Evolution, Ecology & Control of Plant Viruses

Program and Book of Abstracts

12th International Symposium on Plant Virus Epidemiology

Evolution, Ecology and Control of Plant Viruses

28 January - 1 February 2013
The Ngurdoto Mountain Lodge
Arusha, Tanzania

Symposium organized by
International Committee on Plant Virus Epidemiology and
International Institute of Tropical Agriculture

in partnership with

Mikocheni Agricultural Research Institute (MARI), Tanzania
National Agricultural Research Organization (NARO), Uganda
West and Central African Council for Agricultural Research and Development (CORAF/WECARD)
Bioversity International
AVRDC - The World Vegetable Center

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About ICPVE

The International Committee for Plant Virus Epidemiology (ICPVE) is a subject committee of the International Society for Plant Pathology (ISPP). The ISPP was founded in 1968 in the United Kingdom, for worldwide development of plant pathology. The ISPP sponsors International Congress of Plant Pathology, and International Meetings of its Subject Committees. ICPVE, since formation in 1979, has conducted eleven international symposia in different parts of the world. This 12th IPVE Symposium in Arusha, Tanzania, is the first to be held in the Africa.

List of IPVE Symposia Series:

1. UK, Oxford, 28 - 31 July 1981
2. Australia, Corowa, 25 - 27 August 1983
3. USA, Orlando, 6 - 8 August 1986
4. France, Montpellier, 1 - 5 September 1989
5. Italy, Valenzano (Bari), 27-31 July 1992
6. Israel, Jerusalem, 23 - 28 April 1995
7. Spain, Aguadulce (Almeria), 11 - 16 April 1999
8. Germany, Ascherleben, 12 - 17 May 2002
9. Peru, Lima (CIP), 4 - 7 April 2005
10. India, Hyderabad (ICRISAT), 15 - 19 October 2007
11. USA, Ithaca (Cornell University), 20 - 24 June 2010
12. Tanzania, Arusha (IITA), 28 January – 1 February 2013

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Program & Book of Abstracts

Compiled by
P Lava Kumar, Katherine Lopez, and Catherine Njuguna
International Institute of Tropical Agriculture

Dear Participants,

On behalf of the International Committee on Plant Virus Epidemiology (ICPVE) and the International Institute of Tropical Agriculture (IITA), Mikocheni Agricultural Research Institute (MARI), Tanzania, National Agricultural Research Organization (NARO), Uganda, West and Central African Council for Agricultural Research and Development (CORAF/WECARD), Bioversity International, and AVRDC - The World Vegetable Center, we welcome you to the 12th International Symposium on Plant Virus Epidemiology (IPVE), in Arusha, Tanzania. We are delighted to have you and we thank you for your participation in this triennial event of the ICPVE.

The 12th IPVE Symposium marks a special milestone in ICPVE's history—hosting at least one symposium in every continent is a unique feat for which we are very proud. This symposium focuses on links between changes in virus evolution and ecology, and its impact on virus emergence and virus disease control. The scientific program built around these themes deals with the changing phases of plant virus epidemiology, climate change effects on plant viruses, modeling to predict virus disease spread, virus evolution and ecology, virus-vector interactions, advances in diagnostics, surveillance and control. We are pleased to host a special session of IPM-CRSP programs on virus disease management in developing countries. There is also a special session on strengthening plant virology in sub-Saharan Africa, where virus diseases have remained a primary threat to a number of staple crops.

We hope that this symposium presents a great opportunity to young scientists and students to learn and interact with eminent scientists from across the globe, and build new partnerships for advancement of virology in the continent. We included a field trip to give you an opportunity to observe smallholder agriculture, and enjoy the rich landscapes and nature around Arusha.

We acknowledge the contribution and help of all the members of the Organizing Committee—for generously contributing their time and other resources. We specifically wish to thank our sponsors: CGIAR's RTB and SP-IPM programs, CORAF/WECARD, Plant Virus Ecology Network (PVEN), the USAID-funded IPM-CRSP and Africa RISING projects, Agdia-Biofords, BASF, and Inqaba Biotec for their generous support to this event, including facilitating the participation of over 50 scientists and students to this meeting. Special thanks to IITA's communication team who worked closely with the organizing team in publicizing this event and in generating the communication and meeting materials.

We hope that you will find this symposium engaging and informative. We wish you a productive and successful event.

Lava Kumar
Chair, 12th IPVE Symposium
Organizing Committee

Alberto Fereres
Chair, International Committee
on Plant Virus Epidemiology

Organizing and Program Committee

Chief Patron
Nteranya Sanginga
Director General
International Institute of Tropical Agriculture (IITA)

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Lawrence Kenyon (AVRDC, Taiwan)
James Legg (IITA, Tanzania)
Pascal Lepoint (Bioversity, Burundi)
Neema Lazaro (IITA, Tanzania)
Katherine Lopez (IITA, Nigeria)
Victor Manyong (IITA, Tanzania)
Irene Mwasaga (Africa RISING, IITA, Arusha)
Samiran Mazumdar (IITA, Nigeria)
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International Institute of Tropical Agriculture

Headquarters: IITA, PMB 5320, Ibadan, Nigeria
www.iita.org

Message

It is with pride that IITA is organizing the 12th International Plant Virus Epidemiology Symposium, with the theme 'Evolution, ecology and control of plant viruses' in Arusha, Tanzania.

Plant viruses are among the major factors that affect productivity and cause vast economic losses to staple crops in Africa and other developing regions across the tropics. Sustained efforts by IITA and its partners against plant viruses have resulted in dramatic successes in controlling cassava mosaic, maize streak, and a few others. However, new viruses, new strains of existing viruses, along with changing contexts due to agricultural intensification and climate change have been creating new challenges and demanding even greater effort to overcome hurdles to increase agricultural productivity, food availability, and economic development.

Since its establishment in 1967, IITA has worked on the characterization of viruses, development of diagnostics and disease distribution maps, released numerous disease-resistant varieties of cassava, yam, cowpea, maize, and also trained a number of virologists and partners working on viruses and their control. These efforts have substantially contributed to the realization of improved food security and enhancement of farmers' productivity and livelihood.

We will further intensify efforts to raise over 20 million Africans out of poverty and redirect over 25 million hectares of underutilized, marginal, and degraded lands to more productive and sustainable use by 2020. To achieve this mission, IITA adopted a refreshed strategy which focuses on the four CGIAR system-level outcomes: increased food security, reduced rural poverty, enhanced nutrition, and more sustainable management of natural resources. Our new strategy is in line with the new CGIAR mission and contributes to the Africa Union's Comprehensive Africa Agricultural Development Programme (CAADP).

This goal cannot be achieved without adequate efforts to tackle virus disease problems. This symposium is therefore very timely in taking stock of the knowledge, technologies, and learning, and in developing strategies and new partnerships for managing virus diseases.

I thank the International Committee on Plant Virus Epidemiology for hosting this event in Africa, and compliment our co-organizing partners, Mikocheni Agricultural Research Institute (Tanzania), CORAF/WECARD, National Agricultural Research Organization (Uganda), Bioversity, and AVRDC - The World Vegetable Center, and all the sponsors for their efforts in ensuring the success of this event.

Dr Nteranya Sanginga
Director General

Mikocheni Agricultural Research Institute
P.O Box 6226, Dar es Salaam, Tanzania

Message

Plant viruses can only be seen within the most powerful microscope but their devastating effects are impossible to ignore. Many countries have suffered losses caused by plant viruses and Tanzania is no exception. As societies continue to evolve and modernize agriculture, so do plant viruses, potentially becoming even more devastating. To keep up with constant threat of emerging and re-emerging plant viruses, it is necessary to identify, predict and monitor sources of outbreaks worldwide to minimize small infection proportions from becoming devastating pandemics.

MARI recognizes the importance of controlling plant viruses in Tanzania and other African countries through application of biotechnology to understand virus epidemiology, ecology, to monitor and diagnose plant viruses. MARI is also leading research aimed at understanding new sources of virus infections, development of molecular virus diagnostic tools and studying virus disease prevalence for informed decision making. MARI is working towards building and strengthening regional capacity in terms of human and infrastructure in plant virus disease research to provide practical solutions to farmers and increase crop productivity and income.

The 12th IPVE Symposium is therefore a good forum for researchers and other stakeholders to share research results, new knowledge and establish a networking mechanism in the control of plant viruses. I would like to thank the International Committee on Plant Virus Epidemiology (ICPVE) and the International Institute of Tropical Agriculture (IITA) for organizing this event in Tanzania and making us part of the organizing team. MARI is proud to be part of the organizing committee in this Symposium which is held in Tanzania where farmers are ravaged by many crop viruses. It is hoped that results shared during this Symposium will eventually be able to help farmers to control viruses of important crops and minimize losses which they currently incur.

Wish you a successful symposium.

Dr Joseph Ndunguru
Officer in-charge

West and Central African Council for Agricultural Research and Development
CORAF/WECARD, 7 Av. Bourguiba, B.P. 48, cp 18523, Dakar, Senegal
www.coraf.org

Message

On behalf of CORAF/WECARD, I would like to thank the International Committee on Plant Virus Epidemiology (ICPVE) and the International Institute of Tropical Agriculture (IITA) for taking the initiative to organize the 12th International Symposium on Plant Virus Epidemiology in Arusha, Tanzania. The symposium theme, *Ecology, epidemiology and control of plant virus diseases,* is very much in line with CORAF/WECARD priorities, which recognizes the importance of appropriate pest management approaches to improve agricultural productivity and competitiveness in West and Central Africa. It is indeed a great pleasure for CORAF/WECARD to be part of the co-organizers and organizing committee. I would also like to extend thanks to all the co-organizing partners for being part of this initiative.

CORAF/WECARD is constituted by the National Agricultural Research Institutions of 15 countries in West Africa and 7 in Central Africa, with a total population of over 318 million people, 60-70% of whom depend on agriculture for their livelihoods. CORAF/WECARD has been mandated by the Regional Economic Communities (RECs), including the Economic Community of West African States (ECOWAS) and the Economic Community of Central African States (ECCAS), to lead the implementation of the African Union's **Comprehensive Africa Agriculture Development Programme** (CAADP) **Pillar IV** (*Improving agriculture research, technology dissemination and adoption*) within the subregion. The Framework for African Agricultural Productivity Program (FAAP) is an implementation tool of CAADP **Pillar IV,** which is helping stakeholders to bring political, financial, and technical resources together to strengthen Africa's capacity for research and the delivery of agricultural innovations. Increasing the use of improved seeds, fertilizer, integrated pest management (IPM), soil and water management, pre and postharvest practices, climate information and market access, are critical in raising agricultural productivity and production and, therefore, in responding to the objectives of the agricultural policies of the RECs and the CAADP.

This Symposium is therefore seen as a great opportunity for stakeholders to share research results and new knowledge, and to establish a networking mechanism in the control of plant viruses. We look forward to interacting with partners and to working together to identify future priorities and strategies to meet the complex challenges posed by plant viruses.

May we have a successful symposium!

Dr Harold Roy-Macauley
Executive Director

National Agricultural Research Organization

Lugard Avenue, P.O. Box 295, Entebbe, Uganda
www.naro.go.ug

Message

I am very delighted that the National Agricultural Research Organization (NARO, Uganda) is a co-organizer of the 12th International Symposium on Plant Virus Epidemiology, 28 January to 1 February 2013, in Arusha, Tanzania. I must applaud the organizers for choosing to host this event in Africa, where several plant viruses are endemic, yet efforts at control are hampered by momentous challenges. It is my hope that the 12th IPVE symposium will provide a platform for effective knowledge sharing, initiating collaborations and strengthening partnerships.

Plant viruses are a matter of great concern globally, but effective control requires a clear understanding of their ecology and epidemiology. In Uganda, viruses significantly affect most of the major crops: banana, cassava, maize, rice, groundnut, sweet potato, citrus, passion fruit, vegetables, and beans. Notably, during the past two decades, two major epidemics have ravaged cassava in Uganda: cassava mosaic disease and cassava brown streak disease. As a relevant national institution, NARO has successfully spearheaded research programs for the control of the disease. I wish to thank all our collaborators for the support in addressing these two and other similar problems.

In conclusion, I reaffirm NARO's commitment to working with all stakeholders in addressing critical challenges to agricultural productivity, including finding solutions to the persistent plant virus problems. I wish to extend my appreciation to the ICPVE and IITA for taking the lead in organizing the 12th IPVE symposium.

On behalf of NARO, I wish all a very successful symposium.

Dr Emily K. Twinamasiko
Director General

Bioversity International

Montpellier, France
www.bioversityinternational.org

Message

Viral diseases threaten banana productivity worldwide. In sub-Saharan Africa this threat to food security and income among smallholders is particularly severe and spreading. First reported decades ago in Central Africa, banana bunchy top virus (BBTV) is now moving both east and west with devastating effects. The 12th IPVE symposium and the follow-up workshop on BBTV offers banana virologists from around the globe an opportunity to meet with colleagues in Africa to launch the Global Alliance for BBTD control in Africa.

Bioversity's Programme for Commodity Systems and Genetic Resources brings its focus on agroecological intensification to this Alliance, drawing on advances in Asia for the management of viruses in banana through the regional network BAPNET. The regional banana networks of Africa facilitated by Bioversity, BARNESA and Innovate Plantain, will provide an important platform to mobilize and disseminate practical science-based results across the continent. We congratulate the organizers, particularly the virologists from IITA, for bringing this important scientific event to Africa and are proud to be part of the effort.

My best wishes to the participants for an enjoyable and stimulating visit to the Kilimanjaro area.

Dr Dietmar Stoian
Programme Leader
Commodity Systems and Genetic Resources

AVRDC - The World Vegetable Center

PO Box 42, Shanhua, Tainan 74199, Taiwan
www.avrdc.org

Message

Diseases caused by viruses are major constraints to crop production worldwide, particularly in the tropics and subtropics. Better understanding of the epidemiology of these diseases is essential for developing durable and sustainable control measures, maximizing the use of crop management methods and host plant resistance, thus reducing dependence on pesticides. Understanding their epidemiology may help us predict the potential impact of climate change on these diseases and crop health, and allow us to develop strategies to mitigate the impact. This symposium is a forum to share the latest research results and knowledge on the epidemiology of many of the most important virus diseases. It is also an opportunity to foster networking and collaboration in plant virus epidemiology, particularly in sub-Saharan Africa, building upon global experiences and best practices.

AVRDC - The World Vegetable Center is committed to managing plant diseases in vegetable crops to ensure better productivity as part of our mission to alleviate poverty and malnutrition. As a virologist and as current Deputy Director General for Research at AVRDC, which is a supporting partner to the symposium, I regret I am unable to participate in the discussions and networking. However, I wish you an interesting and productive symposium and a pleasant stay in Tanzania.

Dr Jacqueline Hughes
Deputy Director General - Research

Overview of the Program

27 January 2013: Sunday

1600 hrs onwards: Participants arrival and registration

28 January 2013: Monday

0815-0900	Registration and conference kit distribution
0900-1000	Inauguration
1030-1200	Session - 1. Changing phase of plant virus epidemiology
1200-1330	Lunch break
1330-1500	Session - 2. Climate change and Modeling (I)
1500-1530	Refreshment break
1530-1700	Session - 2. Climate change and Modeling (II)
1700-1830	Poster session - 1
1830 onwards	Welcome cocktail and dinner

29 January 2013: Tuesday

0815-1000	Session - 3. Virus vectors and virus-vector interactions (I)
1000-1020	Refreshment break
1020-1220	Session - 3. Virus vectors and virus-vector interactions (II)
1220-1330	Lunch break
1330-1510	Session - 4. IPM (CRSP, special session)
1510-1730	Refreshment break and Poster session - II
1730-1900	Session - 5. ICPVE business meeting
1900 onwards	Executive Dinner

30 January 2013: Wednesday: Excursion

31 January 2013: Thursday: Concurrent sessions

	Conference hall - 1	**Conference hall - 2**
0815-1000	Session - 6: Diagnostics and surveillance (I)	Session - 7: Epidemiology and ecology (I)
1000-1020	Refreshment break	
1020-1205	Session - 6: Diagnostics and surveillance (II)	Session - 7: Epidemiology and ecology (II)
1205-1330	Lunch break	
1330-1500	Session - 8: Disease control (II)	Session - 9: Virus evolution (II)
1500-1530	Refreshment break	
1530-1615	Session - 8: Disease control (II)	Session - 9: Virus evolution (II)
1615-1800	Poster Session - III	
1900 onwards	Dinner	

1 February 2013: Friday

0815-1000	Session - X: Plant virology in sub-Saharan Africa
1000-1030	Refreshment break
1050-1230	Session - X: Plant virology in sub-Saharan Africa
1230 onwards	Lunch break and departures

Abstracts of the Oral Presentations

28 January 2013, Monday

1030-1200: Session - 1. Changing Phase of Plant Virus Epidemiology

OP-01 **A century of plant virus epidemiology**

Keynote ***J. Michael Thresh***
Natural Resources Institute, University of Greenwich, Chatham Maritime, Kent, UK

OP-02 **Trends in plant virus epidemiology: opportunities from new or improved technologies**

Keynote ***Roger A. C. Jones***[1,2]
[1]*School of Plant Biology, University of Western Australia, 35 Stirling Highway, Crawley, Perth, WA 6009, Australia;* [2]*Department of Agriculture and Food, Locked Bag No.4, Bentley Delivery Centre, WA 6983, Australia*

OP-03 **Plant viruses modify the behavior and performance of their vectors enhancing their fitness, transmission and spread**

Keynote *MicheleDo CarmoSousa, E. Garzo, B. Dáder, Aranzazu Moreno &* ***Alberto Fereres***
Institute of Agricultural Sciences, ICA, CSIC, Serrano 115 dpdo, Madrid, Spain

1200-1330: Lunch break

1330-1700: Session - 2. Climate Change and Modeling

OP-04 **Climate change adaptation in disease management: a framework for evaluating the likely utility of decision support systems and index insurance**

Keynote ***Karen A. Garrett***[1*]*, Girly M. Ramirez*[1] *and Bala Natarajan*[2]
[1]*Department of Plant Pathology, Kansas State University, Manhattan, KS, 66506, USA;* [2]*Department of Electrical and Computing Engineering, Kansas State University, Manhattan, KS, 66506, USA*

OP-05 **Influence of climate change on plant virus disease infections and epidemics**

Keynote ***Roger A. C. Jones***[1,2]
[1]*School of Plant Biology, University of Western Australia, 35 Stirling Highway, Crawley, Perth, WA 6009, Australia;* [2]*Department of Agriculture and Food, Locked Bag No.4, Bentley Delivery Centre, WA 6983, Australia*

OP-06 **The effect of elevated temperature on the titre of *Barley yellow dwarf virus*-PAV in wheat cv. Yitpi**
Narelle Nancarrow[1]*, Kyla Finlay*[1]*, Angela Freeman*[2]*, Piotr Trebicki*[2]*, Simone Vassiliadis*[1]*, Brendan Rodoni*[1]*, Jo Luck*[3]*, Alan Yen*[1] *and* ***Fiona Constable***[1*]
[1]*Department of Primary Industries (DPI), Knoxfield, Victoria, Australia;* [2]*DPI, Horsham Centre, Horsham 3400, Australia;* [3]*Plant Biosecurity Cooperative Research Centre, PO Box 666, Melbourne, Victoria, Australia*

OP-07 **Influence of ambient ecology on the incidence and severity of groundnut rosette virus disease in Uganda**
I. O. Mugisa[1]*, J. Karungi*[1]*, B. Akello*[2]*, M. Ochwo*[1]*, M. Biruma*[2]*, D. K. Okello*[2] *and G. Okello*[1]
[1]*Makerere University, College of Agricultural and Environmental Sciences, P.O Box 7062 Kampala, Uganda;* [2]*National Semi-Arid Resources Research Institute, P.O Box Soroti, Uganda*

1500-1530: Refreshment break

OP-08 **Sustainable plant resistance management in agricultural landscapes**

Keynote ***Frédéric Fabre***[1]*, Elsa Rousseau*[1,2]*, Ludovic Mailleret*[2,3] *and Benoît Moury*[1]
[1]*INRA, UR 407 Unité De Pathologie Végétale, F-84140 Montfavet, France;* [2]*INRA, UR 880 URIH, 400 route des Chappes, BP 167, F-06903 Sophia Antipolis, France;* [3]*INRIA, Biocore Team, F-06902 Sophia Antipolis, France*

OP-09 **Geospatial and temporal analyses of *Bean pod mottle virus* epidemics in soybean**

Keynote ***Forrest W. Nutter, Jr****.*[1]*, Emanuel Byamukama*[2] *and Sharon Eggenberger*[1]
[1]*Department of Plant Pathology and Microbiology, 351 Bessey Hall, Iowa State University, Ames, Iowa 50011 USA;* [2]*Department of Plant Pathology, University of Nebraska, Lincoln, Nebraska, 68583 USA*

OP-10 **Biology-rich climate based model for predicting thrips-borne Tomato Spotted Wilt in tobacco in North Carolina**
George G. Kennedy *and Thomas Chappell*
Department of Entomology, North Carolina State University, Raleigh, NC, USA 27695-7630

OP-11 **Temporal and spatial spread of chickpea chlorotic dwarf virus (CpCDV) in chickpea in northern Sudan**
Abdelmagid Adlan Hamed
Gezira Research Station, Agricultural Research Corporation, Wad Medani, Sudan

1700-1830. Poster session - 1

29 January 2013, Tuesday

0815-1205: Session 3. Virus Vectors and Virus-Vector Interactions

OP-12 Keynote **Circulative, nonpropagative transmission: a carefully tuned orchestra of virus, vector and host proteins**
Stewart M. Gray[1], *Michelle Cilia*[1], *Michael S. Bereman*[2], *Stacy Deblasio*[1], *Juan Chavez*[2], *Dawn Smith*[1], *Michael J. MacCoss*[2] *and James E. Bruce*[2]
[1]*USDA, ARS and Dept of Plant Pathology & Plant-Microbe Biology, Cornell University, Ithaca, NY, USA;* [2]*Department of Genome Sciences, University of Washington, Seattle, WA, USA*

OP-13 Keynote **Virus-induced modifications in host plants attract vectors and increase probability of virus spread to healthy plants**
Nilsa A. Bosque-Pérez
University of Idaho, Department of Plant, Soil, and Entomological Sciences, Moscow, ID 83844-2339, USA

OP-14 Keynote **Same vehicle, different engine: the dynamics of *Bemisia tabaci* populations driving cassava virus disease pandemics in sub-Saharan Africa**
James P. Legg[1], *Peter Sseruwagi*[2], *Simon Boniface*[1], *Geoffrey Okao-Okuja*[3], *Rudolph Shirima*[1], *Simon Bigirimana*[4], *Gervais Gashaka*[5], *Hans-Werner Herrmann*[6], *Simon Jeremiah*[7], *Hannington Obiero*[8], *Innocent Ndyetabula*[9], *Willy Tata-Hangy*[10], *Charles Masembe*[11] *and Judith K. Brown*[6]
[1]*Internationaol Institute of Tropical Agriculture (IITA), Dar es Salaam, Tanzania;*[2] *Mikocheni Agricultural Research Institute (MARI), Dar es Salaam, Tanzania;* [3]*National Agricultural Crops Resources Research Institute, Namulonge, Uganda;* [4]*Institut des Sciences Agronomiques du Burundi, Gitega, Burundi;*[5] *Rwanda Agricultural Board, Rubona, Rwanda;*[6]*The University of Arizona, Tucson, USA;* [7]*Lake Zone Agricultural Research and Development Institute;* [8]*Kenya Agricultural Research Institute, Kakamega, Kenya;* [9]*Maruku Agricultural Research Institute;* [10]*IITA, Kinshasa, Democratic Republic of Congo;* [11]*Makerere University, Uganda*

OP-15 Keynote **Transmission of cassava and tomato begomoviruses in South Africa by native and introduced *Bemisia tabaci* haplotypes**
Marie E. C. Rey[1], *Lindy L. Esterhuizen*[2], *Ken G. Mabasa*[1,3], *Schalk W. van Heerden*[4], *Henryk Czosnek*[5], *Judy K. Brown*[6] *and Henriette van Heerden*[6]
[1]*School Molecular and Cell Biology, University of Witwatersrand, South Africa;* [2]*Department of Biochemistry, University of Johannesburg, South Africa;* [3]*ARC-Vegetable and Ornamental Plant Institute, Pretoria, South Africa;* [4]*Sakata Vegenetics Pty (Ltd), South Africa;* [5]*Department of Field Crops and Genetics, Hebrew University of Jerusalem, Israel;* [6]*Department of Plant Sciences, University of Arizona, United States of America;* [7]*Department of Veterinary Tropical Diseases, University of Pretoria, South Africa*

OP-16 Keynote **Different gene copy number of a multipartite virus in host plant and in insect vector**
Stéphane Blanc[1*], *Anne Sicard*[1], *Yannis Michalakis*[2] *and Sérafin Gutierrez*[1,2]
[1]*INRA, UMR BGPI INRA-CIRAD-SupAgro, Cirad TA-A54/K, Campus International de Baillarguet, 34398 Montepllier cedex 05, France;* [2]*UMR MIVEGEC 5290, CNRS-IRD-UM1-UM2, IRD, 911 Avenue Agropolis, B.P. 64501, 34394 Montpellier Cedex 05, France*

1000-1020: Refreshment Break

OP-17 **Insect and endosymbiont proteins are involved in the transmission of begomoviruses by the whitefly *Bemisia tabaci***
Murad Ghanim
Department of Entomology, the Volcani Center, Bet Dagan, Israel

OP-18 **Enigmatic virus-vector relations of *Sweet potato mild mottle virus* in agro- and natural ecosystems in the center of evolution in East Africa**
***Arthur K. Tugume*[1]*, *Settumba B. Mukasa*[2] *and Christopher A. Omongo*[3]
[1]Department of Biological Sciences, College of Natural Sciences, Makerere University, Kampala, Uganda; [2]Department of Agricultural Production, College of Agricultural and Environmental Sciences, Makerere University, Kampala, Uganda. [3]National Crops Resources Research Institute (NaCRRI), Namulonge, Uganda

OP-19 **Direct effects of the begomovirus *Tomato yellow leaf curl virus* in the settling and feeding behavior of its vector *Bemisia tabaci* Gennadius (Hemiptera: Aleyrodidae)**
Ana Moreno-Delafuente , Elisa Garzo, Aranzazu Moreno and ***Alberto Fereres****
Institute of Agricultural Sciences, ICA, CSIC, Serrano 115 dpdo, Madrid, Spain

OP-20 **Ecology of the banana aphid *Pentalonia nigronervose*, the vector of *banana bunchy top virus***
***Rachid Hanna*[1]*, *Sergine Ngatat*[1]*, *Michel R. Ndjab*[1]*, *Apollin Fotso Kuate*[1]*, *Armand R. F. Doumtsop*[1] *and *P. Lava Kumar*[2]
[1]International Institute of Tropical Agriculture (IITA), BP 2008 (Messa), Yaoundé, Cameroon; [2]IITA, PMB 5320, Ibadan, Nigeria

OP-21 **Spread of an emerging vectored disease of sugarcane varies according to local constraints in the French Caribbean islands**
***Jean H. Daugrois*[1]*, *Carine Edon Jock*[1]*, *Nadia Adjanoh-Lubin*[1] *and *Philippe Rott*[2]
[1]CIRAD, UMR BGPI, Station de Roujol, 97170 Petit-Bourg, Guadeloupe, France; [2]CIRAD, UMR BGPI, 34398 Montpellier Cedex 5, France

OP-22 **Influence of plant virus co-infection on transmission and within-host dynamics**
Alison G. Power, *Katherine Marchetto and Jasmine Peters*
Department of Ecology and Evolutionary Biology, 331 Corson Hall, Cornell University, Ithaca, NY 14883, USA

OP-23 **Virus-vector transmission relationships for cassava brown streak viruses and the whitefly vector, *Bemisia tabaci***
***M. N. Maruthi*[1]*, *Simon Jeremiah*[2]*, *Ibrahim Umer Mohammed*[1] *and *James Legg*[2]
[1]Natural Resources Institute, University of Greenwich, Chatham Maritime, Kent ME4 4TB, UK; [2]International Institute of Tropical Agriculture (IITA), PO Box 34441, Dar es Salaam, Tanzania

OP-24 **Transmission of torradoviruses by their whitefly vectors**
Martin Verbeek*, Petra J. van Bekkum and Rene A.A. van der Vlugt*
Plant Research International, part of Wageningen UR (University and Research centre), P.O. Box 69, 6700 AB Wageningen, The Netherlands

1220-1330: Lunch break

1330 - 1510: Session-4. IPM (CRSP, special session)

OP-25 **Management of aphid, beetle, seed and contact-transmitted RNA viruses in tropical ecological cropping systems.**
Sue A. Tolin
Department of Plant Pathology, Physiology & Weed Science, Virginia Polytechnic Institute & State University - Virginia Tech, Blacksburg, Virginia 24061, USA

OP-26 **Comparative case studies of whitefly (*Bemisia tabaci*) vector-begomovirus diversity: associated effects on virus disease epidemiology in diverse study systems in Central America and sub-Saharan Africa**
***J.K. Brown*[1]*, *M. Palmieri*[2] *and *J. P. Legg*[3]
[1]School of Plant Sciences, The University of Arizona, Tucson AZ 85721 USA, [2]Universidad Del Valle, Guatemala City, Guatemala; [3]International Institute of Tropical Agriculture (IITA), Dar Es Salam, Tanzania

OP-27 **Epidemiology and management of intractable virus diseases in subsistence agriculture: The case of a thrips-transmitted tospovirus in South Asia**
Naidu Rayapati
Department of Plant Pathology, Irrigated Agriculture Research and Extension Center, Washington State University, Prosser, WA 99350, USA

OP-28 **Diversity, biology and management of begomovirus diseases of horticultural crops in West Africa**
***Robert L. Gilbertson*[1]**, *Alexandra Campbell*[1], *Li-Fang Chen*[1], *Maria Rojas*[1], *Moussa Noussourou*[2] and *Kadiatou Gamby*[2]
[1]*Department of Plant Pathology, University of California-Davis, CA, USA;* [2]*Institut D'Economie Rurale, Bamako, Mali*

OP-29 **Emergence and diversity of begomoviruses infecting solanaceous crops in Southeast Asia**
***Lawrence Kenyon**, Wen-Shi Tsai, Su-Ling Shih and Li-Mei Lee*
AVRDC – The World Vegetable Center, PO Box 42, Shanhua, Tainan 74199, Taiwan ROC

1510-1730: Refreshment Break and Poster Session - 2

1730-1900: Session 5. ICPVE business meeting

- **ICPE Chairman's remarks**

OP-30 Keynote **Meeting Redcliffe Nathan Salaman, first professor of plant virus diseases**
Karl Maramorosch
Entomology Department, Rutgers-The State University of New Jersey, New Brunswick, NJ 08901, USA

- **ICPVE Awards and Honors**

30 January 2013, Wednesday

- **Excursion**

31 January 2013, Thursday [concurrent sessions]

0815-1205: Session 6. Diagnostics and Surveillance

OP-31 Keynote **Virus diagnosis in plant virus disease prevention and control**
Stephan Winter
Plant Virus Department, Leibniz-Institut DSMZ, German Collection of Microorganisms and Cell Cultures GmbH, Braunschweig, Germany

OP-32 Keynote **A tree shrub in the family *Sapindaceae* is a natural host of a cassava mosaic begomovirus in Tanzania**
***Joseph Ndunguru,** Fred Tairo, Catherine Gwandu, Peter Sseruwagi and J. Kayeke*
Mikocheni Agricultural Research Institute, Box 6226, Dar es Salaam, Tanzania

OP-33 Keynote **State of the art multiplex Luminex *x*MAP and *x*TAG-detection of plant viruses**
***René A.A. van der Vlugt*[1]**, *Henry van Raaij*[1], *Marjanne de Weerdt*[1], *Sharon van Brunschot*[2], *Igor Koloniuk*[3], *José van Beckhoven*[1] *and Jan Bergervoet*[1].
[1]*Plant Research International, Droevendaalsesteeg 1, 6708 PB, Wageningen, the Netherlands;* [2]*CRC for National Plant Biosecurity, LPO Box 5012, Bruce, ACT, 2617, Australia;* [3]*Department of Plant Virology, Institute of Plant Molecular Biology, Biology Centre of Academy of Sciences of the Czech Republic, v.v.i., Branišovská 31, 370 05, ČeskéBudějovice, Czechoslovakia*

OP-34 Keynote **Next generation sequencing as a universal tool for virus detection and identification : characterising Maize Lethal Necrosis in Kenya**
***N. Boonham*[1]**, *I. P. Adams*[1*], *D. W. Miano*[2], *Z. M. Kinyua*[2], *A. Wangai*[2], *E. Kimani*[3], *N. Phiri*[4], *R. Reeder*[5], *V. Harju*[1], *R. Glover*[1], *U. Hany*[1], *R. Souza-Richards*[1], *P. Deb Nath*[1,6], *T. Nixon*[1], *A. Fox*[1], *A Barnes*[1], *A. Skelton*[1], *R. Thwaites*[1], *R. Mumford*[1] *and J. Smith*[1]
[1]*Food and Environment Research Agency, Sand Hutton, York, YO41 1LZ, UK;* [2]*Kenya Agricultural Research Institute, P.O. Box 14733 – 00800, Nairobi, Kenya;* [3]*Kenya Plant Health Inspectorate Service, Nairobi, Kenya;* [4]*CAB International, Africa Regional Centre, Nairobi, Kenya;* [5]*CAB International, Egham, UK;* [6]*Assam Agricultural University, Assam, India*

OP-35 Keynote **Viral diagnostics: from continental viromes to field level diagnostic methods**
***Jan F. Kreuze*[1*]**, *Segundo Fuentes*[1], *Giovanna Muller*[1], *Dina L. Gutierrez*[1], *Neil Boonham*[2] *and Zhangjun Fei*
[1]*International Potato Center (CIP), Apartado 1558, Lima 12, Peru;* [2]*Food and Environment Research Agency, Sand Hutton, York, YO41 1LZ, UK*

OP-36 **Occurrence and distribution of potato viruses in the major potato growing areas in Kenya**

H. K. Were[1], G. C. Cowan[2] and ***L. Torrance[2]***
[1]Masinde Muliro University of Science and Technology, P.O. Box 190-50100 Kakamega, Kenya; [2]Cell and Molecular Sciences Department, The James Hutton Institute, Invergowrie, By Dundee DD2 5DA, UK

1000-1020: Refreshment Break

OP-37 **Unravelling complex viral infections in cassava (*Manihot esculenta* Crantz.) from Colombia**

Monica Carvajal[1], *Cristian Olaya[1], Ivan Lozano[1], Mauricio Castaňo[1], Maritza Cuervo[2] and Wilmer Cuellar[1]*
[1]Virology Laboratory and [2]Germplasm Health Laboratory, International Center for Tropical Agriculture (CIAT), AA 6713, Cali, Colombia

OP-38 **Characterisation of badnaviruses and endogenous pararetroviruses in West African yam breeding lines**

Aliyu Turaki[1], P. Lava Kumar[2], A. Lopez-Montes[2] and Susan E. Seal[1]
[1]Natural Resources Institute, University of Greenwich, Central Avenue, Chatham Maritime, Kent ME4 4TB, UK; [2]International Institute of Tropical Agriculture, Oyo Road PMB 5320, Ibadan, Nigeria

OP-39 **Valuing pest diagnostics for laboratory and field deployment in seed certification and surveillance: a case study on Cassava brown streak disease**

Julian Smith[1]*, Jenny Tomlinson[1], Ian Adams[1], Douglas Miano[2], Phillipe Abidrabo[3,4], Steve Walsh[5] and Neil Boonham[1]*
[1]The Food and Environment Research Agency, Sand Hutton, York, YO41 1LZ, United Kingdom; [2]Kenya Agricultural Research Institute, P.O. Box 14733-00800, Nairobi, Kenya; [3]National Crops Resources Research Institute, P.O. Box 7084, Kampala, Uganda; [4]Agricultural and Environmental Sciences, Makerere University, P.O. Box 7062, Kampala, Uganda; [5]Catholic Relief Services, East Africa Regional Office, P.O. Box 49675-00100, St Augustine's Court, Karuna Close, Westlands, Nairobi, Kenya

OP-40 **Detection of *Banana bunchy top virus* and development of transgenic banana plants in Hawaii**

W. Borth[1], E. Perez[1], K. Cheah[2], Y. Chen[1], W. S. Xie[1], H. G. Xiao[1], D. Gaskill[1], S. Khalil[1], D. Sether[1], M. Melzer[1], M. Wang[1], R. Manshardt[2], D. Gonsalves[3] and ***Johan S. Hu[1]***
[1]Plant & Environmental Protection Sciences, University of Hawaii at Manoa, Honolulu, HI, USA; [2]Tropical Plant and Soils Sciences, University of Hawaii at Manoa, Honolulu, HI, USA; [3]USDA-ARS, PBARC, Hilo, HI, USA

OP-41 **Monoclonal antibodies in the detection and diagnosis of plant viruses**

Anjali A Karande
Department of Biochemistry, Indian Institute of Science, Bangalore 560012, India

OP-42 **Relative incidence and distribution of viruses in plants grown from different portions of seed yams (*Dioscorea* spp.)**

C. K. Nkere[1,3,4]*, Susan E. Seal[2], G. I. Atiri[3], J. T. Onyeka[4] and P. Lava Kumar[1]*
[1]International Institute of Tropical Agriculture (IITA), PMB 5320, Ibadan, Nigeria; [2]Natural Resources Institute, University of Greenwich, Central Avenue, Chatham Maritime, Kent ME4 4TB, UK; [3]Department of Crop Protection and Environmental Biology, University of Ibadan, Ibadan, Nigeria; [4]National Root Crops Research Institute (NRCRI) Umudike, PMB 7006, Umuahia, Nigeria

0815-1205: Session 7. Epidemiology and Ecology

OP-43 Keynote **Molecular epidemiology provides new insights on ZYMV occurrence in France**

Hervé Lecoq, *Catherine Wipf-Scheibel, Karine Berthier and Cécile Desbiez INRA, UR407 Pathologie Végétale, F84140 Montfavet, France*

OP-44 Keynote **Ecological and evolutionary implications of sequence variation of Asclepias asymptomatic virus in non-cultivated plant**

Ulrich Melcher
Department of Biochemistry & Molecular Biology, Oklahoma State University, Stillwater OK, USA

OP-45 Keynote **Tanzania: the biodiversity hotspot of *Rice yellow mottle virus***

Anatolia Mpunami[1], Innocent Ndikumana[2], Judith Hubert[3], Agnès Pinel-Galzi[4], Nkori Kibanda[5], Frederica Mwalyego[6], Paul Tembo[1], Boniface Kola[5], Mohammed Mkuya[5], Zakaria Kanyeka[7], Mutegi Rosemary[7], Susan N'chimbi Msolla[8], Paul Njau[8], Yacouba Séré[3], Denis Fargette[4] and ***Eugénie Hébrard[4]***

[1]Mikocheni Agricultural Research Institute, Dar-es-Salaam, Tanzania; [2]Crop Production Unit, Rwanda Agriculture Board, Kigali, Rwanda; [3]AfricaRice Center, Dar-es-Salaam, Tanzania; [4]UMR Résistance des Plantes aux Bioagresseurs, Institut de Recherche pour le Développement, Montpellier, France; [5]KATRIN Research Institute, Ifakara, Tanzania; [6]Uyole Agricultural Research Institute, Mbeya, Tanzania; [7]International Rice Research Institute, Dar-es-Salaam, Tanzania; [8]Sokoine University of Agriculture, Morogoro, Tanzania

OP-46 Keynote **Viruses of kiwifruit: new and old viruses associated with an emerging crop and their potential for spread**

Michael N. Pearson[1], *Arnaud G. Blouin[2], Ramesh R. Chavan[1], Claudio Ratti[3], Roberta Biccheri[3] and Daniel Cohen[2]*

[1]School of Biological Sciences, The University of Auckland, Private Bag 92019, Auckland, New Zealand; [2]The New Zealand Institute for Plant & Food Research Limited, Private Bag 92169, Auckland, New Zealand; [3]DiSTA – Patologia Vegetale, Università di Bologna, Viale G. Fanin, 40 - 40127 Bologna, Italy

OP-47 Keynote **Viral dynamics: notes from plant-infecting ssDNA viruses**

Darren P. Martin[1], Gordon W. Harkins[2], Aderito L. Monjane[3], Pierre Lefeuvre[4], Jean-Michel Lett[4], Eric van der Walt[5], Dionne N. Shepherd[3], Edward P Rybicki[3], John E.Thomas[6], Daisy Stainton[7], Simona Kraberger[7] and ***Arvind Varsani[7,8,9]***

[1]Institute of Infectious Disease and Molecular Medicine, University of Cape Town, Cape Town, South Africa; [2]South African National Bioinformatics Institute, University of the Western Cape, Bellville, Cape Town; [3]Department of Molecular and Cell Biology, University of Cape Town, Cape Town, South Africa; [4]CIRAD, UMR 53 PVBMT CIRAD-Université de la Réunion, Pôle de Protection des Plantes, Ligne Paradis, 97410, Saint Pierre, La Réunion, France ; [5]Kapa Biosystems, P.O. Box 12961, Mowbray, 7705, South Africa; [6]The University of Queensland, Centre for Plant Science, Queensland Alliance for Agriculture and Food Innovation, Ecosciences Precinct, PO Box 46, Brisbane QLD 4001, Australia; [7]School of Biological Sciences, University of Canterbury, Ilam, Christchurch, New Zealand; [8]Electron Microscope Unit, University of Cape Town, Cape Town, South Africa; [9]Biomolecular Interaction Centre, University of Canterbury, Ilam, Christchurch, New Zealand

1000-1020: Refreshment break

OP-48 **Molecular biodiversity of cassava mosaic begomoviruses in East and Southern Africa**

Peter Sseruwagi[1], *Fred Tairo[1], Ibrahim R.M. Benesi[2], Nurbibi Cossa[3], Elijah Miinda Ateka[4], Marie Claire Kanyange[5], Titus Alicai[6], Patrick Chiza Chikoti[7] and Joseph Ndunguru[1]*

[1]Mikocheni Agriculture Research Institute (MARI), P.O. Box 6226, Dar es Salaam, Tanzania; [2]Chitedze Agricultural Research Station, Department for Agricultural Research Services (DARS), Malawi; [3]Mozambique National Institute of Agronomic Research (IIAM) Avenida Das F.P.L.M No. 2698, C.P. 3658, Maputo, Mozambique; [4]Department of Horticulture, Jomo Kenyatta University of Agriculture and Technology, P. O. Box, 62000 - 00200, Nairobi, Kenya; [5]Rwanda Agricultural Board (RAB), P.O. Box 5016 Kigali, Rwanda; [6]National Crops Resources Research Institute (NaCRRI), P. O. Box 7084, Kampala, Uganda; [7]Zambia Agriculture Research Institute, Mt. Makulu Central Research Station, Chilanga, Zambia

OP-49 **Epidemiology and genetic variability of *Watermelon mosaic virus* infecting cucurbits in Southern United States**

Akhtar Ali *and Osama M. Abdalla*

Department of Biological Science, The University of Tulsa, Tulsa Oklahoma, USA

OP-50 **A novel combination of a new umbravirus species, a new satellite RNA and *Potato leafroll virus* causes tobacco bushy top disease in Ethiopia**

Adane D. Abraham[1,2]*, Wulf Menzel[1], Berhanu Bekele[2] and Stephan Winter[1]*

[1]German Collection of Microorganisms and Cell Culture – DSMZ, Braunschweig, Germany, [2]Ethiopian Institute of Agricultural Research, Addis Ababa, Ethiopia

OP-51 **Diversity and distribution of *Sweet potato leaf curl virus* in Kenya**
D. W. Miano[1,2], *S. Maina[3], J. Irungu[4], E. Mbogo[4] and K. Monjero[4]*
[1]Department of Plant Science and Crop Protection, University of Nairobi, P. O. Box 29053 00625, Kangemi, Kenya; [2]Kenyatta university, Biotechnology and Biochemistry department, P.O. Box 43844-00100, Nairobi, Kenya; [3]Kenya polytechnic university college, Biotechnology and Biochemistry department, P.O. Box, 52428-00200, Nairobi, Kenya; [4]Kenya Agricultural Research Institute, Biotechnology centre, P.O. Box 57811-00200, Nairobi, Kenya

OP-52 **Epidemiology of four cucurbit viruses affecting zucchini production in Flanders (Belgium)**
Mathias De Backer[1], Thijs De Langhe[2], Luc De Rooster[2], Sofie Darwich[3], Danny Callens[3], Martine Maes[1] and ***Kris De Jonghe[1]***
[1]Plant Sciences Unit – Crop Protection, Institute for Agriculture and Fisheries Research (ILVO), B. Van Gansberghelaan 96 bus 2, 9820 Merelbeke, Belgium; [2]Research Station for Vegetable Production (PSKW), Duffelsesteenweg 101, 2860 Sint-Katelijne-Waver, Belgium; [3]Inagro, Ieperseweg 87, 8800 Rumbeke-Beitem, Belgium

OP-53 **Field epidemiology of cassava brown streak viruses in Tanzania**
S. C. Jeremiah[1,2]*, M. N. Maruthi[3], J. N. Ijumba[4] and J. P. Legg[2]*
[1]Ministry of Agriculture, Food Security and Cooperatives, Ukiriguru Agricultural Research Institute, P.O. Box 1433, Mwanza, Tanzania; [2]International Institute of Tropical Agriculture (IITA), P.O Box 34441, Dar es Salaam, Tanzania; [3]Natural Resources Institute, ME4 4TB, Chatham Maritime, United Kingdom; [4]Nelson Mandela African Institute of Science and Technology, P.O. Box 447, Arusha, Tanzania

OP-54 **Epidemiology and evolutionary studies of criniviruses associated with tomato yellows disease in Greece**
C.G. Orfanidou[1], C. Dimitriou[1], L.C. Papayiannis[2], V.I. Maliogka[1] and ***N.I. Katis[1]***
[1]Aristotle University of Thessaloniki, School of Agriculture, Lab of Plant Pathology, 54124 Thessaloniki, Greece; [2]Agricultural Research Institute, PO Box 22016, Nicosia 1516, Cyprus

1205-1330: Lunch break

1330-1615: Session 8. Disease Control

OP-55 Keynote **Is the ability to revert an alternative to distribution of virus-free planting material of sweetpotato to East African farmers?**
Richard W Gibson[1] *and Peter Wasswa[1, 2]*
[1]Natural Resources Institute, University of Greenwich, Chatham Maritime, Kent, ME4 4TB, UK; [2]Makerere University, Uganda

OP-56 Keynote **Do recombinants appearing in natural populations of watermelon mosaic virus represent new agronomic threats?**
Cécile Desbiez, *Catherine Wipf-Scheibel, Charlotte Chandeysson and Hervé Lecoq*
INRA, UR407 Pathologie Végétale, F84140 Montfavet, France

OP-57 Keynote **Viruses of sweetpotato in Israel and their control**
Gad Loebenstein, *Jacob Cohen and Victor Gaba*
Department of Plant Pathology and Weed research, Agricultural Research Organization, Bet Dagan, Israel

OP-58 **Whitefly-transmitted viruses: cultural strategies in vegetable crops**
Alvin M. Simmons *and Shaaban Abd-Rabou*
[1]U.S. Department of Agriculture, Agricultural Research Service, U.S. Vegetable Laboratory, Charleston, South Carolina, USA; [2]Ministry of Agriculture and Land Reclamation, Agricultural Research Center, Plant Protection Research Institute, Dokki, Egypt

OP-59 ***Strategies for managing banana bunchy top disease in the Rusizi valley, Burundi***
Pascale Lepoint[1], *François Iradukunda[1], Guy Blomme[1] and Charles Staver[2]*
[1]Bioversity International Africa; [2]Bioversity International Montpellier

1500-1530: Refreshment break

OP-60 **Mapping the quantitative and qualitative resistance to cassava mosaic disease using next-generation sequencing marker data**
Ismail Y Rabbi*[1]*, *Melaku Gedil[1], Peter Kulakow[1], Martha Hamblin[2] and Jean-Luc Jannink[2]*
[1]International Institute of Tropical Agriculture (IITA), PMB 5320, Oyo Road, Ibadan, Nigeria; [2]Institute for Genomic Diversity, Cornell University, Ithaca, NY 14853, USA; [3]Department of Plant Breeding and Genetics, Cornell University, Ithaca, NY 14853, USA

OP-61 **Transgene viral siRNA profile and its effect on cucurbit viral resistance**
Diana Leibman, Sabrina Haviv, Victor Gaba and ***Amit Gal-On***
Department of Plant Pathology, ARO, The Volcani Center, Bet Dagan 50250, Israel

OP-62 **Quantitative resistance loci reduce the breakdown frequency of a major resistance gene. A relevant way for durable resistance breeding**
Julie Quenouille[1,2], Estelle Paulhiac[1], ***Benoît Moury[2]*** *and Alain Palloix[1]*
[1]INRA, UR1052 Génétique et Amélioration des Fruits et Légumes, F-84140 Montfavet, France; [2]INRA, UR407 Pathologie Végétale, F-84140 Montfavet, France

1330-1615: Session 9. Virus Evolution

OP-63 Keynote **Effects of genetic changes to the begomovirus/betasatellite complex causing cotton leaf curl disease in South Asia post resistance breaking**
Rob W. Briddon
National Institute for Biotechnology and Genetic Engineering, Jhang Road, Faisalabad, Pakistan

OP-64 Keynote **Evidence of purifying selection in the coding regions of wild type *Maize streak virus* (MSV) and pathogen survival (and host-pathogen interaction)**
Daniel O. Pande*[1]*, *Mathews Mito Dida[1], Adérito L. Monjane[2], Dionne N. Shepherd[2], Arvind Varsani[2,3,4], Darren P. Martin[2,5]*
[1]Department of Botany and Horticulture, Maseno University, P.O. Box 333, Maseno, Kenya; [2]Department of Molecular and Cell Biology, University of Cape Town, Rondebosch, 7701, Cape Town, South Africa; [3]School of Biological Sciences, University of Canterbury, Private Bag 4800, Christchurch, 8140, New Zealand; [4]Electron Microscope Unit, University of Cape Town, Rondebosch, 7701, Cape Town, South Africa; [5]Computational Biology Group, Institute of Infectious Disease and Molecular Medicine, University of Cape Town, Observatory, 7925, Cape Town, South Africa

OP-64 **Sequence diversity of global chrysanthemum stunt viroid variants: multiple polymorphic positions scattered throughout the genome**
Ju-Yeon Yoon and ***Peter Palukaitis***
Department of Horticultural Sciences, Seoul Women's University, Seoul, Korea

OP-66 **Micro-evolution of *Beet necrotic yellow vein virus* during a single crop season using next-generation sequencing**
Y. Galein[1], A. Champeil[2], A., H. Escriou[2], M. Richard-Molard[2] and* ***C. G. Bragard[1]***
[1]Université catholique de Louvain, Applied microbiology-Phytopathology, Earth & Life Institute, Croix du Sud, 2 L7.05.03, 1348 Louvain-la-Neuve, Belgium; [2]ITB- Institut Technique de recherche sur la Betterave - 45 rue de Naples 75008 Paris, France

OP-67 **Temporal and spatial changes in the betasatellite associated with the begomoviruses causing cotton leaf curl disease**
Sohail Akhtar, *Muhammad NoumanTahir, Ghulam Rasool Baloch, Shaista Javaid, Ali Qaiser Khan, Imran Amin, LuqmanAmrao, R. W. Briddon and ShahidMansoor*
Agricultural Biotechnology Division, National Institute for Biotechnology and Genetic Engineering, Faisalabad, Pakistan

1500-1530: Refreshment break

OP-68 **Evidence of high genetic variability in cassava geminiviruses and epidemiological implications**
Vincent N. Fondong *and Kegui Chen*
Delaware State University, 1200 North DuPont Highway, Dover, DE 19901, USA; Department of Biological Sciences, Delaware State University, 1200 North DuPont Highway, Dover, DE 19901, USA

OP-69 **Cucumber mosaic virus and plant virus evolution**
Justin S. Pita[1, 2*] *and Marilyn J. Roossinck*[1, 2]
[1]*The Huck Institutes of The Life Sciences, Center for Infectious Disease Dynamics, Pennsylvania State University, University Park, PA 16802, USA;* [2]*Department of Plant Pathology and Environmental Microbiology, 211 Buckhout Lab, University Park, PA 16802*

OP-70 **Oman – a nursery for recombination between exotic Old World begomoviruses of diverse origins**
Akhtar J. Khan*[1]*, *Sohail Akhtar*[1]*, Abdulrahman M. Al-Matrushi*[1]*, Adel A. Al-Shehi*[1] *and Rob W. Briddon*[2]
[1]*Department of Crop Sciences, College of Agricultural & Marine Sciences, Sultan Qaboos University, Al-Khod 123, Oman;* [2]*National Institute of Biotechnology & Genetic Engineering, Jhang Road, Faisalabad, Pakistan*

1615-1800: Poster Session -3

1 February 2013, Friday

0815-1200: Session 10. Plant Virology in sub-Saharan Africa

OP-71 Keynote **War on African cassava viruses: a novel strategy against mighty foes of cassava**
Claude Fauquet
Executive Director GCP21, Member Danforth Plant Science Center, 975 N. Warson Rd., St Louis, MO63132, USA

OP-72 Keynote **Ever increasing diversity of tospoviruses: implications for Africa**
***Hanu R. Pappu*[1]** *and Subramanian Sevgan*[2]
[1]*Department of Plant Pathology, Washington State University, Pullman, WA 99164, USA;* [2]*IPM cluster, icipe, African insect science for food and health, Nairobi, Kenya*

OP-73 **The Bioscience Eastern and Central Africa (BecA) Hub and its role in enhancing science and technology capacity in Africa**
Jagger Harvey*, Francesca Stomeo and Appolinaire Djikeng*
Biosciences Eastern and Central Africa (BecA) Hub, International Livestock Research Institute (ILRI), Nairobi, Kenya

OP-74 **Q-bank plant virus database and collection**
René A. A. van der Vlugt*[1], Annelien Roenhorst*[2]*, Wulf Menzel*[3] *and S. Winter*[3]
[1]*Plant Research International, part of Wageningen UR (University and Research centre), P.O. Box 69, 6700 AB, Wageningen, The Netherlands;* [2]*National Plant Protection Organization, National Reference Centre Geertjesweg15, 6706EA Wageningen, The Netherlands;* [3]*Leibniz-Institut DSMZ-Deutsche Sammlungvon Mikro- organismen undZellkulturen GmbH Inhoffenstraße 7 B, 38124 Braunschweig, Germany*

- **Workshop on partnerships for plant virology capacity development in sub-Saharan Africa**

1200-1230: Concluding remarks (invitation to 13th IPVE, close of 12th IPVE)

Abstracts of the Poster Presentations

28 January 2013: Monday: Session I

PP-001 **Variability and sequence diversity of *Citrus tristeza virus* isolates from Pakistan**

***Sagheer Atta*[1,3,4]**, *Mengji Cao*[1,3], *Yan Zhou*[1,2], *Xuefeng Wang*[1,3] *and Changyong Zhou*[1,2]

[1]*National Citrus Engineering Research Center, Citrus Research Institute, Southwest University, Chongqing, 400712, China;* [2]*Key Laboratory of Horticulture Science for Southern Mountainous Regions, Ministry of Education, Southwest University, Chongqing 400716, China;* [3]*College of Plant Protection, Southwest University, Chongqing 400716, China;* [4]*Institute of Agricultural Sciences, University of the Punjab, Lahore, Pakistan*

PP-002 **Spatial and temporal analyses of the impacts of *Plum pox virus* in Pennsylvania and Ontario, Canada**

***Forrest W. Nutter, Jr.*[1]** *and Andrew V. Gougherty*[1]

[1]*Department of Plant Pathology and Microbiology, 351 Bessey Hall, Iowa State University, Ames, Iowa 50011 USA*

PP-003 **Controlling cassava brown streak disease (CBSD) through genetic engineering**

Evans Nyaboga[1], *Joshua Njiru*[1], *Nigel J. Taylor*[2], *Claude M. Fauquet*[2] *and* ***Leena Tripathi*[1]**

[1]*International Institute of Tropical Agriculture (IITA), C/o Internationa Livestock Research Institute, PO Box 30709-00100, Nairobi, Kenya;* [2]*Donald Danforth Plant Science Center, St. Louis, MO 63132 USA*

PP-004 **Strain diversity of plant RNA viruses in Ukraine**

Irena Budzanivska *and Valery Polishuk*

Taras Shevchenko Kyiv National University, Kyiv, Ukraine

PP-005 **Spread of some virus diseases among representatives of wild flora in Chernobyl region**

***V. P. Polischuk*[1], *O. V.* *Shevchenko*[1], *I. V. Chyzhevskiy*[2] *and I. G. Budzanivska*[1]

[1]*Virology Department, Taras Shevchenko' Kyiv National University, 64 Volodymyrska st., Kyiv 01033, Ukraine;* [2]*State Specialized Scientific Production Enterprise, Chernobyl Radio-Ecological Centre", 07270, 6 Shkilna st., Chernobyl, Ukraine*

PP-006 **Recombinant strains of Potato virus Y outcompete the ordinary strain in the United States potato crop to become predominant in most seed production areas**

***Stewart M. Gray*[1]**, *Alexander Karasev*[2], *Jason Ingram*[1], *Dawn Smith*[1], *Olga Nikolaeva*[2] *and Cassandra Sago*[2]

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PP-007 **Molecular characterization of a new badnavirus infecting enset (*Ensete ventricosum*: Musaceae) in Ethiopia**

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PP-008 **Current status of occurrence and geographical distribution of cassava mosaic and cassava brown streak disease and associated viruses in Mozambique**

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PP-009 **Variability of Cassava Brown Streak Disease Symptoms in Tanzania**

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PP-010 **Molecular characterization of begomovirus associated with tomato and pepper in southern region of Oman**

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PP-011 **Affects of virus infection on seed yams**

S. Asala[1,2,3], *P. Lava-Kumar*[2], *P. Ogunsania*[2], *M. D. Alegbejo*[1], *B. D. Kashina*[1] *and O. O. Banwo*[1]
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PP-012 **Expansion of *Banana bunchy top virus* pandemic into West Africa**

P. Lava Kumar[1], *R. Hanna*[2], *A. Owati*[1], *B. Lokossou*[3], *R. O. Adegbola*[1,4], *O. O. Awosusi*[5], *C. Onyeani*[5], *A. M. Pefoura*[6], *G. I. Atiri*[4] *and E. A. Asiedu*[7]
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PP-013 **Distribution and diversity of viruses infecting soybean in Nigeria**

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PP-014 **The epidemiology of a complex virus pathosystem in a perennial fruit crop**

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PP-015 **Molecular variability in the coat protein gene of the different isolates of *Apple mosaic virus***

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PP-016 **Influence of modifications of Potato virus X coat protein (XCP) on its expression and systemic movement**

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PP-017 **Epidemiology of cassava mosaic disease in the Bukavu, Kisangani and Gandajika region of Democratic Republic of Congo**

M. Muengula-Manyi[1,2], *E. Bisimwa*[3], *G. Monde*[4], *P. Tshilenge-Djim*[1], *S. Winter*[5], *C. Bragard*[2] *and A. Kalonji-Mbuyi*[1,6]
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PP-018 **Development of transgenic sweet potato (*Ipomea batatas* (L.) Lam.) with broad virus resistance in South Africa**

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PP-019 **Does potato virus S infection compromise late blight resistance in potato? Epidemiological implications**

Yu-Hsuan Lin and ***Hanu R. Pappu***
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PP-020 **Endogenous plant pararetroviral sequences in natural and managed ecosystems: epidemiology and evolution**

Sahar Eid, Christie Almeyda and ***Hanu R. Pappu***
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PP-021 **Influence of host type and insect pests on incidence, severity and spread of viral diseases on passion fruit in Uganda**

Mildred Ochwo-Ssemakula[1], *Tadeo Kaweesi[1,2], Michael Abigaba[1], Alfred Otim[2], Michael Otim[2], Samuel Kyamanywa[1], Mark Erbaugh[3] and Peter Sseruwagi[4]*
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PP-022 **Use of artificial microRNAs for engineering resistance against thrips-transmitted tospoviruses (*Tospovirus, Bunyaviridae*)**

Neena Mitter[1], Keith Chua[1], Sahar Eid, Roger Mitchell[3] and ***H. R. Pappu[2]***
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PP-023 **Climate change and *Banana bunchy top virus*: spread from the lowland Rusizi valley to surrounding higher altitudes in Burundi**

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PP-024 **Molecular characterization of begomoviruses and associated satellites that infect vegetable crops in Southwestern Cameroon**

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PP-025 **Intergeneric recombination between a new, spinach-infecting curtovirus and a new geminiviral species in the proposed genus *Becurtovirus*: first New World exemplar**

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PP-026 **Mapping the regional epidemiology of cassava viruses in east and central Africa**

J. P. Legg[1], *H. Bouwmeester[2], R. Shirima[1], S. Jeremiah[3], I. Ndyetabula[4], H. Obiero[5], G. kamilo[6], S. Bigirimana[7], G. Gashaka[8], W. Tata-Hangy[9], G. Okao-Okuja[10], T Alicai[10] and P. Lava Kumar[11]*
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PP-027 ***Lettuce big-vein associated virus*** **is the causal agent of a syndrome of necrotic rings and spots in lettuce**

Martin Verbeek, *Annette M. Dullemans, Petra J. van Bekkum and René A. A. vander Vlugt*
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PP-028 **Exploiting the combination of natural and genetically engineered resistance to viruses impacting cassava production in Africa: Production of transgenic cassava with broad-spectrum CMD and CBSD resistance**

Herve Vanderschuren, Isabel Moreno, Ravi Bodampalli Anjanappa, ImaZainuddin and ***Wilhelm Gruissem***
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PP-029 **Epidemiological studies of tomato yellow leaf curl disease in Greece and Cyprus**

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PP-030 **Cassava brown streak disease: the expanding pandemic**

R. Shirima[1], *S. Bigirimana[2], G. Gashaka[3], W. Tata-Hangy[4], P. Barumbanze[2], P. Ndayihanzamaso[2], M.C. Kanyange[3], M. Mutumwinka[3], C. Mukakanyana[3], C. Nyirahorana[3], J. Uwimana[3], S. Ntivuguruzwa[3], A. Sifa[3], J. Kazindu[3], J. Ndahimana[3], J. Umfuyisoni[3], J. Uwimana, H. Ughento[4], E. Musungayi[4], D. Swai1, H.M.Obiero[5], Ismael Njaro[5], Michael Akhwale[5], Morris Otunga[5], John Mpapale[5] and J.P. Legg[1]*
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PP-031 **Recent emergency of CBSD threatens cassava production in Tanzania**

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PP-032 **Molecular and biological characterization of a new pathotype of *Pepino mosaic virus***

Beata Hasiów-Jaroszewska[1], *Julia Byczyk[1], Natasza Borodynko[1], Henryk Pospieszny[1] and Inge M Hanssen[2]*
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PP-033 **Transient expression of *Pepino mosaic virus* TGB3 and CP genes in *Nicotiana benthamiana* and *Solanum lycopersicum***

Beata Hasiów-Jaroszewska[1], Julia Byczyk[1], *Paulina Jackowiak[2], Przemysław Wieczorek[1], Henryk Pospieszny[1] and Marek Figlerowicz[2,3]*
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PP-034 **silencing suppressor encoded by DNA-β satellite associated with Calendula officinalis yellow vein Lakshmangarh virus**

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Department of Science, Faculty of Arts, Science and Commerce, Mody Institute of Technology and Science, Lakshmangarh, Sikar-332311, Rajasthan, India

PP-035 **Virus checks for safe exchange of cassava germplasm for crop improvement and food security**

Badara Gueye, *P. Lava Kumar, Peter Kulakow and Michael Abberton*
International Institute of Tropical Agriculture (IITA), PMB 5320, Ibadan, Nigeria

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PP-036 **Viruses of sweetpotato in Israel and their control**

Gad Loebenstein, *Jacob Cohen and Victor Gaba*
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PP-037 **On the effect of acid rains on pink hydrangea**

Vahida Šeremet
Tuzla, Akifa Šeremeta 14, Bosna and Herzegovina

PP-038 **Characterization of elite sweet potato genotypes for sweet potato virus disease (SPVD) resistance and high dry matter content in Tanzania**

*Catherine Gwandu**, Fred Tairo,** Emmarold Mneney and Alois Kullaya*
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PP-039 **Genetic resistance and gene action of maize germplasm to *Maize streak virus***

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PP-040 **Molecular characterization of integrated DNA molecules associated with cassava mosaic disease in East Africa**

H. Gabriel[1], *P. Sseruwagi[1], F. Tairo[1], H. Vanderschuren[3], M. E. C. Rey[2] and J. Ndunguru[1]*
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PP-041 **The mode of transmission of *Rice yellow mottle virus***

M. E. Abo[1], *A. A. SY[2], M. D. Alegbejo[3], A. S. Afolabi[6], A. Onasanya[5], F. E. Nwilene[5] and Y. Sere[4]*
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PP-042 **Aphids infesting potato in Kenya**

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PP-043 **Cassava production enhancement in semi-arid and arid regions in Kenya**

K. Monjero[1], *J. Irungu[1] and D. Miano[1]*
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PP-044 **Mechanisms underlying resistance to groundnut rosette virus complex and its vector(s) in Uganda**

G. Otim[1], *M. S. Ochwo[1], B. Akello[2], M. Biruma[2], D. K. Okello[2] and I. O. Mugisa[1]*
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PP-045 **Evaluation of diverse oilseed *Brassica* germplasm from Australia, China and India to identify *Turnip mosaic virus* resistance phenotypes**

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PP-046 **Two genotypes of sub-Saharan Africa 1 *Bemisia tabaci* (Gennadius) (Hemiptera: Aleyrodidae) associated with cassava in East Africa exhibit distinct biological differences in fecundity and development**

H. Mugerwa[1,3], *M. E. C. Rey[3], F. Tairo[2], J. Ndunguru[2] and P. Sseruwagi[2]*

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PP-047 **Demonstration of long-term retention of potyviruses within *Myzus persica*e using nested RT-PCR: implications for transmission of non-persistent plant viruses**

Ahmad Al-Mrabeh*[1,2,3]*, *Ethan Hack[1], Graham Cowan[2], Angharad Gatehouse[1] and Lesley Torrance[2]*
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PP-048 **Assessment of seed-transmitted viruses in wild *Vigna***

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PP-049 **Molecular analysis of the complete genome of Hungarian *Potato virus S* isolate and the mapping of its of its genetic relationships.**

E. Pajtli[1], A. Zambo[1], Zs. Polgar[2], I. Wolf[2], I. Czernak[2] and ***L. Palkovics*[1]**
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PP-050 **Identifying cassava resistant varieties and resistance genes for cassava brown streak disease**

M. N. Maruthi, *Ibrahim Umer Mohammed, Hale Ann Tufan and Rory Hillocks*
Natural Resources Institute, University of Greenwich, Chatham Maritime, Kent UK

PP-051 **Exploiting reversion and tissue culture techniques for eliminating cassava brown streak viruses from infected cassava plants**

M. N. Maruthi, *Ibrahim Umer Mohammed and Rory Hillocks*
Natural Resources Institute, University of Greenwich, Chatham Maritime, Kent UK

PP-052 ***Barley yellow dwarf virus* species PAV and PAS: a comparative analysis of resistance traits**

Jana Jarošová[1,3], Eva Svobodová[1], Jana Chrpová[2], Václav Šíp[2] and ***Jiban Kumar Kundu*[1]**
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PP-053 **Stability of resistance in transgenic HoneySweet plum to *Plum pox virus* strain Rec**

Jana Jarošová[1], Eva Svobodová[1], Jaroslav Polák[1], Ralph Scorza[2], Michel Ravelonandro[3] and ***Jiban Kumar Kundu*[1]**
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PP-054 **Dispersal of TSWV and antipredator behaviour of *Frankliniella occidentalis* in presence of natural enemies**

Belén Belliure[1], Juan Antonio López-Adánez[2], M. Ángeles Marcos-García[2] and ***Alberto Fereres*[1*]**
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PP-055 **Behavioral events associated to the inoculation of a phloem-restricted semipersistent aphid-transmitted virus**

*Carmen Maria Ambros, Raquel Urbon****, Alberto Fereres,*** *and Aranzazu Moreno*
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PP-056 **Enhancing cassava productivity through host plant resistance breeding against cassava mosaic disease and cassava brown streak disease using genetic engineering and marker assisted selection - a Kenyan project**

Wilson M. Thagana*[1]*, *Richard O. Oduor[1] and William M. Muiru[2]*
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PP-057 **The spreading and movement of *Wheat dwarf virus* in its leafhopper vector (*Psammotettix alienus* Dahlb.)**
Yajiao Wang[1], Yan Liu[1], Taiyun Wei[2] and ***Xifeng Wang[1]***
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PP-058 **Facets of *Tomato spotted wilt virus* transmission by tobacco thrips, *Frankliniella fusca***
Rajagopalbabu Srinivasan[1], *Anita Shrestha[1], David Riley[1] and Albert Culbreath[2]*
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PP-059 **The population genetic structure of North Carolina populations of *Thrips tabaci* and its implications for competency of *T. tabaci* to transmit *Tomato spotted wilt virus***
Alana L. Jacobson *and George G. Kennedy*
Department of Entomology, North Carolina State University, Raleigh, NC, USA 27695-7630

PP-060 **Ecological and evolutionary perspectives on thrips-transmitted *Iris yellow spot virus* outbreaks in the USA**
Romana Iftikhar, Vikas Koundal and ***Hanu R. Pappu***
Department of Plant Pathology, Washington State University, Pullman, WA, USA

PP-061 **Complementation between two viruses in an otherwise restrictive host: implications for evolution and epidemiology of insect-borne viruses**
Sudeep Bag[1], Neena Mitter[2], Sahar Eid[1] and ***Hanu R. Pappu[1]***
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PP-062 **Epidemiology of aphid vectors of potato viruses in north-eastern hills of India**
Shahid Ali[1], *MS Kadian[2], Masood Akhtar[3] and Oscar Ortiz[4]*
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PP-063 **Global status of thrips-transmitted *Iris yellow spot virus* (*Tospovirus*) incidence in onion**
Hanu R. Pappu *and Sudeep Bag*
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PP-064 **Overview of CIALCA activities on banana bunchy top in the Great Lakes Region**
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PP-065 **Dynamics of thrips and tospoviruses as influenced by management practices in Uganda: a case of tomato and pepper**
Chris Tananси Muwanika[1], ***Charles Ssemwogerere[1],*** *Mildred Ochwo-Ssemakula[1], Jeninah Karungi[1], Samuel Kyamanywa[1], Naidu Rayapati[2] and Joe Kovach[3]*
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PP-066 **Effect of soil amendments and mulching on occurrence of tomato viral diseases and their vectors in Uganda**
Chris Tananси Muwanika[1], *Jeninah Karungi[1], Mildred Ochwo-Ssemakula[1], Samuel Kyamanywa[1] and Joe Kovach[2]*
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PP-067 **Development of biomarkers for vector competent aphid and whitefly populations in sub-Saharan Africa**
D. Igwe[1]*, S. Ngatat[2], M. Cilia[3,4], M. S. Bereman[5], M. J. MacCoss[5], M. Ghanim[6], S. Gray[3,4], R. Hanna[2] and P. Lava Kumar[1]*
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14853, USA; [5]Department of Genome Sciences, University of Washington, Seattle, Washington 98195, USA; [6]Department of Entomology, Agricultural Research Organization, The Volcani Center, Bet Dagan, 50250, Israel

PP-068 **Establishment of Banana bunchy top virus-free banana seed systems in Malawi**

Misheck M. M. Soko, *Victor E. Mshani and Dickson L. N. Banda*
Bvumbwe Research Station, P.O. Box 5748, Limbe, Malawi

PP-069 **Trend of virus infection on sweetpotato varieties for highland production in central Rift Valley of Kenya**

Laura Karanja[1], *Joyce Malinga[1], Samuel Mwaura[1], Anne Gichangi[1], David Lelgut[1] and John Ndung'u[1]*
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PP-070 **Hollyhock, a new reservoir of a monopartite begomovirus-satellite complex infectious to cotton plants**

M. Zia-Ur-Rehman[1, 3], M. S. Haider[1, 2] and ***J. K. Brown[3]***
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PP-071 **Farmers' knowledge of passion fruit virus diseases and their management in central Uganda**

Atukunda Robinah[1]*, Sseruwagi Peter[2], Ochwo M. Ssemakula[1], Karungi Jeninah[1], Kyamanywa Samuel[1] and Mark Erbaugh[3]*
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PP-072 **Strategies for developing banana planting material free from Bunchy top virus infection in Bas-Congo, DR Congo**

Patrick Mobambo[1,2], *Germaine Vangu[3], Charles Staver[2] and Pascale Lepoint[2]*
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PP-073 **Breeding maize for improved MSV resistance: genomic characterization of MSV strains found in Ghana**

Allen Oppong[1,3], *Darren P. Martin[2], Hans Adu-Dapaah[3], Joseph L. Lamptey[3], Kwadwo Ofori[1], Charles The[1], Samuel K. Offei[1] and Arvind Varsani[4,2]*
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PP-074 **Spread of cassava brown streak disease in Uganda as influenced by host resistance and prevailing disease pressure**

Kasifa Katono[1,2]*, Titus Alicai[2], Yona Baguma[2], Richard Edema[1], Anton Bua[2] and Christopher A. Omongo[2]*
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PP-075 **Susceptibility of *Musa* genotypes to banana bunchy top disease in Cameroon and implications for disease management**

Sergine Ngatat[1], *Rachid Hanna[1*] and P. Lava Kumar[2].*
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PP-076 **Managing the spread of cassava viruses through clean 'seed' systems**

*C. Hermence[1]****, K. Mtunda[2],*** *M. Muhanna[2], S. Boniface[1], S. Jeremiah[3], E. Kanju[1] and J. P. Legg[1]*
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PP-077 **Community action in cassava brown streak disease control through clean seed**

K. J. Mtunda[1], *J. P. Legg[2], I. Ndyetabura[3], S.Jeremiah[2], K.Mvanda[4], G. Mutasingwa[5] and E. Shumbusho[6]*
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PP-078 **Transgenic approach for improving resistance of plum cultivars for Sharka disease**

S. Dolgov[1], *R. Mikhailov[1], O. Shulga[2], P. Kharchenko[2] and A. Firsov[1]*
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PP-079 **Viruses in social-ecological systems: Strategies for farmer selection in smallholder seed systems**

Sara Thomas[1]*, Greg A. Forbes[2] and Karen A. Garrett[1]*
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PP-080 **Effect of cassava brown streak disease on predominant cassava varieties in Malawi**

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PP-081 **Seed transmission of *Tomato torrado virus* in tomato**

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Institute of Plant Protection – National Research Institute, Virology and Bacteriology Department, Poznan, Poland

31 January 2013: Thursday: Poster Session III

PP-082 **Identification and molecular analysis of natural resistance to cassava brown streak disease (CBSD)**

Ravi Bodampalli Anjanappa[1], M. N. Maruthi[2], Edward Kanju[3], Haidari Nawabu[3], ***Wilhelm Gruissem[1]*** *and Herve Vanderschuren[1]*
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PP-083 **Transmission of cassava brown streak viruses by *Bemisia tabaci* whiteflies**

S. C. Jeremiah[1], *M. N. Maruthi[2], J. N. Ijumba[3] and J. P. Legg[4]*
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PP-084 **Diversity and distribution of viruses infecting chilli pepper in Nigeria**

O. Arogundade[1,2,3], *O. S. Balogun[2], S. O. S. Akinyemi[1] and P. Lava Kumar[3]*
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PP-085 **Incidence and distribution of cassava mosaic begomoviruses in Côte d'Ivoire**

Marie N. Y. Toualy[1,2], ***HortenseAttaDiallo[1]****, S. A. Akinbade[2] and P. Lava Kumar[2]*
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PP-086 **Detection and characterization of several distinct walnut isolates of *Cherry leaf roll virus* (CLRV) in Poland**

Mirosława Cieślińska *and Grzegorz Hodun*
The Research Institute of Horticulture, Konstytucji 3 Maja 1/3, Skierniewice, Poland

PP-087 **Diagnostic tools for cassava mosaic and cassava brown streak viruses**

R. C. Aloyce[1,2], *F. Tairo[3], J. Ndunguru[2], P. Sseruwagi[1] and M. E. C. Rey[2]*

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PP-088 **PP-088: Quantitative detection of *African cassava mosaic virus* and *East African cassava mosaic virus* using TaqMan Real Time PCR**

*G. Otti, **A. Owati**, G. Melaku and P. Lava Kumar*
International Institute of Tropical Agriculture (IITA), PMB 5320, Ibadan, Nigeria

PP-089 **The incidence and characterization of *Cherry leaf roll virus* (CLRV) in *Sambucus* spp. plants in Poland**

***Hanna Berniak** and Maria Kamińska*
Research Institute of Horticulture, Konstytucji 3 Maja 1/3, 96-100 Skierniewice, Poland

PP-090 **Inheritance of multiple virus resistance in cowpea**

***K. E. Ogunsola[1-3],** C.A. Fatokun[1], C.O. Ilori[2], O. Bokuar[1], G. I. Atiri[2] and P. Lava Kumar[1]**
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PP-091 **Molecular identification and characterization of a begomovirus associated with *Phaseolus lunatus* L. in Nigeria**

***B. D. Kashina[1],** N. Mogens[2] and L. N. Steen[2]*
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PP-092 **The distribution and molecular variability of *Zucchini yellow mosiac virus* and *Papaya ringspot virus* in the Pacific Islands**

*Karl Crosby[1], Colleen M Higgins[2], Viliami Kami[3] and **Michael N Pearson[1]***
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PP-093 **First molecular evidence of cassava brown streak disease in Democratic Republic of Congo**

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PP-094 **Prevalence of cassava viral diseases in different agro-ecological zones in the western part of Democratic Republic of Congo**

***Z. Bakelana[1,4],** J. Harvey[1], L. Calvert[1], L. Purdie[1], R. Skilton[1], T. Holton[1], E. Magembe[1], M. Macharia[1], J. Legg[2], N. Mahungu[2], K. Tata-Hangy[2], D. Lutete[3] and K. Tshilenge[5]*
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PP-095 **Occurrence and distribution of cassava brown streak viruses in Western Kenya**

***Aggrey K. Osogo[1]** and H. K. Were[1]*
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PP-096 **Prevalence and distribution of begomoviruses infecting cassava in Western Kenya**

***Claris N. Omuse[1],** V. K. Ogemah[1], J. Muoma[1] and H. K. Were[1]*
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PP-097 **Genetic diversity and geographic distribution of cassava mosaic geminiviruses in Mozambique**

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PP-098 Occurrence and distribution of viruses infecting tomato and pepper in Alibori in northern Benin

Regina Kotchofa
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PP-099 Occurrence of a new strain of *Tomato leaf curl Sudan virus* in association with the old betasatellite from Oman

Akhtar Jamal Khan and ***Sohail Akhtar***
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PP-100 The use of FTA® Classic Card Technology for building epidemiologic intelligence of plant viruses

R. A. Naidu[1], *S. Poojari[1], O. J. Alabi[1], G. Karthikeyan[2], T. Damayanti[3], G. Kodetham[4] and P. Lava Kumar[5]*
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PP-101 Multiplex RT-PCR assays for the simultaneous detection of cassava mosaic virus and cassava brown streak viruses

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PP-102 Diagnosis and molecular characterization and of viruses expressing similar necrotic symptoms in blackgram (*Vigna mungo* L. Hepper) and greengram (*Vigna radiata* L. Wilczek)

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PP-103 Presence and distribution of *Banana bunchy top virus* (BBTV) in South-Western Democratic Republic of Congo

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PP-104 Viruses of tomato and pepper in southwest Nigeria and their distribution

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PP-105 Diagnosis and characterization of viruses implicated in mixed infections of *Amorphophallus paeoniifolius*

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PP-106 Distribution of banana bunchy top disease (BBTD) across the main plantain and banana growing regions of the Democratic Republic of Congo

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PP-107 **Passion fruit woodiness virus disease in Kenya: genome characterisation of the casual agent**

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PP-108 **Quarantine viruses of strawberry**

Kris De Jonghe[1], *Sébastien Morio[1], Thibaut Olivier[2], Ellen Demonty[2], Stéphan Steyer[2], Gertie Peusens[3], Tim Beliën[3] and Martine Maes[1]*
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PP-109 ***Distribution of CBSD causing viruses in different cassava tissues***

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PP-110 **Molecular characterization of DNA satellites associated with cassava mosaic geminiviruses**

Francis M. Mwatuni, Elijah M. Ateka, Laura Karanja and Samuel K Mwaura
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PP-111 **A satellite virus associated with Brome mosaic virus isolated from winter wheat and triticale plants in the Russian Central Cernozem region**

Frank Rabenstein[1], *Angelika Ziegler[1], Bernd Schlieter[2] and Nikolay Danilkin[3]*
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PP-112 **Potato virus distribution in different agroecological conditions of Uzbekistan**

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PP-113 **Developing banana bunchy top virus-free planting material in Kisangani, Province oriental, DR Congo**

Faustin Ngama Boloy[1], Bonaventure Ibanda Nkosi[2], ***Benoît Dhed'a Djailo[2]****, Charles Staver[3] and Pascale Lepoint[3]*
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PP-114 **Incidence, symptom severity and distribution of tomato viral diseases in Uganda**

W. Arinaitwe[1], *M. Ochwo-Ssemakula[1], P. Sseruwagi[2], S. Kyamanywa[1], M. Sally[3], Q. Feng[3] and M. Erbaugh[4]*
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PP-115 **Host range and incidence of *European mountain ash ringspot-associated virus* in the Czech Republic and other European countries**

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PP-116 **Incidence, symptom severity and geographic distribution of cassava mosaic disease and associated viruses in Tanzania**

Fred Tairo, *Peter Sseruwagi, Nesie Luambano, Doreen Mgonja, Cyprian Rajabu, Habibu Mugerwa, Happyness Gabriel, Catherine Gwandu Geoffrey Oisso, Margret Lupembe and Joseph Ndunguru*
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PP-117 **Two generic PCR primer sets for the detection of members of the genus *Torradovirus***

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PP-118 **Next Generation Sequencing as a quality tool for plant virus collections**

René A.A. van der Vlugt[1], *Annette Dullemans[1], Annelien Roenhorst[2], Ko Verhoeven[2], Marleen Botermans[2] and Bart van de Vossenberg[2]*
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PP-119 **Sources of PVY infections in potato fields**

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PP-120 **Plant virome ecology in African farming systems: assessing food security**

Francesca Stomeo[1], *Mark Wamalwa[1], Jagger Harvey[1], Douglas W. Miano[2], Dora Kilalo[3], Neil Boonham[4], Ian Adams[4] and Appolinaire Djikeng[1]*
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PP-121 **Status of cassava brown streak in Western Kenya**

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PP-122 **Cassava mosaic disease and associated viruses in Zambia: Occurrence and distribution**

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PP-123 **Diagnostics in biosecuring agriculture from transboundary plant viruses: a case study of India**

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PP-124 **Simultaneous detection of DNA viruses infecting sweetpoptato (*Ipomoea batatas*) by multiple PCR**

A. Berrocal, G Rossel, ***S. Fuentes,*** *A. Perez, W. Cuellar and J. Kreuze*
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PP-125 **First serological characterization and molecular phylogeny of *Rice yellow mottle virus* in Southern Benin**

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PP-126 **Stable internal reference genes for normalization of real-time RT-PCR in tobacco (*Nicotiana tabacum*) during virus infection**
Ju-Yeon Yoon, *Eseul Baek and Peter Palukaitis*
Department of Horticultural Sciences, Seoul Women's University, Seoul, Korea

PP-127 **Status of yam viruses in West Africa**
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PP-128 **The prevalence of cassava mosaic begomoviruses in Malawi**
W. Changadeya[1], *W. Kamowa-Mbewe[1, 2,3], P. Lava Kumar[3], J. P. Legg[4] and P. Ntawuruhunga[5]*
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PP-129 **Genetic diversity of the Polish isolates of *Tomato black ring virus* (TBRV)**
Natalia Rymelska, *Beata Hasiów-Jaroszewska, Henryk Pospieszny and Natasza Borodynko*
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PP-130 ***Potato Virus Y* on Tomato in Poland**
Natasza Borodynko, *Beata Hasiów-Jaroszewska, Natalia Rymelska, Julia Byczyk, Henryk Pospieszny*
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PP-131 **Production and conservation of virus-free cowpea germplasm**
A. A Adesida-Oludare*, P. Ogunsanya, O. Oluwole, O. Oyatomi, E. Iwu, B. Gueye M. Abberton and P. Lava Kumar*
International Institute of Tropical Agriculture (IITA), Ibadan, PMB 5320, Nigeria

PP-132 **Sweetpotato virus degeneration study in Lake Zone of Tanzania**
Nessie D. Luambano *and Joseph Ndunguru*
Mikocheni Agricultural Research Institute, P. O. Box 6226, Dar es Salaam, Tanzania

PP-133 **Impact of banana bunchy top disease in Chiawa, Zambia: need for more integrated disease control programs**
Rabson M Mulenga
Zambia Agriculture Research Institute, Mount Makulu Central Research Station, Private Bag 7, Chilanga, Zambia

PP-134 **Molecular detection and identification of begomoviruses and its associated satellite molecules affecting some important plants in India**
S. K. Snehi, *A. Srivastava, S. Kumar and S. K. Raj*
Plant Molecular Virology Lab, CSIR-National Botanical Research Institute, Lucknow-226001, Uttar Pradesh, India

PP-135 **Molecular detection, identification, genetic diversity and distribution of begomoviruses causing severe mosaic disease on *Jatropha* species in India**
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PP-136 **Status of mungbean research and development in Bangladesh**
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Abstracts of the Oral Presentations

Keynote presentation

OP-1: A century of plant virus epidemiology

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A 60-year involvement with Plant Virus Epidemiology provides an appropriate standpoint from which to consider some of the main developments over this period and over an even longer time-scale to the early years of Plant Virology at the beginning of the 20th Century. In 1953, Plant Virology was in a very rudimentary state. Only a few particularly stable viruses had been purified and characterised, the role and relative significance of virus proteins and nucleic acids had not been established and viroids and phytoplasmas had not been distinguished as separate groups of pathogens. Nevertheless, plant virus epidemiology was already well established and there were several distinguished practitioners. Transmission by contact, seed and several types of insect or mite vector had been demonstrated. Moreover, detailed information was available from field studies on particularly important viruses including ones transmitted by thrips (tomato spotted wilt), leafhoppers (maize streak, beet curly top), plant hoppers (sugarcane Fiji disease), aphids (potato virus Y, potato leafroll, sugarbeet yellowing, groundnut rosette), mealybugs (cacao swollen shoot) whiteflies (cassava mosaic, tobacco leaf curl, cotton leaf curl) and an eriophyid mite (blackcurrant reversion). The role of weeds and wild plants in the epidemiology of several viruses including cucumber mosaic, beet curly top and pineapple yellow spot had been established. Furthermore, the importance of an holistic ecological approach to the complexities of virus/host/vector interrelationships had been stressed by early workers including Walter Carter and R L Piemeisel in the US and Hille Ris Lambers and other vector entomologists in Europe. General epidemiological principles were also emerging from the mathematical approach adopted by several early workers including J G Bald in Australia, J E Vanderplank in South Africa and P H Gregory and Marion Watson in the UK.

There have been many important developments over the last 60 years and some of the earliest were the demonstration of transmission by pollen (1965) and additional types of vector including soil-inhabiting nematodes (1958) and fungi (1960). This stimulated a surge of interest in these topics and contributed towards a solution to long-standing problems of cereals, beet, potato, hop, grapevine, raspberry, cherry and many other fruit crops. Another major development was the publication in 1963 of "Plant Diseases: Epidemics and Control". It was the first of a seminal series of publications by J E Vanderplank that introduced many new concepts and transformed approaches to the analysis and interpretation of disease progress curves and other types of data. Despite such progress it became apparent in the 1970s that epidemiology and "biological" studies more generally were being neglected in favour biochemical research on the physico-chemical properties of viruses.

In an attempt to remedy this unsatisfactory situation and to foster a more balanced approach the Plant Virus Epidemiology Committee of the International Society of Plant Pathology was established in 1980. The first of what has become a regular series of Symposia was held in Oxford, UK in 1981. The Arusha meeting will be the 12th such meeting and the continuing series of six publications contain material presented at previous meetings. They record many of the recent developments and trends on such topics as vectors, modelling, forecasting, integrated disease management, molecular epidemiology and the underlying causes of recent epidemics including those due to viruses transmitted by thrips or whiteflies. Overall, it can be argued that the long tradition of plant virus epidemiology has been maintained and continues to contribute towards meeting the massive challenge of not only maintaining but also increasing food production.

Keynote presentation

OP-2: Trends in plant virus epidemiology: opportunities from new or improved technologies

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The current era is one of rapidly accelerating technological advancement. To address looming world food insecurity and threats to plant biodiversity resulting from climate change and rapid population growth, it is important that new or improved technologies which help us understand and control epidemics of damaging plant viruses are adopted as speedily as possible. This is because such technologies provide opportunities not only to obtain new types of knowledge about plant virus epidemics, but also to collect and process diverse types of standard epidemiological data sets much more effectively and efficiently than previously. This talk will discuss some of the new or improved technologies recently adopted in plant virus epidemiology for (i) knowledge enhancement, (ii) data collection and processing, and (iii) provision of more effective prediction and decision support over deployment of control measures that minimise yield and quality losses. It will also identify new technologies not yet adopted by plant virologists that have potential for use to improve understanding of plant virus pathosystems or the effectiveness of epidemic management. Technologies that can be used to understand and address virus epidemics in cropping scenarios that are either high value, large-scale or small-scale, subsistence types will be covered, as well as technologies that could be used with virus epidemics that threaten indigenous flora.

Keynote presentation

OP-3: Plant viruses modify the behavior and performance of their vectors enhancing their fitness, transmission and spread

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Plant pathogens can influence the behavior and fitness of their insect vectors, by two different ways: directly-mediated by the presence of the virus in the vector's body- and indirectly-mediated by changes occurring in the plant as a consequence of infection. It has been proposed that plant viruses may modify the behavior of their insect vectors adapting to each type of virus-vector relationship in a way that transmission efficiency is optimized. We will report results of two different studies on the direct and indirect effects of virus infection on their insect vectors (aphids and whiteflies). The first study was conducted using *Cucurbit aphid-borne yellow virus* (Luteovirus, CABYV) transmitted by the melon aphid, *Aphis gossypii* Glover in a persistent manner. We compared the probing, feeding behavior and performance of viruliferous and non-viruliferous aphids in two hosts plants: a CABYV-susceptible (cucumber, *Cucumis sativus* L.) and a CABYV-resistant host (cotton, *Gossypium hirsutum* L.).The results show that viruliferous aphids fed more efficiently increasing the probability of virus inoculation and their population growth was enhanced on cucumbers but not on cotton, suggesting that changes were due to plant-mediated indirect effects of virus infection rather than to direct interactions between the virus and its vector. In the second study we analyzed the impact of cucumber plants infected by either a persistent (CABYV) or a non-persistent (*Cucumber mosaic virus*) virus on the performance and behavior of its aphid vector, *A. gossypii*. Results show that virus-infected plants enhanced the performance and modified the flight, settling and probing behavior of their aphid vector in a way that virus transmission and spread is optimized. Our work shows that plant viruses that use different transmission strategies (persistent or non-persistent) induce specific changes in their host plants that modify the behavior and performance of their aphid vectors leading to a mutualistic-type of relationship that enhances their fitness and spread.

Keynote presentation

OP-4: Climate change adaptation in disease management: a framework for evaluating the likely utility of decision support systems and index insurance

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The same core models of the relationship between weather and loss to viruses are needed for climate change scenario analysis, decision support systems (DSS), and other potential applications such as index insurance. We have developed a framework for evaluating the likely effectiveness of DSS and index insurance for pests and diseases, as a function of a number of key factors. First, we consider the time series of weather conditions, in terms of baseline temporal autocorrelation and the type of non-stationarity imposed by climate change, and how these patterns make DSS and index insurance more and less feasible. Second, the framework within which the DSS is constructed is considered, in terms of the number of years of data available and how good initial parameter estimates are. We use these system traits to identify parameter combinations or scenarios where DSS and index insurance are likely to be effective or not. We are beginning the work of placing particular diseases and geographic locations in the theoretical parameter space. Ultimately we plan to use this framework to identify pathosystems and locations that are particularly good targets for implementing tools such as DSS and index insurance. We also are addressing the general question of when DSS developed in baseline climate scenarios can still work well in new climate scenarios, versus when DSS must be modified to maintain utility.

Keynote presentation

OP-5: Influence of climate change on plant virus disease infections and epidemics

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An assessment of the influence of climate change on plant virus disease infections and epidemics was motivated by (i) the magnitude of the threat to world food security and diversity of natural vegetation posed by viral pathogens of plants at a time of accelerating climate change, and (ii) the inadequate attention given to this subject by researchers studying climate change and plant disease. Background information on critical features of viral pathosystems and the general influence of environmental factors upon them will be described briefly. Then, use of comprehensive climatic and biological frameworks to determine the likely influences of direct and indirect climate change parameters on the many different host, vector and pathogen parameters that represent the diversity of viral pathosystems will be described. This approach proved a powerful way to identify the relevant international research data available and many information gaps where research is needed in the future. The analysis suggested that climate change is likely to modify many critical viral epidemic components in different ways often resulting in epidemic enhancement but sometimes having the opposite effect, depending on the type of pathosystem and circumstances. With vector-borne pathosystems and new encounter scenarios, the complication of having to consider the effects climate change parameters on diverse types of vectors and the emergence of previously unknown pathogens added important additional variables. The increasing difficulties in controlling damaging plant viral epidemics predicted to arise from future climate instability warrants considerable research effort to safeguard world food security and biodiversity.

Reference:
Jones RAC, Barbetti MJ (2012). Influence of climate change on plant disease infections and epidemics caused by viruses and bacteria. CAB Reviews 7, No. 22, 1-32 (on-line publication) http://www.cabi.org/cabreviews.

OP-06: The effect of elevated temperature on the titre of *Barley yellow dwarf virus*-PAV in wheat cv. Yitpi

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Barley yellow dwarf virus-PAV (BYDV-PAV) is a phloem- limited luteovirus (family *Luteoviridae*) that is transmitted by *Rhopalosiphum padi* (the oat aphid) and *Sitobion* (*Macrosiphum*) *avenae*. BYDV-PAV is associated with yellow dwarf disease, one of the most economically important groups of diseases of cereals worldwide. In this study the impact of current and future predicted temperatures for the Wimmera wheat growing district in Victoria, Australia on the titre of BYDV-PAV in wheat was assessed. Ten day old wheat seedlings were inoculated with BYDV-PAV and grown at ambient (5.0-16.1°C, night-day) or elevated (10.0-21.1°C, night-day) temperature treatments, simulating the current Wimmera average and future daily temperature cycles respectively during the wheat-growing season. Whole above-ground plant samples were collected from each temperature treatment at 0 (day of inoculation), 3, 6, 9, 12, 15, 18, 21 and 24 days after inoculation. Nucleic acid was extracted using a KingFisher 96 magnetic extractor and an Agencourt Chloropure magnetic extraction kit and DNase treated. The RNA was analysed using a specific one-step multiplex normalised reverse transcription quantitative PCR (RT-qPCR) assay to accurately measure BYDV-PAV titre in wheat. Physical measurements, including plant height, dry and wet weight and tiller number were also taken at each sampling point. The titre of BYDV-PAV in wheat plants grown at elevated temperature peaked at days 12-15, decreased until day 21 and then stabilised. The titre of BYDV-PAV in wheat plants grown at ambient temperature continued to increase until days 15 to 18 and then stabilised. The titre of BYDV-PAV in plants grown at elevated temperature was significantly greater than the titre of the virus in wheat plants grown at ambient temperature on days 6, 9, 12 and 15. Plants grown at elevated temperature were significantly bigger and symptoms associated with BYDV-PAV were visible earlier than plants grown at ambient temperature. These results have important implications for the epidemiology of yellow dwarf disease under future climates in Australia.

OP-07: Influence of ambient ecology on the incidence and severity of groundnut rosette virus disease in Uganda

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Groundnut rosette virus disease (GRVD) is the most destructive disease of groundnut (*Arachis hypogaea*) in Uganda and across Sub-Saharan Africa. Epidemics are sporadic and unpredictable, causing substantial losses which significantly reduce production, crippling the rural economy. The disease is principally transmitted by aphids (*Aphis craccivora*). Much information has been obtained on the main features of GRVD since its discovery in 1907. However, gaps remain in the available knowledge for instance on certain epidemiological aspects of the disease. This study was aimed at establishing the influence of ambient ecology on the incidence and severity patterns of GRVD in Uganda. Trials were established in four groundnut growing locations each located in different agro-ecological zones within the country. Four groundnut genotypes (2 susceptible and 2 resistant to GRVD) were used as treatments in a RCBD that had 4 replicates. Disease progress was assessed at 4, 8 and 12 weeks after planting. Data on environmental factors: rainfall, temperature, relative humidity and wind speed were obtained from standard meteorological stations and supplemental weather equipment (data loggers) at the sites. Aphid numbers were assessed at regular intervals during the trial. Soil samples and yield data were also obtained for each planting season. Levels of GRVD infection appeared to be related to some ambient ecological factors, particularly rainfall and wind speed. Disease incidence, severity, AUDPC values and aphid vector populations were generally higher in conditions of lesser rainfall and lower wind speeds. Correlation coefficients between GRVD incidence and rainfall, wind speed, temperature and aphid numbers were as high as -0.99 and significant ($p=0.05$). Ambient ecology, therefore, to some extent affects GRVD incidence. This information could facilitate the development of disease forecasting methods and sustainable disease management packages. It could also explain the sporadic disease epidemics that cause serious crop losses and sometimes total crop failure.

Keynote presentation

OP-08: Sustainable plant resistance management in agricultural landscapes

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The deployment of virus resistant crops often leads to the emergence of resistance-breaking pathogens that suppress the yield benefit provided by resistances. The theoretical analyses presented here are designed to provide guidelines for farmers aiming altogether to optimise the deployment of a resistant cultivar in a landscape over several years according to management strategies aiming either to minimise the overall yield losses due to the virus (economical strategy) or to keep the frequency of the resistance-breaking virus in the reservoir hosts under a preset threshold (patrimonial strategy). Assuming gene-for-gene interactions, epidemics are modelled by linking genetic and epidemiological processes in a landscape composed of a mosaic of resistant and susceptible fields, subjected to seasonality, and of a reservoir hosting viruses year round. We explored how time constant optimal cropping ratio (i.e. the proportion of resistance cultivar deployed in a landscape) defined according to either economical or patrimonial objectives depend on resistant cultivar choice and on landscape epidemiological context (defined by the landscape structure and the mean epidemic incidence observed before resistance deployment). If the choice of the resistance gene is the main factor determining optimal cropping ratio, epidemiological contexts are also important. In some of them, patrimonial and economical strategies have close economical efficiencies, implying that both management objectives are achievable at the same time. In others, patrimonial strategies have weak economical efficiencies, meaning that both management objectives are incompatible. A way to remove such incompatibility is to design time varying strategies where the proportion of resistant fields in the landscape can change. Indeed, such strategies can at the same time comply with a patrimonial objective while substantially restoring the economical efficiency of time constant strategies and can even over performed them in landscape where epidemics are primarily driven by between fields infection events.

Keynote presentation

OP-09: Geospatial and Temporal Analyses of *Bean pod Mottle virus* Epidemics in Soybean

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A state-wide survey was carried out from 2005 through 2007 to quantify, map, and analyze the spatial dynamics and seasonal patterns of *Bean pod mottle virus* (BPMV) prevalence and incidence within Iowa. Field- and county-scale BPMV prevalence and incidence data were mapped using GIS software. BPMV prevalence was highest in the 2006 soybean growing season, when BPMV was detected in 38.7% of all soybean fields, 91.9% of all counties, and 100% of the agricultural climate districts. The prevalence of BPMV at the field scale was 9.1% and 25.5% in 2005 and 2007, respectively. BPMV incidence at the field scale was highest in 2006, when mean state-wide end-of-season incidence was 24.4%. End-of-season BPMV incidence at the field scale was 4.1% and 10.9% in 2005 and 2007, respectively. Spatial analyses indicated that BPMV incidence was spatially clustered at the county scale in all three growing seasons. Prevalence at the county scale was clustered in 2005 and 2007, but not in 2006. Semi-variogram analyses at the field scale indicated the presence of significant spatial dependence (clustering) for distances of up to 23.4 km in 2005, 297.7 km in 2006, and 45.2 km in 2007. Data for county-scale incidence displayed a north (low incidence) to south (high incidence) BPMV gradient in each year of the survey. High BPMV prevalence and incidence at the county scale in 2006 had a significant carryover effect on BPMV prevalence and incidence in 2007. Soybean fields with narrow row spacing (≤38 cm) were associated with higher levels of BPMV incidence. Soybean fields infected with BPMV had a higher probability of infection by phomopsis pod and stem blight than did non-BPMV infected fields. This study provides new quantitative tools and information to better understand the temporal and geographical distribution of BPMV disease risk at several spatial scales.

OP-10: Biology-rich climate based model for predicting thrips-borne Tomato Spotted Wilt in tobacco in North Carolina

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Abstract: Tomato spotted wilt causes major economic losses in tobacco, tomato and pepper in North Carolina, USA but its occurrence is highly variable among locations and over years. The causative agent, *Tomato spotted wilt virus* (TSWV), is spread by the tobacco thrips, *Frankliniella fusca,* in a persistent manner. Previous research in our program demonstrated the role of tobacco thrips in spread of TSWV among the winter host plants that serve as sources for spread to crop and non-crop summer hosts. It also characterized the effects of winter and spring temperatures and rainfall on the development, population growth, and dispersal of tobacco thrips in winter and spring. We will present the results of recent work to develop a statistical model of TSWV prevalence in tobacco as season's end as a function of weather and weather-mediated thrips activity. This model explains 84% of the variation in final TSWV prevalence in tobacco in a data set representing 8 years and 29 counties in NC. A key component of the model is an interaction involving estimated vector populations in the preceding year, which influence inoculum potential in the current year, and specific weather parameters that profoundly influence vector abundance and dispersal in the current year. The interaction illustrates the interdependence of virus abundance and vector activity in determining final prevalence of TSWV in tobacco.

OP-11: Temporal and spatial spread of chickpea chlorotic dwarf virus (CpCDV) in chickpea in northern Sudan

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Chickpea chlorotic dwarf virus (CpCDV) (family *Geminiviridae*, genus *mastrevirus*) has present in chickpea fields in northern Sudan since early 1990s causing great losses to chickpea production. Nothing was known about the epidemiology of this virus. Thus seasonal, spatial and temporal spreads of the chickpea chlorotic dwarf (CpCD) disease were investigated for the first time in field trials conducted at Hudeiba Research Station Farm, northern Sudan. High levels of disease incidence were found to occur in plots that grown during summer in year 2004 and 2005, while low incidence was noticed during winter months. The low spread of the disease was consistently associated with low numbers of leafhopper vector, *Orosius orientalis*, and vice versa. Ordinary runs analysis indicated that the arrangement of infected chickpea plants within rows was random throughout the life cycle of the crop regardless of sowing dates. Disease progress and rate curves (*dy/dt*) indicated that logistic, monomolecular, logistic and monomolecular growth models would best describe disease progress in chickpea crop grown in May, June, November and December 2005, respectively. Logistic was the best model to describe the disease in May 2006, while monomolecular was the best for describing disease spread in June, November and December 2006. However, the monomolecular model was chosen for the purpose of comparing the disease epidemics. Estimated rates of infection were 0.214, 0.081, 0.012 and 0.001 with respect to the day of the year for the chickpea that grown in May, June, November and December 2005, respectively. For the year 2005 the rates of disease progress were 0.122, 0.083, 0.006 and 0.001 in the crop that grown in May, June, November and December 2006, respectively. The highest rates of virus progress was clearly shown to be during summer, so the key to the management of the disease in the River Nile State is to choosing the third week of November as the optimum sowing date.

Keynote presentation

OP-12: Circulative, nonpropagative transmission: a carefully tuned orchestra of virus, vector and host proteins

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Nonpropagative, circulative plant viruses replicate in and associate with phloem tissue where they are available to sap sucking aphid vectors. Once ingested into the aphid, the virus must actively associate with and move across specific gut and salivary tissues. Combining genetics with proteomics, we have identified a suite of virus, vector and host proteins that orchestrate these complex and interactive processes. Multiple domains in two virus structural proteins mediate virion movement in phloem and insect tissues via physical interactions with plant and aphid proteins. These specific interactions may well represent the molecular Achilles heel of circulative viruses if precision virus management strategies can target and disrupt the molecular interactome. Aphid vector competency is regulated by a multitude of aphid and symbiont genes operating in an additive fashion that ultimately give rise to clonal aphid populations disparate in their transmission efficiency phenotype. These genes encode proteins associated with cell binding, uptake, vesicle transport and immune responses, and some interact directly, or in complex, with virions. Their specific roles in transmission are under investigation. A more practical application is that several of the aphid proteins serve as robust biomarkers for vector competence. These predict which aphid populations are efficient virus vectors and should be targeted for control. Tissue tropism of the virus in the plant is critical for virus transmission. Cytosolic forms of two virus proteins mediate the retention and movement of virus in phloem tissues from which aphids acquire virus during prolonged feeding. The identified host-virus interactome increased transmission efficiency by either influencing virus uptake directly or facilitating virus ingestion via an alteration of the phloem environment. The genes coding for the plant proteins interacting with virus and/or mediating phloem retention may be exploited as components of novel forms of resistance that disrupt phloem-virus or aphid-virus interactions.

Keynote presentation

OP-13: Virus-induced modifications in host plants attract vectors and increase probability of virus spread to healthy plants

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Plant virus infection can alter the suitability of host plants for their insect vectors. Most reports indicate that virus-infected plants are superior hosts for vectors compared to non-infected plants with respect to vector growth rates, fecundity and longevity. Some insect vectors preferentially respond to virus-infected plants compared to noninfected ones, while others avoid infected plants that are inferior hosts. Thus, it appears vectors can exploit changes in host plant quality associated with viral infection. Enhanced vector performance and preference for virus-infected plants might also be advantageous for viruses by promoting their spread. Our research has focused on two of the most important members of the virus family Luteoviridae that infect wheat, [*Barley yellow dwarf virus* (BYDV)], or potato, [*Potato leafroll virus* (PLRV)], and their respective aphid vectors, the bird-cherry oat aphid, *Rhopalosiphum padi,* and the green peach aphid, *Myzus persicae.* Our recent studies have examined preferences of viruliferous and nonviruliferous aphids for virus-infected or sham-inoculated plants (plants challenged with nonviruliferous aphids). In both pathosystems, nonviruliferous aphids prefer virus-infected plants, while viruliferous aphids prefer sham-inoculated plants. This shift in preference from infected to noninfected plants following virus acquisition could accelerate the rate of virus spread. Modeling exercises confirm this prediction. Recent research findings will be presented and potential impacts on vector ecology and virus disease epidemiology will be highlighted.

Keynote presentation

OP-14: Same vehicle, different engine: the dynamics of *Bemisia tabaci p*opulations driving cassava virus disease pandemics in sub-Saharan Africa

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Super-abundant populations of the whitefly vector of plant viruses, *Bemisia tabaci* (Genn.) sibling species group, have driven the expansion of pandemics of cassava mosaic and cassava brown streak viruses throughout East and Central Africa. Early studies indicated the association between a distinct haplotype (Ug2) of *B. tabaci* and the 'front' of the severe cassava mosaic disease (CMD) pandemic that emerged in the late 1990s. Here, mtCO1sequences were determined for *B. tabaci* collected from > 600 sites in six countries of East and Central Africa between 1997 and 2010. The results provide unique insights about the dynamics of cassava-associated *B. tabaci* haplotypes. Eight phylogenetically distinct *B. tabaci* haplotype groups were identified from cassava crops in the pandemic zone. More than 96% of *B. tabaci* individuals represented the three most frequently occurring haplotype groups: SSA2 (=Ug2), SSA1-SG1 (=Ug1) and SSA1-SG2 (=Ug1). SG1 and SG2 were sub-groups 1 and 2 of the group previously designated Ug1. At the outset of the study, in 1997, the SSA2haplotypegroup was associated with the outbreak of severe CMD in Uganda. After 2003 the SSA2 haplotype group became rare and did not spread beyond Uganda and western Kenya. By contrast, from 2000 onwards, the SSA1-SG1 haplotype group became prevalent in pandemic zones. Its pattern of spread and displacement of SSA1-SG2 closely mirrored the geographical expansion of the CMD pandemic. A similar but less clearly defined association is also apparent between the change in distribution over time of SSA1-SG2, and the development and spread of the CBSD pandemic through the Great Lakes region of East and Central Africa. Mismatch analyses revealed significant change in the genetic structure of SSA1 from 2000onwards, providing evidence of a population expansion. These data suggest that initially stable and neutrally evolving *B. tabaci* SSA1 populations may have inherited genes conferring superior fitness from SSA2, with which they have been shown to interbreed. The genetic basis for the apparent enhanced fitness of these putative hybrid populations remains uncharacterized, although there is evidence that SSA2-SG1 has a broader host range compared to some cassava-colonizing *B. tabaci*, which are host-restricted. These results highlight the continued threat of *B. tabaci* to cassava production in sub-Saharan Africa, and emphasize the need for determined efforts to develop more effective management strategies.

Keynote presentation

OP-15: Transmission of cassava and tomato begomoviruses in South Africa by native and introduced *Bemisia tabaci* haplotypes

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The whitefly *Bemisia tabaci* cryptic species complex contains some important agricultural pest and virus vectors. The sub-Saharan African region harbours indigenous and possibly less invasive *B. tabaci* types, that vector many begomoviruses to crops including tomato and cassava, and which cluster in the major sub-Saharan Africa non-silver leafing clade (SSAF) that includes four subclades (SSAF1-4). Despite their economic importance, studies on the biology and distribution of *B. tabaci* in SA have been limited, and therefore a survey was undertaken to investigate the diversity and distribution of *B. tabaci* cryptic species in eight geographical locations (provinces) in SA, between 2002 and 2009, using the mitochondrial cytochrome oxidase I (mtCOI) sequences. Phylogenetic analysis revealed the presence of members from two endemic sub-Saharan Africa (SSAF) subclades co-existing with two introduced putative species. The SSAF-1 subclade includes cassava host-adapted *B. tabaci* populations, whereas the whiteflies collected from cassava and non-cassava hosts formed a distinct subclade, referred to as SSAF-5, and represent a new subclade among previously recognized southern Africa clades. Two introduced cryptic species, belonging to the Mediterranean and Middle East-Asia minor 1 clades were identified and include the B and Q types. The B type showed the widest distribution, being present in five of the eight provinces explored in SA, infesting several host plants and predominating over the indigenous haplotypes. This is the first report of the occurrence of the exotic Q type in SA alongside the more widely distributed B type. The presence of several whitefly genotypes in South Africa has implications for transmission of begomoviruses and will be useful in the development of knowledge-based disease management practices.

Keynote presentation

OP-16: Different gene copy number of a multipartite virus in host plant and in insect vector

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Multipartite viruses are enigmatic entities for both evolutionary biology and systems biology. Their genome is divided into several segments, each encapsidated separately. As opposed to monopartite, multipartite genomes have been proposed to increase stability of viral particles with shorter nucleic acid segments, or to allow faster replication. The most popular view, however, is that "multipartitism" facilitates genetic exchanges through shuffling of segments, exemplifying the evolution of sex in viruses. An obvious counterpart cost, is a decreased probability to gather at least one copy of each gene within individual cells for efficient infection. This cost is obviously minimized when the relative frequencies of the segments are equal, and rapidly increases when they diverge. Thus, unless otherwise selected, all genomic segments are predicted by these theories to accumulate with equi-molar ratios in order to minimize the cost. Here, through the demonstration that the genome segments of a nanovirus vastly diverge in frequencies, we provide empirical evidence that multipartitism's major benefit is elsewhere. It opens the possibility to control differentially the gene "copy number variation" (CNV), a phenomenon recognized as a key regulator of phenotypic changes in any organism. We have monitored in planta the 8 single-gene segments composing the genome of *Faba bean necrotic stunt virus* (FBNSV). We show that each adjusts to a different frequency, ranging from 2% to 25%, and that the virus repeatedly converges to the same "genome formula" in a given host plant, where each gene is associated to a specific relative copy number. We further show that the genome formula is host plant-specific and, surprisingly, we demonstrate that the copy number of the FBNSV genes is changing within the body of aphid vectors, different aphid species inducing different genome formulae. This latter result clearly indicates that a simple model of non-circulative non-propagative aphid-transmission does not apply to nanoviruses.

OP-17: Insect and endosymbiont proteins are involved in the transmission of begomoviruses by the whitefly *Bemisia tabaci*

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Tomato yellow leaf curl virus (TYLCV) (*Geminiviridae: Begomovirus*) and other begomoviruses are exclusively vectored by the whitefly *Bemisia tabaci* (Gennadius) (Hemiptera: Aleyrodidae). TYLCV induces several effects on the whitefly and its transmission depends upon a 63-kDa GroEL protein produced by the vector's endosymbiotic bacteria. *B. tabaci* is a species complex comprising several genetically distinct biotypes that show different secondary-symbiont fauna. The aims of our studies are to explore specific proteins that aid in the transmission of begomoviruses by *B. tabaci.* Virus-transmission assays by *B. tabaci* populations from Israel showed that the B biotype efficiently transmits the virus, while the Q biotype scarcely transmits it. Yeast two-hybrid and protein pull-down assays as well as membrane feeding experiments with *in-vitro* synthesized GroEL proteins showed that a GroEL protein produced by the secondary endosymbiont *Hamiltonella* from *B. tabaci* B biotype, but not other GroEL proteins from other bacteria, interacts with TYLCV coat protein. Transcriptome microarray analysis comparing viruliferous and non-viruliferous whiteflies from the B and the Q biotypes with TYLCV and the bipartite *Squash leaf curl virus* (SLCV) identified several host proteins with possible roles in virus transmission. A Heat Shock Protein 70 (HSP70) was a strong candidate that was induced following virus acquisition and retention, interacted *in vivo* and *in vitro* with TYLCV, and specifically co-localized with TYLCV and *Watermelon chlorotic stunt virus* (WmCSV) in midgut epithelial cells. Membrane feeding of whiteflies with anti-HSP70 antibodies and TYLCV virions showed increase in TYLCV transmission, suggesting an inhibitory role for HSP70 in virus transmission, a role that might be related to protection against begomoviruses. Taken together, these results show that endosymbiont and insect host proteins interact with transmitted begomoviruses by *B. tabaci*, and may significantly influence their spread in the field.

OP-18: Enigmatic virus-vector relations of *Sweet potato mild mottle virus* in agro- and natural ecosystems in the center of evolution in East Africa

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Sweet potato mild mottle virus (SPMMV) is a type member of the genus *Ipomovirus* (family *Potyviridae*). The virus ranks third in importance among the viruses threatening cultivated sweetpotato in the Lake Victoria basin of East Africa, but also infects natural wild vegetation (Convolvulacea) there. An earlier study showed that SPMMV is transmitted by the whitefly, *Bemisia tabaci*; however, subsequent studies over three decades have not confirmed the whitefly-transmissibility of SPMMV. In East Africa, the odds of co-occurrence of SPMMV and the whitefly-transmitted *Sweet potato chlorotic stunt virus* (SPCSV; genus *Crinivirus*) are low and statistically insignificant, yet both viruses were previously reported to be whitefly-transmitted in sweetpotato. Could this be a reflection of different whitefly vector species/biotypes or transmission efficiencies, or both? Moreover, natural co-infections of SPMMV and the aphid-transmitted *Sweet potato feathery mottle virus* (SPFMV; genus *Potyvirus*) in sweetpotato crops in East Africa are up to 3-times more common than infections of SPMMV alone. Could this imply that SPFMV facilitates aphid-transmission of the non-aphid transmissible SPMMV, given that SPMMV is a definite HC-Pro-encoding ipomovirus? Because of these 'unknowns' the epidemiological relationships between SPMMV and its potential vectors remains cryptic, which challenges the designing and implementing effective virus disease control measures, particularly the damaging sweetpotato virus disease (SPVD) complex. SPMMV is a unique virus that has evolved, and is geographically confined, in East Africa. Geographical ranges of plant viruses are constrained more by virus-vector relations than by virus-host interactions, alluding a 'localized vector'; however, activities to unravel the vector transmitting SPMMV are only underway.

OP-19: Direct effects of the begomovirus *Tomato yellow leaf curl virus* in the settling and feeding behavior of its vector *Bemisia tabaci* Gennadius (Hemiptera: Aleyrodidae)

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Plant viruses can produce direct and plant-mediated indirect effects in their insect vectors, modifying their performance and behavior leading to enhanced spread. Here we report that the acquisition of the begomovirus *Tomato yellow leaf curl virus* (TYLCV) directly alters the settling, probing and feeding behavior of its vector, the whitefly *Bemisia tabaci* Gennadius. In this study, the settling, probing and feeding behavior of viruliferous and non-viruliferous female adults of *B. tabaci* (Q-biotype) was compared. Whiteflies were subjected to an acquisition access time of 72h in TYLCV-infected or non-infected tomato plants to obtain viruliferous and non-viruliferous insects, respectively. Insects that were exposed to virus-infected plants were checked by PCR to verify their status (viruliferous or non-viruliferous). Results of the Ethovision video tracking bioassays indicated that viruliferous whitefly adults remained more time motionless after alighting on aubergine plants than non-viruliferous whiteflies. The Electrical Penetration Graph technique showed that in fact, TYLCV-viruliferous *B. tabaci* fed more often from phloem sieve elements and made a larger number of phloem contacts (increased number of E1, E2 and sustained E2 per insect, $p<0.05$) in aubergine plants than non-viruliferous whiteflies. Furthermore, the duration of the salivation phase in phloem sieve elements (E1) preceding sustained sap ingestion was longer in viruliferous than in non-viruliferous whiteflies ($p<0.05$). This particular probing behavior is known to enhance the inoculation efficiency of TYLCV by B. tabaci as shown in previous studies. Our results show evidence that TYLCV modifies the settlement, probing and feeding behavior of its vector *B. tabaci* in a way that enhances virus transmission and spread. This outcome provides a better understanding of TYLCV-*B. tabaci* interactions that has direct implications in the epidemiology and management of the disease.

OP-20: Ecology of the banana aphid *Pentalonia nigronervose*, the vector of *banana bunchy top virus*

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The banana aphid *Pentalonia nigronervosa* is a serious pest of banana and plantain (*Musa* spp.) largely because it is the only known vector of *Banana bunchy top virus* (BBTV), the causal agent of banana bunchy top disease (BBTD). In surveys conducted in sub-Saharan Africa, we showed that the banana aphid was widely distributed with relatively high infestation levels in most locations, with nearly 3-folds higher infestations on plantains than on bananas. Twenty four ant species belonging to 22 genera were found associated with the aphid. Parasitism was absent from all surveyed locations and all subsequent field research, including foreign explorations in Southeast Asia. On-going studies on the genetic variability of the aphid could help us in pinpointing with greater precision its probable origin and better targeting of explorations for natural enemies that can be used for its control. In laboratory and field experiments, we showed that banana aphid abundance on *Musa* genotypes is positively related to the presence of the B genome. An experiment is underway to test these early observations using *Musa* genotypes with various combinations of A and B genomes. In long term population dynamics studies in Cameroon the aphid has shown at least two peaks per year with one peak in the beginning of the long dry season and another during the short dry season, with aphid abundance decreasing with plantation age. Aphid dispersal, colonization and abundance were not affected by vegetation cover. Thermal response studies showed that the aphid's lower and upper thermal thresholds are at about 10° C and 30° C respectively, with implications for changes in aphid distribution and abundance in response to global warming. Knowledge of aphid ecology along with information on aphid-BBTV interactions are being used in developing an integrated strategy for the management of BBTD that includes aphid population suppression.

OP-21: Spread of an emerging vectored disease of sugarcane varies according to local constraints in the French Caribbean islands

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Sugarcane yellow leaf was diagnosed for the first time in Guadeloupe in 1996 and in Martinique in 1997. Affected plants show early leaf yellowing, which starts from the leaf midrib. This emerging disease, transmitted by aphids and cane cuttings, is caused by a polerovirus called *Sugarcane yellow leaf virus* (SCYLV). SCYLV is distributed worldwide and occurrence of at least seven genotypes has been reported, three of which were identified in the French West Indies. In order to control epidemics of this disease, which affected almost 30% of sugarcane plants in commercial fields in Guadeloupe in 2010, we need to understand its local spread. Previous studies showed that (i) spread of yellow leaf by the vector in virus-free fields is regulated by rainfall that impacts primary infection due to immigrant aphids, and (ii) virus genotypes vary in virulence and infection capacity. Based on these results, spread of the disease since its emergence in commercial fields in the French West Indies was characterized using SCYLV diagnosis by tissue blot, computing of climate data, and identification of virus genotypes with genotype specific primers. In Guadeloupe, SCYLV incidence in fields has increased progressively over the last decade, from 0.6% in 2000 to 1.7% in 2003, 14% in 2005, and 28% in 2010. On the other hand, in Martinique, virus incidence has been high from the early years of emergence (30% in 1999) and it has remained at this level (32% in 2005). Data analyses showed that rainfall, impacting vector dynamics, is one of the key factors in disease epidemics. Resistance of sugarcane varieties to yellow leaf and interactions between sugarcane varieties and SCYLV genotypes also affect disease incidence. Spread of an emerging vectored disease such as yellow leaf appears, therefore, to be regulated by vector dynamics, as well as host and pathogen genetics.

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Op-22: Influence of plant virus co-infection on transmission and within-host dynamics

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Infections of a single host by multiple pathogens are common in nature but relatively poorly studied compared to single infections. In surveys of wild grasses in natural grasslands along a 2000 km latitudinal gradient in the western United States, we found high levels of co-infection by multiple barley/cereal yellow dwarf viruses (B/CYDVs), all persistently transmitted by aphids. In order to understand the epidemiological implications of these mixed infections, we carried out laboratory experiments to explore the consequences of coinfection for transmission by vectors. First, we studied coinfection in *Bromus hordeaceus,* an annual grass, with two pairs of viruses: 1) BYDV-PAV & BYDV-MAV transmitted *by Sitobionavenae;*and 2) BYDV-PAV & CYDV-RPV transmitted by *Rhopalosiphum padi*. We used quantitative ELISA to measure virus populations in infected plants and used bioassays to assess transmission success into and out of coinfected plants by vectors of the component viruses. Experiments are ongoing but early results indicate that vector transmission success can vary significantly between single infections and coinfections. We also investigated the consequences of coinfection with BYDV-PAV and barley stripe mosaic virus (BSMV) in barley. BSMV is transmitted horizontally by contact and vertically through pollen, ovule and seed, so we expected that BSMV would be less virulent than BYDV-PAV. We also expected that coinfection with BYDV-PAV would have negative effects on BSMV fitness through reduced seed output, thereby reducing the ability of BSMV to transmit to new hosts. Our laboratory transmission experiments provided no evidence that infection with one virus inhibited the successful replication of the other virus. We detected no significant differences between coinfections and single infection in titers of either virus, in horizontal transmission of either virus, or in vertical transmission of BSMV. However, compared to single infections or delayed secondary infections, simultaneous coinfection resulted in significantly higher virulence and reduced seed production, presumably leading to lower rates of spread for BSMV. These results suggest that coinfection may have strong impacts on hosts without displaying strong competitive effects within hosts.

OP-23: Virus-vector transmission relationships for cassava brown streak viruses and the whitefly vector, *Bemisia tabaci*

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The virus-vector transmission relationships for cassava brown streak viruses and the whitefly vector, *Bemisia tabaci* was investigated using a combination of laboratory and field experiments. Laboratory-based studies included investigations on the three modes (non-persistent, semi-persistent and persistent mode) of *Cassava brown streak virus* (CBSV) transmission by *B. tabaci* with virus acquisition periods ranging from 5 min to 4 days. CBSV was acquired and transmitted to 16% of healthy cassava plants within 5 min of feeding on a diseased plant while feeding for 24 h achieved the maximum transmission efficiency of 45%. Investigations on virus inoculation time indicated that whiteflies require a minimum of 30 min feeding time for CBSV transmission (7%) while the transmission efficiency increased up to 40% when insects were allowed to feed for 24 h. Additional experiments on latent period and the number of whiteflies required to achieve optimum transmission indicated that CBSV has no latent period in whiteflies and that between 25-30 whiteflies are needed to inoculate each plant to achieve a maximum 50% infection levels. These results indicate that whiteflies transmit CBSVs poorly which is unlike cassava mosaic viruses where 100% transmission can be achieved by whiteflies. Field studies included monitoring the spread of cassava brown streak disease (CBSD) in the field in Tanzania and Uganda which coincided with increases in *B. tabaci* numbers. When put together, results of the field and laboratory experiments indicated that CBSV is semi-persistently transmitted by the *B. tabaci* with transmission rates achieved between 40-60% when 25 whiteflies were given 24 h each acquisition and inoculation access periods. The implications of these results on our understanding of the current spread of CBSD in the field will be discussed.

OP-24: Transmission of torradoviruses by their whitefly vectors

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Tomato torrado virus (ToTV) is the type species of the recently created genus *Torradovirus*, assigned to the family *Secoviridae*. Other members of this genus are *Tomato marchitez virus* (ToMarV), Tomato chocolàte virus (ToChV) and Tomato chocolate spot virus (ToChSV). Torradovirus particles are spherical with a diameter of approximately 30 nm and are composed of three capsid proteins (with molecular masses of approximately 35, 26 and 23 kDa). The torradovirus genome is bi-partite with a total size of approximately 13.5 kb (~8 kb for RNA1 and ~5.5 kb for RNA2). It has been demonstrated that ToTV is transmitted by the whiteflies *Trialeurodes vaporariorum* and *Bemisia tabaci.* However, data on the mode of transmission of torradoviruses were lacking. In this paper we will report on the studies we conducted on the transmission of ToTV, ToMarV and ToChV by their vectors *T. vaporariorum* and *B. tabaci*(biotype B). The minimal acquisition access period (AAP), minimal inoculation access period (IAP) and retention times were determined in laboratory experiments. Additionally, we determined the binding place of virus particles in the whitefly vector. The results of our transmission studies and localisation studies of torradovirus in the vector give a clear indication for the so far unknown transmission mechanism of torradoviruses when vectored by whiteflies.

IPM-CRSP Special Presentation

OP-25: Management of aphid, beetle, seed and contact-transmitted RNA viruses in tropical ecological cropping systems.

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Plant viruses transmitted by vectors or through seed or germplasm cause diseases that become major constraints to food security in tropical developing countries. In the last year, collaborators in the IPM CRSP identified and detected viruses in tomato, pepper, eggplant, potato, sweetpotato, okra, onion, pumpkin and other cucurbits, country and yardlong bean, tree tomato, passion fruit, and other plants including weeds. Diseases caused by viruses pose extreme challenges to developing country scientists because of limited capability and resources to diagnose and understand the virus/vector/host pathosystem, essential for disease management within increasingly dynamic crop ecosystems of tropical and sub-tropical countries. The lack of capacity and infrastructure to conduct rapid diagnostic assays is being alleviated somewhat by collaborative research and training and by improved diagnostics. Knowledge of the many economically important viruses in an area as documented through surveys, enables targeting research toward understanding the complexity of virus biology in diverse cropping ecosystems and dissemination by vectors. Management in tropical cropping ecosystems must be holistically designed and transferred to different regions/countries, and have socioeconomic acceptance and impact. The basic concepts of managing viruses by reducing initial inoculum and delaying infection and rate of spread remain applicable, but require different approaches depending on the vector ecology (e.g. aphids, thrips and whiteflies) and cropping systems. Globally prevalent and aphid-transmitted potyviruses and *Cucumber mosaic virus* are also often seed-transmitted. Beetle transmitted viruses, common in many crops in Africa, can also be seed-borne. Mechanically-transmitted viruses, mainly *Tobacco mosaic virus* and *Tomato mosaic virus*, have been detected in tomato in many countries including Uganda. The role of contact transmission though cultivation and harvesting practices in epidemiology of these viruses, and well as seed production systems to reduce levels of seed-borne and/or seed-transmitted viruses, should be considered in management of tropical virus diseases.

IPM-CRSP Special Presentation

OP-26 Comparative case studies of whitefly (*Bemisia tabaci*) vector-begomovirus diversity: associated effects on virus disease epidemiology in diverse study systems in Central America and sub-Saharan Africa

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Members of the whitefly *Bemisia tabaci* (Genn.) sibling species group feed on eudicots and transmit plant viruses in the genus, *Begomovirus* (Geminiviridae) in dry subtropical locales and fringe temperate zones. Taxonomically, begomoviruses form major phylogeographical clades comprising Old and New World species, respectively. *Bemisia tabaci* haplotypes group into 6 major phylogeographical clades based on the mitochondria cytochrome oxidase I gene. Even so, *B. tabaci* in the same clade can be polyphagous or monophagous. Our studies have focused on monophagous and polyphagous haplotype-begomovirus complexes. In Guatemala (New World), several polyphagous *B. tabaci* haplotypes transmit numerous begomoviruses in vegetable crops and endemic/wild hosts. Here, whitefly vectors comprise endemic/local haplotypes (N/C American clade), and the B biotype, an introduced haplotype from the North Africa Mediterranean-Middle East clade adapted to dry-arid, irrigated agroecosystems. The second study is centered in sub-Saharan Africa where cassava is the staple food, and cassava-adapted haplotypes transmit a complex of Old World begomoviruses. In 1990, a new virus-vector complex emerged and spread rapidly in cassava crops, resulting in a pandemic affecting >12 countries. In both systems changes in virus-vector distributions and prevalence were documented. In Guatemala, initial changes were related to the exotic B haplotype having a host range overlapping with, but distinct from, the endemic *B. tabaci*. Next, changing distributions of *B. tabaci* and associated begomoviruses, and a non begomovirus-vector, *Trialuerodes vaporariorum* were observed that appear to be related to microclimate alteration. In contrast, the African cassava mosaic pandemic, studied since ~1997, is associated with the upsurgence of the 'more fit' offspring (high fecundity, long-distance dispersal, high vector competency) of parental haplotypes putatively from eastern and western Africa, in comparison to extant local *B. tabaci* haplotypes that adapted to cassava after its introduction there from South America about 400 years ago.

IPM-CRSP Special Presentation

OP-27: Epidemiology and management of intractable virus diseases in subsistence agriculture: The case of a thrips-transmitted tospovirus in South Asia

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In recent years, thrips-transmitted tospoviruses (genus: *Tospovirus*, family: *Bunyaviridae*) have emerged as a significant limiting factor for the production of vegetable, food, feed and fiber crops worldwide. Although *Tomato spotted wilt virus* has been considered a major constraint to production of field crops and vegetables in the U.S. and Europe, *Peanut bud necrosis virus* (PBNV; = *Groundnut bud necrosis virus*) has emerged as a significant constraint to tomato production in South Asia, especially in India. PBNV was recently reported from Bangladesh and Indonesia indicating possible wide spread occurrence of the virus outside India. The genome sequence of PBNV has been determined and diagnostic methods developed for the detection of virus in plants. *Thrips palmi* is the principal vector of PBNV. Although *T. palmi* has been documented in different continents, available information indicates that PBNV is largely confined to Asian continent. Practical challenges to management of PBNV in subsistence agriculture are posed by the broad host-ranges of PBNV and its vector that include legume and solanaceous crops and non-crop species, limitations and disadvantages of chemical control of thrips, overlapping cultivation of different crops that are susceptible to PBNV and perpetuate its vector, and the lack of genetic sources of resistance to PBNV in tomato. In addition, indiscriminate use of pesticides by farmers is leading to the buildup of resistance to pesticides in thrips. Consequently, the IPM-CRSP of the USAID is pursuing environmentally benign IPM strategies as an alternative to pesticide-based tactics for mitigating negative impacts of PBNV on tomato production. Raising clean tomato seedlings and roguing of symptomatic seedlings during and soon after transplanting were found beneficial in reducing virus incidence and avoiding crop losses. Farmer participatory IPM packages were found to reduce incidence of PBNV and offer economic benefits to resource poor farmers without incurring extra costs for spraying pesticides to control thrips vectors.

IPM-CRSP Special Presentation

OP28: Diversity, biology and management of begomovirus diseases of horticultural crops in West Africa

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The worldwide explosion in begomovirus diversity and diseases is due to the widespread distribution of indigenous begomoviruses in non-cultivated crops and the polphagous whitefly vector (*Bemisia tabaci* biotype B), together with the remarkable genetic flexibility of these viruses. These factors drive the local evolution of begomoviruses in tropical and subtropical regions. One such region is West Africa, where begomovirus diseases have emerged as constraints on production of horticultural crops, such as tomatoes, okra and peppers. Through IPM-CRSP research, progress has been made in characterizing these viruses and understanding their biology and ecology. Six tomato-infecting begomoviruses and two betasatellites have been identified and associated with three distinct disease phenotypes. In okra, two begomoviruses and one betasatellite cause okra leaf curl disease. One of the okra-infecting begomoviruses and the betasatellite have been associated with a leaf curl and yellowing disease in the common weed *Sida* spp., which may serve as a reservoir for these viruses. In contrast, a single begomovirus appears to be responsible for a pepper leaf curl and yellow vein disease. Molecular tools (DNA probes and PCR primers) have been developed and used to investigate virus biology (host range, reservoir hosts, prevalence in whiteflies, etc.). Infectious clones have been generated and used to complete Koch's postulates, assess host range and screen germ plasm for resistance. This information has been used to develop a sustainable IPM package for tomato-infecting begomoviruses in the irrigated rice-vegetable production system in West Africa. The key aspects of this package include implementation of a two-three month tomato/pepper-free period, planting early maturing hybrid tomatoes, and applying extensive sanitation following harvest. This IPM package has been successful in reducing the incidence and severity of begomovirus diseases of tomato in a major irrigated rice-vegetable perimeter in Mali.

OP-29: Emergence and diversity of begomoviruses infecting solanaceous crops in Southeast Asia

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Over the last 30-40 years diseases caused by whitefly-transmitted geminiviruses (begomoviruses) have emerged to be important constrains to the production of solanaceous crops in many tropical and sub-tropical regions of the World. The most studied of these is *Tomato yellow leaf curl virus* (TYLCV), which has spread to many other areas from its likely origin in the Mediterranean basin region. Through collaboration with partners and when opportunity has arisen, virologists at AVRDC – The World Vegetable Center, since the mid 1980s, have tried to survey and monitor solanaceous vegetable crops in different countries of Southeast Asia for emergence of diseases caused by viruses, and in particular begomoviruses. Despite the rather non-systematic sampling (Countries/ locations/ crops/ seasons), it is evident that the incidence of diseases caused by begomoviruses has increased across the region, but most of the increase has been of local species and not of TYLCV. In this poster/paper we will present the compiled information from AVRDC and other labs across the region and will speculate on what factors have and are influencing the emergence of these diseases across the region.

Special Lecture in the ICPVE Business Meeting

OP-30: Meeting Redcliffe Nathan Salaman, first professor of plant virus diseases

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In 1953, I wrote to Professor Salaman that I would like to visit him, and he invited me . He told me that he obtained his M.D. degree in 1904 but acute tuberculosis suddenly terminated his medical career. Imminent death was predicted, but, as he jokingly said, the prognosis was incorrect. Advised to refrain from heavy work, he merely observed his gardener every day. He noticed diseased potato plants and took a few to the Ministry of Agriculture in London. When he told there that he was able to transmit the disease symptoms by grafting, he was asked to give a lecture about this to students in Cambridge. This started a series of lectures and resulted in his appointment as first plant virus disease professor. Among his most prominent students were Sir Frederick C. Bawden and Kenneth M. Smith. The latter became Salaman's successor as virology professor in Cambridge. In 1908 Salaman discovered that *Solanum demissum* had a high level of resistance to potato late blight, and he established this plant as the primary source of vertical, R-gene late blight resistance. Salaman also pioneered the concept of controlling potato virus diseases by producing a virus-free stock through selection and testing, and then multiplying this seed on a commercial scale. Salaman was among the first to demonstrate the acquired immunity, produced by one virus strain against another related strain. The work that was of greatest interest to Salaman was his study of the influence of the potato on human populations. He was President of the Union of the Jewish Literary Society and Governor of the Hebrew University of Jerusalem. He was at all time a genial and kindly man and he showed these qualities to great advantage when acting as host at his home. It was my privilege to enjoy these qualities during my memorable visit.

Keynote presentation

OP-31: Virus diagnosis in plant virus disease prevention and control

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Diagnosis of plant viruses for disease prevention and control is integral part of agricultural production systems and regulatory frameworks that exist in western industrial countries. Production of propagation materials is not possible without adequate measures in place to maintain high product quality. Ensuring freedom of (virus) diseases in planting materials thus is central to voluntary or mandatory certification schemes for production of plant propagation materials. While this is a complex challenge for countries were regulatory frameworks exist, it is generally not practiced in countries of the South and as illustrated with recent outbreaks of virus diseases in East Africa (maize, cassava) this has serious consequences and impact. Several recent incidences of newly emerging diseases (viroids in ornamentals in Europe, new viruses of tomato, maize, cassava in Europe and in Africa) illustrate that agricultural systems are dynamic and require constant surveillance to respond timely and with adequate measures to reduce impact of diseases and, to permit forecasting. To evaluate virus situations, a number of methods with various levels of resolution are available. For virus detection ELISA is generally the most appropriate method as it is simple to apply and robust hence best for virus indexing in nurseries to ensure virus freedom. However ELISA does not have a resolution power comparative to molecular methods. These are mostly based on PCR permitting subsequent sequence analysis to further resolve virus identity and the structure of virus populations. Quantitative PCR can be applied for high throughput virus testing while a global assessment of the entire pathogen content of a given sample is provided with next generation sequencing applications. This makes the choice of the most appropriate method for a diagnostic problem most critical and this will be discussed over the range of diagnostic challenges, from indexing to ensure virus freedom to dynamics of virus populations and epidemiology.

Keynote presentation

OP-32: A tree shrub in the family *Sapindaceae* is a natural host of a cassava mosaic begomovirus in Tanzania

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Cassava mosaic disease (CMD) was described for the first time in Tanganyika (now Tanzania) by a German scientist, Warburg in 1894 near Usambara mountains. However, natural hosts of cassava mosaic begomoviruses (CMBs), the causal agents of CMD have not been identified in Tanzania. Using Roche 454 Sequencer, we sequenced the complete DNA-A of a CMB from a shrub in the family *Sapindaceae* collected near the Usambara Mountains in 2012. Blast Searches and nucleotide sequence as well as phylogenetic analyses of the begomovirus sequence confirmed it to be a cassava mosaic begomovirus belonging to the *East African cassava mosaic virus* (EACMV) clade. Genome organization structure of the CMB was typical of published bipartite CMBs with AV2, AV1, AC1, AC2, AC3, and AC4 ORFs. With species demarcation in begomoviruses made from full length DNA-A, with sequences of 89% identity as a species distinction cut-off point, the CMB isolated from the shrub was found to be a new species with a sequence identity of <75% to the reference CMB sequences in the geneBank. We have named the CMB as *East African cassava mosaic Tanzania virus* (EACMTV), a shrub clone. The geographical distribution of the shrub stretches from Somaliland to northern Mozambique on the mainland, and Reunion and Zanzibar Island as shown in the Flora Zambesiaca of 1876. The shrub was found colonized by whitefly, *Bemisia tabaci,* the insects which transmit CMBs. This is the first report of the occurrence of a CMB in a shrub species in Tanzania and may provide light as to the foci of cassava mosaic begomoviruses in East Africa.

Keynote presentation

OP-33: State of the art multiplex Luminex xMAP and xTAG-detection of plant viruses

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Multiplex detection of viruses in a single sample would be an elegant way to improve DAS-ELISA efficiency and reduce costs. The Luminex *x*MAP technology allows such multiplex serological virus detection while retaining the standard DAS-ELISA 96-well format and workflow. Different Luminex colour-coded xMAP beads, each specifically coated, capture virus particles. Virus-specific conjugated antibodies, in combination with the unique bead colour-code identify a unique combination, allowing specific detection of each individual virus. In sensitivity comparable to DAS-ELISA, detection is completed in less than 3 hours with higher specificity. When specific antibodies are not available, viral or viroid nucleic acid is detected on the same platform using Luminex *x*TAG beads. Similar colour-coded bead sets, labelled with virus–specific oligonucleotides probes, capture specific (RT)-PCR fragments. Similarly to TaqMan probes, Template Specific Primer Extension (TSPE) adds an extra level of specificity to the *x*TAG test format while allowing a much higher level of multiplexing than TaqMan. We developed Luminex *x*MAP and *x*TAG tests for a variety of plant viruses and viroids that allow the multiplex detection of more than 10 analytes in a single sample. They offer a state of the art, true multiplex and cost-effective alternative to the current DAS-ELISA and TaqMan formats.

Keynote presentation

OP-34: Next generation sequencing as a universal tool for virus detection and identification: characterising Maize Lethal Necrosis in Kenya

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Rapidly identifying the causal agents of plant disease can be slow as conventional methods such as isolation and culture, plant inoculations, electron microscopy, ELISA or PCR are often performed sequentially to collect a chain of evidence that leads to an identification. In particular when dealing with new or unexpected findings some methods (e.g. PCR or ELISA) can too specific to a particular species or even strain of a virus whilst alternatives such as electron microscopy (EM) or sap inoculation of indicator species do not usually give species level diagnosis. Next generation sequencing offers an alternative solution where sequence data is generated in a non-specific fashion and identification is based on similarity searching of the sequences of other viruses present in Genbank. This method enables both detection and identification to be performed in a single step, speeding up the process. Conventional and next generation sequencing techniques were applied to a damaging and apparently new disease of maize, which was first identified in Kenya in the autumn of 2011. ELISA (for a range of viruses) and EM provided negative results, whilst inoculation of other cereal species identified the presence of a sap transmissible virus but the symptoms did not allow identification of it. RNA and DS-RNA were both purified from symptomatic field material and sequenced using a Roche 454 GS-FLX+. Database searching of the resulting sequence identified the presence of *Maize chlorotic mottle virus* (MCMV) and *Sugarcane mosaic virus* (SCMV) a combination previously reported to cause maize lethal necrosis disease. Over 90% of both viral genome sequences were obtained, allowing strain characterisation and the development of specific real-time PCR assays which were used to confirm the presence of the virus in symptomatic material from 6 different fields in 2 different regions of Kenya. The availability of these assays should aid the assessment of the disease and may be used for routine diagnosis. The method based on NGS generated a much faster result than the conventional techniques and concomitantly provided sequence from which a rapid assay could be developed to enable testing of further field samples to assess prevalence in the field as well as be used in attempts to control the disease and prevent reoccurrence and future early detection.

Keynote presentation

OP-35: Viral diagnostics: from continental viromes to field level diagnostic methods

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The power of modern high throughput DNA sequencers is enabling a new generation of virological studies in which metagenomes of ecosystems can be determined to understand evolution and variability of viruses. We are currently applying a technology based on siRNA sequencing and assembly to determine the 'virome' of sweetpotato throughout Africa. Results of such surveys enable us to get a glimpse of viral diversity and variability across the continent, inform us of viral distribution on which to base containment measures and guide further research into impact and significance of identified viral entities. Such technologies however are still too expensive and knowledge intensive to be applied by most national diagnostic laboratories (NDL) which still mostly rely on ELISA and sometimes PCR methods for testing single viruses at a time. Platforms for the sensitive detection of multiple viruses at the same time such as microarrays may be practical and efficient solutions for NDLs with the need to test many plants against many viruses with sufficient sensitivity. Results from validation experiments of ClonDiag tube arrays for potato and sweetpotato will be presented. On the other hand, for diagnostics at the field level, simple and straight forward methods are needed that are robust, require minimum equipment but still are sensitive and easy to interpret. Loop-mediated isothermal Amplification (LAMP) is a highly sensitive and specific nucleic acid amplification method that does not to require complex thermal cycling equipment. Reagents can be lyophilized and reactions performed with low cost re-usable heat-packs, whereas color changes or lateral flow devices may be used to identify positive reactions. The challenges to bring the technology to field use rely on optimizing the way of detecting positive reactions and developing of simple enough nucleic acid extractions that can be used under field conditions.

OP-36: Occurrence and distribution of potato viruses in the major potato growing areas in Kenya

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Potato plays an important role in food security in Kenya but yields are low (< 10t/ha) and this is partly attributed to lack of availability of healthy planting material with consequent yield loss through diseases. No wide scale survey has been done to determine the occurrence and distribution of common potato viruses in Kenyan potato crops. In this study, seed and ware potato crops growing on 101 farms in 21 districts were examined. Approximately 36% of plants in farmers' fields displayed disease symptoms (mean of all crops) with the incidence in seed crops between 4 and 36%. Six viruses (PVY, PVA, PVS, PVM, PVX and PLRV) were detected by DAS-ELISA in potato samples and they were found infecting potato plants in all districts. PVS was detected most often, PVY was second and PLRV was the third most commonly occurring virus. PVS, PVY, PVX, PVM and PLRV were also detected in *Solanaceous* weeds growing in or near potato fields. Nucleotide sequencing revealed the presence of recombinant strains of PVY (NTN and Wilga). The work showed that potato planting material is a major source of virus infection, although *Solanaceous* weed species were also virus reservoirs. On farm surveys revealed that farmers do not recognize viruses as a problem. Seed and ware crops are not clearly separated and are often produced in close proximity; a seed crop may be planted on land that in the previous growing season was used to produce a ware crop, so that ground keepers are a source of disease contamination for the next crop. The results will be discussed in the context of the scope for improved crop management and virus disease control.

OP-37: Unravelling complex viral infections in cassava (*Manihot esculenta* Crantz.) from Colombia

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Cassava (*Manihot esculenta* Crantz.) is the third most important source of calories for human nutrition in the tropics. Viral diseases continue to cause significant losses in cassava crops, challenging food security in developing countries. In the Americas, Cassava frogskin disease (CFSD) reported since the early 70's in Colombia and characterized by mild to severe symptoms in roots and in leaves of some cultivars, may be the most significant disease affecting yield in this region. Although several pathogens have been associated to CFSD, the causing agent of the disease remains to be identified. In order to first characterize the viral content of cassava plants displaying CFSD symptoms, we utilized a combination of biological, serological, molecular and metagenomic approaches for the detection and identification of viruses infecting field collected cassava. The results revealed the presence of members of families *Alphaflexiviridae, Luteoviridae, Reoviridae,* and *Secoviridae.* Among these, a distinct reovirus strain found only in material collected in the Amazon region, a novel *Potexvirus*, serologically unrelated to CsCMV and CsVX, a bipartite *Secoviridae* distinct to *Cassava green mottle virus* and a new *Polerovirus* were found in different cassava-growing regions of Colombia. A preliminary phylogenetic study showed different geographical distributed strains for each virus group. Although mixed virus infections were commonly found in plants displaying root symptoms associated to CFSD, not all different virus species were associated to leaf mosaic in the cassava landrace 'Secundina', commonly used as a virus indicator plant. Virus isolation and detection by multiplex RT-PCR in cassava leaf and root tissue, genome characterization and co-infection studies are currently being carried out at CIAT. We will discuss the implications of these results on previous CFSD-transmission studies, cassava virus indexing and the relevance of previously reported CFSD-associated pathogens.

OP-38: Characterisation of badnaviruses and endogenous pararetroviruses in West African yam breeding lines

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Cultivated yams (*Dioscorea* spp.) are propagated vegetatively through their tubers, which results in the accumulation of tuber-borne virus infections, and their perpetuation from one crop to the next. These infections reduce the productivity of the plants and are an impediment to the international movement and exchange of yam germplasm. The only effective method of controlling these virus diseases is to use virus-free planting material. The 26 virus species that have been reported to infect yams worldwide fall into nine taxonomic genera, but only three of these (*Badnavirus, Potyvirus* and *Cucumovirus*) have been shown to be widespread in recent surveys across West Africa. Badnaviruses were detected in over 95% of landraces and breeding lines suggesting its wide distribution in West Africa. Analysis of >150 partial PCR-amplified badnavirus RT-RNaseH sequences has grouped them into 12 species clusters each sharing <80% nucleotide identity to each other. As such species differences were not identifiable from their single RT-RNaseH PCR products, denaturing gradient gel electrophoresis (DGGE) was evaluated for its usefulness to discriminate these sequences. Seventeen RT-RNaseH PCR products from West African yam breeding lines produced 11 discrete DGGE bands that represented sequence variants. DGGE was found to be a successful technique for rapid identification of the true diversity of yam badnavirus sequences in a given sample. The existence of badnavirus PCR-positive, but ISEM/ELISA negative results indicated that some breeding lines and landraces contain integrated badnavirus sequences, and this has been supported by nucleic acid hybridization studies. Future research is on-going to determine which of these sequences represent dead integrants, and which are activatable sequences that will pose a serious threat to yam germplasm health and movement.

OP-39: Valuing pest diagnostics for laboratory and field deployment in seed certification and surveillance: a case study on Cassava brown streak disease

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The failings of African agriculture are not essentially about gaps of knowledge and a need for research, but as much about a failure of systems, processes, planning and pre-emptive action; about organisation, strengthening what is already available, in enabling for innovation to take hold and in being prepared to mitigate potential shock events. This is most evident in areas of plant health and in the provision of seed certification and pest surveillance. Africa appears ever-prone to planting non-certified unhealthy seed and the next big pest epidemic. This paper sets out through the example of cassava and Cassava brown streak disease a summary of efforts made to provide seed to farmers that is of known CBS virus (CBSV and UCBSV) status. The paper takes note of innovation in diagnostics for CBSVs, suitable for laboratory and field use, and of some surveillance approaches. Consideration is also given to the robustness of field inspection and visual symptom recognition of CBSD and works with the concepts of risk evaluation about the trade-off between any stated position on assurance and cost. The role of centralised and decentralised testing for CBSVs is critically appraised, along with a perspective on potential roles for the private sector and government institutes. Finally, the possibility to achieve surveillance as an outcome of certification is addressed. To date the research and development agenda has struggled with these areas, and more specifically engaging effectively with plant health institutes that by mandate are not natural research partners. Much of what has gone before has been prefaced by research and not functionality and service delivery of actors within a cropping system or production pathway.

OP-40: Detection of *Banana bunchy top virus* and development of transgenic banana plants in Hawaii

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Banana bunchy top is the most devastating viral disease of bananas in Hawaii and many areas of Asia, Africa, and the Pacific. It is caused by the *Banana bunchy top virus* (BBTV). Sensitive and reliable assays including ELISA, PCR, and quantitative PCR were developed and examined for detection of BBTV-infection from symptomatic and asymptomatic banana plants. Nucleic acid sequences of BBTV isolates from China and the Philippines were compared with that of the Hawaiian BBTV isolate. We have produced nearly 300 transgenic banana plants with various constructs derived from BBTV that are predicted to enhance BBTV resistance. These plants have been bioassayed for BBTV resistance using viruliferous aphids; 20 of these plants have survived BBTV challenge without developing bunchy top symptoms in the greenhouse. We have successfully returned all twenty putatively BBTV-resistant banana lines to tissue culture, have initiated field experiments for thirteen of these transgenic lines, and are currently multiplying seven lines in preparation for planting in the field. We have obtained a one-acre plot at the Waimanalo Field Station on the island of Oahu to be used for field-testing of the transgenic lines. Permits detailing the conditions for field-testing of the transgenic banana lines have been obtained from the USDA-APHIS-BRS, the HDOA, and the University of Hawaii Institutional Biosafety Committee. Evaluation of BBTV resistance and characterization of these banana plants in field experiments are in progress.

OP-41: Monoclonal antibodies in the detection and diagnosis of plant viruses

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Plant pathogenic viruses and bacteria are responsible for the increasing economic losses worldwide. Identification of the pathogen would be the first step towards management of the associated diseases. The use of serological methods for the detection of plant viruses was in use for several decades. However, as many plant viruses remain latent in the planting material, highly sensitive, specific and reliable methods are required. Advances in biotechnology and molecular biology over the last three decades have made this possible. Recent immunological methods make use of panels of well characterized monoclonal antibodies that have been utilized extensively not only in the detection of viruses but also in classifying them. The utility of these reagents would depend on the method employed for detection, but since monoclonal antibodies are biochemically well defined and homogeneous, their use ensures uniform results from different laboratories particularly in quarantine screening and virus strain identification. The presentation will discuss and summarize the use of monoclonal antibodies in plant disease diagnosis.

OP-42: Relative incidence and distribution of viruses in plants grown from different portions of seed yams (*Dioscorea* spp.)

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Yam (*Dioscorea* spp.) is a multi species clonally propagated crop cultivated for its edible tubers in West Africa. Tubers – whole yams or sliced portions (minisetts) - are used as planting materials. This study determined the frequency of four widely prevalent yam viruses in West Africa, *Dioscrea* badnaviruses (DBV, *Badnavirus*), *Yam mosaic virus* (YMV, *Potyvirus*), *Yam mild mosaic virus* (YMMV, *Potyvirus*) and *Cucumber mosaic virus* (CMV, *Cucumovirus*), in plants grown from different portions of the seed yam tubers. Each of the 349 seed yam tubers from virus infected plants representing 38 varieties was sliced into three equal portions (apex, middle and base) of about 50 g each and they were planted in a screen house. Grown-out plants (N=1047) were evaluated for three RNA viruses using a multiplex RT-PCR and a PCR using generic primers to badnaviruses. The rate of sprouting was highest for tubers portions from apex (92%) whilst the sprouting from middle and base tuber portions were 61.6% and 66.8%, respectively. The virus incidence (symptoms) was between 42.1 – 100% in different varieties assessed and the incidence of YMMV, CMV, YMV and DBV respectively were 5.5%, 10.1%, 67.8% and 95.2%. Frequency of virus infections ranged from 5% to 97% in plants grown from different tuber portions. Several grown-out plants from virus infected tubers were asymptomatic but tested positive to viruses in PCR assays. Some asymptomatic plants that tested negative to RNA viruses at early growth stage developed symptoms and tested virus positive at later stages. Differences in virus incidence in plants generated from infected tubers provide a scope for generating virus free planting material.

Keynote presentation

OP-43: Molecular epidemiology provides new insights on ZYMV occurrence in France

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Zucchini yellow mosaic virus (ZYMV) causes locally severe but sporadic epidemics in France, contrasting with other non-persistent aphid-borne viruses such as *Watermelon mosaic virus* (WMV) or *Cucumber mosaic virus* (CMV) which occur much more regularly. In order to better understand parameters that could explain this particular behavior, ZYMV occurrence and spread were monitored over a four-year period in a multilocal layout. The layout included four identical zucchini squash plots, planted on the same day with the same batch of seedlings and located 0.5 to 4 km apart. ZYMV, WMV, CMV and *Cucurbit aphid-borne yellows virus* (CABYV) epidemics were monitored within each plot at weekly intervals using DAS-ELISA and ZYMV populations were characterized by direct sequencing of the N-terminal part of the coat protein after RT-PCR amplification. ZYMV occurred irregularly, and, depending on the plot, developed either early, late or no epidemics. Three out of the five different strain types known from France were observed in the layout throughout the four years, but generally a single very homogeneous population (often composed of a single haplotype) was observed per plot. Only in one occasion, two distinct populations were detected in the same plot, and with different haplotypes for each population. These results will be discussed in relation with the potential of ZYMV dissemination by aphids, the origin of primary inoculum and the potential interactions between different virus populations.

Keynote presentation

OP-44: Ecological and evolutionary implications of sequence variation of Asclepias asymptomatic virus in non-cultivated plant

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The Plant Virus Biodiversity and Ecology project of the Tallgrass Prairie Preserve in the Great Plains of the USA generated partial sequences of many plant associated viruses in the years 2005 to 2009. Among the viruses whose sequences were detected was a previously undiscovered tymovirus, which is called Asclepias asymptomatic virus (AsAV) because its sequences were found at highest titer and prevalence in the green milkweed *Asclepias viridis*. Min et al. (2012) have shown that considerable nucleotide sequence variation exists among plants, while within plant variation is limited (with the exception of a few plants which appeared to be infected with more than one AsAV strain). Efforts to obtain further insights into the evolution and ecology of this virus, as a model for viruses of non-cultivated plants, will be reported. Nucleotide distances between pairs of viral sequences obtained from milkweed plants were narrowly distributed around 3.5%, (0.46% standard deviation). These differences were distributed among 26% of the residues of the AsAV genome. Of the positions exhibiting polymorphism, 52% were multiply polymorphic. Nucleotide distances between viral sequences from non-milkweed plants and a milkweed plant-derived standard sequence were bimodally distributed with a major peak at 4.0% These distributions will be discussed in the contexts of time of virus colonization of the preserve and limits to virus divergence.

Keynote presentation

OP-45: Tanzania: the biodiversity hotspot of *Rice yellow mottle virus*

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Tanzania is the center of origin of *Rice yellow mottle virus* (RYMV), a threat for rice crop in Africa and Madagascar. Despite the limited number of regions previously surveyed, an exceptionally high level of viral molecular diversity has been revealed in Tanzania. Half of the six major RYMV strains are located in the country while the other three strains are spread all over Central and West Africa. The distribution areas of the three East-African strains, S4, S5 and S6 appeared contrasted. While the S5 strain was restricted to Kilombero Valley in the Morogoro region, the S4 and S6 strains were reported to be widely spread. However, the detailed distribution of the two lineages S4 in the lake regions - S4-lv around the Lake Victoria and S4-lm along the Lake Malawi - is not available and the data on the strain S6 – which showed the highest nucleotide diversity - are still limited. In addition, since rice cultivation is present all over the country, the viral diversity could have been underestimated and some other strains may remain unknown. To evaluate the diversity country wise and the prevalence of the RYMV strains, a set of isolates was collected during three surveys covering all ecological zones. More than 220 RYMV isolates were characterized by ELISA and 50 isolates were selected for coat protein sequencing. Tanzanian isolates belonged to two serotypes Ser4-Ser5, and three strains S4-S6. No new strains were identified but several new lineages were revealed. Distribution areas of each strain were mapped. Boundaries and overlapping regions were located suggesting strain circulation and expansion. Moreover, specific nucleotide polymorphisms were identified for some serotype variants and new lineages. This study provides additional information on the abundance and the distribution pattern of the disease in this biodiversity hotspot of RYMV.

Keynote presentation

OP-46: Viruses of kiwifruit: new and old viruses associated with an emerging crop and their potential for spread

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Kiwifruit (*Actinidia spp.*) originates from China but commercial production started in New Zealand in the 1920's. It is now grown as a commercial crop in many countries including China, Italy, Chile, Greece, France, Japan, Iran USA and Spain. The first definitive identification of a kiwifruit virus was an interception of *Apple stem grooving virus* in budwood being imported into New Zealand from China in 2003. Since this interception germplasm held in quarantine and breeders collections, in NZ and Italy has been surveyed for additional viruses in order to determine the potential threat from the spread of new viruses via Actinidia bud wood. To date twelve virus species have been identified in kiwifruit, using a combination of biological properties, serology and sequencing. These viruses represent a wide range of virus families and genera and include: common and widespread viruses such as *Alfalfa mosaic virus*, *Cucumber mosaic virus, Ribgrass mosaic virus* and *Turnip vein clearing virus*; and known viruses with restricted host ranges such as *Apple stem grooving virus, Cherry leafroll virus*, *Cucumber necrosis virus* and *Pelargonium zonate spot virus*. In addition we have identified acitrivirus, two vitiviruses and a potexvirus, that appear to be new strains or species that may be specific to Actinidia. Sequences of Actinidia viruses have been compared with isolates from other crop hosts and common weed hosts to provide information on potential sources and reservoirs of these viruses. The general unawareness of viruses in kiwifruit and consequent lack of measures to mitigate their spread is of concern for both international movement of germplasm and propagation and distribution of existing and new cultivars. Between them these viruses exhibit a wide range of biological properties, including host range and modes of transmission. The potential for spread of these viruses is discussed.

Keynote presentation

OP-47: Viral dynamics: notes from plant-infecting ssDNA viruses

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Over the past five years an overwhelming diversity of plant–infecting circular single stranded DNA viruses (ssDNA) has been catalogued. This has primarily been attributed to new molecular tools for non-specifically amplification of circular DNA coupled with cheap sequencing. The high resolution of data, for example for mastreviruses and begomoviruses, has enabled our team to address important aspects of viral evolution and spread using Bayesian phylogeographic analysis to reconstruct the plausible history and diversification of these viruses at a continental and global scale. For example, 1) *Maize streak virus strain-A* (MSV-A) which seems to have emerged in Southern Africa in the 1860s though recombination of mastreviruses infecting indigenous grasses (MSV-B and ancestral MSV-F/G-likes) an, has spread transcontinentally at an average rate of 32.5 km/year, 2) *Tomato yellow leaf curl virus* (TYLCV) a pathogen crippling tomato production globally most probably arouse in the Middle East between 1930s and 1950s, with a global spread occurring in the 1980s and recombination playing a major role in its evolution. One of the more striking discoverers, from our evolution experiments and also analysis of sequences available in public databases by others, is that plant-infecting ssDNA viruses are evolving at rates (between 2 and 3 x 10^{-4} substitutions/site/year) similar to those of RNA viruses. Our recombination experiments on mastreviruses reveal that these viruses are extremely efficient at exploring fitness landscapes, the mechanistic predispositions of different genomic regions to recombination can strongly influence the accessibility of high-fitness recombinants and the frequency with which these genomes arise correlates directly with the escalating selection pressures imposed by increasingly resistant host varieties. To add to the evolutionary complexity of ssDNA viruses, we have found multi-component nanoviruses, primarily *Banana bunchy top virus* (BBTV), to be evolving through, not only genetic drift, but also through a degree of intra- and inter component recombination and reassortment. In summary, plant-infecting ssDNA viruses are highly capable of exploring sequences space efficiently.

OP-48: Molecular biodiversity of cassava mosaic begomoviruses in East and Southern Africa

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A total of 16 full length DNA-A sequences of Cassava Mosaic Begomoviruses (CMBs), the causal agents of Cassava Mosaic Disease (CMD) were obtained from DNA samples collected from Tanzania (4), Rwanda (4), Uganda (1), Zambia (2), Kenya (3), Malawi (1) and Mozambique (1) using the Roche 454 sequencer. Genome organization structure of the CMBs was typical of the bipartite CMBs with AV2, AV1, AC1, AC2, AC3 and AC4 open reading frames (ORFs). Phylogenetic relationship analysis grouped three of the CMBs with the published *African cassava mosaic virus* (ACMV) and thirteen with *East African cassava mosaic virus* (EACMV) genetic groups. With species attributions in begomoviruses made from full length DNA-A, where a sequence of 89% identity is the species distinction cut-off point, two new CMB species were identified: one each from Uganda and Zambia. The two species have been named here as *East African cassava mosaic Uganda virus* (EACMUV) and *East African cassava mosaic Zambia virus* (EACMZmV), respectively. The highest percentage nucleotide sequence homology to the reference CMB sequences in the geneBank was 72% for EACMUV and 75% for EACMZmV. Our results highlight the need for further research to understand and develop durable management strategies for the emerging CMBs for improved cassava productivity in sub-Saharan Africa.

OP-49: Epidemiology and genetic variability of *Watermelon mosaic virus* infecting cucurbits in Southern United States

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Cucurbits (cantaloupe, cucumber, pumpkin, squash and watermelon) are widely grown in southern United States. Many viruses are known to infect cucurbits and responsible for serious losses in cucurbit production annually. About 700 cucurbit samples were collected from nine southern States during 2008- 2011 growing seasons. All samples were tested against the antisera of *Watermelon mosaic virus* (WMV) by dot-immunobinding assay (DIBA). The results showed that the most dominant virus infecting cucurbits in Southern United States is WMV with an average incidence of 30 %. Coat protein genes (CP) of 57 DIBA positive WMV samples collected in nine Southern states were amplified using reverse transcription-polymerase chain reaction (RT-PCR) followed by cloning and sequencing. Phylogenetic analysis of both nucleotide and amino acid sequences of these 57 isolates and previously WMV isolate reported from Florida (1990), showed high degree of variation in nt sequences of CP genes. All WMV isolates from USA were also compared with the available sequences of WMV isolates in the GenBank database and are discussed.

OP-50: A novel combination of a new umbravirus species, a new satellite RNA and *Potato leafroll virus* causes tobacco bushy top disease in Ethiopia

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The causal agents of a recently emerged virus-like disease of tobacco with bushy top symptoms resulting in serious losses in Ethiopia have been determined. Double stranded RNA isolated from plants with natural or experimental infections yielded banding patterns typical of umbraviruses and a satellite RNA (satRNA). cDNA cloning and sequencing of the larger (~4.5 kb) fragment indicated that it represents an umbravirus with a genome of 4236 nucleotides and the corresponding four ORFs whereas the smaller band (~0.5 kb) is that of a new satRNA with 521 nucleotides. Besides, *Potato leafroll virus* (PLRV) was consistently associated with symptomatic field samples and no other luteovirus could be detected. The experimental host range of the umbravirus and satRNA is restricted to the family *Solanaceae* including several *Nicotiana* species and tomato. The three agents always occurred together in field samples and are transmitted by the aphid *Myzus periscae nicotianae* from naturally or experimentally infected tobacco plants to healthy solanaceous species. Transcapsidation tests using sap extracts or purified virions from plants with mixed infection indicated that both the umbravirus and the satRNA are encapsidated in PLRV capsid proteins. Phylogenetic analysis, pairwise sequence comparison and biological data suggested that the umbravirus represents a distinct species most closely related to *Groundnut rosette virus* and the name Ethiopian tobacco bushy top virus (ETBTV) is suggested. It is found that while the Chinese *Tobacco bushy top virus* sequence in the database belongs to a distinct species, the partial sequence of the Zimbabwan isolate A2 indicates that it belongs to the same species as ETBTV. The new satRNA showed no match in BLAST search but shared significant sequence identity to other umbravirus satRNAs. Hence, tobacco bushy top disease in Ethiopia is caused by a novel combination of new umbravirus and a new satRNA assisted by PLRV for aphid transmission.

OP-51: Diversity and distribution of *Sweet potato leaf curl virus* in Kenya

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A study was carried out to determine the distribution and diversity of *Sweet potato leaf curl virus* (SPLCV) in major sweetpotato growing regions of Kenya. Leaf symptoms with typical curling symptoms were collected from three regions of western, central and coast. Polymerase chain reaction was used to amplify AC1, AC2, and AC4 regions. The virus was found to be widely distributed all over the country with the highest incidence of over 70% being recorded in the coast region followed by western region at about 60%. Amplified PCR products were sequenced and analyzed using OMEGA5 software. Phylogenetic relationships derived using nucleotide and amino acid sequences showed that all the isolates were closely related to the US isolate. The study recommends evaluation of the economic importance of the virus in sweet potato production in the region.

OP-52: Epidemiology of four cucurbit viruses affecting zucchini production in Flanders (Belgium)

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Cucumber mosaic virus (CMV, *Cucumovirus*), *Zucchini yellow mosaic virus* (ZYMV, *Potyvirus*), *Watermelon mosaic virus* (WMV, *Potyvirus*) and *Papaya ringspot virus* (PRSV, *Potyvirus*) are an increasing threat for cucurbit cultivation in temperate and tropical regions. They are transmitted in a non-persistent manner by a variety of aphid species and easily infect large areas in a limited time span. The symptoms, including mosaic, mottling, leaf distortion and chlorosis, not only result in a decreased yield but also seriously affect fruit quality. Since zucchini production in Flanders (Belgium) increased 5 to 10 times during the last decade, the economic impact of the damage caused by these viruses gained importance as well. To obtain insights into the epidemiology of the viruses, we performed preliminary virus screenings from 2007 to 2009, followed by a more intensive survey from 2010 to 2012. During this survey a clear shift in virus occurrence was observed between the different culture years. From 2007 to 2012, the importance of ZYMV gradually decreased while CMV became more important and is currently the most prevalent virus in Flanders, followed by WMV, ZYMV and PRSV. The viral shift did not only occur over the years, but also within a single growing season. Additionally, a substantial part of mixed virus infections were observed. Based on the results of this survey, inoculation experiments were set up to study introduction pathways and survival of the viruses and to assess the influence of mixed infections and cultivar choice on symptom development, yield and fruit quality. The results of this thorough epidemiological study of the zucchini viruses, together with a simultaneously performed epidemiological study of the aphid vector will result in a more sustainable control strategy of this emerging problem.

OP-53: Field epidemiology of cassava brown streak viruses in Tanzania

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A replicated field trial was conducted from 2010-2011 to investigate the field spread of cassava brown streak viruses (CBSVs), causing cassava brown streak disease (CBSD). CBSVs-free planting material was obtained through the screen-house bulking of virus-indexed tissue culture plants of cv. Kiroba obtained from NRI, UK. The experiment consisted of four replicated blocks, separated by a distance of >200m. Within each block, five 20-plant test plots were planted in a line, downwind of a larger 'spreader' plot planted with CBSD-infected cassava of the same variety. Test plots were therefore spaced at different distances from the 'spreader'. Following planting, monthly records were made of CBSD foliar incidence and *Bemisia tabaci* whitefly adult abundance by inspecting/counting all test plot plants. Average final CBSD incidences for test plots were: 47.2% (1m from spreader); 37.3% (6m); 18.3% (11m); 9.5% (16m) and 10.2% (21m), although there were large differences between individual blocks. A follow-up experiment was planted under controlled conditions within a 8mx20m screen-house using a similar design. Here, one half of the area was planted with CBSD-infected spreader plants, whilst into the other half were introduced CBSD-free plants of cv. Kiroba in pots. These test plants were arranged in four plot tiers at increasing distance from the spreader plants. More than 1000 adult *B. tabaci* adults were then introduced to the portion of the spreader plot most distant from the test plants. CBSD incidence and whitefly abundance were subsequently recorded for all plants in all test plots over a period of seven months, at weekly intervals. By four months after planting, CBSD incidences were 65% in the nearest and 8.3% in the farthest test plots from the spreader. The distribution of adult *B. tabaci* followed a similar gradient. Three months later, 100% of plants were infected in all three plots nearest to the spreader, whilst CBSD incidence was 90% in the plot most distant from the spreader. These results confirm the CBSD spread gradient demonstrated through the field experiments and highlight the central role played by the whitefly vector in CBSD epidemiology. The steep gradients encountered during the early stages of disease spread highlight the potential importance of phytosanitary measures and isolation as control measures for CBSD.

Op-54: Epidemiology and evolutionary studies of criniviruses associated with tomato yellows disease in Greece

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Tomato chlorosis virus (ToCV) and *Tomato infectious chlorosis virus* (TICV) are members of the genus *Crinivirus* (family *Closteroviridae*) reported to be related with tomato yellows disease (TYD). ToCV is transmitted by *Bemisia tabaci* Gennadious, *Trialeurodes vaporariorum* Westwood and *Trialeurodes abutilonea* Haldeman, whereas TICV is transmitted solely by *T. vaporariorum*. During 2009-2012 a study on the viruses involved in TYD etiology and their epidemiology was carried out in Greece collecting samples from glasshouse and open field tomato crops. Surveys were also conducted on other crops showing yellows symptoms and on weeds (showing or not symptoms), while their whitefly vectors species were also identified. In total 1206 tomato and 4 lettuce samples showing yellowing symptoms were collected, as well as 1339 samples of weed species (42 different species within 17 families) and 1041 adult whiteflies. Results showed that *T. vaporariorum* is the predominant whitefly species in Greece (76%), followed by *B. tabaci* (biotypes B and Q) (24%). Regarding their spatial distribution *T. vaporariorum* is the main species encountered in the North while *B. tabaci* is the predominant species in the southern part of the country. TICV prevails in tomato crops (87%), while ToCV incidence is very low (16%) and rather confined in southern Greece. Mixed infections with both viruses were very rare (2%). Weed species seem to play an important role in the epidemiology of both viruses, as 26 species from 16 families proved to be natural reservoirs of ToCV and TICV. It is worth mentioning that ToCV was detected for the first time in lettuce plants showing mild yellowing symptoms. Sequence analysis of the CP and CPm genes from Greek tomato and weed isolates of ToCV and TICV showed that even though both viruses have very wide host ranges their populations show very low evolutionary divergence.

Keynote presentation

OP-55: Is the ability to revert an alternative to distribution of virus-free planting material of sweetpotato to East African farmers?

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Projects have tried or are trying to distribute virus-free planting material of sweetpotato varieties to farmers in East Africa. There are now also various methods of achieving rapid multiplication and cheap protection against vectors. Nevertheless, this is being done with little knowledge of how quickly viruses such as *Sweet potato feathery mottle virus* (SPFMV) spread to cause degeneration in East African varieties. There is, however, evidence from elsewhere that SPFMV spreads very quickly, indicating that it may quickly overwhelm initial freedom from virus infection. Surprisingly, there is survey evidence that a high proportion of the planting material of many landraces is virus free despite crops being grown unprotected for generations; we also present evidence that this is also true for several released Ugandan varieties. Greenhouse experiments over a 10 week period using both qPCR and indicator plants (*Ipomoea setosa*) show that some of these varieties have an ability to revert from SPFMV-infected to healthy, probably through an inbuilt RNA silencing mechanism. This explains the low equilibrium level of infection in unprotected crops and indicates that for these varieties the benefits of starting with virus-free material are likely to be small.

Keynote presentation

OP-56: Do recombinants appearing in natural populations of watermelon mosaic virus represent new agronomic threats?

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Watermelon mosaic virus (WMV, *Potyvirus*) is very common in France where it has been present for at least 40 years. Since the early 2000s, new "emerging" (EM) strains of WMV, highly divergent molecularly from the "classic" (CL) strains present before and probably originating from recent introductions, were detected in southeastern France. Since both types of strains did not appear to be present in the same geographic locations before, this situation constituted a unique opportunity to study the frequency of appearance and the potential spread of recombinants in the few years following the introduction of the new strains. Analyzing isolates from experimental plots in Montfavet (Southeastern France) as well as from epidemiological surveys performed from 2004 to 2008 all around France (about 2000 WMV isolates) revealed at least 7 independent recombination events, either between CL and EM strains or between different EM subgroups. Most recombinants were found in a few plants from the same field, but, with one notable exception, did not seem to spread or be maintained locally for several years. Mixed infections of CL and EM isolates were also performed in experimental conditions in order to compare the frequency and nature of recombination events to those of natural situation. The fitness of natural recombinants relative to potential "parental" strains was also tested in controlled conditions. The epidemiological and evolutionary consequences of recombination in WMV populations will be discussed. This work represents one of the first estimation for the frequency of appearance of recombinants in natural populations of a plant RNA virus.

Keynote presentation

OP-57: An R-gene associated with the *Tobacco mosaic virus* local lesion response in tobacco induces partial resistance to several fungal pathogens in tomato

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The inhibitor of virus replication (IVR) gene associated with the *Tobacco mosaic virus* (TMV) local lesion response in tobacco is an R-gene that codes for a putative protein with a molecular mass of 22 kDa. The IVR gene product is rich in leucine and is considered to be a leucine-rich-repeat protein. When tomato (*Solanum lycopersicum*) cv. VF36 plants were transformed with a cDNA clone encoding the IVR gene, they became partially resistant to seedling infection by *Alternaria alternata*, *Pythium aphanidermatum* and *Rhizoctonia solani in vitro.* Resistance to damping-off was observed in transgenic seedlings planted in soil infested with *R. solani* and *P. aphanidermatum*. The foliar diseases gray mold (*Botrytis cinerea*), early blight (*Alternaria solani*) and powdery mildew (*Oidium neolycopersici*) were also controlled in mature tomato plants. The finding that an R-gene associated with virus localization also induces resistance against some fungal diseases is unique and suggests that some R-genes have a wider range of action than originally targeted for.

OP-58: Whitefly-transmitted viruses: cultural strategies in vegetable crops

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Whitefly-transmitted viruses are important problems in agriculture on a global scale. The sweetpotato whitefly, *Bemisia tabaci* (Gennadius), is a notable vector because of the extensive number of viruses that it transmits and the extensive number of host plants that it feeds on. To help develop strategies to manage whitefly-transmitted viruses and *B. tabaci* in vegetable crops, experiments on several cultural techniques were conducted in Egypt. Mulching with white polyethylene, intercropping with corn (*Zea mays* L.), and crop rotation with corn resulted in reduced whitefly populations and reduced incidences of viruses in cucumber (*Cucumis sativus* L.), squash (*Cucurbita pepo* L.) and tomato (*Solanum lycopersicum* L.). However, no benefit in virus incidence and whitefly abundance was obtained from modifying the planting time by one month earlier than standard planting. The viruses affecting the crops were *Cucumber vein yellowing virus* in cucumber, *Squash leaf curl virus* in squash, and *Tomato yellow leaf curl virus* in tomato. Experiments were also conducted on some cultural irrigation practices (drip, furrow and sprinkler) in cucumber, green bean (*Phaseolus vulgaris* L.), squash and tomato. A daily drip irrigation treatment resulted in the lowest incidences of plants with whitefly-transmitted virus symptoms and lowest whitefly populations, while the highest infections and infestations were observed for a weekly sprinkler irrigation treatment and a biweekly furrow irrigation treatment, respectively. Regardless of cultural treatment, there was a high correlation between virus incidence and whitefly abundance. This study demonstrates that certain cultural strategies can affect incidences of whitefly-transmitted viruses and whitefly populations in vegetable crops in Egypt.

OP-59: *Strategies for managing banana bunchy top disease in the Rusizi valley, Burundi*

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Banana bunchy top disease (BBTD), caused by the banana bunchy top virus (BBTV), was reported for the first time in Burundi in 1987. Ever since, the disease has continued its spread throughout the Rusizi valley, slowly reaching higher altitudes, as no specific measures are being taken for its control. Acquisition of sufficient BBTV-free planting materials via natural regeneration is a challenge in the Rusizi valley as disease incidence is reported to reach up to 30% in certain Provinces such as Cibitoke. A dual strategy tested in Munyika pilot village (Rugombo commune, Cibitoke province) was used to reduce the spread and impact of BBTD with on one hand targeted awareness raising and management practices focusing on symptom and vector identification, good cultural practices and prompt eradication campaigns carried out with collaborative support from farmers; however with limited success. On the other hand, BBTV-free planting material of preferred local and hybrid cultivars was selected using serological tests and multiplied using macropropagation technologies. The resulting BBTV-free plantlets were planted in March 2011 in Gitebe (Mugina commune, Cibitokeprovince) under experimental and farmers conditions in order to evaluate reinfection rates in disease hotspots under various management conditions. Plantlets were established in an experimental plot where prompt eradication of newly diseased mats was adhered to and in farmers' fields where management and adherence to BBTD management practices was left to individual willingness. Twenty months after planting, a reinfection rate of 12 and 23% was observed respectively in the experimental and farmer fields located adjacently to BBTD affected plots. In April 2010 a parallel study carried out in Munyika II (Rugombocommune, Cibitokeprovince), a farmer-led FHIA-03, FHIA-17 and FHIA-23 trial using tissue culture planting material was established 80m outside of existing banana plantations. Three percent of plantlets were lost within the first year, however, with prompt eradication of cases and strict adherence to BBTD disease management practices, no cases have been observed since.

OP-60: Mapping the quantitative and qualitative resistance to cassava mosaic disease using next-generation sequencing marker data

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Cassava mosaic disease (CMD), caused by several begomoviruses, is the most important disease of cassava (*Manihot esculenta* L.) in Africa – where millions of people rely on the crop for their daily carbohydrate intake. Polygenic resistance to this devastating disease was obtained from wild species, *M. glaziovii*, more than 80 years ago through a backcross breeding strategy. Using these ancient backcross clones, the International Institute of Tropical Agriculture (IITA) developed a large number of varieties, named Tropical Manihot Series (TMS) that were deployed in many African countries, including East Africa where severe pandemics of CMD nearly destroyed cassava farming systems in the 1990's. We sought to identify these important quantitative trait loci (QTL) that played such an important role in fight against CMD using a genome-wide association study approach (GWAS). Specifically, we genotyped-by-sequencing 650 TMS-clones held by IITA. Mixed-model analysis using the high density marker data from GBS and historical phenotypic data uncovered three major loci that explained more than 60% of the quantitative resistance to CMD. A scan of the cassava genome sequence near the markers found to have the strongest association with the resistance revealed several candidate disease resistance genes. We also developed a bi-parental population to map a dominant, monogenic resistance thought to have spontaneously arisen in a West-African landrace, and that seems to confer near-immunity to all known types of cassava mosaic viruses. This population was genotyped-by-sequencing and phenotyped under high-disease pressure. Using classical QTL mapping analysis, a single locus that co-located with a previously mapped QTL in a different mapping population was identified. We demonstrate the capability of GWAS and classical linkage analysis using marker data obtained from next-generation sequencing technologies in locating disease resistance loci in the clonally-propagated cassava. Identified markers can be used expedite development of clones with durable resistance by combining quantitative and single-gene resistance.

OP-61: Transgene viral siRNA profile and its effect on cucurbit viral resistance

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Viral resistance based on gene silencing has been developed in transgenic plants for many viruses. However, little is known concerning the transgene-small-interfering RNA (t-siRNA) population causing viral resistance. Transgenic cucumber and melon plants were constructed bearing a hairpin construct including a fragment of the *Zucchini yellow mosaic potyvirus* (ZYMV) HC-Pro gene. Transgenic lines accumulatingt-siRNA exhibited resistance to systemic ZYMV infection. In resistant lines t-siRNA comprised 12-44% of total small RNA in cucumber, determined by Illumina sequencing. The majority of t-siRNA in transgenic melon and cucumber was 21 and 22 nts, Unevent-siRNA densities along the transgene sequence were characterized, reflecting accumulation oft-siRNA in "hot spots". One transgenic line exhibited resistance to systemic infection of four different RNA viruses, independent of homology between the transgene sequence and the virus. This line accumulated an exceptionally high level of t-siRNA, 43% of total plant siRNA, in addition to increased level of RNA-dependent-RNA-polymerase 1 (RDR1). Our data show for the first time a correlation between a broad RNA virus resistance and an increased level of RDR1 mRNA expression. We suggest a new model in which a high level of t-siRNA increases RDR1 expression leading to the induction of broad viral resistance, independent of involvement of salicylic acid.

OP-62: Quantitative resistance loci reduce the breakdown frequency of a major resistance gene. A relevant way for durable resistance breeding

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The combination of major resistance genes with quantitative resistance factors is hypothesized as a promising breeding strategy to preserve the durability of resistant cultivars. In three pathosystems, experimental data demonstrate that the durability of a major resistance gene depends on the plant genetic background but the genetic factors involved are still unknown. Using the pepper (*Capsicum annuum*)/*Potato virus Y* (PVY)) pathosystem, we aimed to identify genetic factors directly involved in *pvr2[3]* resistance breakdown frequency and to compare them with genetic factors affecting quantitative resistance. For QTL mapping experiments, 156 doubled haploid lines carrying the *pvr2[3]* resistance allele were tested for *pvr2[3]* resistance breakdown frequency, virus accumulation and symptom intensity. Four loci including additive QTLs and epistatic interactions explained together 70% of the variance of *pvr2[3]* breakdown frequency. Comparative mapping of the different traits showed that three of the four QTLs controlling the breakdown frequency of the *pvr2[3]* allele were also involved in quantitative resistance, indicating that QTLs for quantitative resistance have a pleiotropic effect on the durability of the major resistance gene. This study provides the first mapping of QTLs directly affecting resistance durability and opens the way for sustainable resistance breeding.

Keynote presentation

OP-63: Effects of genetic changes to the begomovirus/betasatellite complex causing cotton leaf curl disease in South Asia post resistance breaking

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Cotton leaf curl disease (CLCuD) has been a problem for cotton production across Pakistan and north-eastern India since the early 1990s. The appearance of the disease has been attributed to the introduction, and near monoculture of highly susceptible cotton varieties. During the intervening period the genetic make-up of the virus(es) causing the disease has changed dramatically. The most prominent of these changes has been in response to the introduction of CLCuD-resistant cotton varieties in the late 1990s, which provided a brief respite from the losses due to the disease. During the 1990s the disease was shown to be caused by multiple begomoviruses and a single, disease-specific betasatellite. Post-resistance breaking the complex encompassed only a single begomovirus, *Cotton leaf curl Burewala virus* (CLCuBuV), and a recombinant version of the betasatellite. Surprisingly CLCuBuV virus lacks an intact C2 gene. The C2 gene is found all begomoviruses and encodes a product of ~134 amino acids that is important in virus-host interactions; being a suppressor of post-transcriptional gene silencing (host defence) and a transcription factor that modulates host gene expression, including microRNA genes. This presentation will outline recent studies which have highlighted the differences between CLCuBuV and the earlier viruses showing the latter virus to be a much "fitter" pathogen. These studies are part of on-going efforts to define the molecular basis for resistance breaking in cotton, which continues to be elusive.

Keynote presentation

OP-64: Evidence of purifying selection in the coding regions of wild type *Maize streak virus* (MSV) and pathogen survival (and host-pathogen interaction)

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Maize streak disease, caused by *Maize streak virus* (MSV) reduces maize yields in an infected maize plant by up to 100% even in high potential zones, making it one of the most serious biotic threats to African food security. The MSV-A strain which today causes devastating disease in maize likely emerged in the mid-1800s in Southern Africa following a recombination event between two wild-grass adapted MSV strains. Determining the evolutionary changes that occurred in MSV-A during and immediately after its emergence, would provide vital information on how and why virulent viruses emerge as agricultural pests. To deduce the selection pressures acting on MSV-A and other related mastreviruses, we calculated for all amino acid encoding sites within their genomes the ratio of the rates of non-synonymous (d_N) and synonymous (d_S) substitutions (i.e. the d_N/d_S ratio) using the codon-based maximum likelihood selection detection methods REL, IFEL, and SLAC implemented on the Datamonkey web-server (Kosakovsky Pond and Frost, 2005a,b). We looked for amino acid sites in MSV-A genes that seem to be evolving under negative selection (and are therefore likely important for MSV-A survival) that correspond to sites in other groups of grass adapted streak viruses (wild grass adapted MSV strains, *Pannicum streak virus*, *Australasian streak viruses*, *Wheat dwarf virus* and dicotyledonous host infecting mastrevirus) with amino acids different to those in MSV-A. We found two sites in *mp* gene (both within the region before the putative trans-membrane domain), two in the *cp* gene (both within the DNA binding domain) and five in *rep* gene (two just before and after the VRDYILK rolling circle replication motif, one between the RCR motifs and the oligomerisation domain, one between the RB binding domain and the transactivation domain and one after the myb-like transactivation domain) that are evolving under negative selection for a particular amino acid that is different from that found in the nearest grass adapted relatives of MSV-A. Among these sites are likely to be the mutations that have specifically adapted MSV-A to infecting maize. We also found two sites evolving under positive selection in the *cp* gene (one within the DNA biding domain and one at the putative nuclear localisation signal) that are changing extraordinarily frequently, possibly in response to the wide-range of host species that MSV-A is known to infect in the field.

OP-65: Sequence diversity of global chrysanthemum stunt viroid variants: multiple polymorphic positions scattered throughout the genome

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The extent of natural sequence variation among isolates of chrysanthemum stunt viroid (CSVd) was examined by sequencing cDNA clones, by "deep sequencing," and by comparison with the global sequences obtained from the GenBank. First, the nucleotide sequences from cDNA clones of three CSVd isolates (one each from the USA, China and Australia) were determined and analyzed. The cDNA clones of the US and Australian isolates were found to be quasi-species, while those of the Chinese isolate contained only a single variant. Sequence variation also was examined within two Korean isolates by comparing the sequences obtained either from ~100 cDNA clones of each vs. by "deep sequencing" using 454 pyrosequencing technology. Both approaches showed that there was little variation within the populations of molecules examined, with the major variations detected at largely the same positions in both Korean isolates. This lesser variation may be a reflection of a recent introduction of these isolates to Korea. Finally, a comparison of the nucleotide sequences of 117 isolates and cDNA clones obtained from 16 countries showed that in some cases identical CSVd isolates were found in several countries and from multiple locations within the same country. CSVd isolates differed as much in sequence between countries as within countries. Sequence variation was observed at 103 nucleotide positions scattered through the CSVd genome, and was not associated predominantly with a single variable region, as was the case with several other viroids. Although the sequence variation *in toto* was largely random, some regions did not show sequence variation, including the (left) terminal conserved region and the right-hand loop. In addition, seven sites (positions 47, 49, 50, 64, 65, 254 and 298) showed variation in a large proportion of various CSVd isolates, with the minority nucleotide alternatives occurring in ~14 % to 32 % of the populations.

OP-66: Micro-evolution of *Beet necrotic yellow vein virus* during a single crop season using next-generation sequencing

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In order to understand the impact of the sugar beet varieties on the evolution of the *Beet necrotic yellow vein virus*, 454 deep-sequencing was used to generate sequences from BNYVV RNA-2, RNA-3 and RNA-5 targeted amplicons. The samples were collected in field plots where the disease distribution had been characterized, with mostly presence of the BNYVV P-type associated with the tetrad SYHG and the fifth genomic RNA. Trial plots were selected from a long term experiment conduced jointly with the French technical institute in the historic BNYVV epidemic epicenter, in Yèvre-la-Ville, Loiret, France, from 2008 to 2012. Three different varieties were used with different BNYVV resistance background: susceptible (Rz1rz1rz2rz2), tolerant (Rz1rz1rz2rz2) and resistant (Rz1rz1Rz2rz2). The estimated disease root impact in September varied from 2 % in the "resistant" variety, 6 % in the tolerant and 22 % in the susceptible one. Amplicons were obtained using tagged primers positioned in conserved BNYVV genome region. The genes targeted were anticipated to be involved in the interaction plant virus: the p25 of BNYVV RNA-3, the p14 of BNYVV RNA-2 and the p26 of BNYVV RNA-5 to create a library composed of nine cDNA samples. All cDNA were then pooled together for emulsion PCR. The nine different tags allowed to retain the link to the original sample, the gene and the variety. The 454 deep-sequences were analyzed for all samples. Approximately, 6000-7000 sequences per sample for each amplicon/ variety combination were obtained. The analysis of conventional sequences obtained early and at the end of the sugar beet growing season, together with sequences from bioassays using a susceptible (rz1rz1rz2rz2) variety as well as deep sequencing results reveals variations according to the sugar beet genotype as well as to the spatial dispersion of the virus.

OP-67: Temporal and spatial changes in the betasatellite associated with the begomoviruses causing cotton leaf curl disease

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Cotton leaf curl disease (CLCuD) is the most devastating disease of cultivated cotton in Pakistan and western India. The disease is caused by a complex of begomoviruses and single-stranded DNA satellites. Two classes of satellites occur in association with the begomoviruses; alphasatellites and betasatellites. The contribution of alphasatellites to the complex has not been clearly defined. Betasatellites are small (~1.4 kb) and encode only a single product (a protein known as βC1 that is a pathogenicity determinant involved in overcoming plant host defence based on gene silencing. During the 1990s CLCuD in Pakistan/India was associated with at least seven begomoviruses but only a single species of betasatellite – Cotton leaf curl Multan betasatellite (CLCuMB). In 2003, following the introduction of resistant cotton varieties during the late 1990s, a resistance breaking strain of CLCuD appeared in cotton. This consisted of a single begomovirus (*Cotton leaf curl Burewala virus* [CLCuBuV]) and a variant of CLCuMB (CLCuMB^{Bur}). The precise molecular basis for resistance breaking remains unclear. Nevertheless, both CLCuBuV and CLCuMB^{Bur} were shown to have a recombinant origin and to possess some unusual characteristics. In Sindh, which was not severely affected by the CLCuD epidemic during either the 1990s or by the resistance breaking strain, we have recently shown the presence of another unusual variant of CLCuMB – which we named CLCuMB^{Shahdadpur}. Here we show the appearance of an additional recombinant variant of CLCuMB which is spreading in cotton in Pakistan. The possible significance of these findings is discussed.

OP-68: Evidence of high genetic variability in cassava geminiviruses and epidemiological implications

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Cassava geminiviruses occur in all cassava growing areas of Africa and are considered to be the most damaging vector-borne plant pathogens. At least seven species of these viruses have been identified. We investigated genetic variation in East African cassava mosaic cassava Cameroon virus (EACMCV) from naturally infected cassava and from experimentally infected *Nicotiana benthamiana*. Results showed that the populations of EACMCV in cassava and in *N. benthamiana* were genetically heterogeneous. Mutation frequencies in the order of 10^{-4}, comparable to that reported for plant RNA viruses, were observed in both hosts. We also produced an EACMCV mutant that induces reversion and second site mutations, thus suggesting that a high mutation frequency facilitates the maintenance of genome structure and function. This is direct experimental evidence showing that cassava geminiviruses exhibit a high mutation frequency and that a single clone quickly transforms into a collection of mutant sequences upon introduction into the host. These data and virus recombination is strong evidence for emergence of new and more virulent virus species.

OP-69: Cucumber mosaic virus and plant virus evolution

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The journal *Molecular Plant Pathology* recently considered which viruses should appear in a "top 10" list of plant viruses based on their perceived importance scientifically or economically. *Cucumber mosaic virus* (CMV) was ranked number four on that list generated by the international community (*Molecular Plant Pathology* (2011) 12 (9), 938-954). This is not surprising because CMV is an extremely successful virus that infects plants all around the world. The variety of available strains of CMV and the divided genome of the virus provide a useful and convenient system to study many general principles of virus evolution and ecology. We used this system to elucidate the forces behind RNA virus population diversity. We identified the genes that are related to the differing population diversity levels in different strains of CMV and mapped the regions that are associated with high and low diversity levels. Furthermore, we used the CMV system to understand the mechanisms underlying the fixation of newly generated variants in a viral population, a process that constitutes a key aspect of evolutionary dynamics. We found that the increase in relative fitness of such variants in CMV population is associated with a better adaptation to the replicase complex, a process that is probably a major driving force in the deep evolution of RNA viruses. Understanding the evolutionary mechanisms underlying CMV adaptability, and uncovering the process whereby a new mutant introduced in a population can reach fixation will impact research on the control of emerging viruses.

OP-70: Oman – a nursery for recombination between exotic Old World begomoviruses of diverse origins

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Recent results show begomoviruses to be an important constraint for the cultivation of vegetable crops in Oman. The viruses identified have diverse geographic origins and include *Tomato yellow leaf curl virus* (TYLCV) originating from Iran isolated from tomato, *Chili leaf curl virus* originating from South Asia infecting peppers and tomato, *African cassava mosaic Zanzibar virus* originating from Zanzibar/East Africa affecting cassava as well as the begomovirus-associated satellites Tomato leaf curl betasatellite (ToLCB) originating from South Asia and Ageratum yellow vein Singapore alphasatellite originating from Singapore, both of which were identified in tomato. Recombination is a major driver of geminivirus diversification and the confluence of distinct viruses and associated components in Oman provides a unique opportunity for the interaction of evolutionarily distinct viruses and associated components. Already this has led to the appearance of new, recombinant begomovirus species/strains unique to Oman, including *Tomato leaf curl Oman virus* and *Okra leaf curl Oman virus*, as well novel associations of satellites with viruses, such as the only known strain of TYLCV to interact with a betasatellite. Additionally Oman is a major hub for commerce by both air and sea, which is likely how the viruses were introduced into Oman but more importantly provides a possible means for global spread of these pathogens.

Keynote presentation

OP-71: War on African cassava viruses: a novel strategy against mighty foes of cassava

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Cassava is infected by at least 30 different viruses worldwide, but it is in Africa that the devastation is the greatest. Cassava mosaic disease (CMD) is present in all cassava growing African countries. CMD is caused by at least 10 different geminiviruses, transmitted by whiteflies and by cuttings from infected plants. An estimated 45Mt of cassava are lost each year to CMD on the African continent and it is considered the first and most important constraint continent-wide. A pandemic caused by a new recombinant geminivirus exploded in Uganda in the 90s and for years completely suppressed the cassava production in the region, exemplifying that a situation could worsen! Cassava brown streak disease (CBSD), first described in 1935, re-appeared in East Africa in 2003, causing a severe epidemic in the whole region, to the point where this disease is now the worst constraint for cassava in East Africa and a major threat for the rest of Africa. CBSD is caused by two species of ipomoviruses, also transmitted by whiteflies and by cuttings. CBSD is dramatic because it does not impact the growth of the infected plants but completely compromises the harvest, as all the roots are necrotic. CBSD is a threat for millions of farmers in East Africa today and the rest of Africa tomorrow. CMD and CBSD are considered the two most important constraints for cassava in Africa suppressing a minimum 30% of the total cassava harvest. The **Global Cassava Partnership for the 21st Century** (GCP21), a recognized global organization within the cassava community, is **Declaring War to Cassava Viruses in Africa**. GCP21, with a number of experts, will draw a comprehensive and coordinated plan to decrease these constraints and to prevent CBSD from reaching West Africa, the largest cassava producing region in Africa and in the world. This plan will be developed through a conference held at the Rockefeller Center of Bellagio in 2013. The outcome of this conference will be a detailed plan established by cassava experts in virology, entomology, breeding, biotechnology and seed systems, with the participation of donors and developers to fund the necessary research and development plan to control and potentially eradicate these diseases.

Keynote presentation

OP-72: Ever increasing diversity of tospoviruses: implications for Africa

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The tospovirus group (*Bunyaviridae*, *Tospovirus*) used to be a monotypic genus consisting of *Tomato spotted wilt virus* (TSWV) for several decades. *Impatiens necrotic spot virus* (INSV) was the second distinct tospovirus described from the US in 1980s. Subsequently, new and distinct tospoviruses have been described from several continents and countries. Availability of virus-specific antisera, genomic information, and development of descriptors for describing new viruses have improved clarity in taxonomy and identification of tospoviruses to the species level, especially over the last ten years. There are more than 30 distinct tospovirus species described so far affecting a wide range of horticultural crops and some staples both in protected and open field cultivation. The basis for this diversity within the *Tospovirus* genus could be due to several reasons: expansion of cultivation of new crops in the vicinity of other susceptible crops, expanding host range of thrips vectors, the divided genome of these viruses which make them amenable to genetic reassortment either in the host plant or their thrips vectors. On a regional basis, tropical regions of Asia and South America continue to have the greatest diversity of tospoviruses. In case of Africa, while Groundnut ring spot virus was one of the first tospoviruses reported from South Africa. Recent years have seen the reports of *Iris yellow spot virus*, TSWV, and most recently *Tomato yellow ring virus* from East Africa, Mauritius and Reunion islands. Since several thrips vectors are already established in many parts of Africa and with increasing acreage under vegetables and ornamentals, inoculum build up could lead to more frequent outbreaks of tospoviruses and it is possible that new tospoviruses could emerge or be introduced into the continent. Regular surveillance and surveys for various known tospoviruses should provide important information on the diversity of tospoviruses in Africa and their potential impact on various crops that are susceptible to tospovirus infection.

OP-73: The Bioscience Eastern and Central Africa (BecA) Hub and its role in enhancing science and technology capacity in Africa

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The Biosciences eastern and central Africa-International Livestock Research Institute (BecA-ILRI) Hub exists to increase access to affordable, world-class research facilities and to create and strengthen human resources in biosciences and related disciplines in Africa. Developed under the framework of Centers of Excellence for Science and Technology as part of the AU-NEPAD (African Union-New Partnership for Africa's Development) African Biosciences Initiative, the BecA-ILRI Hub is located at, and managed by ILRI in Nairobi, Kenya. Established as a biosciences research and capacity building platform, the Hub employs modern biotechnology to address key constraints to agriculture in eastern and central Africa. The Hub provides state of the art molecular, nutritional, genomics, diagnostics and bioinformatics capabilities and capacity building opportunities to the region and beyond. Our activities have significantly expanded over the past few years with major support from the Syngenta Foundation for Sustainable Agriculture; the Australian Agency for International Development (AusAID), through a partnership with the Commonwealth Scientific and Industrial Research Organisation (CSIRO); the Bill & Melinda Gates Foundation; and the Swedish Ministry of Foreign Affairs through the Swedish International Development Agency. Our current research activities focus on food security, food safety, disease diagnostics in crops and livestock, biosciences for climate change, functional and viral genomics, pathogen discovery, environmental metagenomics, plant virome studies and other areas. The Hub's research and capacity building portfolio will be discussed, with highlights of several past and ongoing virus research projects and opportunities for collaboration. More information is available at http://hub.africabiosciences.org.

OP-074: Q-bank plant virus database and collection

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The Q-bank Plant virus database and collection is part of the larger Q-bank initiative (www.q-bank.eu) to support national and international plant health policies. Q-bank is a dynamic open-access database containing relevant data (sequence data, morphological data including photographs, nomenclatural and diagnostic data) on plant pathogenic quarantine organisms and look-alikes (fungi, bacteria, arthropods, viruses, phytoplasmas, nematodes and invasive plants) Data of Q-bank are curated by an international network of curators and specimens are available from publicly accessible reference collections. The Q-bank plant virus database contains information on plantviruses with respect to their taxonomy and phytosanitary status, biological and molecular characteristics (including sequence data and blast options), protocols (EPPO) and (molecular) test methods, antiserum suppliers, pictures and availability of specimens (reference material).The Q-bank plant virus database offers a platform to share knowledge on regulated and other relevant plant virus species, to make virus specimens available for diagnostics and research activities and to create a 'network' between plant virologists. The fact that next to this digital information the isolates themselves are available from a collection distinguishes Q-Bank from other databases and makes it a unique and valuable reference in plant virology. To strenghen the database and collection, plant virologists are kindly requested to provide isolates of regulated or otherwise interesting isolates for inclusion in Q-bank.

Abstracts of the Poster Presentations

PP-001: Variability and sequence diversity of *Citrus tristeza virus* isolates from Pakistan

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Citrus tristeza virus (CTV) is one of the major threats to citrus production and fruit quality worldwide. In Pakistan more than 95% of the citrus trees are grown on sour orange rootstock which is highly susceptible to CTV. We studied the genetic variability of four genomic regions (*p18*, *p20*, *p23* and *p25*) of 21 CTV isolates collected from the citrus orchards. High divergence was revealed among the isolates from Pakistan and also with reference isolates. An inter-isolate identity range of 93.1 to 100% at the nucleotide level and 89.8 to 100% at the amino acid level were found. Phylogenetic analysis of the predominant sequence variants of each isolate revealed almost similar grouping of isolates for each genes. The groups revealed by phylogenetic trees include sequences of severe quick decline, seedling yellows and stem-pitting (SP) and also mild isolates. The high percentage of mixed infections is alarming for further diversification and spread of severe variants into new citrus growing areas of Pakistan and the neighboring countries.

PP-002: Spatial and temporal analyses of the impacts of *Plum pox virus* in Pennsylvania and Ontario, Canada

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Plum pox virus (PPV) was first detected in the United States in Pennsylvania in 1999, and in Ontario, Canada in 2000. Although both countries implemented PPV eradication programs, PPV has been officially declared eradicatedonly in Pennsylvania. Though similar in many aspects, the impact of the two eradication programs on the spatial and temporal dynamics of PPV remains unknown. The goals of this research, therefore, were to quantify the impacts of the US and Canadian PPV Eradication Programs on both the spatial and temporal dynamics of PPV epidemics in Pennsylvania and Ontario. The frequency of PPV-positive trees detected over time (year) decreased in both countries, however, *Plum pox virus* incidence decreased approximately 1.5 times faster in Pennsylvania than in Ontario. Marked point pattern analysis revealed that PPV-positive *Prunus* blocks in Pennsylvania were clustered for distances of 0.7 to 4.3 km, whereas in Ontario, PPV-positive blocks were clustered for distances of 1.0 to 25.0 km. Multi-year spatiotemporal analyses revealed that PPV-positive *Prunus* blocks in Ontario were clustered for distances of 0.1 to 3.0 km in 2007, and for distances of 0.1 to 17.0 km in 2008 and 2009. This indicates that the location of PPV-positive blocks that were detected in one year were spatially dependent upon the locations of PPV-positive blocks detected the previous year. Distances to 50% and 95% (D_{50} and D_{95}) of newly detected PPV-positive blocks from the previous year's PPV-positive blocks in Pennsylvania revealed that 95% of new PPV-positive blocks between 2002 and 2006 were found to occur within 10 to 20 km from the previous year's PPV-positive blocks. In Ontario, 95% of new PPV-positive blocks occurred within 500 to 900 m from PPV-positive blocks detected the previous year. Although highly successful in reducing PPV incidence from 2001 to 2008, Canada has shifted from or eradicated-based policy to a management-based strategy. This study provides important new information concerning the impact of PPV eradication programs on the spatial and temporal dynamics of PPV epidemics in Pennsylvania and Ontario.

PP-003: Controlling cassava brown streak disease (CBSD) through genetic engineering

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Cassava brown streak disease (CBSD) has emerged as the most significant threat to cassava production in East and Central Africa in the past one decade. The disease is caused by two viral species of the genus *Ipomovirus*, family *Potyviridae*, called *Cassava brown streak virus* (CBSV) and *Ugandan Cassava brown streak virus* (UCBSV). Both viruses are transmitted through vegetative stem cuttings and by whitefly, *Bemisia tabaci*. As CBSD resistance has not been found in cassava genotypes traditionally grown by farmers, development of transgenic varieties holds significant potential to control CBSD pandemic. One of the most promising transgenic methods to confer resistance against CBSD is the use of RNA interference (RNAi) technology that has been demonstrated to control numerous diseases caused by both DNA and RNA viruses. The coat protein (CP) of potyviruses plays an important role in the encapsidation of the viral genome and the regulation of viral RNA replication, insect transmission, cell-to-cell and systemic movement in the host, and is also one of the most conserved genes across related viral species. The *CP* gene has therefore been an important target for the RNAi strategy designed to control RNA viruses. The RNAi construct pILTAB5001 (near full length-CP) was generated from the coat protein (CP) sequences of both UCBSV and CBSV, and transgenic cassava produced in the CBSD susceptible cultivar 60444. Transgenic lines will be evaluated for their ability to accumulate CP specific siRNAs and challenged in the glasshouse to UCBSV and CBSV-infected rootstocks. In order to tackle both CBSD and Cassava mosaic disease (CMD), the technology will be mobilized into a farmer-preferred cassava genotype naturally resistant to CMD. Progress towards the optimization of transformation protocol of east African farmer-preferred cultivars and control of CBSD by RNAi-mediated technology will be presented.

PP-004: Strain diversity of plant RNA viruses in Ukraine

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This study determined the divergence of different RNA plant viruses in Ukraine and provides data on their molecular-biological and phylogenetic analysis. The origin of the analyzed Ukrainian plant viruses was determined and hypothetical mechanisms of evolution for Ukrainian isolates of RNA plant viruses were tested. Study of gene sequences of capsid proteins of ten Ukrainian RNA viruses (from 8 genera and 5 families) isolated in field and laboratory conditions confirmed no evidence for direct dependence of molecular divergence of viruses from the climate conditions, type of host plant, geographical spread or effect of abiotic factors (heavy metals). The established trend of low genetic variability of viruses, despite high mutational ability of *RNA* viruses, indicates the impact of negative selection to maintain the stability of viral nucleotide sequences. Analysis of the phylogenetic trees topology shows the direction of isolation and low probability for the evolution of new strains. Our data have shown high genetic conservatism for most phytoviral populations that favors modern hypothesis of evolution for plant RNA viruses. High relationship level between all Ukrainian isolates has been reveled, indicating their high homogeny (for all studied viruses except ACLSV). It was shown that the results of phylogenetic analysis are affected by the chosen method for construction of phylogenetic trees and mathematical model used. Also they are depend on section of viral genome selected for study, database used (complete presence of different strains in the databases), relationship of strains and isolates in study and sample size.

PP-005: Spread of some virus diseases among representatives of wild flora in Chernobyl region

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Chemical stress factors including heavy metals and radionuclides may induce a number of biologically significant phenomena in the course of plant virus infections. The development of virus infections in higher plants under effect of chronic radioactivity was shown to correlate with atypical visual symptoms of the disease and possibly genetic changes of virus genome. However speculative changes in the development and spread of virus diseases at the level of population remain unknown. In recent years serious attention has been paid to virus infections of wild plants because they may be the reservoirs for viruses and due to the potential of virus genetic changes invoked by continuous co-existence with atypical host. The aim of this work was to evaluate natural spread of virus diseases among wild plants growing under chronic effect of radioactivity of different intensities. TEM studies demonstrated occurrence of virus (or virus-like) particles of different morphology (rod-shaped, filamentous, spherical, bacilli-like, etc.) in 8 samples. Bioassay employing sap-inoculated *Nicotiana tabacum* cv. Samsun indicator plants showed virus-specific symptoms on plants inoculated with sap from 10 samples in forms of leaf mosaics and deformation, and enations. We should stress that TEM and bioassay outcomes here were nearly complimentary. Indirect ELISA carried out with TMV-specific polyclonal antisera confirmed TMV infection for 5 samples which is in agreement with previous results. The highest TMV content was noted for *Lupinus perennis* plants. However this plant species has not been registered as TMV host. PCR was conducted using primers to the genus *Tobamovirus*. Phylogenetic analysis of sequenced cDNA showed affiliation of isolated virus to TMV species. Hypothetically, TMV adaptation to *L. perennis* plants may have been favoured also by chronic effect of radioactivity (both on the plant and on the virus).

PP-006: Recombinant strains of Potato virus Y outcompete the ordinary strain in the United States potato crop to become predominant in most seed production areas

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The recombinant strains of PVY, $PVY^{N:O/NWi}$ and PVY^{NTN}, were first reported infecting the United States potato crop about a decade ago. Surveys conducted in the late 1900s did not identify these strains, although, diagnostic methods used at the time may have been inadequate to define all strain types. Over the past 8 years extensive surveys of the US seed potato crop have been conducted to determine the relative incidence and distribution of the various PVY strains. The ordinary strain, PVY^{O}, predominated in most seed production areas at the start of the surveys, but it is being displaced in almost all regions by the recombinant strains. Fortunately the tuber necrotic strain, PVY^{NTN}, still makes up a small proportion of the total recombinant population in all growing regions. Studies on U.S.-favored potato cultivars indicate that many express mild foliar symptoms when infected with recombinant strains in contrast to moderate to severe foliar symptoms when infected with the ordinary strain. Furthermore, the ordinary strain has a greater impact on tuber production and yield, relative to the recombinant strains and can be self-limiting in some cultivars. The recombinant strains are also transmitted more efficiently than the ordinary strain. These attributes increase the fitness of the recombinant strains and also help drive their selection by current seed certification and plant breeding schemes that are based on visual symptom assessments.

PP-007: Molecular characterization of a new badnavirus infecting enset (*Ensete ventricosum*: Musaceae) in Ethiopia

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Enset (*Ensete ventricosum* Cheesman) and banana (*Musa* spp.) are two related crops widely cultivated in Ethiopia on which virus-like diseases are commonly observed. Badnaviruses represent the main group of viruses infecting banana and related crops. To identify a virus with bacilliform particles associated with enset leaf streak disease, we used a rolling circle amplification strategy followed by using its product as template in a PCR with degenerated badnavirus primers. The sequence obtained was used to design an outward directed virus-specific primer pair which was used in an inverse long PCR which gave a product of ca. 6 kbp. The full length viral circular dsDNA genome so obtained from overlapping sequences has 7163 nucleotides encoding three ORFs with predicted proteins of 21.5 kDa, 14.5 kDa and 202.5 kDa arranged in a manner typical of badnaviruses. Sequence analysis showed that the virus is genetically most closely related to Sugarcane bacilliform Guadaloupe D virus recently reported from sugarcane with 73.6% overall nucleotide identity followed by *Banana streak Mysore virus* (60.5%). Based on current badnavirus species demarcation criteria, the virus is sufficiently distinct that it should be considered a new species for which the name Enset leaf streak virus (ELSV) is suggested. In addition to the full length genome, a circular DNA segment missing 1244 nt and thus appeared to be a defective badnavirs DNA has been described from the enset plant studied. ESLV was also detected in 6 out of 40 randomly collected enset samples using virus specific primers in PCR suggesting it is fairly widely distributed. On banana, the widespread occurrence of *Banana streak OL virus* is reported for the first time in Ethiopia on several samples but the new enset badnavirus (ESLV) was not detected. The results suggest that distinct badnavirus species naturally infect enset and banana crops in Ethiopia.

PP-008: Current status of occurrence and geographical distribution of cassava mosaic and cassava brown streak disease and associated viruses in Mozambique

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A study was conducted to establish the incidence, symptom severity and geographical distribution of cassava mosaic disease (CMD) and cassava brown streak disease (CBSD) in six major cassava producing provinces in Mozambique in May 2010. Two hundred and seventy four fields were assessed in: Cabo Delgado (33), Nampula (41), Zambezia (41), Inhambane (58), Maputo (27) and Gaza (74). Sampling was done along two diagonals across each field by scoring 30 plants per field for CMD and CBSD incidence, symptom severity and adult whitefly population. In addition, 115 CMD- and 150 CBSD-symptomatic leaf samples were collected for DNA and RNA analysis using PCR and RT-PCR, respectively. Results obtained indicate that CMD incidence was highest in Gaza (68.1%) and lowest in Nampula (6.3%) province. CMD symptoms were generally mild (2.8 to 3.3) in all six provinces. More than 50% of the surveyed fields had high CMD incidence (76-100%). CMD was mainly caused by use of cutting-infected planting material. Using virus specific primers, only 36% (42 out of 115) of the CMD-infected leaf samples were detected with CMBs and were positive for *East African cassava mosaic virus* (EACMV). None of the samples were positive for *African cassava mosaic virus* (ACMV) and mixed infections (ACMV+EACMV). Only 10 out of 150 samples were positive for CBSV. In contrast, CBSD incidence was highest in Zambezia (61.3%) and lowest in Cabo Delgado (23.6%). CBSD symptoms were generally low in all the three provinces with severity ranging between 2.4 and 2.8. CBSD incidence was highest in Zambezia province (76-100%). Adult whitefly population ranged from 0.02 - 4.7 per plant in the six provinces. Zambezia had the highest (4.7) population.

PP-009: Variability of Cassava Brown Streak Disease Symptoms in Tanzania

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Cassava brown streak disease (CBSD) has devastated African cassava growers particularly in the East African coasts for nearly a decade since was first reported in 1936. The disease caused by two distinct *Ipomoviruses*, the *Cassava brown streak virus* and *Ugandan cassava brown streak virus* both of the *Potyviridae* family. Viral infection of the susceptible plants usually leads to manifestation of foliar, stem and root symptoms. Hence, understanding the diversity of CBSD symptoms remain a vital component of diagnosis particularly in areas with lowly developed or limited access to laboratory technologies. The current study aimed at examining the current diversity of CBSD symptoms in field grown cassava. In an extensive survey covering 81 locations throughout Tanzania, four major types of foliar and three root symptoms associated with CBSD were identified. The newly described CBSD symptoms includes; spotty foliar chlorosis, water-mark lesion on senescent leaves, brown necrotic internal tissue at the base of the leaf petiole and chalky root necrosis in the roots. The study indicated that CBSD symptoms continue to evolve suggesting the need for continued update on the disease symptoms

PP-010: Molecular characterization of begomovirus associated with tomato and pepper in southern region of Oman

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Begomoviruses (family *Geminiviridae*) are associated with diseases of many plant species including tomatoes and peppers causing economic losses worldwide. In 2011 tomato and pepper crops showing symptoms reminiscent to begomovirus were collected from Dhofar, Southern Governorate of Oman. Following PCR-based detection of begomoviruses, multimeric viral genomes were amplified by rolling circle amplification (RCA) using plant genomic DNA as template, which were then cloned and sequenced. All begomovirus isolates from different wilayats of Dhofar Governorate infecting both pepper and tomato were closely related to each other with nucleotide sequence identity more than 97%. The similarity analysis revealed them to be the strains of ChLCV-Multan sharing >92% identity. The viral genome was found to be typical of monopartite begomovirus encoding six ORFs, two in sense and four in antisense directions. Biological indexing of ChLCV-OM was conducted using agro-inoculation test on *Nicotiana benthamiana,* which resulted in severe symptoms. Phylogenetically ChCLV (oman isolate) clustered closely with ChCLV-Multan and ChLCV-Narwan and showed maximum nt identity of 92% with ChCLV-Multan followed by 91% with ChLCV-Narwan. Repeated attempts to clone any other begomovirus from these samples could not be successful. These results indicate that ChLCV-OM is the dominant begomovirus species on tomato and pepper crops, in southern region of Oman.

PP-011: Affect of virus infection on seed yams

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Yam (*Dioscorea* spp.) is an important food crop grown for its edible tubers in West Africa. The crop is propagated vegetatively using whole or sliced portions of tubers. This study was conducted to assess the affects of viruses over successive cycles of yam propagation. Field trials were organized using two improved varieties, TDa 05/00129 and TDr 89/02665, and popular landraces, Gbakunmo, Elemsu and Orin in Kwara State, and Makakusa, Dan-anachia and Army in Federal Capital Territory (FCT) Abuja, in the Guinea savanna agro ecologies of Nigeria. Trials were conducted in RBCD design in 30 sq. m plots for three years (2010 to 2012). Seed yams procured from researchers and farmers were used for trials in 2010. Seed yams harvested from these trials were used for planting in 2011 season and harvest from this crop was used for planting in 2012 season. Seed yams were treated with chemicals to protect from fungal pathogens, insect and nematode pests. Seed yams and germinated plants were tested for *Yam mosaic virus* (YMV), *Yam mild mosaic virus* (YMMV), *Dioscorea* badnavirus (DBV) and *Cucumber mosaic virus* (CMV). Germination percent varied from 66% to 97%. Sequential use of infected seed yam tubers decreased germination rate in some cultivars. Cultivar Orin showed maximum decline (up to 90% reduction in germination) compared to TDa 05/00129-1 which was least affected. Virus incidence increased over the three generations possibly because of use of infected tubers. There was no change in mean symptom severity score measured on 1 to 5 scale (1 = no symptoms and 5 = severe mosaic symptoms). Reduction in total yield per plot observed was due to poor germination but average yield per plant was unaffected. However, control trials were not organized due to unavailability of virus-free seed yams. Nonetheless, data from this study provides empirical evidence for progressive degeneration of virus infected seed yam stocks.

PP-012: Expansion of *Banana bunchy top virus* pandemic into West Africa

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Banana bunchy top disease (BBTD) caused by the *Banana bunchy top virus* (BBTV) was first reported from sub-Saharan Africa (SSA) from Democratic Republic of Congo (DRC) in the 1950s. BBTD occurrence since then was reported in 11 countries in central and southern Africa (Angola, Burundi, Cameroon, Central African Republic, Congo Republic, DRC, Equatorial Guinea, Gabon, Malawi, Rwanda and Zambia). The disease is known to be widely prevalent in Central African countries and Malawi in Southern Africa; whereas its distribution is limited to a few production zones in Angola, Cameroon and Zambia. Until very recently, *Cucumber mosaic virus* and *Banana streak virus* were the only viruses reported to occur in *Musa* spp in West Africa. In 2011, an outbreak of BBTD was reported in Dangbo District, Ouémé Region, in the southeastern part of the Republic of Benin. BBTD incidence was over 90% in the affected communities. The BBTD-affected regions in the Republic of Benin border with Ogun State in south-western part of the Nigeria. Investigations in 2012 at 31 locations in Ogun State confirmed spread of BBTV into Nigeria. Analysis of the nucleotide sequences of DNA-S and DNA-R segments indicate that BBTV isolates in Benin and Nigeria are genetically identical to 'South Pacific' phylogroup and they formed a unique clade along with other BBTV isolates from SSA. Prior to this finding, BBTD occurrence in southern Cameroon, close to Gabon border, was the western most frontier of BBTV in SSA. Current situation suggests that virus-infected planting materials as most likely source of virus spread into West Africa. The few infected plants mostly likely served as sources for further virus spread by the banana aphid, *Pentalonia nigronervosa* – the vector of BBTV wide spread in all the banana production zones in Africa, and also through local exchange of planting materials between farmers, leading to the first BBTV epidemic in West Africa. Delimitation surveys in Benin and Nigeria are necessary to assess the extent of spread. The current situation in West Africa underscores need for creating greater awareness about the diseases and strict implementation of phytosanitary measures, including restrictions on the movement of planting material from disease-affected regions, to prevent further spread of this disease. Efforts are also necessary to produce and supply virus-free planting materials to rehabilitate banana production in the affected regions, and prevent the use of infected planting material for banana propagation.

PP-013: Distribution and diversity of viruses infecting soybean in Nigeria

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Nigeria ranks 1 in soybean production in Africa. Several virus diseases were reported to infect soybean in Nigeria, but knowledge on their incidence and distribution is not know. This survey was therefore conducted to determine the incidence and distribution of soybean-infecting viruses in all the 15 major soybean producing states in five agroecologies in Nigeria. Random sampling procedure was used for surveys in 235 farmers' fields in two successive cropping seasons. Leaf samples collected were tested for viruses known to infect soybean by ELISA and PCR. Fifteen viruses were detected in soybean samples. Virus incidence was highest (85%) in Benue state and least in Kogi state (30%). *Cowpea mild mottle virus* (42.9%; 31.7%), *Soybean mosaic virus* (23.8%; 14.4%), *Blackeye cowpea mosaic virus* (9.0%; 23.1%), *Bean pod mottle virus* (1.5%; 18.4%), *Cucumber mosaic virus* (10.1%; 7.1%) and *Cowpea aphid-borne mosaic virus* (10.1%; 3.3%) were most frequently detected viruses. Mixed infections were detected in >60% of the samples. *Cowpea severe mosaic virus*, *Tobacco streak virus* and *East African cassava mosaic virus* were detected in several samples. This finding was the first report of the occurrence of these thee viruses in soybean in Nigeria. Partial nucleotide sequence of select isolates revealed 98-100% identity within the species, but less than 90% with nucleotide sequences of corresponding species reported from outside Africa. Alternative hosts, particularly weeds and wild legumes, and seed-borne viruses seems to play a major role in recurrent virus infections in soybean.

PP-014: The epidemiology of a complex virus pathosystem in a perennial fruit crop

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Grapevine leafroll disease (GLRD) is one of the most important biotic constraints to the production of grapes worldwide. GLRD produces contrasting symptoms in red- and white-fruited wine grape cultivars of *Vitis vinifera*. In red-fruited cultivars, symptomatic leaves show 'green' veins and inter-veinal reddening. In white-fruited cultivars, GLRD symptoms consist of mild yellowing, rather than reddening, of leaves. GLRD affects plant vigor and longevity and impact fruit yield and berry quality. A survey of vineyards in Washington State indicated the presence of *Grapevine leafroll-associated virus 1* (GLRaV-1), GLRaV-2, GLRaV-3, GLRaV-4, GLRaV-5, and GLRaV-9 and their genetic variants in several own-rooted wine grape cultivars showing GLRD symptoms. In addition, seven grapevine viruses (*Grapevine rupestris stem pitting-associated virus*, *Grapevine virus A*, *Grapevine virus B*, *Grapevine virus E*, *Grapevine fanleaf virus*, *Grapevine fleck virus* and *Grapevine Syrah Virus 1*) and four viroids (*Australian grapevine viroid*, *Hop stunt viroid*, and *Grapevine yellow speckle viroid-1* and *-2*) were detected in some wine grape cultivars exhibiting GLRD symptoms as mixed infections with GLRaVs. However, GLRaV-3 was found to be the most widespread and predominant among the viruses and viroids documented in Washington vineyards. Data on spatial distribution of GLRD showed clustering of infected vines along rows in vineyard blocks planted with different cultivars indicating secondary spread between neighboring vines within rows. Studies on spatio-temporal spread of GLRD indicated spread of the disease from heavily infested older blocks to neighboring healthy, young plantings. Grape mealybug *(Pseudococcus maritimus* Ehrhorn, Pseudococcidae) is the only species documented in Washington vineyards and it was shown to transmit GLRaV-3. The status of European fruit lecanium scale (*Parthenolecanium corni*, Coccidae), present in Washington vineyards, as a vector of GLRaVs is not known. The epidemiologically relevant data is being used to develop guidelines for the management of GLRD in grower vineyards.

PP-015: Molecular variability in the coat protein gene of the different isolates of *Apple mosaic virus*

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Sequences of the capsid protein (CP) gene of 24 ApMV isolates from different asymptomatic hop varieties and geographic locations were determined and analysed. The identities of the CPs of ApMV isolates from hops to all available ApMV isolates showed remarkably low variation ranging from 0% up to 4.8% and 4.2% at the nucleotide and amino acid level, respectively. Phylogenetic analysis indicated two branches, branch 1 containing ApMV isolates from Czech hybrid varieties and branch 2 including 21 remaining virus isolates. Each of the putative subclusters of branch 2 included isolates from both within and from outside of Europe, thus, sequence analysis showed that CP gene was highly conserved irrespective of geographic origin. Comparison of the analysed putative CPs among ApMV isolates from hop and further species showed also extensive conservation (>95.5% identity) irrespective of the hosts (*Prunus persica, P. armeniaca, Sambucus nigra* and *Coryllus avellana*). Nevertheless, when the previously published data of ApMV isolates were included, the situation has significantly changed. A comparison of complete CP nucleotide and deduced amino acid sequences showed identity ranging from as low as 85.7 % and 81.1 %, respectively. ApMV strains could be classified into three subgroups in both nucleotide and amino acid levels: subgroup I with ApMV isolated from almond tree, subgroup II with pome fruit isolates together with one cherry isolate and subgroup III with all remaining isolates from hop, European elder, mountain ash, hazelnut, peach, apricot, prune and mahaleb cherry.

PP-016: Influence of modifications of Potato virus X coat protein (XCP) on its expression and systemic movement

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Our results confirmed that N-terminal modifications of XCP do not influence the viral life cycle, whereas the simple C-terminal XCP fusion impedes the viral replication. We designed several C-terminally modified XCP chimeras and tested their viabilities in various *Nicotiana benthamiana* genotypes. Our results showed the negative impact of 3´-terminal modification of XCP on the chimera´s life cycle. To ensure chimeric constructs stability, the second copy of the last 60 nucleotides of XCP followed by the 3´-untranslated region was added downstream of the recombinant sequence. Simultaneously, the first copy of the last 60 nucleotides of XCP was mutated in order to prevent recombination between the two identical sequences. The movement protein of *Tobacco mosaic virus* expressed in transgenic *N. benthamiana* plants positively affected the cell-to-cell spread of C-terminally modified XCP chimeras. Further, we proposed the production of heterologous peptides situated in four different loops connecting α-helices and β-strands which are assumed to be located on the exterior part of XCP particles. We studied the conditions leading to the highest expression and stability of transiently expressed heterologous proteins and simultaneously we evaluated the effect on virus systemic movement. As a host system we used nontransgenic and transgenic *N. benthamiana* plants. As a model peptide we chose the immunodominant *Human papillomavirus* type 16 (HPV16) E7 epitope (aa 44-60) in fusion with His tag to screen the yields and immunological properties of expressed proteins. We hope that our research concerning the properties of the PVX and its ability to express heterologous epitopes on XCP surface will be valuable for further biotechnological use of this virus.

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PP-017: Epidemiology of cassava mosaic disease in the Bukavu, Kisangani and Gandajika region of Democratic Republic of Congo

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In DR Congo, cassava (*Manihot esculenta* Crantz) is both a source of food and income for about 70% of the population. However, cassava is severely affected by cassava mosaic disease (CMD). To manage the viral disease, various strategies such as the use of healthy cuttings and resistance varieties have been suggested to farmers. Unfortunately and despite such strategies, in many provinces of DR Congo, the level of CMD pressure is alarming. In this paper, we report the results of epidemiological surveys conducted with the aim to evaluate the CMD pressure in relationship with the different ecosystems where cassava crop was planted. A total of 566 farmers' fields were investigated in Bukavu, Yangambi and Gandajika region, respectively, for the cassava varieties, disease severity and incidence, as well as infestation and abundance of *B. tabaci* whiteflies. The presence of CMD-associated begomoviruses was assessed by ELISA and with PCR followed by sequencing. The targeted areas offer a wide range of altitude, climate and soil in this region variation within DR Congo, covering different agroecosystems like the evergreen forest, mixed secondary forest, the savannah areas and intensive agricultural areas around the dwellings. In general, CMD pressures remained weak in high altitude and evergreen forest, and moderate in savannah region while it become more marked in low altitude and in secondary forest. Molecular analysis did not reveal a high diversity of cassava begomoviruses species in the areas investigated but indicated spatial repartitions. The widespread occurrence of both *African cassava mosaic virus* and *East African cassava mosaic virus* in the investigated areas was also confirmed.

PP-018: Development of transgenic sweet potato (*Ipomea batatas* (L.) Lam.) with broad virus resistance in South Africa

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Sweetpotato (*Ipomoea batatas*(L.)Lam.) is an important crop for food security. Given that the plant is vegetatively propagated, pathogens such as viruses accumulate to levels where they become a major limiting factor toproduction wherever the crop is grown. A survey to determine the occurrence and distribution of viruses infecting sweetpotato was conducted in major growing areas in the province of KwaZulu-Natal (KZN), in South AfricaThe survey revealed that sweet potato feathery mottle virus (SPFMV), sweet potato chlorotic stunt virus (SPCSV), sweet potato mild mottle virus (SPMMV), and sweet potato virus G (SPVG), occuring singly or in combination, were the most prevalent viruses infecting sweet potato in KZN. In order to address the problem of the multiplicity and synergism of sweet potato viruses in KZN, this study aimed to develop transgenic sweetpotato cv. Blesbok plants with broad virus resistance. Untranslatable coat protein gene segments of SPFMV,SPCSV,SPVGand SPMMVin a sense orientation were fused to a silencer DNA, the middle half of the nucleocapsid gene of Tomato spotted wilt virus, and used as a chimeric construct to develop transgenic sweetpotato with multiple virus resistance. in. The construct was introduced into apical meristen explants by *Agrobacterium*-mediated transformation. A total of 24 putative transgenic plants were produced.Polymerase chain reaction and Southern blot analyses confirmed that the chimeric construct was incorporated into the genomic DNA of six of the 24 putative transgenic plantsand that all plants were derived from the same transgenic event. The six transgenic sweet potato plants were challenged by graft inoculation with virus infected *Ipomoea setosa* Ker. Although virus presence was detected using NCM-ELISA, all transgenic plants displayed delayed and milder symptomsin the lower leaves when compared to the untransformed control plants. These results lay the foundation for sustainable control of virus diseases in sweetpotato.

PP-019: Does potato virus S infection compromise late blight resistance in potato? Epidemiological implications

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Potato (*Solanum tuberosum*) is one of the most important crops grown in Washington State. In 2011, Washington growers raised 160,000 acres of potatoes with an average yield of 61,500 lb per acre, 9.8 billion lb total, with a farm gate value of over $734 million. Late blight, caused by *Phytophthora infestans*, is an extremely devastating disease of potato worldwide. Defender is the only cultivar with foliar and tuber resistance to this disease in the U.S. However, under field conditions this cultivar exhibits high susceptibility to infection by *Potato virus S* (PVS, family *Betaflexiviridae*, genus *Carlavirus*). This phenotype was reproduced under controlled conditions and tuber/seed transmission was demonstrated. Moreover, PVS infection resulted in similar severe symptoms in late blight resistant (LBR) breeding line LBR4106 (A95053-61). To better understand this phenomenon and to characterize PVS at biological and molecular levels, the complete nucleotide sequence of the PVS isolates from cvs Defender and LBR4106 were determined. *Nicotiana occidentalis*-37B was recognized as a good biological indicator for identifying severe phenotypes of PVS. Host response studies of PVS were done by screening LBR breeding lines, selected commercial cultivars, and the pedigree of LBR breeding lines. Results indicated LBR potatoes appear to be susceptible to PVS infection. To further investigate the potential interactions between these two pathogens and the resulting response, detached leaves of Defender and Ranger Russet were inoculated with *P. infestans* and/or PVS. The amount of sporulation and the extent of lesion expansion were measured to estimate the severity of late blight. The incidence of late blight increased with PVS infection in Defender suggesting potential interaction between PVS and Defender impacting the late blight resistance. Genetic diversity studies of PVS were carried out by analysis PVS isolates on a world-wide basis.

PP-020: Endogenous plant pararetroviral sequences in natural and managed ecosystems: epidemiology and evolution

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The central mountain ranges of Mexico are home to the greatest diversity for genus *Dahlia*. First described in 1791, the genus has 35 recognized wild species in addition to the cultivated forms, known as either *D. pinnata* or *D. variabilis*. Majority of these wild dahlia species were found in the Mexican mountain ranges. Two distinct caulimoviruses, *Dahlia mosaic virus* (DMV), and *Dahlia common mosaic virus* (DCMV), and an endogenous plant pararetroviral sequence (DvEPRS, formerly known as DMV-D10) were reported to be associated with dahlia mosaic, a serious disease affecting cultivated dahlia (*D. variabilis*). To better understand the incidence of these pararetroviruses, selected wild *Dahlia* species in their natural habitats from west - central Mexico were tested for the three caulimoviruses. Virus species-specific primers and PCR were used followed by cloning and sequencing of the amplicons. Results showed that the wild dahlia species in their natural habitat contained DMV-D10. Viral sequences were found in 91% of the samples (n=56) representing four different wild species. Genetic diversity studies were performed using a dataset of 7 full-length EPRSs isolated from cultivated and wild *Dahlia* spp. Assessment of all open reading frames (ORFs) using phylogenomic and population genetics approaches showed that genetic diversity of EPRSs occurring in dahlia is very diverse. Phylogenetic analyses showed that EPRSs formed one clade, indicating a lack of clustering by geographical origin and no divergence due to source (cultivated vs. wild). Population genetic analyses found negative selection for all ORFs, with the replicase region more variable than other ORFs. Recombination events were found and provided evolutionary evidence for genetic diversity. The discovery of plant pararetroviruses in wild dahlia species in their natural habitats suggests a possible emergence, co-existence and co-evolution of pararetroviruses and their host plants.

PP-021: Influence of host type and insect pests on incidence, severity and spread of viral diseases on passion fruit in Uganda

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A number of questions on the role of insect vectors in transmission of viral diseases on passion fruit in Uganda remain unanswered. In the absence of host resistance the usefulness of clean planting material is being considered in disease management. Temporal and spatial spread of viral diseases on passion fruit was investigated using three passion fruit types: *Passiflora flavicarpa* (yellow), *Passiflora edulis* (purple) and *Passiflora maliformis (*hard shell) in a field trial set up at the National Crops Resources Research Institute in Uganda from 2009B to 2012B. No significant differences were recorded in incidence and severity of viral diseases among the passion fruit types. The rate of disease spread was twice as fast in the yellow (0.32 ±0.07 gompit/day), compared to the hard shell (0.15±0.03 gompit/day). Infection patterns highlighted the role of insect vectors in transmission. Four major types of insect pests were recorded: mites, thrips, whiteflies and aphids. There were significant differences among populations of all four insect pests recorded on the passion fruit types. Mites (24.5) and thrips (15.6) were the most abundant pests per plant. Colonization of passion fruit plants occurred early in the season at 7 and 35 days after transplanting (DAT), respectively. In contrast, aphids infested the crop later (77 DAT). Viral diseases significantly affected yield; more fruits were diseased in the hard shell (25%), compared with the purple (18.1%) and yellow (16.7%). Significant differences were registered in marketable fruit weights among the three passion fruit types. Fruit weights were reduced by 62.4% in purple, 58.7% in hard shell and 49.4% in yellow passion fruit. Results support aphids as transient vectors of viral diseases in passion fruit. Management strategies for viral diseases should therefore target pest exclusion from passion fruit fields. The response of passion fruit type to viral diseases highlights the importance of planting clean seedlings for delayed infection.

PP-022: Use of artificial microRNAs for engineering resistance against thrips-transmitted tospoviruses (*Tospovirus, Bunyaviridae*)

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MicroRNAs (miRNAs) are a highly conserved class of small non–coding RNAs, which are both highly specific and effective to achieve silencing of genes in a wide range of living organisms including animals, humans and plants. We are using artificial microRNAs (amiRNA) technology for introducing resistance to *Tomato spotted wilt virus* (TSWV), one of the most economically important virus threats to a wide range of crops in many arts of the world. Growing TSWV resistant varieties is the most cost-effective, sustainable and environmentally friendly approach for reducing its impact. Toward that goal, amiRNAs were developed targeting viral RNA sequences encoding the nucleocapsid protein (N) and the silencing suppressor (NSs) genes of TSWV. An *Arabidopsis thaliana* miR159 precursor was modified to express virus-specific amiRNAs. Transient expression of amiRNAs in *Nicotiana benthamiana* by agroinfiltration has confirmed expression of virus-specific amiRNAs by Northern blot analysis. The ability of the amiRNA constructs to confer resistance to TSWV has been confirmed in virus challenge experiments. Stable Arabidopsis and tobacco plants have been generated with selected constructs and challenge experiments of these plants with TSWV showed that the amiRNA constructs conferred resistance to TSWV infection. We are investigating various construct design features to improve the efficiency of expression of the mature amiRNAs that would provide effective resistance against tospoviruses.

PP-023: Climate change and *Banana bunchy top virus*: spread from the lowland Rusizi valley to surrounding higher altitudes in Burundi

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Banana is a major staple crop and represents the main source of income for small-scale farmers in Burundi, in addition it contributes to soil protection. Unfortunately, this crop is threatened by different biotic constraints that limit its potential production such as virus diseases. The banana bunchy top virus (BBTV) was reported for the first time in 1987 in the Rusizi valley in Burundi. Since then, the first comprehensive survey was conducted from September to October 2008. The results indicated that the disease and its vector, *Pentalonia nigronervosa*, were mainly present in regions located in three provinces namely Bujumbura-rural, Bururi and Cibitoke; with an average occurrence of 24% and 42%, respectively. Although the occurrence of *P. nigronervosa* was higher (40%) at lower altitudes such as in Cibitoke and Bururi; the aphid was equally found (25%) at higher altitude sites of Bujumbura Rural. A subsequent survey, spanning all 16 provinces of Burundi, was carried out in October 2012. This survey confirmed the on-going spread of BBTV across the country irrespective of altitudes. These results showed the expansion of BBTV into two new provinces including Bubanza (41,4%) and Makamba (12,9%) where BBTV was recently reported. The incidence of the disease also increased from 30% to 48,3% in Cibitoke and from 14 to 20% in Bururi and remained stable in Bujumbura rural (26 to 25,8%). BBTV spread is known to be caused by the exchange of banana suckers between farmers across different regions and virus transmission through the aphid vector that is associated to banana plantations. Quarantine regulations and integrated cropping practices (ICP) aimed at reducing aphid populations should be encouraged in the context of small-scale farmers in Burundi.

PP-024: Molecular characterization of begomoviruses and associated satellites that infect vegetable crops in Southwestern Cameroon

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Begomoviruses are plant-infecting viruses, which are transmitted by the whitefly vector *Bemisia tabaci*. They have a genome of single-stranded DNA that consists of either a single (monopartite) or two components (bipartite) with a component size of approximately 2.8 kb. Many monopartite begomoviruses in the Old World have been found to be associated with betasatellite and alphasatellite molecules, which are about half the size of their helper begomovirus genome. Betasatellites have been shown to be necessary for inducing severe disease symptoms. In Cameroon, *B*. *tabaci* has been associated with suspected begomovirus infections in many crop and weed species. Despite their growing importance, only begomoviruses infecting cassava have been studied in Cameroon in any detail. Thus, there was a need for additional information on diversity and distribution of begomoviruses and satellites in vegetable crops and dictyledonous weeds, which likely serve as virus reservoirs. Sequencing of viral genomes showed that the okra plants were infected by viruses of two previously known begomovirus species (*Cotton leaf curl Gezira virus* and *Okra yellow crinkle virus*) as well as a new recombinant begomovirus species (Okra leaf curl Cameroon virus). In addition, a betasatellite (*Cotton leaf curl Gezira betasatellite*) and two alphasatellites (Okra leaf curl Mali alphasatellite and Okra yellow crinkle Cameroon alphasatellite) were identified. Tomato plants with leaf curling were shown to contain isolates of a new begomovirus, Tomato leaf curl Cameroon virus, and an alphasatellite, Tomato leaf curl Cameroon alphasatellite (ToLCCMA). To study the potential begomovirus complexes infecting weeds, begomoviruses and satellites in plants of the weed *Ageratum conyzoides* with leaf curl symptoms were characterized. Sequence analyses showed that they were infected by isolates of a new begomovirus (Ageratum leaf curl Cameroon virus), two new betasatellites (Ageratum leaf curl Cameroon betasatellite and Ageratum leaf curl Buea betasatellite), an alphasatellite (ToLCCMA) and two types of defective recombinants between a begomovirus and ToLCCMA. Putative recombinations were detected in begomovirus genomes for all three plant species studied, indicating that recombination is an important mechanism for their evolution. A close relationship between the begomoviruses infecting tomato and *A*. *conyzoides*, and the detection of the same alphasatellite in them support the idea that weeds are important reservoirs for begomoviruses and their satellites. This study has revealed a huge complexity of begomoviruses and DNA satellites previously largely unknown in West and Central Africa. With this high diversity, recombination potential and transmission by *B*. *tabaci*, begomoviruses and their associated DNA satellites pose a serious threat to crop production in the region.

PP-025: Intergeneric recombination between a new, spinach-infecting curtovirus and a new geminiviral species in the proposed genus *Becurtovirus*: first New World exemplar

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A novel new, curtovirus species, *Spinach severe curly top virus* (SSCTV), was associated with symptomatic spinach plants collected from a commercial field in south-central Arizona during 2009. In addition, a second viral molecule of about 2.9 kb was amplified, cloned and sequenced from the same spinach plants. The latter isolate, herein named Spinach curly top Arizona virus (SCTAV), was found to share 77% pairwise sequence identity with *Beet curly top Iran virus* (BCTIV), a leafhopper-transmitted geminivirus, placed in the newly erected genus, *Becurtovirus*. The SCTAV genome encodes three viral sense genes V1, V2, and V3, and two complementary sense genes C1 and C2. No C3 or C4 ORFs were present in the genome sequence. The genome organization of SCTAV is not like extant New World curtoviruses, but instead is most similar to that of BCTIV, to date known only from Iran. Consistent with the latter observation is that SCTAV and BCTIV both contain the same unique nonanucleotide, TAAGATT/CC, and a replication associated protein, Rep (or C1) that is more closely related to mastrevirus Rep, than to other curtoviruses reported to date. Both SSCTV and SCTAV were found to have a recombinant genome containing derived SCTV (AY548948) ancestral sequences in the virion sense portions of the genome. Tobacco *Nicotiana benthamiana* (Domin) plants inoculated with the cloned genome of each spinach isolate, respectively, 90% of the plants inoculated with SCTAV developed severe curling symptoms, whereas, only 20% of the SSCTV-inoculated plants were infected, developing only mild curling symptom. When plants were co-inoculated with both viruses, the frequency of infection remained higher for SCTAV than for SSCTV (80% vs 20%), indicating no evidence of synergistic effects between the two viruses with respect to efficiency of infection.

PP-026: Mapping the regional epidemiology of cassava viruses in east and central Africa

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Cassava viruses are the most important constraint to cassava production in East and Central Africa. In 2007, a major multi-partner programme, co-ordinated by Catholic Relief Services (CRS) and known as the Great Lakes Cassava Initiative (GLCI), was launched with the aim of tackling cassava disease threats. At the outset, regular monitoring and surveillance of cassava viruses were identified as important components of the overall disease management approach. Consequently, international and national research partners in each of the six target countries (Burundi, Democratic Republic of Congo, Kenya, Rwanda, Tanzania and Uganda) conducted extensive surveys in each of three years: 2009, 2010 and 2011. By assessing both young (3-6 month old) and mature (> 10 months old) cassava crops, these surveys were able to characterize all of the major pest and disease constraints, but most importantly, both the foliar and tuberous root damage caused by cassava brown streak disease (CBSD). The two virus diseases – cassava mosaic disease (CMD) and CBSD – were determined to be the most important constraints in all countries assessed. An overall decline in incidence of CMD was associated with a concomitant increase in the proportion of CMD-resistant varieties being cultivated. By contrast, the pattern of change of CBSD was more mixed, with reductions from 2009-2011 in eastern and northern Tanzania and most of western Kenya, but increases in Uganda, Burundi and eastern DRC. Areas of increase mainly corresponded to parts of the region affected by CBSD for the first time. Priority indeces were developed for both CMD and CBSD to identify districts/regions most immediately threatened by the impacts of these diseases. In addition to their value as tools for the prioritization of research for development efforts, the diverse set of maps generated has also contributed significantly to improving understanding of the epidemiology of cassava viruses and to guiding the quality management process for improved planting material dissemination programmes. The > 150 maps generated are available to interested parties for free download via the IITA website.

PP-027: *Lettuce big-vein associated virus* is the causal agent of a syndrome of necrotic rings and spots in lettuce

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Lettuce big-vein associated virus (LBVaV, genus *Varicosavirus*) was shown to be responsible for characteristic necrotic symptoms observed in combination with big-vein symptoms in lettuce breeding lines when tested for their susceptibility to Lettuce big-vein disease (BVD) using viruliferous*Olpidiumvirulentus* spores in a nutrient film technique (NFT) system. Lettuce plants showing BVD are generally infected by two viruses: *Mirafiori lettuce big-vein virus* (MiLBVV, genus *Ophiovirus*) and LBVaV. New mechanical inoculation methods were developed to separate the two viruses from each other and to transfer both viruses to indicator plants and lettuce. After mechanical inoculation onto lettuce plants MiLBVV induced vein-band chlorosis, which is the characteristic symptom of BVD. LBVaV caused a syndrome of necrotic spots and rings which was also observed earlier in lettuce plants inoculated on the NFT system, resembling symptoms described for Lettuce ring necrosis disease (RND). This observation is in contrast with the general thought that LBVaV only causes latent infections in lettuce. *De novo* next generation sequencing demonstrated that LBVaV was the only pathogen present in a mechanically inoculated and symptomatic lettuce plant, providing evidence that LBVaV was the causal agent of the observed necrotic syndrome and thus fulfilling Kochs postulates for this virus. We will refer to the necrotic syndrome caused by LBVaV in lettuce as LBVaV-associated necrosis (LAN).

PP-028: Exploiting the combination of natural and genetically engineered resistance to viruses impacting cassava production in Africa: Production of transgenic cassava with broad-spectrum CMD and CBSD resistance

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We have previously demonstrated that cassava mosaic disease (CMD) resistance can be engineered in transgenic cassava by expression of hairpin-RNAs targeting viral sequences. Here we report on the production of transgenic cassava resistant to both viral species associated with cassava brown streak disease (CBSD), namely *cassava brown streak virus*(CBSV) and *Ugandan cassava brown streak virus* (UCBSV). Transgenic cassava lines expressing hairpin RNAs homologous to conserved regions of the CBSV and UCBSV genomes were generated using the cassava TMS60444 model genotype for genetic transformation. Virus resistance was evaluated using the stringent top grafting method to confirm that transgenic lines had stable resistance against both CBSV and UCBSV in multiple experiments with increasing viral loads. In order to establish both CBSD and CMD resistance in farmer- and consumer-preferred cassava, we have subsequently applied our technology to the TME7 genotype that has natural resistance to CMD. All transgenic TME lines showed resistance when inoculated with CBSV and UCBSV. Co-inoculation with geminiviruses did not alter the engineered CBSV resistance. Our work demonstrates that CMD and CBSD resistances can be combined to produce virus-resistant farmer- and consumer-preferred cassava.

PP-029: Epidemiological studies of tomato yellow leaf curl disease in Greece and Cyprus

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Tomato yellow leaf curl disease (TYLCD) is one of the most important viral diseases of tomato crops worldwide. In the eastern Mediterranean basin *Tomato yellow leaf curl virus* (TYLCV) and *Tomato yellow leaf curl Sardinia virus* (TYLCSV) are currently involved to TYLCD epidemics. During 2006-2011, an extensive survey was conducted in Greece and Cyprus to investigate the epidemiology and characterization of the virus species and the whitefly vectors involved in TYLCD. Approximately 7000 samples of symptomatic tomato plants and 4500 weeds, as well as 3000 *B. tabaci* individuals were collected and analyzed. Transmission efficiency of TYLCV and TYLCSV was evaluated using four *B. tabaci* colonies harboring different bacterial endosymbionts. Results showed that TYLCV was the most prevalent *Begomovirus* species (94.5%) in Greece, whereas TYLCSV was found only in 5.5% of the samples tested. In Cyprus, TYLCV was the only species found to be associated with TYLCD. Molecular identification of *B. tabaci* biotypes showed that Q was the only one found in the mainland of Greece, Peloponnese and the island of Crete. In Cyprus and the Greek islands located in the eastern Mediterranean, both B and Q biotypes co-exist and they are involved in TYLCD spread. Forty nine weed species belonging to 15 botanical families were found to be naturally infected with TYLCV. Transmission studies showed that TYLCV isolates had a broader host range as well as higher transmission efficiency than TYLCSV. Moreover, TYLCV transmission efficiency to tomato plants was positively correlated with the presence of the endosymbiont *Hamiltonella* sp. Finally, transmission assays from infected weeds and other cultivated plants onto tomato, showed that these alternative hosts could serve as important virus reservoirs, contributing significantly to disease outbreaks.

PP-030: Cassava brown streak disease: the expanding pandemic

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Since the early 2000s the attention of many agricultural researchers in East and Central Africa has been focused on combating Cassava Brown Streak Disease (CBSD). Although the disease was first reported as far back as the 1930s, it was largely confined to coastal East Africa. Following the first report of significant spread in mid-altitude (>1000 masl) areas of Uganda in 2007, there have been a series of subsequent 'new reports' of its occurrence in western Kenya, north-western Tanzania, Burundi, Rwanda and eastern Democratic Republic of Congo (DRC). The two species of CBSVs: *Cassava Brown Streak Virus* (CBSV) and *Ugandan Cassava Brown Streak Virus* (UCBSV) have been recorded in the endemic coastal areas of Kenya, Tanzania and Mozambique as well as in Uganda and north-western Tanzania. More recently, we have demonstrated the co-occurrence of these two species in south-western Tanzania and in western Kenya. Contrastingly, new reports from Rwanda, Burundi and eastern DRC demonstrate the occurrence of only UCBSV. The molecular diversity of UCBSV isolates has been examined, using short (*ca*200-300nt) CP sequences in an attempt to determine the epidemiological characteristics of CBSD spread through the Great Lakes region. Two distinct and very homogeneous phylogenetic clades of UCBSV were observed in Rwanda, one of which was identical to a Ugandan UCBSV sequence. By contrast, sequences from both Burundi and eastern DRC were more variable and showed no direct affinity with Ugandan or Rwandan UCBSVs. These results suggest that both transmission mechanisms (via planting material and via the whitefly vector) are likely to be important in the on-going spread of the CBSD pandemic, and that the original source(s) of this region's UCBSV isolates cannot be definitively deduced. Currently, there are no reported occurrences of cassava brown streak viruses in non-*Manihot* hosts. Further and more extensive sequencing work is likely to provide clearer answers about the long and short-term evolutionary history of UCBSV and its strains.Additionally, field-based epidemiology studies will be important for improving understanding of both the local and regional spread of CBSD. New knowledge gained from both molecular and field-based studies of cassava brown streak viruses will be vital for developing effective management strategies.

PP-031: Recent emergency of CBSD threatens cassava production in Tanzania

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Cassava brown streak virus disease (CBSD) has been recognized in Tanzania since the 1930s. Previous studies indicated that CBSD was limited to low altitude areas along the Indian Ocean coast from Tanga to Mtwara and Zanzibar. Recent studies have revealed significant changes in the distribution of CBSD in Tanzania, which pose a great threat to cassava production, food security and income due to the losses caused by the disease, which can be as high as 70–100%. Field surveys were conducted in Tanzania from 2004 to 2011 in the Lake Zone of the north-west and the coastal lowlands to assess the level of CBSD spread in farmers' fields. Cassava fields of three to six months and more than nine months of age were sampled and assessed for the incidence and severity of CBSD symptoms on leaves and roots. The results obtained differed from one year to the next and between areas. The results indicated that in the Lake Zone, the average CBSD foliar incidence was 0.1% in 2006. This incidence increased sharply to 23.7% in 2009 and 39.8% the following year, although the value declined in 2011 to 23.4%. In the coastal lowlands, CBSD foliar incidences ranged from 8.4% in 2004 to 46.5% in 2009 survey, 44.6% in 2010 and 29.8% in 2011. Mean CBSD shoot severity values ranged from 2.7 in 2006, to 2.8 in 2010. By contrast, in the Lake Zone, average foliar symptom severity was 2.1 for all years. Root symptom incidence increased significantly in the Lake Zone (9.3% in 2009 to 28.9% in 2011) as well as in the coastal region (14.4% in 2009 to 28.9% in 2011). Although fluctuations are apparent in incidence and severity values obtained from annual surveys of CBSD, there is a clear general trend towards an increased prevalence of CBSD in Tanzania. Most notable has been the new appearance and continuing geographic spread of CBSD in north-western Tanzania. This highlights the need for concerted efforts to improve the control of CBSD in the country. These efforts should involve various stakeholders at the different levels of the cassava value chain.

PP-032: Molecular and biological characterization of a new pathotype of *Pepino mosaic virus*

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Pepino mosaic virus is one of the most important pathogens infecting greenhouse tomato crops worldwide. The virus is known for its high level of genetic and biological variability. Therefore, the characterization of a new PepMV pathotypes is important for understanding the process of disease emergence caused by this virus. In recent years new pathotypes of PepMV, causing severe yellowing symptoms, were found in Belgium and Poland. Unlike previously described PepMV isolates, the new pathotypes systemically infect *Solanum tuberosum* causing yellowing symptoms. A wide variety of tomato cultivars was inoculated and they all displayed the same severe, yellowing symptoms independent of environmental conditions. RNA sequence analyses revealed that the new pathotypes are grouped within the CH2 genotype. A specific point mutation, located in the coat protein gene, distinguished the yellowing isolates from previously described CH2 isolates. The point mutation results in an amino acid substation and alters the surface properties of the coat protein, as 3-dimensional modeling of the coat protein indicates that the altered amino acid is located on the surface of protein. It may suggest that these positions or this region of the protein play a role in virus infection by interaction with one or more host factors.

PP-033: Transient expression of *Pepino mosaic virus* TGB3 and CP genes in *Nicotiana benthamiana* and *Solanum lycopersicum*

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Triple gene block 3 (TGB3) and coat protein (CP) genes of *Pepino mosaic virus* (PepMV) were found to act as determinants in development of symptoms on infected plants. In order to perform gene expression two expression vectors were used. We aimed to express TGB3 and CP from necrotic (PepMV-P19) and mild (PepMV-P22) isolates. In the first step, viral expression system based on *in planta* assembly of functional viral vectors from separate pro-vector modules was used. The primers for cDNA of TGB3 and CP amplification contained gene-specific sequences, restriction sites for Sal I and Sac I enzymes and sequence encoding Xpress epitope (Invitrogen) that can be detected by the Anti-Xpress antibody. The pro-vectors were delivered to *Nicotiana benthamiana* and *Solanum lycopersicum* leaves using *Agrobacterium tumefaciens* (agroinfiltration). Construct encoding GFP was used as a control. Total protein was isolated using phenol extraction at 7 and 14 dpi. The western blot technique was performed using Anti-Xpress and viral CP specific antibodies. Positive results were obtained only with specific antibody against viral CP. In the second approach we aimed to develop another system to obtain higher expression of these two proteins. We used expression vector based on modified pCAMBIA construct (Cambia). In this approach cDNAs of analyzed genes were cloned within multi cloning site of the plasmid under control of 35S enhanced promoter of CaMV followed by omega leader sequence and NOS terminator. As previously, TGB3 and CP cDNAs were cloned into vector and used for agrobacterium transformation and agroinfiltration. The total plant protein was extracted using Nucleo Spin RNA/Protein (Aqua Lab) and western blot technique was performed with CP and Anti-Xpress antibodies. The positive results with CP gene expression indicated that in both cases the level of gene expression was efficient. The production of TGB3 specific antibody is further step in our research.

PP-034: RNA silencing suppressor encoded by DNA-β satellite associated with Calendula officinalis yellow vein Lakshmangarh virus

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Calendula officinalis is a short-lived aromatic herbaceous perennial ornamental plant which is widely cultivated in Indian gardens and can be grown easily in sunny locations in most kinds of soils. Begomovirus-associated symptoms such as yellowing of leaf veins was observed on several ornamental plants of *C. officinalis* growing in the gardens of Lakshmangarh, Rajasthan (India). Begomovirus infectivity was confirmed using universal primers of coat protein region designed for DNA-A component (GenBank Acc. No. JN998443). DNA-β (GenBank Acc. No. JQ693147) was also detected using β satellite universal primers. A 650 nucleotides fragment corresponding to the DNA-β of Calendula officinalis yellow vein Lakshmangarh virus (CoYVLV) was cloned in sense and anti-sense orientation with short introns. Primers were designed to amplify the full length DNA-β C1 region. The BamHI (5´-ATGGATCCACCACACAGACACCTTCAAAGG-3´) and XbaI (5´-GTATTCTAGATCTCTGTGAACTATATCTTCT-3´) restriction site was introduced in upstream and downstream for sense orientation and Xho I (5´-GTATCTCGAGTCTGTG AACTA TATCTTCT-3´ and Nco I (TAAAAACCATGGAGACACCTTCAAACGACAAC-3´) as antisense orientation. The resulted amplicon were cloned in the pCambia 1300. The resulting binary construct was introduced into *Agrobacterium tumefaciens* LBA4404 by electroporation with a Gene Pulser apparatus (Bio-Rad). Seeds of T1 lines were grown on MS and two weeks old seedlings were infected with the infectious clones of CoYVLV using Bio-Rad particle delivery system. The siRNA isolation and analysis was performed. The DNA probe used for siRNA northern hybridization corresponds to the Nonanucleotide sequence within the CoYVLV. *Nicotiana benthamiana* plants were transformed by *Agrobacteium*-mediated gene transfer and were tested for siRNA expression. CoYVLV infected transgenic lines showed small RNAs of approximate sizes, 23 nt higher expression intensities. Results show that this β gene encodes virulence factor and suppresses host defense system. Our results of sense-antisense orientation derived from DNA-β confer immunity to the virus.

PP-035: Virus checks for safe exchange of cassava germplasm for crop improvement and food security

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Cassava mosaic begomoviruses and cassava brown streak ipomoviruses are responsible for cassava mosaic disease, (CMD) and cassava browns steak disease (CBSD) respectively. In sub-Saharan Africa they pose a major risk to international and domestic exchange of cassava (*Manihot esculenta*) germplasm for breeding or propagation material production programs. The IITA Genetic Resources Center (GRC), in collaboration with the Germplasm Health Unit and the Cassava Breeding Unit, has established a procedure for conservation and distribution of cassava germplasm (botanic seeds, in vitro plants and other propagation materials) free of the viruses responsible for CMD and CBSD. Over the past 40 years IITA GRC conserved 3499 accessions of cassava in a field bank in Ibadan (Nigeria), about 80% (2787 accessions) of which has been duplicated in the medium term in vitro (slow growth) bank. In addition, 761 improved cassava lines developed by the cassava breeding programs are also conserved in medium term in vitro storage. Cassava germplasm was introduced or reintroduced into the in vitro system following a procedure that combines heat-treatment, regeneration through meristem culture and virus indexing and selection of materials that are negative to viruses responsible for CMD and CBSD. Virus-tested germplasm is distributed to partners and stakeholders following an internationally accepted phytosanitary procedures aimed at reducing the risk of pest and pathogen spread through the propagation material. Since March 2010, in vitro plantlets of 287 accessions of improved cassava varieties were supplied to partners in 11 countries (Nigeria, Tanzania, Zambia, Malawi, DRC, Swaziland, Switzerland, Uganda, USA, Cameroon and Kenya). Information on cassava germplasm accessions and the procedure to acquire germplasm from IITA is available at http://genebank.iita.org/.

PP-036: Viruses of sweetpotato in Israel and their control

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Sweepotatoes were introduced to Israel in 1920 and grown mainly in home gardens. In the early 1950's the crop was expanded with new cultivars. Yields started to be high with more than 60 t/ha but later declined to 15 t/ha due to virus diseases. Renewed research in the 1990s led to the identification of the main viruses and the development of a scheme to provide growers with virus-tested planting material. The following viruses were identified: *Sweet potato feathery mottle virus* (SPFMV); *Sweet potato sunken virus* Genus *Crinivirus* (SPSVV) [Possible synonym: *Sweet potato chlorotic stunt virus* (SPCSV)]. *Cucumber mosaic virus* (CMV) causes stunting, chlorosis and yellowing. Infection by CMV was dependent on the presence SPSVV. It is interesting to note that CMV was not reported from Kenya or Tanzania though SPCSV-Kenya is widespread there. Apparently SPSVV and SPCSV-Kenya differ also in their ability to facilitate replication or translocation of some CMV strains in sweetpotato. This scheme when rigorously applied resulted during 2000-2008 in yields of 45-60 t/ha. After that yields declined. The relationship between SPSVV and other criniviruses affecting sweetpotato and the scheme for supplying growers with virus tested planting materials will be discussed. Possible reasons for yield decline, in addition to farmers using non-certified planting material, will also be discussed.

PP-037: On the effect of acid rains on pink hydrangea

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Acid rains rich in sulphuric acid can greatly affect changes in plants. They provide a medium favourable for the development of new diseases which can lead to the annihilation of the species. By eliminating the cause, i.e. by treating the earth with the base we neutralize the secondary acidity, and make it possible for the plant to develop normally. I have demonstrated with the "pozegaca plumtree" that "sarka" plum pox potyvirus can be prevented. The domestic red rose "rose centifolia" yields again lovely, fragrant flowers with abundant leaves. I have supported this theory also with pink hydrangea, i.e. the effect of the acid rains on the change of the colour in the hydrangea, as well as return to its natural colour. In the town of Tuzla (Bosnia and Herzegovina) (44º32´23''N; 18º40'24'' E) the thermoelectric generation power plant has been in operation for over 50 years. In the close vicinity of the power plant on Husino hydrangea has changed its pink colour to blue. On the locality Slatina and Brdo cca 5 km away from the power plant to the east the hydrangea changes its colour so that its flowers are both blue and pink on the same bush. At the same location, i.e. Brdo in my yard where I treated the ground with the base the hydrangea continues to be pink. This is the proof that plants can be healed, and that their natural qualities can be returned to them.

PP-038: Characterization of elite sweet potato genotypes for sweet potato virus disease (SPVD) resistance and high dry matter content in Tanzania

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Sweet potato genotypes with high dry matter content and resistant to sweet potato virus disease (SPVD) were characterized using four simple sequence repeat (SSR) markers. The germplasm included 20 genotypes identified as having high dry matter content and 25 accessions tolerant to SPVD in a study conducted in Tanzania in 2008. The total number of alleles within the 57 genotypes across 4 loci was 395, with an average of 4 alleles per locus. The unweighted pair group method with arithmetic mean (UPGMA) and analysis of molecular variance (AMOVA) using generated SSR data, grouped the 57 genotypes into two major clusters, with mean pair-wise genetic distance of 0.55. No specific grouping was observed in relation to SPVD resistance, dry matter content and geographic location. The four microsatellites markers distinguished the 57 Tanzanian sweet potato genotypes into two major clusters. The relatively high level of genetic diversity indicates broad genetic base for sweet potato breeding in Tanzania. The results obtained demonstrate the efficiency of SSR marker technique for the assessment of genetic relationships and distinguishing between Tanzanian sweet potato genotypes. The findings of this of this study provide valuable information to breeders to facilitate cost effective germplasm conservation and development of improved sweet potato varieties resistant to SPVD and containing high dry matter.

PP-039: Genetic resistance and gene action of maize germplasm to *Maize streak virus*

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Maize streak virus (MSV, genus *Mastrevirus*, family *Geminiviridae*) transmitted by leafhoppers (*Cicadulina* spp.) can cause severe yield losses in susceptible maize (*Zea mays* L.) varieties. MSV is endemic in all the maize producing regions in sub-Saharan Africa (SSA). Use of maize lines and hybrids with appreciable levels of MSV tolerance remains the most effective and reliable control option. Knowledge of resistance background and mode of gene action is critical for breeding MSV-tolerant varieties. Two hundred and fifty maize inbred lines and their F_1 hybrids derived from the cross with MSV–tolerant inbred Tzi3 were arranged in alpha lattice design with two replications under screenhouse and field conditions, respectively. At 2 to 3 leaf stage seedlings were inoculated using viruliferous leafhoppers (*Cicadulina triangula*). Disease severity (scale 1 – 5; 1 means <10 % of leaf area covered with streak symptoms; 5 implies >75 % of leaf area covered with streaks) and yield components were recorded. Resistance classes were based on Area Under the Disease Progress Curve (AUPDC) determined by plotting the data on disease severity over time. Twenty seven (10.8%), 49 (19.6%) and 53 (21.2%) lines were highly resistant, resistant and moderately resistant, respectively. Amongst the hybrids, 28 were highly resistant, whereas 45 (18%) each were resistant and moderately resistant. The highest grain (6 t/ha) and cob yield (5.6 t/ha) were recorded in the highly resistant (Plot 1445 × Tzi3) and resistant hybrids (Plot 1452 × Tzi3), respectively. Cob weight per plant (257.9 g), grain weight per plant (173.6 g), and kernel number per plant (578) were highest in the moderately resistant hybrids (Plot 1381 × Tzi3). Resistance was polygenically inherited and under the influence of both dominant and recessive genes. Simple recurrent selection would facilitate maize breeding for MSV resistance in SSA.

PP-040: Molecular characterization of integrated DNA molecules associated with cassava mosaic disease in East Africa

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Cassava mosaic disease (CMD) caused by cassava mosaic begomoviruses affect cassava in the major cassava growing areas in East Africa. The disease is associated with DNA molecules (DNA-II and DNA-III) which contribute to CMD symptom enhancement. They have been shown to break resistance in TME3 and increase cassava begomovirus accumulation in susceptible cassava varieties and *Nicotiana benthamiana* plants. DNA-II and DNA-III are integrated into cassava genome. These DNAs were isolated from cassava plants expressing unusual CMD symptoms in East Africa countries and were investigated using the polymerase chain reaction and DNA sequencing. DNA-II and DNA-III sequences resembled published sequences of cassava begomovirus associated satDNAII and satDNAIII. The diversity of these DNA molecules was investigated using pairwise sequence comparison. Generally, there was little genetic divergence as the sequences were 88% - 100% identical to each other. This study revealed that both DNA-II and DNA-III are widely distributed in the major cassava growing areas in Tanzania and other East Africa countries.

PP-041: The mode of transmission of *Rice yellow mottle virus*

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The investigation on the mode of transmission of *Rice yellow mottle virus* (RYMV, genus *Sobemovirus*) was carried out in the screen house and field in Cote d'Ivoire between 1995 and 1997. The study was based on visual assessment utilizing Standard Evaluation Scale (SES) for rice and enzyme-linked immunosorbent assay (ELISA) of leaves, other organs and components of rice plants. RYMV was detected in the husk/hull of rice seed but was not transmitted through rice seeds. However, it was transmitted through plant debris and empty spikelets from infected rice plants. The virus was also transmitted when rice roots from infected plants became intertwined with non-infected plants, leaf contact from closely spaced plants, rice stubble and hands contaminated with the virus. Ratooning of the rice roots increased the incidence of RYMV. The beetles, *Trichispa sericea* Guerin*, Chaetocnema pulla* Chapuis*, Chnootriba similis* Thunberg (*Epillachna similis* Mulsant) and a long horned grasshopper (*Conocephalus lonipennis* de Haan) transmitted the virus. *Trichispa sericea* and *C. similis* transmitted it in a semi-persistent manner, while *C. pulla* transmitted it in a persistent manner. The virus was not however transmitted by any of the nematodes screened. *Oryza sativa, O. glaberrima* and *O. barthi* were identified as systemic hosts while *O. longistaminata, Echinochloa crus-pavonis, E. pyramidalis* and *E. ciliaris* were found as local lesion hosts. The virus did not infect the dicotyledonous plants, cultivated cereals and other grasses screened thereby confirming that RYMV has a narrow host range.

PP-042: Aphids infesting potato in Kenya

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Aphid-transmitted viruses probably cause greater economic loss in potato production than all other insect-related damage. Some 40 virus species are known to infect potato, and of these, 13 are aphid-transmitted. Monitoring of aphid populations in potato fields is therefore essential to determine areas with low aphid occurrence suitable for potato seed production and the right moments for haulm destruction. While plenty of information on such areas is available in traditional seed potato producing countries of America and Europe, there is none available for Kenya. The current study determined the best locations for seed potato multiplication in Kenya by monitoring aphids in major potato producing areas using two methods: yellow water traps and aphid-leaf counts. Ten aphid species, *Aphis gossypii* (Glover), *Aphis fabae* (Scopoli), *Aulacorthum solani* (Kaltenbach), *Acyrthosiphon pisum* (Koch), *Brevicoryne brassicae* L., *Cavariella aegopodii* (Scopoli), *Macrosiphum euphorbiae* (Thomas), *Myzus persicae* (Sulzer), *M. ascalonicus* (Doncaster), *Rhopalosiphum maidis* (Fitch) were caught in YWTs while four aphid species, *A. fabae*, *A. gossypii*, *M. persicae* and *M. euphorbiae* were also found colonising potato leaves in Kenya. The populations of the aphid species varied significantly, *R. maidis* had the greatest numbers, followed by *B. brassicae*, *A. gossypii*, *M. euphorbiae*, *M. persicae*, *A. fabae* in this order while *A. solani* was the least abundant. The populations of *A. fabae*, *A. solani*, *C. aegopodii* and *M. ascalonicus* did not vary between seasons and sites but *A. gossypii*, *A. pisum*, *B. brassicae*, *M. euphorbiae*, *M. persicae* and *R. maidis* populations varied significantly between the five sites, and between the three seasons. Njabini and Nairobi consistently had low aphid numbers and may be the sites most suitable for potato seed multiplication.

PP-043: Cassava production enhancement in semi-arid and arid regions in Kenya

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Cassava (*Manihot esculenta*) is a perennial woody shrub of Euphorbiaceae family which is mainly grown in tropical and subtropical-marginal area. Cassava does well in high nutrient soils but can still do in low nutrient soils. Underground root storage can last for 24–36 months hence important in maintaining families in arid and semiarid areas. It's important as human food, animal feed, paper and textile binding agent. Africa produces about 54%. Its production is affected by diseases – CMD, CBSD, blight, anthracnose, root rot and pests – green mite, mealy bug and grasshopper. Production is also affected by poor variety selection by farmers, climatic factors, perishability, infrastructure and labor. KARI in conjunction with the Ministry of Agriculture is in support and production enhancement in arid and semiarid areas. Disease diagnostics has been deployed, TC cleaning of germplasm and giving out healthy planting materials. Work has been done in reduction of postharvest physiological deterioration by transformation. This has greatly improved cassava shelf life hence advantaged cassava marketing; transportation from farms to market. With the adoption of transformed varieties towards shelf life, CBSD and CMD, cassava production will increase two-fold. There is awareness creation of cassava germplasm for varied areas and the improved cultivars produced by KARI for CBSD/CMD resistance. Adoption of new varieties has increased within the region.

PP-044: Mechanisms underlying resistance to groundnut rosette virus complex and its vector(s) in Uganda

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Groundnut Rosette virus disease (GRVD) causes a significant reduction in yields of groundnut in Uganda and across sub-Sahara Africa (SSA). The disease is caused by a virus complex of three agents, Groundnut Rosette Virus (GRV), Satellite RNA (Sat-RNA) and Groundnut Assistor Virus (GRAV) luteovirus, transmitted in a persistent manner by the aphid vector (*Aphis craccivora*). Management practices and technologies (resistant varieties) developed to reduce the impact of the disease are currently not effective. The resistant groundnut varieties widely used by small holder farmers in Uganda are succumbing to GRVD. Knowledge on underlying resistance mechanisms of groundnut to GRVD and the aphid vector still remains a gap in breeding for durable disease resistance sought by breeders. This study was to determine the underlying resistance mechanisms of groundnut to GRVD and aphid vector(s) in groundnut varieties in Uganda. Fifteen groundnut varieties with reported resistance to GRVD were used in this study, two susceptible groundnut varieties (JL24 and Acholi white). Experiments were conducted in the field and screen house. Data on instars, nymph, winged and wingless aphids, adult aphid body scores and adult aphid numbers were determined at regular intervals. The study showed that, aphid preference differs significantly among the groundnut varieties. Resistant varieties are less preferred than susceptible varieties in choice tests. The mortality of aphids significantly varied among the groundnut varieties. High mortality of instars, nymph and adult aphids were recorded in resistant varieties than in susceptible varieties. It can then be concluded that, the low preference of resistant groundnut varieties are due to the expression of antixenosis; high mortality of the instars, nymphs and adult aphids are antibiosis response by the varieties. This information may then be used in breeding for multiple and durable resistance to manage groundnut rosette disease in Uganda.

PP-045: Evaluation of diverse oilseed *Brassica* germplasm from Australia, China and India to identify *Turnip mosaic virus* resistance phenotypes

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Among the *Brassica* oilseeds crops, *B. juncea* (Indian mustard) and *B. napus* (canola) have the highest economic value. *Turnip mosaic virus* (TuMV) causes one of the major diseases of *Brassica* oilseed crops worldwide. To identify useful TuMV resistance phenotypes, diverse *Brassica* oilseed germplasm lines from Australia, China and India [70 *B. napus* (Australia – 41 and China – 29) and 60 *B. juncea* (Australia -17, China -12 and India -31)] were evaluated by mechanical inoculation with infective sap containing an isolate of TuMV belonging to pathotype 8. Overall, plants within 93% of *B. napus* lines were resistant to systemic infection with TuMV. Three different phenotypes were found: localised hypersensitivity, R_N, was the commonest (43%), especially among the Australian lines. Extreme resistance, O, occurred less frequently (26%), but was commonest within Chinese lines. None of the lines exhibited resistance to systemic movement without necrosis, phenotype R, alone. Plants in 31% of lines segregated for two phenotypes [R_N and O (17), R_N and R (2), and R and O (1)]. The remaining two lines segregated for all three phenotypes (R, O and R_N). With *B. juncea* lines, 7 different phenotypes were obtained: +, susceptible; $R_{N/+}$, systemic infection with necrosis limited to inoculated leaves; $+_N$, systemic infection with some necrosis; $+_{ND,}$ systemic hypersensitivity; $R_{N/st/+,}$ a severe variant of $R_{N/+}$; $+_N^1$, a mild variant of $+_N$; and $+_{St}$, a severe variant of +. Twenty lines developed uniform reactions belonging to only one phenotype: + (2), $R_{N/+}$ (7), $+_N$ (10) and $R_{N/st/+}$ (1), 31 lines developed two different phenotypes, and the remaining nine developed three different phenotypes. Phenotype $+_{ND}$ was commoner with Chinese than Australian or Indian *B. juncea* lines. Of the resistance phenotypes found, O in *B. napus* and $+_{ND}$ in *B. juncea* held the greatest promise for use in breeding oilseed *Brassica* for TuMV resistance.

PP-046: Two genotypes of sub-Saharan Africa 1 *Bemisia tabaci* (Gennadius) (Hemiptera: Aleyrodidae) associated with cassava in East Africa exhibit distinct biological differences in fecundity and development

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A study was conducted to determine the number of eggs laid and development of two genotypes of sub-Saharan Africa 1 (SSA1) *Bemisia tabaci* associated with cassava in East Africa on healthy and CMBs-infected (ACMV & EACMV) plants under screenhouse conditions at Mikocheni Agricultural Research Institute (MARI), Dar es salaam, Tanzania in 2011/12. The two genotypes: subclade I and II of SSA1were obtained from Lake Victoria Basin (LVB) and Coast Region (CR), respectively, in Tanzania, and their colonies established at MARI. Single female adults of each genotype of 1-5 days old were allowed to feed and oviposit on the healthy and CMBs-infected cassava for 3 days. LVB genotypes performed significantly ($P<0.05$) better than CR genotypes in mean number of eggs laid, developing instars and hatched adults on all the treatments in both the first and repeat trials. LVB and CR genotypes produced: 33.52 and 23.59 (eggs), 27.02 and 16.74 (1^{st} instars), 24.44 and 14.66 (2^{nd} & 3^{rd} instars), 23.83 and 13.62 (4^{th} instars), and 22.29 and 13.13 (hatched adults), and 30.94 & 23.63 (eggs), 22.40 & 17.32 (1^{st} instars), 19.91 and 15.21 (2^{nd} & 3^{rd} instars), 19.11 and 14.12 (4^{th} instars) and 18.05 and 13.55 (hatched adults) in the first and repeat trials, respectively. Interestingly, the number of eggs laid, developing instars and hatched adults did not differ significantly on healthy and CMBs-infected cassava in both the first and repeat trials in our study. Mortality (K_T) was highest on EACMV-infected cassava in the first (13.61) and repeat (16.22) trials for the LVB genotypes. In contrast, the highest mortality (K_T) occurred on the ACMV-infected plants for the first (13.34) and repeat (13.70) trials for the CR genotypes. Generally, healthy cassava plants had the highest percentage survival compared to the CMBs-infected for both LVB and CR genotypes. The results obtained in our study clearly show that the LVB and CR genotypes differ in their biology (fecundity and development). Secondly, there was no apparent boost in whitefly numbers by the CMBs-infected plants. On the contrary, it is the healthy cassava that supported consistently the most whitefly populations.

PP-047: Demonstration of long-term retention of potyviruses within *Myzus persica*e using nested RT-PCR: implications for transmission of non-persistent plant viruses

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Viruses within the genus *Potyvirus* are transmitted by vector aphids nonpersistently by a mechanism that is thought to involve short acquisition and retention times. The present study challenges the concept that these viruses are only retained within the aphid vector for short periods. Using an ultrasensitive nested polymerase chain reaction technique (N-RT-PCR), RNA of potato virus Y (PVY) was detected in individual *Myzus persicae* for up to 14 days after they were given access to virus and then transferred daily to healthy plants. Virus RNA was detected in different parts of dissected aphids including the stylet, head and body. Similarly, RNA of potato virus A (PVA) and a non-transmissible strain of PVY (PVY^C) were detected in aphids for up to 7 days following initial acquisition. However, PVA was detected in a smaller proportion of aphids than PVY. The N-RT-PCR technique was shown to detect virus at the attogram level and was approximately 100 times more sensitive than RT-PCR. To our knowledge, detection of PVA and transmissible and non-transmissible strains of PVY in aphids for 7 to 14 days is a novel finding. These results should stimulate a reassessment of the molecular mechanisms of uptake and retention of potyviruses and the determinants involved in aphid transmission of this important group of viruses. Importantly, this finding has relevance for the application of molecular diagnostic tools for forecasting aphid transmission to field-grown potato plants.

PP-048: Assessment of seed-transmitted viruses in wild *Vigna*

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Several viruses are known to be seed-transmitted in cowpea (*Vigna unguiculata*) and its wild relatives (*Vigna* spp.). In this study, antigen coated plate enzyme-linked immunosorbent assay (ACP-ELISA) was used to test for viral infections in 201 leaf samples regenerated from seeds of wild *Vigna* plants obtained from different locations of Nigeria. Cocktail of antibodies against different legume viruses such as *Blackeye cowpea mosaic virus* (BlCMV*), Cowpea aphid-borne mosaic virus* (CABMV), *Cucumber mosaic virus* (CMV), *Cowpea mottle virus* (CPMoV), *Bean pod mottle virus* (BPMV), *Cowpea mosaic virus* (CPMV), *Southern bean mosaic virus* (SBMV) and *Cowpea mild mottle virus* (CPMMV). Twenty samples (9.9%) were tested positive to one or more of the viruses but confirmatory test using each antisera detected virus in 70.0% (14) of the samples; whilst 30.0% (6) were negative. Many of the virus infected plants were asymptomatic. Single virus infection was detected in 57.1% of the samples. Of the eight viruses tested, CMV, CPMMV and BPMV were not detected in any of the samples.

PP-49: Molecular analysis of the complete genome of Hungarian *Potato virus S* isolate and the mapping of its of its genetic relationships.

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The Hungarian *Potato virus S* isolate (PVS HU) was found to be 8485 bp in length containing 6 open reading frames (ORF). It was classified in the PVS^{O}-1 genotype group of the PVS^{O} strain. The analysis of the whole genome revealed the closest relationship with two American sequences, with which the isolate exhibited 92.63% and 92.74% homology. These sequences were also found to be closest to the Hungarian isolate phylogenetically. The PVS HU isolate exhibited 92.31% homology with the isolate Leona, 89.39% with Vltava and only 78.61% with a Brazilian isolate, representing a difference of 1828 nucleotides in terms of the whole genome. At the nucleotide level, PVS HU was more than 95% homologous for 5' UTR with European and North American isolates, but this figure was only 91.95% for the Brazilian isolate. With respect to ORF1 the degree of homology was extremely low (76.9%) for the Brazilian isolate, but around 90% for the European and North American isolates. In the ORF2 region the Hungarian isolate only had over 90% similarity to Leona, among the European isolates, and in the case of ORF3 to ORF6 the homology with Vltava was as low as that observed for the Brazilian isolate, suggesting the occurrence of recombination events. Recombination analysis was performed using the complete genomes available in the NCBI database. When the Brazilian isolate was omitted from the analysis, the Hungarian isolate was found to take part in the recombination of the ORF1 region of Leona and Vltava isolates.

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PP-050: Identifying cassava resistant varieties and resistance genes for cassava brown streak disease

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The aim of this study was to identify the natural sources of resistance to cassava brown streak viruses (CBSVs) that cassava brown streak disease (CBSD) using conventional as well as next generation sequencing technologies. Three cassava varieties; Kaleso (resistant to CBSD), Kiroba (tolerant) and Albert (susceptible) were used in the study. Upon inoculation with CBSVs, Kaleso was resistant to the disease and expressed mild symptoms on leaves but had no symptoms on the root. Kiroba was tolerant as it expressed severe leaf and mild root symptoms, while Albert was susceptible with severe symptoms both on leaf and root. Quantitative Real-time PCR was used to estimate virus concentrations in all three varieties which revealed that varieties less affected by CBSD such as Kaleso supported much lower concentrations of CBSVs, in comparison with severely affected Albert. Reduced levels of infection and reduced virus titres in Kaleso are both characteristics of resistance. To uncover the genetic basis of resistance, we used Illumina RNA-sequencing to identify genes differentially expressed in Kaleso, but remain unchanged in control and virus-infected Albert treatments. More than 700 genes were identified that were selectively induced in Kaleso in response to CBSV infection, which included defence-related genes, transcription factors, RNA silencing as well as gene belonging to defence signalling pathways. Differentially expressed genes identified in this study have great potential to improve our understanding of CBSV resistance mechanisms in cassava, but may also be deployed to accelerate CBSV resistance breeding using marker assisted selection.

PP-051: Exploiting reversion and tissue culture techniques for eliminating cassava brown streak viruses from infected cassava plants

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Three cassava varieties differing in levels of resistance; Kaleso (resistant to CBSD), Kiroba (tolerant) and Albert (susceptible) were used to investigate the effect of reversion, tissue culture technique as well as thermo and chemotherapies (Ribavirin) to eliminate infection by cassava brown streak viruses (CBSVs) in them. Heat treatment of plants grown from tissue culture at 30 °C and 35 °C had the maximum effect in which up to 49% virus-free plants was obtained for the resistant and tolerant varieties and 27% for the susceptible variety Albert. Treatment with ribavirin had positive and identical effect on all three varieties in which up to 38% virus-free plants were obtained. The combination of chemo and thermo therapies had the highest effect on the susceptible variety Albert that resulted in the production of up to 35% virus-free plants while the effect on Kaleso (50%) and Kiroba (44%) although was good but less significant. In addition to these artificial therapies, the natural ability of cassava to free itself from virus infection (reversion) was investigated by planting infected stem cuttings of three varieties. Results indicated that cuttings of 15 cm length are ideal size for the maximum exploitation of reversion as up to 37%, 20% and 17% virus-free plants were obtained from Kaleso, Kiroba and Albert, respectively. Exploiting reversion and tissue culture therapies augers well for eliminating CBSVs from elite cassava lines and it can also be a means for CBSD management.

PP-052: *Barley yellow dwarf virus* species PAV and PAS: a comparative analysis of resistance traits

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Barley yellow dwarf virus (BYDV) is one of the most widespread and damaging viral diseases of cereal crops and grasses worldwide. The BYDV species vary strongly in their symptom expression, aphid vector transmission efficiency, host preferences and in their serological and molecular properties. Three BYDV species, PAS, PAV and MAV have been identified so far in the Czech Republic. The species PAS was the most frequently occurring BYDV in cereal crops as well as in grasses. This study was focused on the analysis of resistance traits in wheat and barley to two frequently distributed BYDV species PAS and PAV. The resistance traits were analysed in field experiments and the level of resistance was evaluated by analysing the virus titre using Syber green I based real-time RT-qPCR. Significant differences were found between BYDV species in all tested traits. The virus titre of PAS was greater than that of PAV in all tested varieties of barley and wheat. BYDV-PAV resulted in a greater reduction of plant height and grain weight per spike. High levels of resistance were recorded in winter barley breeding lines (Wbon-116, Wbon-123) and cultivars (Wysor, Doria) containing the resistant *Yd*2 gene to both PAV and PAS. The winter wheat breeding line PSR 3628 (a hybrid of wheat and couch grass) was highly resistant to both tested BYDV species. A significant and positive correlation between symptoms scores (VSS), reduction in plant height and reduction in grain weight per spike was detected. The correlation between infections with BYDV-PAS and BYDV-PAV was especially tight for symptom scores ($r = 0.83$, $P < 0.001$ and 0.91, $P < 0.001$, respectively), but also highly significant for reductions of grain weight per spike and plant height (r ranging from 0.54, $P < 0.01$ to 0.87, $P < 0.001$).

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PP-053: Stability of resistance in transgenic HoneySweet plum to *Plum pox virus* strain Rec

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Plum pox virus (PPV) is one of the most devastating diseases of *Prunus* species. Since few sources of resistance to PPV have been identified, transgene-based resistance offers a complementary approach to developing PPV-resistant stone fruit cultivars. HoneySweet (C5), a transgenic clone of *Prunus domestica* L., containing the PPV coat protein (CP) gene, has been described as highly resistant to the virus. The resistance in C5 to PPV is associated with PTGS and the siRNAs duplex (21–22 nt and 25–26 nt), controlling the specificity of viral RNA silencing in a homology-dependent manner. In our study, a high and permanent infection pressure of PPV-Rec was provided by bud grafting of inoculum in the field trial of C5 plants. Stability of resistance was evaluated by symptoms observation and a relative quantification of virus titre by real-time RT-qPCR in both non-transgenic rootstock (St. Juien) and transgenic C5 scions. In a seven-year-long evaluation (2005-2011) it showed that the PPV titre in C5 remained very low, whereas, in the non-silenced rootstock (St. Julien) the virus concentration was increasing gradually over the tested period (about 1000 fold higher than in C5). Severe yellow spots and rings in leaves were recorded in the non-transgenic rootstock, St. Julien, in contrast to very mild diffuse spots in few leaves of silenced C5 scions. Hence, C5 plants maintained high level of resistance to PPV-Rec over the seven years period after graft inoculation by susceptible St. Julian rootstock in field conditions. The C5 plants became virus free over the time in the field conditions due to the active systematic silencing. Our results show that C5 plants may become virus infected by grafting at a low level and the active silencing confers the resistance to PPV even in a high and continual inoculum pressure in this woody perennial.

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PP-054: Dispersal of TSWV and antipredator behaviour of *Frankliniella occidentalis* in presence of natural enemies

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Natural enemies might induce antipredator behaviour, thus enhancing vector dispersal and virus spread. Predators inducing strong antipredator behaviour promote higher transmission efficiency of a non-persistently transmitted virus than less disturbing predators. The effect of biological control on transmission efficiency could also be affected by the mode of transmission of the virus, since different acquisition and inoculation periods are required to transmit them. We studied the antipredator behaviour of *Frankliniella occidentalis*, main vector of *Tomato spotted wilt virus* (TSWV), in presence of two predators commonly used as biological control agents of thrips: the predatory bug *Orius laevigatus* and the predatory mite *Amblyseius swirskii,* and a predator not feeding normally on thrips, the aphidophagous syrphid fly *Sphaerophoria rueppellii*. Since feeding behaviour of female and male adult thrips are different and affected by the viruliferous state of the insect, we compared antipredator behaviour of female and male adults, as well as of viruliferous and non-viruliferous thrips. Behaviour observations were performed under the stereoscope and recorded with the program Etholog. In a semi-field study, dispersal of thrips towards receptor plants and transmission efficiency of TSWV by thrips in presence and absence of predators was compared. Transmission of TSWV was measured 25 days post inoculation as the number of infected receptor plants divided by the number of total receptor plants. Preliminary results indicate that thrips displayed antipredator behaviour less frequently in front of syrphid larvae than in presence of predatory mites or *O. laevigatus*. Defense rate of viruliferous and nonviruliferous thrips was similar, and it was higher in female that in male thrips. The implications of our results on the epidemiology of TSWV are discussed within the context of a multi-predator system and a plant virus transmitted in a persistent propagative manner.

PP-055: Behavioral events associated to the inoculation of a phloem-restricted semipersistent aphid-transmitted virus

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Most of the knowledge on the behavioural events associated to the transmission of aphid-borne viruses transmitted in a semipersistent manner is restricted to *Cauliflower mosaic virus* that is not a phloem-restricted virus. However, there is hardly any information about the transmission mechanism of phloem restricted semi-persistent aphid-transmitted viruses. For a better understanding of these transmission mechanisms, we studied the stylet activities associated to the inoculation of *Citrus tristeza closterovirus* (CTV) by its aphid vector, *Aphis gossypii* Glover to alemow (*Citrus macrophylla* Wester) test plants. The Electrical penetration graph (EPG) technique was used to assess aphid feeding behavioural events during the inoculation phase of CTV. Aphids were fed on CTV (T-397 isolate) infected Mexican lime plants during 36 hours. Then, aphids were placed on the alemow test plants where different treatments were recorded to analyse the inoculation process: an intercellular penetration prior to any intracelular stylet puncture (pd), one pd, five or more pds, complete sieve element salivation phase (E1) and committed phloem ingestion phase (E2). After the inoculation treatments, each aphid was analysed by real-time RT-PCR to assess its status (either CTV-viruliferous or non-viruliferous). Inoculation rates obtained under each treatment were evaluated by tissue print-ELISA and by real-time RT-PCR,5 months after the experiments. No transmission was obtained when CTV-viruliferous aphids penetrated plant cells prior to the phloem salivation phase (E1). However, our preliminary results show that CTV inoculation is likely associated to stylet contacts with phloem sieve elements (E1 and E2 waveforms) during the inoculation probes in receptor plants. The possible behavioural events associated to the inoculation process of the virus will be discussed in order to elucidate the mechanism and the likely location of the specific cuticular binding sites involved in the transmission process of CTV.

PP-056: Enhancing cassava productivity through host plant resistance breeding against cassava mosaic disease and cassava brown streak disease using genetic engineering and marker assisted selection - a Kenyan project

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Cassava (*Manihot esculenta* Crantz) is an important food crop for more than 800 million people worldwide and is second to maize in importance in coastal, central and western regions of Kenya. In the warm-humid regions, the major constraints to cassava production are cassava mosaic disease (CMD) and cassava brown streak disease (CBSD) which may cause over 90% yield loss. Farmers in the region attain yields of 6-8 t ha^{-1} compared with the potential of 80 t ha^{-1}. CBSD also affects root quality by causing necrosis which renders roots unfit for food, feed and industrial purposes. Host plant resistance is the most practical way of managing CMD and CBSD. Local approaches to improve cassava has mainly focused on conventional breeding that is less efficient and time consuming especially because of the heterozygous nature of the cassava genome hence the objective of the project is to apply targeted plant breeding using genetic engineering of RNA_i of respective coat proteins and marker assisted selection techniques to develop tolerant varieties. Coat proteins of the cassava mosaic virus (CMV) and cassava brown streak virus (CBSV), that have been reported to play a significant role in viral pathogenicity and will be targeted for gene silencing. Sources of resistance to CMD and CBSD have already been identified in the region and will be used in the development of tolerant varieties. Molecular markers for CMD are available, while those for CBSD will be validated and developed. The project is funded by the East African Agricultural Productivity Project (EAAPP) for three years. High-yielding transgenic locally adapted cassava with host plant resistance will be released for commercial production in concert with the national agricultural research systems (NARS). Release of commercial conventional varieties will be fast tracked using marker assisted selection.

PP-057: The spreading and movement of *Wheat dwarf virus* in its leafhopper vector (*Psammotettix alienus* Dahlb.)

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Wheat dwarf virus (WDV) is transmitted as a persistent and non-propagative manner by its leafhopper vector (*Psammotettix alienus* Dahlb.). There are fewer studies about the interaction between WDV and its leafhopper vector. In this study, immune-fluorescence confocal laser scanning microscopy (iCLSM) and transmission electron microscopy (TEM) were used to understanding the distribution and movement of WDV in its leafhopper vector. Following a 5-min acquisition access period (AAP) on diseased wheat plants and different inoculation period (IP) on healthy wheat plants, the digestive system and salivary glands were dissected, and then observed by iCLSM and TEM. The results showed two pathways of WDV movement in its leafhopper vector: (1) through the filter chamber to the salivary glands via hemocoel, and (2) through the anterior and middle midgut to the salivary glands via hemocoel. WDV could spread to the salivary glands at a short time after AAP in the first pathway in which could last only several hours. For pathway II, the spreading time of WDV from anterior and middle midgut to the salivary glands was occurred later than pathway I, but it could last for long time (several days to 2 weeks). When recombinant WDV capsid protein and nonstructural protein REP and REPA incubated with the alimentary canal of leafhopper, only recombinant capsid protein was retained. Same result was obtained by the serological infectivity neutralization (SIN) experiments. It is suggested that the capsid protein of WDV is a key factor for WDV retention in digestive system of leafhopper.

PP-058: Facets of *Tomato spotted wilt virus* transmission by tobacco thrips, *Frankliniella fusca*

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Tomato spotted wilt virus (family *Bunyaviridae*; genus *Tospovirus*) continues to threaten peanut, tomato, and pepper production in southeastern United States. Losses induced by this virus have exceeded$200 million. *Tomato spotted wilt virus* (TSWV) is exclusively transmitted by thrips in a persistent and propagative manner. The tobacco thrips, *Frankliniella fusca* (Hinds), is arguably the most important vector species in our farmscapes. Here, we will attempt to explain the various factors that contribute to its vector competence. First, akin to the virus, *F. fusca* exhibits a high degree of polyphagy without compromising its fitness. Our results indicated that besides crop hosts *F. fusca* can efficiently colonize non-crop hosts and competently acquire and transmit TSWV to and from them, the transmission efficiency ranged from 10% to 80%. Host colonization might be crucial, as TSWV transmitting thrips acquire TSWV only as larvae. Detailed studies conducted to assess the transmission parameters indicated that individual thrips could transmit the virus with just 15-min. inoculation access period. Such a scenario makes it difficult to break the epidemiological cycle. Second, the effect of TSWV-resistant genotypes on thrips fitness, virus acquisition, and transmission were qualitatively and quantitatively characterized. Results indicated that the genotypes differentially affected thrips fitness. However, western blotting and qRT-PCR assessments indicated that TSWV acquisition and transmission were only modestly affected. Third, TSWV infection of *F. fusca* positively and negatively impacted its reproductive fitness. Positive and negative effects included increased oviposition and reduced survival, respectively. These responses seem to be due to direct effects of the virus on thrips and indirect effects mediated by plants. Analysis of biochemical compounds of hosts, particularly amino acids, by ion-exchange chromatography provided evidence for the same. The interactions between TSWV and *F. fusca* seem to be mutualistic to a certain magnitude, and facilitate TSWV transmission and spread.

PP-059: The population genetic structure of North Carolina populations of *Thrips tabaci* and its implications for competency of *T. tabaci* to transmit *Tomato spotted wilt virus*

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Knowledge of population-level genetic differences can help explain variation among populations of insect vectors in their role in the epidemiology of specific viruses. Variation in competency to transmit *Tomato spotted wilt virus* (TSWV) that exists among populations of *Thrips tabaci* has been associated with the presence of cryptic species that exhibit different modes of reproduction and host ranges. However, recent findings suggest that vector competency of *T. tabaci* at any given location depends on the thrips and virus populations that are present. This study characterizes the population genetic structure of *T. tabaci* collected from four locations in North Carolina, and examines the relationship between population genetic structure and variation in TSWV transmission by *T. tabaci*. Mitochondrial COI sequence analysis revealed the presence of two genetically distinct groups with one characterized by thelytokous, parthenogenetic reproduction and the other by arrhenotokous, sexual reproduction. Using a set of 11 microsatellite markers that we developed to investigate *T. tabaci* population genetic structure, we identified 17 clonal groups and found significant genetic structuring among the four NC populations that corresponded to the geographic locations where the populations were collected. Analysis of variation in transmission of *Tomato spotted wilt virus* (TSWV) among isofemale lines initiated with individuals used in this study revealed that 'clone assignment,' 'virus isolate' and their interaction significantly influenced vector competency. These results highlight the importance of interactions between specific *T. tabaci* clonal types and specific TSWV isolates underlying transmission of TSWV by *T. tabaci.*

PP-060: Ecological and evolutionary perspectives on thrips-transmitted *Iris yellow spot virus* outbreaks in the USA

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Iris yellow spot virus (IYSV; family *Bunyaviridae*, genus *Tospovirus*) is becoming an increasingly important constraint to the production of bulb and seed onions (*Allium cepa* L.) in many onion-growing regions of the world. In the US, the virus was first reported in southeastern Oregon and southwestern Idaho where it stayed for over a decade. However, since 2000, the virus has spread rapidly to many other states in the US causing, in some instances, total crop loss to onion seed crops. Our studies identified several new weed species as potential hosts for IYSV during summer. However, we were unable to identify any overwintering plant hosts for the virus so far. To better understand the population structure and variability over time, IYSV isolates were collected during summer 2011 from Colorado, Idaho, New Mexico, New York and Washington. The full length N-gene was cloned and sequenced. The N-gene sequences of these five isolates had 99.6-100% identity with one another. Sequences from the 2011 isolates were aligned with those reported prior to 2011 from various parts of the US. In a phylogenetic tree consisting of all the N-gene sequences reported between 2003-2011 from the U.S., the 2011 Idaho isolate grouped with the previously reported California isolate from 2005, while the remaining 2011 isolates grouped with one another forming one cluster. Phylogenetic analyses also showed clustering of all the five 2011 isolates with those reported between 2003-2006, while isolates from 2008 and 2010 grouped with one another in a separate clade. *In silico* analysis detected recombination in one of the 2011 isolates out of the 27 sequences reported between 2003 to 2011, suggesting evidence of some genetic divergence and evolution in the IYSV N-gene sequences over this time period.

PP-061: Complementation between two viruses in an otherwise restrictive host: implications for evolution and epidemiology of insect-borne viruses

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Tospoviruses cause serious diseases in several important crop field and horticultural crops. New tospoviruses continue to be described and the continued emergence of new viruses was attributed to recombination and/or genome mixing among existing tospoviruses during mixed infections of plants. The genome of tospoviruses consists of three RNAs, large (L), medium (M) and small (S). The S RNA codes for a nonstructural protein (NSs) which was shown to function as a viral suppressor of gene silencing in plants. To determine if inter-virus genetic complementation takes place in plants with mixed infections, we used datura (*Datura stramonium*) which is a differential host for two distinct tospovirus species, *Iris yellow spot virus* (IYSV) and *Tomato spotted wilt virus* (TSWV). Following mechanical inoculation of datura, TSWV causes systemic infection, whereas IYSV infection of datura remains localized to inoculated leaves. We demonstrated that, in plants inoculated with both viruses, the silencing suppressors (NSs) of both TSWV and IYSV were expressed at a much higher level compared to single infections in inoculated as well as systemic leaves. The systemic symptoms produced by TSWV in the presence of IYSV were more severe than those caused by TSWV infection alone. Even though the IYSV infection remained localized to the inoculated leaf, transcript for the IYSV NSs gene could be detected in the younger, uninoculated leaves with the concurrent elevated expression of TSWV NSs transcript indicating complementation between two distinct tospovirus species.

PP-062: Epidemiology of aphid vectors of potato viruses in north-eastern hills of India

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Aphid surveys were carried out in four North Eastern-Hill States during 2008-2011 for seed and commercial potato crop to determine the abundance of aphids as virus vectors. Based on present findings the aphid free or low aphid sites identified were extrapolated on the geographical map of NE-Hills drawn giving clarity of the possible ideal locations for potato seed production at the altitudes between 2000 to 2700 meter amsl. The Shillong Peak/Laitkor Mawri and Mawkriah west in Meghalaya; Hilley Seed Potato Farm, Okhrey, Ribdi and Rawangla Seed Potato Farm in Sikkim; Upper Wanghoo and Warjung villages in Arunachal Pradesh; Upper Ukule Kigwema and Lower Ukule Kigwema villages in Nagaland were identified ideal/suitable sites for quality potato seed production where aphid population was recorded below the threshhold level during the main cropping season.

PP-063: Global status of thrips-transmitted *Iris yellow spot virus* (*Tospovirus*) incidence in onion

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Iris yellow spot virus (IYSV; *Bunyaviridae*, *Tospovirus*) was first described in the 1990s from iris and later found to infect bulb and seed onion crops in Brazil, Israel and the US. The virus is primarily transmitted by *Thrips tabaci* and with a lesser efficiency by *Franklienella fusca*. In the US, the virus was largely confined to a relatively small geographical area in southwestern Idaho and southeastern Oregon till 2000. However, due to factors unknown, the virus had spread rapidly to other parts of the country since 2000 and began to cause serious losses to both seed and bulb crops. Total crop losses were reported in the Columbia Basin of Washington State. New reports of IYSV began to emerge from all continents except Antarctica. The virus infects primarily Alliums such as onion, garlic, and leek. In Africa, IYSV was reported first in Egypt (2005) and subsequently reported from other African nations such as Tunisia (2005), Reunion Island (2006), South Africa (2007), Mauritius (2010), and Kenya and Uganda in 2011. In the Americas, it was first reported from Brazil (1991), and then from USA (1993), Chile (2005), Guatemala and Peru (2006), Canada (2008), Uruguay (2010) and most recently from Mexico (2011). Among Eurasian countries, it was first reported from Israel (1998), and subsequently from the Netherlands (1998), Japan (1999), Slovenia (2001), Iran and Spain (2005), India (2006), France, Germany, Italy, Serbia, UK (2008), Greece and Sri Lanka (2009), and Austria (2011). From Oceania it was reported from both Australia (2003) and New Zealand (2009). International trade of Alliums combined with the availability of ELISA- and PCR-based diagnostic techniques might have resulted in increased number of reports of IYSV incidence from various parts of the world. The potential economic impact of IYSV on Alliums in these regions remains to be seen.

PP-064: Overview of CIALCA activities on banana bunchy top in the Great Lakes Region

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Banana bunchy top disease (BBTD), caused by the banana bunchy top virus (BBTV), was reported for the first time in central Africa in Yangambi(Oriental Province, Democratic Republic of Congo, DRC) in 1958. The disease was reported in Rwanda and Burundi in 1987. A diagnostic/characterization survey carried out in 2007 by the Consortium for Improving Agriculture-based Livelihoods in Central Africa (CIALCA) revealed that several diseases, including BBTD, are causing increasing concern amongst farmers in the region as they continue to spread and reduce yield while no specific control measures are being taken. CIACLA has since invested efforts in surveys on BBTD and its aphid vector distribution, on-station varietal screening and aphid preference trials, artificial inoculations in contrasting agroecologies, farmer participatory research on best management practices and molecular characterization of the pathogen with the aim of better understanding the epidemiology and diversity of the virus and associated vector in addition to farmers' capacity/willingness to manage the diseases in the region. A dual strategy to reduce the spread and impact of BBTD was explored with on one hand, awareness raising and targeted farmer-led eradication campaigns in a pilot village (Munyika, Cibitoke Province), and on the other hand collection and multiplication of BBTV-free planting material of preferred local cultivars and FHIA hybrids using serological and macropropagation technologies. In parallel, backstopping of partner NGOs and NARs on BBTD symptomology, epidemiology and management was carried out through various meetings and trainings of trainers. Based on the experience gained through these studies CIACLA, in collaboration with national/international research centers and the private sector, hopes to revive interest of donors to the BBTD plight and contribute to the identification of a sustainable short to long term strategy to manage BBTD for the benefit of resource-constrained small-holders in sub-Saharan Africa.

PP-065: Dynamics of thrips and tospoviruses as influenced by management practices in Uganda: a case of tomato and pepper

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Surveys were conducted in four major markets in Kampala district, Uganda to test tomato fruits for *Tomato spotted wilt virus* (TSWV) and *Impatiens necrotic spot virus* (INSV) presence using immunostrip assays. Fruit samples analyzed gave positive tests for TSWV and INSV, implying occurrence of tospoviruses in the tomato growing areas that are mainly in Central Uganda. Biological monitoring surveys were conducted in Wakiso and Mpigi districts in Central Uganda for two seasons to document the occurrence of selected tospovirus species, thrips species composition and the effect of management on their occurrence on tomato and pepper. Six thrips species were identified: *Frankliniella occidentalis, Thrips tabaci, Frankliniella schultzei, Scirtothrips dorsalis, Ceratothrips ericae and Megalurothrips sjostedti*. Incidence scores as high as 62.5% and 47.2% were recorded in farmers' fields on tomato and pepper, respectively. Severity of tospovirus-like symptoms in farmers' fields ranged from 21% to 60% (mild to severe). Incidence and severity of symptoms characteristic of tospoviruses as well as thrips were significantly influenced by crop growth stages in both growing seasons in tomato and pepper; the highest occurrence was seen at the flowering and vegetative stages. Viral disease incidence and thrips population was found to be highest during the 2008B growing season with infrequent rains and lower during the 2009A growing season with frequent rains. Most of the pesticides and number of sprays used also had a significant effect on thrips occurrence, with the mean thrips population decreasing with increasing number of sprays in a week ($F_{1, 148}$ = 5.473**) regardless of the dosage. In general, cropping system and varieties grown had no significant on thrips occurrence on tomato and pepper.

PP-066: Effect of soil amendments and mulching on occurrence of tomato viral diseases and their vectors in Uganda

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Field trials were established for two consecutive seasons; 2011B and 2012A, at Makerere University, Uganda to assess the effect of soil amendments and mulches on occurrence of viral diseases and their vectors on tomato, and the effect of soil amendments on physical and biochemical attributes of the plant and how this influences occurrence of viral diseases and their vectors. A randomized complete block design had three replications and five treatments: straw mulch; coffee husks; cattle manure; yellow reflective sheets and untreated control. Data were collected on population dynamics of insect vectors and natural enemies, soil and plant performance parameters. Leaf samples were analyzed for key mineral elements at different growth stages. Fifteen leaf samples with typical virus symptoms were tested for *Tomato yellow leaf curl virus* (TYLCV) using specific primers in polymerase chain reaction (PCR). Results indicated that incidence and severity of tomato viral diseases as well as the numbers of whiteflies and thrips per plant varied significantly with season. The treatments also significantly influenced the incidence and symptom severity of tomato viral diseases in addition to populations of thrips and natural enemies. Straw mulch had the lowest virus incidence (12.91%) and symptom severity (1.09) while the control had the highest virus incidence (23.8%) and symptom severity (1.3). Plots amended with cattle manure had the highest mean yield (40.73 fruits per plant; marketable weight 48g per fruit, and marketable yield 8.17kg/5m^2). The control had the least mean yield (29.4 fruits per plant; marketable weight 25g per fruit and marketable yield 3.7kg/5m^2). In the molecular analyses, TYLCV was detected in seven out of 15 leaf samples tested.

PP-067: Development of biomarkers for vector competent aphid and whitefly populations in sub-Saharan Africa

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Populations of aphid vectors have been shown to differ in their ability to transmit persistent, circulatively transmitted viruses in the family *Luteoviridae* (e.g. *Schizaphis graminum* and Cereal yellow dwarf virus). This feature has also been demonstrated in whitefly and leafhopper vectors transmitting viruses in the family *Geminiviridae*. However, identification of within population differences in vectoring ability is a time consuming process. Recently, a panel of protein biomarkers that can distinguish transmission competent and transmission refractive populations of *S. graminum* were established as quick diagnostic tool. This study is conducted to determine if these biomarkers are conserved in aphid (*Aphis craccivora* and *Pentalonia nigronervosa*) and whitefly (*Bemisia tabaci*) vectors in sub-Saharan Africa. Populations of *A. craccivora* (transmits several legume infecting viruses, including luteoviruses) were collected from cowpea, soybean and other legumes; *P. nigronervosa* (transmits *Banana bunchy top virus*) from banana and plantain; and whiteflies (transmits begomoviruses) from cassava were collected. Genomic DNA, mRNA, and proteins were isolated from these colonies were used for mining the biomarker expressing genes. Mass spectrometry-based proteomics experiments are ongoing to characterize the expression of these biomarkers in aphids and to discover additional, species-specific markers in whiteflies. Preliminary data from this on-going work will be presented

PP-068: Establishment of *Banana bunchy top virus*-free banana seed systems in Malawi

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Banana bunchy top disease (BBTD), caused by the banana bunchy top virus (BBTV), continues to cause havoc in Malawi as it continues to spreads from one district to another covering almost the entire length and width of the country. Surveillance results obtained early 2012, through extension reports across the country indicate that spread is continuing, with no single variety showing resistance to the disease. At present it is estimated that over 90% of the crop is infected and land under banana has reduce by more than 50% due the disease. The progressive reduction in land area under banana and falling production has resulted high pricing of bananas despite the obvious reduced quality of the fruits. Source of disease free planting material remains a big challenge. Banana sucker collection, with the objective of getting clean planting materials for further propagation through a project grant from Bioversity International, was carried out in Malawi starting from 2009 and has yielded some positive results. Asymptomatic suckers collected in the field were tested using TAS-ELISA (Agdia) for BBTV freedom and further multiplied utilizing PIF propagation techniques. A total of 662 plants, comprising 11 preferred varieties were certified BBTV-free and are being further multiplied in the green house with 2 plants per variety maintained in a quarantine house as stock for tissue culture propagation. The resultant plants will be utilized in tolerance screening trials to be sited in different agro-ecological zones and also in the establishment of primary nurseries. The project also managed to build national capacity in virus testing and macro propagation of bananas. Eradication campaigns were also conducted, but with little success.

PP-069: Trend of virus infection on sweetpotato varieties for highland production in central Rift Valley of Kenya

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In Kenya sweetpotato virus disease (SPVD), a synergistic interaction of *Sweetpotato chlorotic stunt virus* (SPCSV) and *Sweetpotato feathery mottle virus (*SPFMV); *Sweetpotato mild mottle virus* (SPMMV); and C*ucumber mosaic virus* (CMV) have contributed to cultivar quality decline and low yields due to vegetative perpetuation of virus infected material. Hence screening for resistance/ tolerance to SPVD is a feasible strategy that can sustain sweetpotato production. The objective of the study was to determine the trend of disease incidence, severity, virus species and their effect on root yields of sweetpotato varieties for highland production. Fourteen varieties were screened for resistance/ tolerance to SPVD at KARI-Njoro (LH3-2166 masl) for a period of six months. A complete randomized block design experiment replicated three times was established. Disease incidence, severity, virus species; their mode of infection; and their effect on yields were assessed using standard procedures. Visual observation and NCM-Elisa were done on 42 samples for SPFMV, SPCSV, SPMMV and CMV. Observed virus disease scores were recorded monthly from June to November 2011 using a score of 1-9. Identification of the virus species was done using NCM-ELISA in the laboratory. Results showed variation in severity of infection among cultivars (score of 4 – 6). Infection was higher and more severe when rainfall was higher but less with lower moisture levels. The moisture level most likely provided the vectors with a constant supply of food. The cycle of infection showed an efficient mechanism for the perpetuation and dissemination of SPVD. The cycle also showed that fourth month is possible time to get fairly clean material for propagation but thereafter there is a build-up of virus diseases. Laboratory results of NCM-Elisa showed that SPFMV had the most incidence of 69%; CMV 60%; SPMMV 55%; SPCSV 33%. Effect on root yields varied with varieties; new varieties (KNSP013, KNSP06/1(2), KNSP010/6(1) and KNSP02/16(1) performed better than the current varieties. Results confirmed that high virus infection reduced yields significantly but some new varieties still yielded high an indication of tolerance. Moisture levels and harvest time of planting material have an effect on incidence and severity. Knowledge on the trend of infection will enable effective control of sweetpotato viruses at highland production.

PP-070: Hollyhock, a new reservoir of a monopartite begomovirus-satellite complex infectious to cotton plants

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Leaf samples were collected from two different, symptomatic hollyhock plants growing in a private garden in Lahore, Pakistan. Plants exhibited vein-yellowing or foliar mosaic symptoms, reminiscent of those caused by whitefly-transmitted geminiviruses (*Begomovirus; Geminiviridae*). Rolling circle and polymerase chain reaction amplification, respectively, revealed the collective presence of two monopartite begomoviruses, one betasatellite satellite, and eight alphasatellite molecules. Pairwise sequence comparisons with the most closely related begomoviruses available in the GenBank database revealed that one begomovirus (2.7 kb) was a newly described species, based on 87.0% shared nucleotide (nt) sequence identity with its closest relative *Mesta yellow vein mosaic virus* (MeYVMV) {FJ159265}. The name *Hollyhock yellow vein mosaic virus* is proposed for this virus. The second begomovirus genome (2.7 kb) was most closely related to *Croton yellow vein mosaic virus* (CYVMV) {FN6445926}, with 89.8% shared nt sequence identity, and is considered a new strain of this already established species. Recombination analysis showed that HoYVMV is a predicted recombinant in that the genome contains sequences also present in *Cotton leaf curl Multan virus* (CLCuMV), *Malvestrum yellow vein virus* (MaYVV) and *Tomato leaf curl Karnataka virus* (ToLCuKV). The betasatellite (1346 nt) was most closely related to *Kenaf leaf curl beta satellite* (KLCuB) {EF620566} at 81.2% nt identity and represents the first betasatellite from hollyhock in Pakistan. Among the eight alphasatellites detected, two were found to represent previously unreported molecules, based on the ICTV demarcation for distinct alpha- or beta-satellites, at 83% shared nt identity. One new variant was only 62.3%, with its closest alphasatellite relative reported from cotton {EU384652}, and is herein named *Hollyhock yellow vein mosaic alphasatellite-1*. The sequence of the second new variant was 80.3% identical with its closest relative, *Sida yellow vein alphasatellite (SiYVA)* {DQ641717}, and herein is named *Hollyhock yellow vein mosaic alphasatellite-2.* Infectivity tests were carried out using the cloned 1.5-mer or dimeric components of the helper virus, HoYVMV, to biolistically inoculate *Nicotiana benthamiana* and cotton plants, indicating that either HoYVMV or CYVMV together with KLCuB are infectious in that they cause severe leaf curling and yellow vein symptoms, characteristic of symptoms observed in hollyhock. This is the first report of a begomovirus-satellite complex isolated from hollyhock plants that is capable of infecting cotton, and therefore poses a potentially serious threat to the cotton crop in Pakistan.

PP-071: Farmers' knowledge of passion fruit virus diseases and their management in central Uganda

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A survey was conducted to assess farmers' knowledge of passion fruit viruses and their management using structured questionnaires and interviews in Buikwe and Mukono districts, central Uganda in 2011. A total of 60 farmers were interviewed with 31 and 29 in Buikwe and Mukono districts, respectively. Majority (80%) of the farmers recognized the passion fruit virus diseases as a major limitation to passion fruit production. About 73% of the farmers recognized the disease and were able to describe the symptoms. Unfortunately, the only small percentage (5%) of farmers who claimed to be aware of the cause of the passion fruit virus diseases, attributed the disease to be due to use of virus-infected planting materials. None of them clearly pinpointed the pathogen to be a virus/es. Among those unaware of the cause, 29%, 6%, and 3% considered the cause to be direct insect feeding damage, heavy rains, and poor soils, respectively. Nearly all the interviewed farmers lack the knowledge of how the passion fruit virus diseases are transmitted. Farmers employed a range of strategies to manage the passion fruit virus diseases. Some (23%) applied pesticides and fungicides to kill the insects found on the plants. Although, this successfully killed off some insects, the lack of knowledge on the target vectors resulted in very limited effect in reducing the disease incidence. About 7% of the farmers practiced roguing, with some limited success. Others simply pruned off the virus symptomatic leaves and branches. Majority (40%) of the farmers used their own experience and knowledge from fellow farmers to deploy management strategies. Almost all the farmers interviewed were willing to adopt weeding and mulching as alternative management strategies for passion fruit virus diseases. This study provided baseline information that will advise efforts for development of an integrated pest disease management package for passion fruit aphid vectors and associated virus diseases in Uganda.

PP-072: Strategies for developing banana planting material free from Bunchy top virus infection in Bas-Congo, DR Congo

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The banana bunchy top virus (BBTV) vectored by the banana aphid, was first reported in Yangambi, Oriental Province, Democractic Republic of Congo (DRC) in 1958. A survey conducted in 2007 motivated by the appearance of BBTD in variety testing trials being run by INERA and Bioversity confirmed the presence of the BBTV in all three administrative Districts of Bas Congo Province. Infestations ranged from 5% to 75%. In Masende village of the Cataracts District, banana and plantain production dropped to virtually zero in two years and a major source of farmer income was eliminated. While banana and plantain are important food and income crops for small farmers in DRC, the country has extremely limited infrastructure for tissue culture production and virus testing. Cultivar diversity is also high in farmers' fields, the Congo basin being a secondary center of diversity for plantain. INERA, University of Kinshasa and Bioversity proposed to pilot test a local seed system approach to reduce the risk of BBTV presence in new planting material based on 5 steps: (1) identify zones which are still relatively virus free; (2) extract suckers from plants without visual symptoms; (3) select only suckers negative based on TAS-ELISA; (4) multiply suckers in high humidity macropropagation chambers with a yield of 6-20 plantlets/sucker; (5) plant plantlets in a field where all banana plants have been destroyed at least 6 months previously. This model was tested in Masende village where farmers were highly motivated to recover their banana income. A first TAS-ELISA done on mother plant samples showed the test is still very important to identify symptomless plants which test positive. A second TAS-ELISA test done on the macropropagated plants prior to transplant showed that no reinfection occurred during the macropropagation process. Macropropagated plants in the field have showed no visual symptoms of re-infection through flowering, although TAS-ELISA testing is pending. This local seed system model shows promise for recovery of BBTV-infested zones, although investment in virus testing is a key component. In conclusion, the Bas-Fleuve District in Bas-Congo has been identified as a main source of potentially BBTV-free banana and plantain planting materials and should be used in conjunction with serological assays for confirmation.

PP-073: Breeding maize for improved MSV resistance: genomic characterization of MSV strains found in Ghana

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Maize is an important cereal in Ghana. Maize cultivation is affected by both biotic and abiotic stresses. Among the most important biotic stresses is *Maize streak virus* (MSV), the causal agent of maize streak disease (MSD). MSD can reduce farmers' maize yields by up to 100% during severe outbreaks. Efforts to control MSD through the development and use of MSV-resistant maize varieties have achieved considerable success in West Africa. However, possibly due to changing climate, pathogen evolution or farmers practices within this region some previously resistant varieties are succumbing to the disease. With improved virus detection and sequencing techniques developed in recent times, new efforts to develop MSV-resistant maize genotypes should include the detailed characterization of MSV strains against which these genotypes will be deployed. Identification of the key MSD-causing MSV strains will enable the screening of novel maize genotypes with the most relevant range of MSV strains. To this end, full genome sequencing of MSD-associated MSV isolates collected from the forest and forest-transition zones of Ghana (where maize is the most cultivated cereal) has been carried out at the Universities of Canterbury New Zealand and Cape Town, South Africa in collaboration with the West Africa Centre for Crop Improvement and the CSIR Crops Research Institute, Kumasi, Ghana. This work has determined that MSV populations in Ghana are genetically less diverse than those seen elsewhere in Western and Southern Africa and has identified the specific groups of MSV lineages that are most relevant for future maize MSV resistance screening efforts in Ghana.

PP-074: Spread of cassava brown streak disease in Uganda as influenced by host resistance and prevailing disease pressure

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Cassava brown streak disease (CBSD) is a major threat to cassava production in Uganda. The disease is caused by two ipomovirus species; *Cassava brown streak virus* (CBSV) and *Ugandan cassava brown streak virus* (UCBSV), both transmitted by the whitefly vector (*Bemisia tabaci*). Since the outbreak of the CBSD epidemic in Uganda in 2004, knowledge on its spread in the field is still limited. In this study, five cassava genotypes with varying levels of tolerance to CBSD were used to evaluate the effect of genotype and location (prevailing disease pressure) on CBSD spread in Uganda. Disease incidences (%), apparent infection rate (*r*), area under disease progress curves (AUDPC) were determined and populations of the whitefly vector *Bemisia tabaci* monitored on a monthly basis. Genotype and location significantly affected CBSD incidence ($P = 0.001$), AUDPC and *r* ($P = 0.05$). In Lira, where CBSD pressure is low, there was no noticeable spread even, in the susceptible genotype. On the contrary, in Namulonge and Kamuli where disease pressure is high and moderate respectively, final disease incidence was maximum (100%) in *I92*/0067, TME 204 and MH 97/2961 while the tolerant variety NASE 3 had significantly low final disease incidence of ≤ 5%. Mean whitefly populations varied with location ($P = 0.001$) and there was interaction between whitefly population and location hence the rapid CBSD spread in Kamuli and Namulonge. There was a high correlation ($r = 0.994$) between foliar CBSD incidence and CBSD root incidence hence high CBSD root incidences in Kamuli and Namulonge. These results clearly showed that high disease pressure in an area, use of susceptible genotypes and high whitefly numbers significantly enhance CBSD spread and development.

PP-075: Susceptibility of *Musa* genotypes to banana bunchy top disease in Cameroon and implications for disease management

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Banana bunchy top disease (BBTD) is a serious threat to banana and plantain production. The disease is now known from 14 countries in Africa. BBTD is caused by *banana bunchy top virus* (BBTV) which can only spread by infected plant propagules or through its only known insect vector, the banana aphid *Pentalonia nigronervosa*. At present, resistance to BBTD in *Musa* has not been yet discovered, but there is a wide range of susceptibility among *Musa* genotypes. We have been following for 26 months in two replicated field experiments the response of 16 *Musa* genotypes to BBTV in the South region of Cameroon where BBTD is widespread. BBTD symptom expression varied widely among the 16 genotypes without any specific patterns related to their genomic composition. Williams (AAA) and the hybrid plantain PITA 23 (AAB) were the most susceptible (nearly 95% infection). A larger group including local plantain landraces (AAB), several hybrid plantains (AAB and AAAB), a cooking banana (AAB) and Grande Nain (AAA) were moderately susceptible with a range of about 30 to 60% infection. The least susceptible group included only two genotypes, Gros Michel (AAA) and Pisang Awak (ABB) which after 26 months had less than 20% infection. The banana aphid was present on all genotypes but the level of a genotype's infection was not related to aphid abundance. There was however a positive linear relationship at whole field level between cumulative aphid abundance and cumulative infection levels across all genotypes, with this relationship being 2-fold higher in one field compared with the other, possibly related to either between-field differences in aphid transmission efficiency and/or BBTD symptom expression. The variation in BBTD susceptibility among the most common *Musa* genotypes in use in Cameroon within and between-field in symptom expression provide options for inclusion in BBTD management strategy.

PP-076: Managing the spread of cassava viruses through clean 'seed' systems

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Cassava is a vegetatively propagated crop, and is therefore vulnerable to the effects of viruses that pass through cuttings from one crop generation to the next. Although largely confined to Africa, cassava mosaic geminiviruses (CMGs) and cassava brown streak viruses (CBSVs) are globally the most economically important viruses affecting cassava in this way. Effective management requires the use of virus-free planting material of resistant varieties managed in a way that minimizes the potential for subsequent infection. There are currently no official sources of virus-free cassava planting material readily available to cassava growers in Africa. This represents a major constraint to the continent's cassava production in general, but more specifically to the establishment of commercial and sustainable cassava 'seed' (=planting material) systems. In order to begin to address this issue, IITA and the Tanzania National Research System are working in partnership with other stakeholders in Tanzania to establish a pilot model for a clean 'seed' system. The key elements of this model include: (i) the consultative design, testing and institutionalization of a formal certification system for cassava 'seed'; (ii) the development, validation and application of robust virus testing procedures to be applied at pre-basic and basic levels of 'seed' production; (iii) the establishment of a country-wide network of pre-basic seed production sites, with a two-stage design comprising 'Reception' and 'Holding' sites; (iv) the strengthening of public and private sector tissue culture work including virus indexing; and (v) the development of linkages with private sector seed production partners to foster commercialization and sustainability. These objectives are currently being vigorously pursued within the framework of two Bill & Melinda Gates Foundation-funded projects in Tanzania. One of these is focusing on the development of the overall 'clean' seed system model, certification systems and the establishment of pre-basic 'seed' sites, whilst the second is exploring several strategies for the sustainable commercialization of cassava 'seed' systems. If these approaches are successful, they will offer great potential for application elsewhere in sub-Saharan Africa, and are likely to have a significant and lasting impact in controlling the effects of CMGs and CBSVs.

PP-077: Community action in cassava brown streak disease control through clean seed

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Cassava in Tanzania is a key food security crop and an emerging cash crop from sale of fresh roots and leaves, processed products and planting materials. However, the productivity of the crop is low and has continued to decrease in recent years. Cassava brown streak disease (CBSD) is among the principal biotic stresses that threatens cassava production and productivity in the country. CBSD affects value addition and increases labour for women who have to remove necrotic tissues from affected roots. The cassava brown streak viruses (CBSVs) that cause CBSD are transmitted by a whitefly vector, *Bemisia tabaci*. Recent research into the transmission of CBSVs by whiteflies has shown that the virus particles are retained for relatively short-periods of times (semi-persistent). This implies that whiteflies can spread CBSD over relatively short distances. This opens up the possibility for controlling CBSD through the careful management of the health of cassava plants (phytosanitation). The three key elements of phytosanitation that can be used to control CBSD are: (i) establishing crops using healthy planting material; (ii) maintaining the health of cassava crops during the active growth period; and (iii) avoiding to plant healthy cassava cuttings near to diseased cassava crops. We recently initiated a project to demonstrate the feasibility to reduce the overall incidence and consequent impact of CBSD by implementing a community-wide phytosanitation programme. The specific objectives of this project are: (1) to demonstrate the benefits of growing CBSD-free planting materials of superior varieties; (2) to increase farmer knowledge about the effects of CBSD, its management and control practices; (3) to engage communities in managing and controlling the further spread of CBSD; and (4) to learn and document systematically community behaviours and social dynamics in managing and controlling CBSD; and (5) to determine disease spread patterns and the impact of phytosanitation on yield. It is expected that CBSD incidences will be reduced, thereby contributing to increased production and productivity of cassava. Implementing partners include the Division of Research and Development (DRD), the Ministry of Agriculture Food Security and Cooperatives, the International Institute of Tropical Agriculture, the Tanzania Official Seed Certification Institute, VECO Tanzania, KOLPING Society Tanzania, Plan International, Rulenge Diocesean Development Office, and Local Government in respective districts.

PP-078: Transgenic approach for improving resistance of plum cultivars for Sharka disease

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Since the first record of Sharka disease in Bulgaria, the disease has progressively spread via infected plant materials throughout Europe were it has destroyed well over 100 million stone fruit trees. The disease has serious agronomic and political consequences due to the enormous economic losses. Because only few PPV resistance genes have been found to naturally occur in *Prunus*, scientists have utilized genetic engineering techniques to develop resistant plums by inserting specific genes from the PPV genome into the DNA of *Prunus* host plants. For improving the plants resistance to plum pox virus (PPV) we used two technologies were based on co-suppression gene and RNA-silencing. Binary vector pCamPPVcp which contained *ppv-cp* gene in sense-orientation and self-complementary fragments of gene *ppv-cp* were used for realization post-transcriptional gene silencing. Seven independent transgenic lines with *ppv-cp* gene and six transgenic lines with a two inverted repeats of *ppv-cp* gene fragment were produced in our laboratory. Stable integration of genes into genome of plants was confirmed by PCR analyses. The accumulation of coat protein was evaluated by Western blot assay in five from six lines. Plum clones were infected by bud-grafting. PPV detection was analyzed RT-PCR by using primers targeting the 3' untranslated region and HC-Pro gene of PPV. Western blot analysis was performed using rabbit polyclonal antibodies to PPV coat protein (Loewe). We observed absence of PPV in four tested lines of St-pCam PPVRNAi. Field testing of transgenic plants is underway in the field plots.

PP-079: Viruses in social-ecological systems: Strategies for farmer selection in smallholder seed systems

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In many smallholder seed systems, seed free of viruses and other pathogens may rarely be available for purchase, or may be too expensive. This is a particular problem for vegetatively-propagated crop species, which accumulate pathogens on propagules. Farmers may reduce pathogens by selecting symptomless mother plants or seed materials, or alternatively, eliminating plants with symptoms. We present a framework building on existing models of crop virus ecology and evolution to support strategies for smallholder farmer selection of healthier seed. This framework includes estimation of the uncertainty associated with model outcomes. We will evaluate the effect of host resistance and environment on virus accumulation, as well as the efficacy of different types of virus management, includingroguing, positive selection, plant replacement, and vector management. We also will evaluate the effects of different strategies on virus evolution toward greater virulence.

PP-080: Effect of cassava brown streak disease on predominant cassava varieties in Malawi

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Cassava brown streak disease (CBSD) has emerged as a major threat to cassava in Eastern and Southern Africa. The occurrence of CBSD in Malawi was first reported in the 1950s. The disease can cause yield losses of up to 70%. However, there is little knowledge about the tolerance and susceptibility of local cultivars to the disease. A national survey was therefore conducted in 90 locations in 12 districts in 2010 so as to understand the effect of the disease on the most widely cultivated varieties in the country. The study showed that most predominant varieties are susceptible to CBSD. The varieties *Sauti* and *Bitilisi* were the most frequently affected, having incidences of above 80%. By contrast, *Mbundumali* had a low average incidence (3.3%) and symptoms were less severe. The most widely cultivated varieties included: *Manyokola, Mbawala, 20-20, Mbundumali,* and *Matakolembwende*. CBSD incidence differed significantly between varieties ($\chi^2 = 20.9$, $P < 0.001$). The average leaf incidence per field was 26.3%, with a maximum of 96.7%. Incidence of CBSD stem symptoms was less in all varieties with a field average of 13.9%. The varieties *Thundulu*, *Mbawala* and *Gomani* were the most severely affected varieties, with an average severity of ≥3.0. Average CBSD foliar severity was 2.5. Differences in CBSD severity between varieties were significant ($\chi^2 = 13.9$, $P < 0.05$). The average abundance of the whitefly vector (*Bemisia tabaci*) was 0.4 per shoot. Whitefly abundance was greatest in *Nyajogwa* and least in *Chitembweri* and *Koloweka*. Numbers of whiteflies were low since the survey was conducted during a period of the year unfavourable to whitefly population increase. Although CBSD continues to be widespread in Malawi, comparison with previous surveys indicates that this status is not deteriorating. Management programmes are still required, however. Based on the results of this survey, these should emphasize the judicious in-country distribution of better-performing local varieties, as well as the development of varieties that combine resistance to both CBSD and the other important cassava virus disease in Malawi, cassava mosaic disease.

PP-081: Seed transmission of *Tomato torrado virus* in tomato

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During the last decade, *Tomato torrado virus* (ToTV) was recognized and identified on tomato plants. The occurrence and spread of the virus were reported in many countries of Europe as well as Central America and Australia. There has been a limited accumulation of the virus in infected plants. The virus is also known for its very low stability, poor mechanical transmission but effective transmission by whiteflies. Taking the above factors into account, the issue that should be solved is how the virus is transmitted over very long distances. ToTV belongs to the family *Secoviridae*. Several viruses transmitted by seeds are described as belonging to this family. The goal of this research was to evaluate whether ToTV can be transmitted through tomato seeds. In 2011, tomato seedlings var. Beta Lux were mechanically inoculated with ToTV-Kra isolate. The seedlings were kept in a greenhouse, at 20-25ºC to observe symptoms and fruit development. Tomato plants with symptoms of necrosis typical for ToTV were selected for seed production. Those seeds which were harvested before sowing were kept in the refrigerator. Seeds treated with a 10% solution of K_3PO_4 were sown individually in small pots with soil, within 4–5 weeks of the fruit being harvested. The tomato plants had been growing for at least 4 weeks before being tested in a greenhouse. In order to find out the presence of ToTV in seedlings, they were subjected to immunocapture real-time RT-PCR. Leaf tissue from 10 plants (combined samples) was homogenized in buffer in plastic bags. All total, 540 pooled samples (from 5400 seedlings) were tested and 17 positives were detected, indicating a transmission rate of 0.315%. Positive samples were subjected to RT-PCR and the identity of the PCR products was confirmed by the sequencing. This preliminary study indicates that ToTV is seed-transmitted in tomato plants.

PP-082: Identification and molecular analysis of natural resistance to cassava brown streak disease (CBSD)

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Cassava production in Eastern and Central African countries is adversely impacted bycassava brown streak disease (CBSD).The disease is caused by two RNA viruses: *Cassava brown streak virus* (CBSV) and *Ugandan Cassava brown streak virus* (UCBSV). So far no durable natural resistance to CBSD has been reported among elite cassava lines. We have identified CBSD resistance in controlled greenhouse conditions against the two CBSD isolates in elite cassava lines selected from cassava germplasm and breeding programs. Using a stringent infection method based on cleft grafting combined with precise virus quantitation we have characterized the observed CBSD resistance. The infection assays resulted in the identification of one elite line that remained symptom-free and that efficiently controlled viral replication for both CBSD-associated viral species. The CBSD resistant elite line remained symptom-free even when tested for combined CBSV and UCBSV infection, suggesting a robust CBSD resistance. Transcriptome responses to CBSV infection were analyzed in resistant and susceptible CBSD lines using Illumina sequencing technology to develop molecular markers associated with CBSD resistance. We identified a number of differentially regulated cassava genes that are involved in defense-related, signaling and metabolic processes. Our studies contribute to better understanding of CBSV—cassava pathosytems and provide further insights into potyvirus-host interactions.

PP-083: Transmission of cassava brown streak viruses by *Bemisia tabaci* whiteflies

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Cassava brown streak viruses (CBSVs) (*Potyviridae*: *Ipomovirus*) are transmitted by *Bemisia tabaci* and disseminated though the use of infected stem cuttings. The transmission characteristics of CBSVs were investigated at Kibaha Research Station, Tanzania and at the UK's Natural Resources Institute in 2010 and 2011. The experiments aimed at characterizing the transmission components: Acquisition Access Period (AAP), Inoculation Access Period (IAP) and Retention Period (RP). For all tests, insectary-reared adult whiteflies (*B. tabaci)* were allowed to starve in collection tubes for 1 h. The insects were then given various AAPs and IAPs, including: 5 min, 30 min, 1 h, 4 h, 24 h, 48 h and life-long feeding. The virus source was CBSD-affected cassava plants infected by a *Ugandan cassava brown streak virus* (UCBSV) isolate from Uganda. For each test, groups of 20-25 *B. tabaci* adults were allowed to feed on the virus source plant before being transferred to each of 15-25 virus-free test plants, cv.Kiroba. Insects allowed to feed on source plants for varying AAPs were given 24 h to feed on test plants before being killed through the application of a contact insecticide, Cypermethrin. Insects used for IAP experiments were allowed to feed on the source plant for 24 h before being transferred to test plants. Following the completion of IAP feeding periods, insects were transferred to a second test plant in order to assess determine the RP. Results revealed that even at the minimum AAP (5 min), 6.7% of test plants were infected. This rose to a maximum of about 40% by 1 h. The minimum IAP was 30 min (6.7% transmission), with transmission efficiency increasing to 40% by 48 h UCBSV was weakly retained, with a maximum retention time of 24 h. These findings collectively suggest a semi-persistent mode of transmission. Additional tests comparing the efficiency of transmission of UCBSV and CBSV revealed no significant difference. These results help to improve our understanding of the epidemiology of CBSVs and will contribute to the development of improved management strategies.

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PP-084: Diversity and distribution of viruses infecting chilli pepper in Nigeria

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Chilli pepper (*Capsicum* spp.) is an important source of income for rural households in Nigeria. It is considered as a high value crop grown by smallholder as well as large-scale commercial farmers in almost every state of Nigeria. The country has a climate that is conducive for year round pepper production. Virus diseases pose major threat to pepper cultivation in Nigeria. They affect both productivity and quality of the produce. Many viral diseases affecting pepper in Nigeria were identified based on symptoms but no data is available on actual identity of the viruses. Prevailing knowledge on virus diseases are based on symptoms and recommendations for disease control are usually adapted from research results from other countries and therefore tend to be general. Surveys to determine the incidence, diversity and distribution of viruses infecting pepper was conducted in six states (Oyo, Ondo, Osun, Ogun, Ekiti and Lagos) in 2010 and 2011. Symptoms observed on infected plants includes mild to severe mosaic, mottling, puckering, reduction in leaf size, vein yellowing, leaf and fruit deformation and stunting. The average disease incidence was 79% and 77% in 2010 and 2011, respectively, whilst the average disease severity score was 2.9 (1 = no symptoms and 5 = very severe symptoms) in both years. Symptomatic leaf samples were collected and tested for viruses reported to infect pepper by antigen coated plate-enzyme linked immunosorbent assay (ACP-ELSA) and reverse transcription polymerase chain reaction (RT-PCR). Samples were also tested for begomoviruses using generic primers by PCR. *Potato virus Y* (PVY)*, Potato virus X, Pepper veinal mottle virus* (PVMV)*, Pepper mild mottle virus, Tobacco mosaic virus, Cucumber mosaic virus* (CMV)*, Tobacco Etch virus* (TEV) and *Tomato mosaic virus* (ToMV) were frequent in pepper. Tests for begomoviruses were negative. Incidence of PVY was the highest (79%), followed by TEV (67%), CMV (61%), PVMV (60%) and ToMV (23%). Mixed infection of more than one virus was found to be common in the farmers' fields. High virus incidence in the farmers' fields suggests high susceptibility of cultivars to virus infections. Deployment of disease resistant cultivars will offer sustainable virus disease control option to farmers.

PP-085: Incidence and distribution of cassava mosaic begomoviruses in Côte d'Ivoire

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Cassava mosaic disease (CMD) cased by whitefly transmitted begomoviruses is a number 1 production constraint to cassava (*Manihot esculenta* Crantz.) in Côte d'Ivoire. In 2009, surveys were conducted in 72 locations spanning major cassava production zones to determine the incidence and distribution of cassava mosaic begomoviruses infecting the crop. Disease incidence (percent plant infected) and symptom severity (based on 1 to 5 scale, with 1 = no symptoms and 5 = severe symptoms) was estimated in each field. At least 5 leaf samples were collected per field and they were tested by polymerase chain reaction (PCR) for *African cassava mosaic virus* (ACMV), *East African cassava mosaic virus* (EACMV), *East African cassava mosaic Cameroon virus* (EACMCV) and *East African cassava mosaic virus-Uganda* (EACMV-Ug), a recombinant virus responsible for CMD pandemic in Eastern Africa. CMD symptoms were recorded in 71 of 72 fields' surveyed (98.6% prevalence). Disease incidence ranged from 4% to 100% (mean 52%). Mean severity was 3.75 for all fields combined. Begomoviruses were detected in 80% of the 335 samples tested. Incidence of ACMV, EACMV and EACMCV was 74.6%, 37.0% and 36.1%, respectively. EACMV-Ug was not detected. Mixed infection of ACMV and EACMV was detected in 31.3% samples. Adoption of high yielding CMD resistant varieties was found to be low due to a number of factors including shortage of planting materials. This study underscores the need for reinvigoration of cassava improvement programs and wide deployment of high yielding CMD resistant varieties in the country.

PP-086: Detection and characterization of several distinct walnut isolates of *Cherry leaf roll virus* (CLRV) in Poland

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Cherry leaf roll virus (CLRV) is a member of the subgroup C of the genus *Nepovirus,* family *Comoviridae.* The virus infects many species of trees and shrubs leading to serious damage especially in sweet cherry and walnut production. CLRV consists of two genomic RNAs and has a bipartite single-stranded positive-sense RNA genome with a long 3´ non-coding region (3´NCR) involved in regulation of replication and translation. Silica capture (SC) method was used for extraction of total nucleic acids from the walnut leaves collected in commercial orchards, germplasm collection and private gardens. Molecular characterization of RT-PCR amplified fragments of the 3'NCR region of the isolates were determined by RFLP, sequencing and phylogenetic analyses. Depending on restriction enzyme (*Alu*I, *Mse*I, *Rsa*I, *Hpa*I), two or three different restriction patterns were obtained after digestion of the amplicons. The analysis of nucleotide sequences of ~370 bp fragments of 3'NCR confirmed the diversity among the Polish CLRV isolates from walnut (GQ871785-89). They were clustered within two groups: D1 and D2 containing the other walnut strains. The walnut isolates differ in their sequences with the CLRV strains from birch, sweet cherry, European ash, mountain ash, elderberry, walnut, raspberry, blackberry, grapevine and rhubarb available in the GenBank. Herbaceous plants of *Chenopodium quinoa*, *C. amaranticolor*, *Nicotiana clevelandii*, *N. benthamiana*, *N. tabacum* 'White Barley' and 'Samsun', and *Cucumis sativus* were infected by sap inoculation with CLRV isolates. The reaction of herbaceous hosts differed in presence or lack of the symptoms and their intensity depending on CLRV isolate used for mechanical inoculation.

PP-087: Diagnostic tools for cassava mosaic and cassava brown streak viruses

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Accurate and efficient detection and identification of plant viruses are fundamental aspects of virus diagnosis leading to sustainable disease management. We described here two techniques; the first based on a single tube duplex and multiplex PCR (d&mPCR), developed for simultaneous detection of *African cassava mosaic virus* (ACMV), *East African cassava mosaic Cameroon virus* (EACMCV) and *East African cassava mosaic Malawi virus* (EACMMV). Secondly a technique based on Restriction Fragment Length Polymorphism (RFLP) analysis of RT-PCR amplified cassava brown streak viruses: *Cassava brown streak virus* (CBSV) and *Uganda cassava brown streak virus* (UCBSV). Four primer pairs were designed from published DNA A component sequences targeting specific amplification of the four cassava mosaic begomoviruses (CMBs). Additionally degenerate primer amplifying 785 bp of the coat protein gene (CP) of CBSV and UCBSV was also designed. Two restriction enzymes: HindIII and EcoR1 were identified by vecto NTI software, which produce different fragments upon digestion of RT-PCR amplicons from CBSV and UCBSV which were used to distinguish them. The d&mPCR enabled the simultaneous detection and differentiation of the four CMBs: ACMV (948 bp), EACMMV (504 bp), EACMCV (435 bp) and EACMZV (260 bp) in single and mixed infection. Analysis by RFLP using HindIII produced three fragments (437 bp, 267 bp and 81 bp) for CBSV, one fragment (785 bp) for UCBSV and four fragments (785, 437, 267 and 81 bp) for CBSV and UCBSV mixed infections. On the other hand, EcoR1 analysis produced one fragment (785 bp) for CBSV, two fragments (525 bp and 224 bp) for UCBSV and three fragments (785, 525 and 224 bp) for the mixed infections. In both d&mPCR and RFLP analyses, results from the PCR/RT-PCR amplicons sequenced agreed with sequence identities of the respective published virus species. Experience from using the d&mPCR and RFLP techniques shows that time was saved and amount of reagents used were reduced. RFLPs confirmed the presence of CBSV and UCBSV in RT-PCR amplicons without requirement for sequencing. Additionally, we report here modified protocols from Dellaporta et al. (1983) and Chang et al. (1993), which ware used to extract DNA and RNA, respectively, from dry and fresh cassava leaves with comparable results. The two diagnostic tools can be used routinely in germplasm indexing, disease surveillance, and disease monitoring programs.

PP-088: Quantitative detection of *African cassava mosaic virus* and *East African cassava mosaic virus* using TaqMan Real Time PCR

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A number of begomoviruses are involved in cassava mosaic disease (CMD) etiology. In Africa, *African cassava mosaic virus* (ACMV) and *East African cassava mosaic virus* (EACMV), EACMV-Kenya, EACMV-Cameroon, EACMV-Malawi, EACMV-Zanzibar and *Southern African cassava mosaic virus* are involved in CMD etiology. Mixed infections of these viruses are frequent in CMD-affected plants. A TaqMan real time PCR (RT-PCR) method is established in this study to determine the relative and absolute concentrations of ACMV and EACMV in dually infected plants and its impact on symptoms, host resistance and virus transmission. The primer pair and probe for ACMV was designed from nucleotide sequences of AC1 gene which amplifies a 171 bp fragment; whilst the primer pair and probe for EACMV detection was designed from nucleotide sequences of AV1 gene which amplifies a 153 bp fragment. Ubiquitin10 (UBQ10) gene was used as an endogenous control. This assay was validated using a range of cassava samples comprising different varieties and geographic locations in different countries. It was hundred times more sensitive than the corresponding conventional PCR and revealed variable concentration of ACMV and EACMV in case of mixed infections in cassava and also in whitefly vector, *Bemisia tabaci*. This tool has great potential in characterization of resistance mechanisms and genetic studies.

PP-089: The incidence and characterization of *Cherry leaf roll virus* (CLRV) in *Sambucus* spp. plants in Poland

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Sambucus spp., are cultivated in Poland for fruit production and as ornamental shrubs. In 2009-2010 symptoms including chlorosis, rings or line patterns on the leaves were observed on *S. nigra*, *S. racemosa* and *S. kamtschatica* plants grown in commercial plantations as well as on natural habitats. Samples from plants showing virus-like symptoms and healthy looking plants were tested using DAS-ELISA for the presence of 11 viruses reported to infect elderberry plants. Results of this assay revealed that 37% of elderberry plants (all showing disease symptoms) tested was infected by *Cherry leaf roll virus* (CLRV). Thirteen virus isolates were selected for further serological and molecular analysis. Serological properties of isolates were determined using DAS-ELISA with CLRV subgroup A, B or E-specific polyclonal antibodies. All but one tested isolates reacted with all subgroup-specific kits used in experiments. The exception in was isolate Sn8 found in wild *S. nigra* that did not react in ELISA with any IgG used in the assay. Silica capture RT-PCR method with primers targeting 3'UTR region of CLRV RNA was followed to amplify a ~390 bp fragment and the amplicons were sequenced. Nucleotide sequences identity among analyzed isolates ranged from 95 to 99%. Phylogenetic analysis showed that these sequences were most closely related with sequences of CLRV found in elderberry plants in Germany. Based on these results isolates were classified as members of subgroup E of *Cherry leaf roll virus*.

PP-090: Inheritance of multiple virus resistance in cowpea

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Cowpea is a major source of dietary protein in sub-Saharan Africa. Viral diseases, which usually occur in multiple infections, cause serious economic yield losses in cowpea. Planting of resistant variety remains the most economical and effective method of controlling viral diseases while genetic studies on mode of inheritance of virus resistance is essential for choosing appropriate breeding procedures. In this study, the patterns of inheritance of cowpea lines to *Blackeye cowpea mosaic virus* (BlCMV), family *Potyviridae*, genus *Potyvirus, Southern bean mosaic virus* (SBMV), genus *Sobemovirus* and tolerance to *Cucumber mosaic virus* (CMV), genus *Cucumovirus* were investigated. Two resistant cowpea breeding lines (IT98K-1092-1 and IT97K-1042-3) and two susceptibles (IT99K-1060 and IT98K-573-1-1) were selected and crossed. The parental lines, F1, F2, BCP1 and BCP2 were screened for virus resistance following mechanical inoculation of plants with each virus in screen-house experiments at IITA. Classification into resistant/ susceptible classes was carried out by weekly severity scores (scale 1-5), area under disease progress curve and virus detection/concentration using ACP-ELISA and RT-PCR. Segregation patterns of the two classes were subjected to Chi-square analysis to determine goodness-of-fit to appropriate genetic ratios. Inheritance of resistance to BlCMV is controlled by a single recessive gene pair in IT97K-1042-3. Duplicate dominant genes condition both resistance to SBMV and tolerance to CMV in IT98K-1092-1. Knowledge of genetic bases of the resistance lines obtained will be useful in developing improved cowpea varieties with resistance to these viruses.

PP-091: Molecular identification and characterization of a begomovirus associated with *Phaseolus lunatus* L. in Nigeria

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Whitefly-transmitted begomoviruses cause devastating diseases in many economically important crops. Lima bean (*Phaseolus lunatus* L.) plants with mosaic and bright yellowing symptoms similar to that of begomovirus infection have been observed over many years in lima bean farms at Malagum, Kaduna State of Nigeria. The DNA A of a begomovirus infecting lima beans in Nigeria was detected by polymerase chain reaction (PCR) using begomovirus-specific degenerate primers PAL1v1978 and PAR1c496. DNA B, DNA β and DNA 1 components were not detected by PCR using their respective specific primers. The complete genome of DNA A component (2.7kb) was sequenced using sequence-specific primers BeFwd1/BeRev1 and B1B6Fwd/B1B6Rev or B7B9Fwd/ B7B9Rev. The sequences were assembled and compared using CLC Genomics software. Virus identification was performed by percent sequence identity and phylogenetic analysis with corresponding sequences of other begomoviruses. The sequence identity of the lima bean virus from Nigeria was 93% identical in DNA A with *Soybean chlorotic blotch virus* (SbCBV, genus *Begomovirus*) previously reported from Nigeria. Based on phylogenetic analysis and percent sequence identity with reference to other begomoviruses the virus associated with lima beans in Nigeria was identified as a strain of SbCBV, but lacking the DNA B component that is also present in SbCBV.

PP-092: The distribution and molecular variability of *Zucchini yellow mosiac virus* and *Papaya ringspot virus* in the Pacific Islands

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Potyvirus is an economically important virus genus and includes species that limit the production of cucurbit crops worldwide. Although considerable global effort has focused on characterizing and understanding these potyviruses very little research has focused on the Pacific. *Zucchini yellow mosaic virus* (ZYMV) and *Papaya ringspot virus* (PRSV) infections of cucurbits were originally detected by ELISA during virus surveys conducted by the Land resources Division of the Secretariat of the Pacific Community. Using dried leaf samples from the original surveys as a source of viral RNA RT- PCR was used to amplify part of the coat protein gene for sequencing. Nucleotide sequences for both ZYMV and PRSV grouped according to geographic origin within the Pacific islands but not according to host plant. The ZYMV sequences allclustered with group A isolates; the Samoan and Tongan sequences in A-IV with Japanese and New Zealand sequences, which are cucurbit trade partners; Vanuatu and Nauru in A-I; and New Caledonian and Federated States of Micronesia grouped in A-II. The PRSV sequences split into two groups; the Commonwealth of the Northern Marinara Islands with the Asia group, with all of the remaining isolates in the Americas group. While these results shed some light on the possible origins of these viruses an issue of more immediate practical importance is to determine whether other hosts carry the same strains and are acting as reservoirs for crop infection or whether the infection cycle is limited to the crop hosts only (e.g., seed transmission). Surveys in Tonga detected ZYMV and PRSV in squash, and watermelon and several weed species. Sequences of ZYMV isolates from watermelon, which is grown year round for local consumption,were>95% similar to thosefrom export squash crops, which are grown for just a few months of the year.

PP-093: First molecular evidence of cassava brown streak disease in Democratic Republic of Congo

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Cassava is a staple food in sub-Saharan Africa, cassava leaves and roots are consumed by more than 60% of population in Democratic Republic of Congo (DRC). The causal agents of Cassava Brown Streak Disease (CBSD) are two distinct ssRNA$^+$ viruses (CBSV and UCBSV, genus *Ipomoviruses,* family *Potyviridae*), and both are transmitted semi-persistently by *Bemisia tabaci* (Aleyrodidae*,* Hemiptera). Cassava is propagated using stem cuttings, and the transportation of infected materials is a major factor in CBSD spread. Cassava affected by CBSD produces non-edible and non-marketable tuberous roots. This pandemic has caused very large economic damage in many African countries. Unfortunately, many of the varieties resistant to CMD are susceptible to CBSD, and there is a need for locally adapted varieties resistant to both diseases. CBSD-like symptoms identified in DRC are not yet confirmed by virus diagnostic techniques. In this study, molecular diagnostics were used to confirm the presence of CBSD and to understand the distribution pattern of this disease in the eastern region of DRC. Cassava leaves (symptomatic or no) were collected in four provinces in the Northeastern DRC for molecular diagnostic for CBSD viruses. Sampling was made in three sites per province. Mean fields incidence (5%) and mean severity disease (3) were scored in ten fields per site. Total nucleic acid was extracted using a modified CTAB procedure. RT-PCR using universal and specific primers was performed by themocyclor GenAmp 9700®. The Nested PCR products were purified from the gels using Fermentas® gel kits. Sequencing was performed after cloning into pJET vector using CloneJET Kits (Fermentas®). Molecular diagnostic of CBSD viruses confirmed the presence of CBSD disease in DRC, and validates the field observations. Of the 128 samples tested, 43% were positive for CBSD. The BLAST analysis of 8 coat protein sequences (280 nt) showed 95-99% identity to CBSV and UCBSV. The mixed infections by both CMD and CBSD viruses (34%) were common and not unexpected since they are both transmitted by the same vector. Moderate CBSD field incidence (5%) in comparison to the molecular incidence (9% in single infection) indicates symptomless infections. This first molecular evidence of CBSD viruses in DRC raises the importance of appropriate diagnostic tests and the need to develop strategies to mitigate cassava viruses.

PP-094: Prevalence of cassava viral diseases in different agro-ecological zones in the western part of Democratic Republic of Congo

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One of the most economically important crop disease in Africa is the cassava mosaic disease (CMD), transmitted by the whitefly *Bemisia tabaci*. During the 2000s, Democratic Republic of Congo (DRC) experienced widespread outbreak of severe CMD associated with the recombinant virus EACMV-Ug. Cassava brown streak disease (CBSD)-like symptoms were first reported from western DRC in 2002. Since that time, several attempts have been made to detect cassava brown streak viruses (CBSVs) in symptomatic leaf and root samples from this region. Although these have used standard, established RT-PCR diagnostic approaches, no CBSV positive samples have so far been obtained from western DRC. The objectives of this study are to identify viruses causing CMD- and CBSD-like symptoms in western DRC using molecular techniques and to determine the spatial distribution of the viruses within western DRC. In order to make a comprehensive effort to test material with CMD or CBSD-like symptoms from western DRC, 1450 leaf samples (asymptomatic and symptomatic) were collected from 145 fields in Bas Congo, Kinshasa, Bandundu and Equateur Provinces. DNA and RNA was extracted from the cassava leaf samples using the CTAB protocol and analyzed for CMVs and CBSVs by PCR. To confirm the identity of PCR products, the amplicons from select samples were cloned using the InsTAclone PCR cloning Kit and sequenced. Sequences were analyzed with the CLC Main Workbench 6.0 software and verified by BLAST search (NCBI database). CMVs were detected in 96.5% of samples using PCR with 4.1% being ACMV positive, 21.3% being EACMV-UG positive and 71.3% with mixed infections (ACMV and EACMV–UG). The nucleotide sequence of amplicons showed 98% and 99% sequence identity with ACMV (GenBank accessions No GU580897.1 and JN053430.1) and EACMV-UG (GenBank accession Nos. FM 877474 and HE814063), respectively. All samples tested negative for CBSVs using primers specific for the two known CBSVs and also with universal potyvirus primers. This suggests that another causative agent could be present in these samples. Deep sequencing of freshly collected infected cassava leaves and roots should help elucidate the causes of CBSD-like symptoms in western DRC.

PP-095: Occurrence and distribution of cassava brown streak viruses in Western Kenya

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A diagnostic survey to investigate the distribution and occurrence of cassava brown streak viruses was conducted in major cassavagrowing areas of Western Kenya in November 2011. The highest mean cassava brown streak disease (CBSD) incidence was in Busia County with 11.5%, Siaya county 7.2%, Bungoma County with 3.7% while the lowest was in Homabay County with 1.5%. High mean severity score of 3 was observed in farmer's fields in Busia (Mungatsi, Matayos and Mundika divisions), while the rest of other areas showed no foliar symptoms.CBSD incidence correlated positively with disease severity on the leaves (r= 0.7, $p_{0.01}$) and stems (r= 0.9, $p_{0.01}$). Polymerase chain reaction (PCR) results using specific primers for *Cassava brown streak viruses* (CBSV) and *Uganda brown streak virus (UCBSV)* detected single infections of CBSV and UCBSV in 70% and 3.6% of the positive reactions, respectively. The study revealed a first record of *Uganda cassava brown streak virus* (UCBSV) in the region. Dual infections of CBSV and UCBSV were not detected in any of the samples in the surveyed fields. The widespread occurrence of CBSV in Western Kenya may result in synergistic association with other plant viruses resulting in severe symptoms expression in affected plants that may greatly reduce cassava production in the

PP-096: Prevalence and distribution of begomoviruses infecting cassava in Western Kenya

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Cassava *(Manihot esculenta* Crantz*)* is an important food staple in Busia, Siaya, Kuria, Kwale, Kilifi and Marakwet counties and is a secondary food crop for many Kenyans. Whitefly-transmitted begomoviruses are the causes of cassava varietal degeneration in the area. The usual practice of retaining some seed cuttings from the current ware crop or buying them from neighbours, leads to high incidence of begomovirus infections. This study was intended to survey for CMD to determine incidence and distribution of the causal begomoviruses. A diagnostic survey of CMD was carried out in main growing areas of Western Kenya. Symptomatic leaf samples and hardwood stem cutting were collected and analysed by ELISA and PCR. Socioeconomic data obtained from the questionnaire was analysed by SAS. Land allocated for cassava production was found to be small and positively correlated to yield. Poor planting methods, diseases, pests and small land allocated to cassava production were found to be the leading causes of poor yields. Phytosanitary measures such as rogueing, uprooting of diseased plants and crop rotation were found to be majorly practised as ways of overcoming the constraints in cassava production. CMD symptoms observed in the field were very severe.CMD incidence was found to lie between 2 – 54% in the surveyed area, although the incidence was not significantly different among the surveyed districts. ACMV, EACMV and EACMV-Ug were detected in most samples and thus found to be widely distributed in the surveyed area with EACMV-Ug highly displacing ACMV. To increase cassava production, it is recommended that cassava farmers be educated on cassava diseases and their control and on proper agronomic practices and marketing.Urgent measures have to be devised to curb the alarming spread of EACMV-Ug that is rapidly displacing ACMV.

PP-097: Genetic diversity and geographic distribution of cassava mosaic geminiviruses in Mozambique

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Cassava mosaic geminiviruses (CMGs) show large diversity because their genomes have a high plasticity, and variations can occur naturally due to inter- and intra-species recombination. Geminiviruses can recombine and exchange sequences between genomic components. Intra- and interspecies recombination events have contributed to begomovirus diversity and evolution. In sub-Saharan Africa, six distinct species of CMGs have been sequenced and many genetic variants or isolates have also been reported. In order to determine the biodiversity of CMGs in Mozambique, 285 infected cassava leaf samples were collected throughout the six provinces in Mozambique in 2005 and 2006. Of these 109 were screened by PCR using core coat protein (CCP) universal primers for begomoviruses. Sixty samples revealed positive CCP amplification. Many of the samples were degraded due to lack of cooling or freezing facilities in some of the remote districts. From the 60 CCP- positive samples, full-length DNA A amplification was performed (either by Rolling Circle Amplification (RCA)-PCR or PCR from Total Nucleic Acid) from 55 of the leaf samples. Restriction Length Fragment Polymorphism (RLFP) analysis was undertaken using the enzymes *EcoR*V, *Dra*I and *Mlu*I. The results showed that 63.4% (35 of the 55 cassava leaf samples) were EACMV, 12.7% (6/55) were ACMV species; 12.7 (7/55) were mixed infections of EACMV and ACMV; and 6 samples were not unidentified by RFLP. However, RFLP was not able to distinguish between EACMV and EACMMV and EACMCV. Six full-length DNA A clones, one from each province, showing unusual RFLP patterns, were cloned and sequenced. Consensus sequences were aligned with other cassava begomoviruses and selected begomoviruses from southern Africa. Phylogenetic analysis (parsimony) revealed that virus isolates from Maputo, Inhambane and Nampula Provinces exhibited 95-97% nucleotide sequence divergence/similarity to *African cassava mosaic virus*-[Nigeria]; the virus isolate from Gaza Province was 99% similar to *South African cassava mosaic virus* - [South Africa]; while the Zambezia Province virus was most closely aligned (94%) with EACMMV (*East African cassava mosaic Malawi* virus- [Malawi: MH]).The isolate from Cabo Delgado aligned most closely (96%) with the *East African cassava mosaic Cameroon virus*- Cameroon, and less closely (87%) to EACMMV. This study reports, for the first time, diversity for cassava begomovirvus species in Mozambique, similar to previous studies in South Africa, and demonstrates the mixture of geminivirus species from east and west Africa. Sequence variation of > 92% indicates that the cassava geminiviruses in Mozambique are genetic variants ACMV-[NG], EACMMV and EACMCV. This is the first report of SACMV in Mozambique.

PP-098: Occurrence and distribution of viruses infecting tomato and pepper in Alibori in northern Benin

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In Benin, tomato and pepper are the most produced crops in dry season in the department of Alibori. Their production is unfortunately undermined by viral diseases leading to a huge yield loss. In this study we assessed both occurrence and distribution of tomato and pepper viral diseases throughout the department of Alibori in northern Benin. Surveys were conducted in 2011 and 2012 in Malanville, Karimama and Kandi districts in order to collect tomato and pepper leaf samples carrying symptoms of viral diseases. Weed samples were also collected. Four hundred and eighty one (481) samples were collected and analyzed by Enzyme-Linked Immuno Sorbent Assay (ELISA) using 11 specific polyclonal antibodies allowed to detect the viruses usually met on tomato and pepper worldwide. Seven (07) viruses -Cucumber Mosaïc Virus (CMV) - Pepper Veinal Mottle Virus (PVMV) - Paprika Mild Mottle Virus (PaMMV) - Tobacco Mosaïc Virus (TMV) - Potato Virus Y-nécrotic (PVY-n) - Pepper Mottle Virus (PepMoV) and Tomato Yellow Leaf Curl Virus (TYLCV) were detected on pepper, and five (05) viruses on tomato - PVY – CMV – TYLCV - TMV and PaMMV. Pepper was more infected than tomato, and mixed cases of infections of types PVMV/PVY-n (8.16%), CMV/PVMV (6.70%) and CMV/PVMV/PVY-n (4.60%) were detected. PVMV (56.74%), CMV (53.37%) and PVY-n (33.71%) were the viruses which prevail on pepper. These viruses were detected on 5 species of weeds, *Euphorbia hirta, Moringa oleifera, Leucas martinicensis, Combretum micranthum and Abelmoschus esculentus*. PVY-n (70.59%), CMV and TYLCV (17.65%) were the most important viruses on tomato. These viruses were detected on tomato or pepper in all the prospected districts. The highest incidence of the viruses was raised on pepper with Malanville (56.18%) followed by Karimama (39.32%). The intensification of tomato and pepper production in Alibori indicates that the impact of the viruses on the yield will be more increased if suitable control methods are not found to eliminate the inoculums sources.

PP-099: Occurrence of a new strain of *Tomato leaf curl Sudan virus* in association with the old betasatellite from Oman

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Tomato leaf curl disease (ToLCD) is one of the devastating diseases of tomato around the globe. Several begomoviruses/begomovirus-betasatellite complexes have been known to be associated with the disease. Different isolates of *Tomato leaf curl Sudan virus* (ToLCSDV) are also involved in this complex. Here we have reported a new strain of ToLCSDV from the North and South regions of Oman. Analysis of the full-length sequences of three begomovirus clones showed them to be the isolates of ToLCSDV. The three isolates are most closely related to the isolates of ToLCSDV from Yemen with more than 92% nucleotide sequence identity, when analyzed phylogenetically. Upon closer inspection, the sequences of ToLCSDV-OM showed them to be the recombinants of ToLCOMV [FJ956700], ToLCSDV-YE [JF919733] and ToLCSDV-Sha [AY044139]. Significant differences were observed in the sequence of Rep proteins when compared with other available sequences. The three virus isolates were found to be associated with a common Tomato yellow leaf curl betasatellite-Oman (ToYLCB-OM [DQ644566]). We propose the name for this new strain as "*Tomato leaf curl Sudan virus*-Oman strain [ToLCSDV-OM]". Significance of this finding, possible ways of introduction of this virus and spread are discussed. To our knowledge, it is the first report of ToLCSDV from Oman.

PP-100: The use of FTA® Classic Card Technology for building epidemiologic intelligence of plant viruses

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Accurate diagnosis of a plant virus is the first step for elucidating its ecology and epidiomiology and deploying appropriate disease management strategies. Due to the lack of adequate facilities in many developing countries for diagnosis of viruses, alternative methods are needed whereby plant samples from farmers' fields can be collected, processed and transported to laboratories having adequate facilities and expertise for reliable and accurate detection of viruses. For this purpose, we evaluated the use of FTA® Classic Cards in sample collection and shipment for identification of plant viruses. Plant samples suspected for virus infections, based on visual symptoms, were collected from crops grown in farmers' fields from India, Bangladesh, Nepal, Cambodia, Tajikistan, Indonesia, and Nigeria, pressed gently on FTA cards, allowed to air dry and brought to a central facility for virus testing. Using a simplified protocol, nucleic acids bound to FTA card matrix were eluted and used in RT-PCR or PCR for the detection of viruses. The amplified DNA fragments were cloned and nucleotide sequence determined. The derived sequences were compared with corresponding sequences available in GenBank to confirm identity of virus(es) present in individual samples. The results showed presence of distinct virus species belonging to the genera *Begomovirus*, *Potyvirus*, *Tospovirus* and *Cucumovirus* in several samples. Since FTA card matrix is impregnated with denaturing agents that protects viral nucleic acids from plant inhibitory compounds, viral nucleic acid bound to these cards is stabilized and inactivated such that FTA cards do not pose any risk of spreading alien pathogens from one country to the other. Thus, FTA cards can be shipped via standard mail or transported at ambient temperature and amenable for processing large number of plant samples for virus diagnosis. The cards can be stored indefinitely for downstream applications such as virus diversity analysis and molecular characterization of viruses.

PP-101: Multiplex RT-PCR assays for the simultaneous detection of cassava mosaic virus and cassava brown streak viruses

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Uniplex and multiplex reverse transcription-polymerase chain reaction (RT-PCR) protocols were developed for the detection of cassava brown streak viruses (CBSVs) in single and mixed infections with cassava mosaic begomoviruses (CMBs) in cassava. CMBs contain ssDNA as their genome (genus *Begomovirus*, family *Geminiviridae*) while CBSVs are made up of positive sense ssRNA (genus *Ipomovirus*, family *Potyviridae*), and they cause the economically important cassava mosaic and cassava brown streak diseases, respectively, in sub-Saharan Africa. Diagnostic methodologies have long been available for CMBs but they are limited for CBSVs especially in mixed infections. In this study, the two CBSVs, *Cassava brown streak virus* (CBSV) and *Cassava brown streak Uganda virus* (CBSUV) occurring singly or in mixed infection with CMBs, *African cassava mosaic virus* and *East African cassava mosaic virus* were detected in a single RT-PCR using both previously described and newly designed virus-specific primers. Protocols were highly efficient for detecting CBSVs compared to the existing methods and have great potential to minimize sample handling and contamination. As well as improving the diagnosis of cassava viruses, the development of multiplex RT-PCR protocols have revealed the common occurrence of mixed infections by CBSV and CBSUV in cassava fields of Tanzania and Kenya, which was contrary to the common belief until recently that these two viruses have existed separately. These protocols have implications for diagnosis and epidemiological studies on cassava virus diseases in Eastern Africa.

P102: Diagnosis and molecular characterization and of viruses expressing similar necrotic symptoms in blackgram (*Vigna mungo* L. Hepper) and greengram (*Vigna radiata* L. Wilczek)

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In the present scenario, viruses causing necrosis, transmitted by thrips has assumed epidemic proportions in different crops and became a serious production constraint in blackgram and greengram. Leaf curl disease caused by *Peanut bud necrosis virus* (PBNV) is considered a major threat. Recently, *Tobacco streak virus* (TSV) has also been reported to be a cause of leaf curl symptoms paving a way for confusion in field diagnosis to assess the disease incidence. Although both the viruses cause necrosis and are transmitted by thrips, the method of transmission and virus vector relationships vary and need different approaches of management practices. Symptomatic leaf samples were collected from various locations of Andhra Pradesh, and subjected to DAC-ELISA against TSV and PBNV polyclonal antisera. The samples tested positive to PBNV (PBNV-BG, PBNV-GG) and the samples positive to TSV (TSV-BG, TSV-GG) expressed typical symptoms in infectivity tests. The nucleocapsid protein (N) gene of PBNV-BG and PBNV-GG and coat protein (CP) gene of TSV-BG and TSV-GG were amplified by RT-PCR yielding a fragment of the expected size, ca. 830 bp and ca. 700 bp, respectively. The determined nucleotide sequences of PBNV and TSV isolates of blackgram and greengram were deposited at GenBank: FJ749261 (PBNV-BG), FJ749262 (PBNV-GG), FJ749259 (TSV-BG) and FJ749260 (TSV-GG). The sequenced region in PBNV isolates of blackgram and greengram contained a single open reading frame of 831 bases that could potentially code for a protein of 276 amino acids while the sequenced fragment of TSV isolates of both the crops contained a single open reading frame of 717 bases that could encode for a protein of 238 amino acids. Each isolate was individually compared with the other corresponding gene sequences of PBNV and TSV isolates from different crops and locations, recorded in India, using BioEdit. Dendrograms based on nucleotide and deduced amino acid sequences of the N gene and CP gene revealed that the PBNV and TSV isolates originating from different hosts and locations in India clustered in different branches according to their sequence identities and PBNV-BG and TSV-BG were most closely related to PBNV-GG and TSV-GG, forming one cluster, respectively. Comparative sequence analysis revealed that PBNV-BG shared maximum sequence identity with PBNV-GG at nucleotide (99.7%) as well as amino acid (100%) levels, while TSV-BG isolate shared hundred per cent sequence identity with TSV-GG at nucleotide as well as amino acid levels. Nucleotide and amino acid identities of PBNV-BG&GG and TSV-BG&GG isolates with twenty other PBNV and TSV isolates, recorded in different ranges *viz.,* PBNV-BG&GG 93.2 to 97.9 % and 96.3 to 97.4% (nucleotide identities), 94.5 to 99.6%, 95.5 to 99.4% (amino acid identities), TSV-BG&GG 98.1 to 99.3 % (nucleotide identities) and 95.7 to 98.3% (amino acid identities). Since, the N-genes and CP genes are highly conserved (>90%) with other PBNV and TSV isolates; It is proposed that PBNV-BG&GG and TSV-BG&GG isolates should be regarded as strains of PBNV and TSV, respectively, already existing in India.

PP-103: Presence and distribution of *Banana bunchy top virus* (BBTV) in South-Western Democratic Republic of Congo

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Banana bunchy top virus (BBTV) is one of the most severe and widespread viruses limiting production and distribution of planting material of banana (*Musa* spp.) crops in the world. In Democratic Republic of Congo (DRC) where these crops play a major role in daily life of almost 70% of population, epidemiological surveys were conducted in experimental stations and farmers' fields in five provinces with the objective to evaluate the presence and distribution of the *Banana bunchy top virus*. A total of 174 *Musa spp.* leaves samples were collected and analyzed by PCR (Kumar et al. 2011). The results of the study revealed the presence of BBTV in all provinces investigated with a frequency of 6.3% in Bandundu, 12% in Kasaï-oriental, 17.8% in Bas-Congo, 1.1 % in Katanga, 7,4% in Kinshasa urban and peri-urban. Our results also revealed that BBTV occur both in dwellings gardens and farmers' fields. In farmers' fields, all cooking and dessert bananas were local types. The high incidence of BBTV seem to be linked to multiple introduction of planting material in the Bas-Congo province between 1990 and 2002 (Bakelana 2005). However, the province of Katanga has not experienced the introduction of planting material. This factor would explain the low incidence of *Banana bunchy top virus* in the province. The results indicate that there is a real need to facilitate access to genetically improved and healthy certified planting material in these provinces.

Kumar, P. L. et al. 2011, *Virus Research* 159, 171-182.
Bakelana, B., 2005, *Musafrica,* Vol (2), 1: 11 -13.

PP-104: Viruses of tomato and pepper in southwest Nigeria and their distribution

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Tomato and pepper are important vegetable crops grown in Nigeria which accounts for 50% of the African production. Understanding the diversity of pathogens infecting these crops is a prerequisite for breeding resistant cultivars where none currently exist as a means of improving the production. During a survey of virus diseases on pepper and tomato crops in three states of southwest Nigeria in 2011, a total of 113 leaf samples comprising 58 tomato and 55 pepper leaf samples were collected from farmers' fields. To determine the identity of the viruses, specific polyclonal antibodies were used in enzyme-linked immunosorbent assay (ELISA) to index for viruses. Four viruses, *Potato virus* Y (PVY), *Tomato mosaic virus* (ToMV), *Cucumber mosaic virus* (CMV), and *Pepper veinal mottle virus* (PVMV) were detected in 3.5%, 10.6%, 13.3%, and 57.5% of the leaf samples respectively. The distribution of viruses on tomato was 5.2%, 6.9% and 43.1% for CMV, PVY and PVMV, while for pepper it was 21.8%, 21.8%, and 72.7% for CMV, ToMV and PVMV, respectively. The most prevalent virus on tomato and pepper was PVMV which occurred in all the states surveyed in Southwest Nigeria, similarly, CMV was detected in pepper crops in all the states surveyed. Mixed viral infections were few, PVY + PVMV occurring only in one tomato leaf sample while PVMV + CMV occurred on three pepper leaf samples. The diseases caused by these viruses cause a significant limiting factor for the sustainable production of these vegetables especially for smallholder farmers of southwest Nigeria. Thus, a complete understanding of a virus pathosystem is vital for developing targeted solutions for stable production of quality vegetables in Southwest Nigeria.

PP-105: Diagnosis and characterization of viruses implicated in mixed infections of *Amorphophallus paeoniifolius*

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Amorphophallus paeoniifolius (Dennst.) Nicolson or elephant foot yam is a tropical tuber crop belonging to the aroid family *Araceae* is an economic food crop in India and generally used as a vegetable and for its medicinal characteristics. Symptoms indicating virus diseases occur wherever plants are cultivated and range from mild mosaic to severe leaf curling, malformation of leaves and stunting of entire plants. Only Dasheen mosaic virus (DMV) has so far been found in this crop. To investigate on the virus status of Amorphophallus, leaf samples were collected from different growing areas in India to identify the putative viruses. In electron microscopy, only filamentous flexuous particles indicating potyviruses were found. RT-PCR with Potyvirus genus-specific primers were resulted in approx. 1.7 kb fragments which upon sequence analysis showed relatedness to DMV but with remarkable sequence variations clustering DMV isolates from Amorphophallus in 2 distinct groups. In PCR using Badnavirus specific primers, 550 bp fragments also were obtained, however sequence analysis provided no evidence for episomal viruses and rather genome integrated sequences of ancestral Badnaviruses have to be assumed. Using RCA putative geminivirus sequences were also amplified however, these findings are pending for further confirmation. At this point it can be assumed that the main virus causing Amorphophallus mosaic disease are isolates of DMV showing a remarkable genome variation which might also be reflected in differences of virus symptoms. Several isolates of DMV were subjected to mechanical transmission trials resulting in an infection of *Nicotiana benthamiana* with one isolate only. This was further propagated in this host and antisera against purified preparation of DMV from Amorphophallus were raised. ELISA and lateral flow assays were developed and proved robust and sensitive for virus detection of samples collected in the field.

PP-106: Distribution of banana bunchy top disease (BBTD) across the main plantain and banana growing regions of the Democratic Republic of Congo

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Bananas and plantains (*Musa* spp.) are important food crops in the Democratic Republic of Congo (DR Congo). Banana bunchy top disease (BBTD), one of the most important constraints for banana and plantain cultivation in DR Congo observed in 1958 at Yangambi research station. Since then, it has been reported in Bas Congo and the Kivus. But disease spread throughout the other *Musa* growing regions has not been studied. Study was then carried out during 2009-2012 to determine the incidence and severity of BBTD in 9 on 11 banana and plantain producing provinces in the Congo basin to assess the geographical spread of the virus and its aphid vector. TAS-ELISA was also carried out for confirmation of the disease. As results, an average of 87% disease incidence was observed across the Oriental province. Disease severity levels were however low. Only 9.6% of mats had advanced disease symptoms. All plantain and banana cultivars grown in farmers' fields were susceptible to the disease. The vector *Pentalonia nigronervosa* was found on 82.3% of all assessed mats and several simple colonies without winged insects were most frequently observed (on 37.8% of mats with aphids). All samples collected in the surveyed provinces with a typical bunchy top appearance (scores 4 and 5) had positive TAS-ELISA results. However, 40% of symptomless plants tested positive. The results suggest that BBTD is widespread and disease severity is relatively low in most of the surveyed provinces with a corresponding limited impact on production in short term. There is however an urgent need to carry out TAS-ELISA testing in order to identify BBTD-free plants for multiplication and distribution of disease-free planting materials to limit the spread of the disease.

PP-107: Passion fruit woodiness virus disease in Kenya: genome characterisation of the casual agent

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Passion fruit production and longevity is hugely constraint by passion fruit woodiness virus disease in Kenya. While reports from other countries have implicated several viruses as the causes of PWD, it is so far unknown which one of them is the primary causal agent in Kenya. In 2008 and 2009 symptomatic and asymptomatic leaf and fruit samples were collected from nine agroecological zones. The presence of viral infection was confirmed using ACP-ELISA and molecular assays. A viral particle was isolated and initially characterized using primers designed from known Australian and East Asian passion fruit woodiness viruses. The 3' and 5'-ends of the isolated viral particle was rapidly amplified using SMARTer RACE kit, cloned and subjected to high throughput sequencing. The contigs assembled from the sequence reads were subjected to BLAST to identify the potential viruses. One large 9,907 nucleotides long contig was assembled and predicted to encode an uninterrupted open reading frame (ORF) of 3,184 amino acids. It was determined to be the genome of a new *Cowpea aphid-borne mosaic potyvirus* (CABMV) referred to as Kenya isolate 1 (K1). The genome of K1 isolate is predicted to be is 99% complete, missing only about 20 nt at the 5'end. The identification of CABMV confirms previous reports elsewhere showing CABMV as one of the main cause of PWD and is implicated as the primary agent of this disease in Kenya. Future work should focus on production of an antibody that reacts to CPs of this virus and develop immunological procedures that will facilitate screening of passion fruit seedlings and rootstocks, leading to effective management of PWD

PP-108: Quarantine viruses of strawberry

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Raspberry ringspot virus (RpRSV), *Strawberry crinkle virus* (SCV), *Strawberry latent ringspot virus* (SLRSV) and *Strawberry mild yellow edge virus* (SMYEV) are quarantine viruses that should be avoided on strawberry (but also on *Rubus* and *Prunus* for RpRSV and SLRSV) propagation material in all strawberry growing regions. In order to assess the prevalence and status of these four regulated viruses in Belgium, an extensive survey was organized during the past two years. Approximately 1000 samples were collected and tested taking into account a balanced geographical distribution based on production and historical/recent outbreak information. Duplex PCR techniques were used to detect the viruses, grouping both aphid transmittable viruses, SCV ans SMYEV, and both nematode transmittable viruses, RpRSV and SLRSV. In both consecutive survey years outbreaks of SCV and SMYEV were observed in strawberry. In the 2011 and 2012 growing season SMYEV was detected at 5 and 3 locations, respectively. SCV was detected twice in 2011 and three outbreaks were pinpointed in 2012. Outbreak sites were dispersed over the whole of the Belgian strawberry growing area and on each site a monitoring strategy was set up, including sampling and testing of the aphid vectors. None of the nematode transmitted viruses was detected during the survey. Their status can therefore be considered as *'absent'.* The obtained status information on the four viruses was put in a database following ISPM8 guidelines and transmitted to the federal authorities and will contribute to review the regulation status of these viral pathogens in Belgium.

PP-109: Distribution of CBSD causing viruses in different cassava tissues

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Cassava brown streak disease (CBSD) is caused by two viruses; *Cassava brown streak virus* (CBSV) and *Ugandan cassava brown streak virus* (UCBSV). The disease expresses yellow vein clearing symptoms in older leaves, but more strikingly necrotic lesions on stems and within storage roots. However, little is known about within-host distribution of the viruses in infected plants in single or mixed infections. Thus, it is not clear whether the variation in symptom expression and the rapid spread of CBSD is attributable to virus distribution in the host and availability to feeding vectors at the tender leaves of the plants. In this study, we investigated within-host distribution of the viruses in naturally CBSD-infected cassava. Leaf and root tissues were sampled from plants of CBSD susceptible cassava cultivars, cv. 60444 and TME 204, and from plants of six transgenic cv. 60444 events growing within Namulonge, a CBSD hotspot in Uganda. Total RNA was extracted from the plant samples and subjected to RT-PCR and quantitative PCR (qPCR) assays using species specific primers to detect and quantify the two CBSD infecting virus species; CBSV and UCBSV. The viruses were detectable in 87.7% of all leaf tissues sampled compared to 58.9% and 53.3% (n = 90) of all peel and root tissues sampled, respectively. UCBSV was undetected in all tissues of transgenic cv. 60444 events, whilst CBSV was detected in 83.3% (n = 60) of these tissues. Of all samples collected from wild type cv. 60444 and TME 204 combined, CBSV/UCBSV dual infection was detected in 41.4%, 27.6% and 51.7% (n = 29) of leaf, peel and root tissues, respectively. Quantitative PCR analyses, on average, showed that younger leaf tissues had lower virus concentrations compared to older tissues. These results show that both CBSV and UCBSV managed to infect all organs in the host, and are not mutually exclusive in all tissues.

PP-110: Molecular characterization of DNA satellites associated with cassava mosaic geminiviruses

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DNA satellites are subviral agents that require proteins encoded by the helper virus for their replication, movement and encapsulation. The interaction of the DNA satellites with begomoviruses leads to different symptom expression of CMD with a likelihood of increasing disease severity. The symptoms manifest themselves by leaves infected by begomoviruses assuming a sickle shape. This study aimed at characterizing the DNA satellites associated with the CMGs in Kenya and further describe symptom modulation of the disease. Plants with severe symptoms associated with begomoviruses were sampled during the survey and tested by PCR using Sat III F/R primers. Selected positive samples were sequenced and characterized by sequence identity analysis, phylogenetic analysis and genetic distance evaluation. The integrated satellites in this study were distantly related to begomoviruses associated DNA III satellites (AY836367) found in other parts of Eastern Africa with a sequence similarity of 30%. They were also distantly related to the EACMV-Di (defective interference) DNA molecules (AY676464) and the Tobacco leaf curl virus defective DNA satellite (AF368275) from Zimbabwe at sequence similarity of 35%. The sequences of the satellites from the study exhibited high levels of variability ranging from 40% to 95% with some showing low similarity (29%) with Genbank sequences of the Mentha leaf DNA II satellites from India. Evolutionary distance analysis showed high variability with over 60 nucleotide substitution. Cassava varieties co-infected with CMGs and the associated DNA satellites were characterized by enhanced symptom severity compared to the same varieties infected with CMGs only. More studies in the CMD symptom modulation in the presence of DNA satellites and the economic importance on the crop need to be initiated.

PP-111: A satellite virus associated with Brome mosaic virus isolated from winter wheat and triticale plants in the Russian Central Cernozem region

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Cereal plants displaying yellow dwarf symptoms contained high concentrations of *Brome mosaic virus* (BMV) as detected by DAS-ELISA and immunoelectron microscopical decoration tests. No Barley yellow dwarf luteovirus or Wheat dwarf geminivirus was detected in the material originating from a German-affiliated breeding company located in the Central-Cernozem region of Russia. BMV isolates from winter wheat and triticale were obtained by mechanical inoculation of test plants. In addition to BMV particles of 28-30 nm in diameter both isolates contained smaller spherical particles of 18 nm in diameter. The wheat isolate (BMV-R-W) was selected for further investigation and propagated in winter barley cv. 'Erfa'. Virus particles were purified by density gradient centrifugation. A broad, more diffuse lower band was observed after ultracentrifugation containing typical BMV particles of approximately 30 nm and a minor upper band filled with smaller particles of around 18 nm in size. RNA extracted from purified BMV-R-W consisted of four RNAs characteristic for normal BMV isolates whereas the particles from the upper band contained RNA of approximately 1200 nucleotides. Sequencing revealed an open reading frame coding for a protein of 155 amino acids. Multiple alignments showed about 50 % identity to P20 protein encoded by Bamboo mosaic virus satellite RNA and to capsid protein of *Panicum mosaic satellite virus*. There are several identical amino acid motifs including an arginine-rich N-terminal domain. Collectively we conclude that a hitherto unknown satellite virus of BMV was identified. Further studies are necessary to support the conclusion that among RNA viruses with jelly roll capsid proteins such a helper virus - satellite virus interaction exists not only for members of *Tombusviridae* (STNV, MWLMV, and PMV) and *Virgaviridae* (STMV) but also for BMV, the type member of the genus *Bromovirus* within the family *Bromoviridae*

PP-112: Potato virus distribution in different agro-ecological conditions of Uzbekistan

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Farmers in Uzbekistan usually do not follow good practices when it is matter of planting potato in their field. They do select small size potatoes for propagation from the stock of potatoes stored in their cellars or cut large tubers seed with the result that they ensure a continuous perpetuation of virus diseases in their fields. Because of these continuous practices and the use of imported seed from Europe that became common in the last twenty years, we wanted to investigate the potato virus distribution in the country as well as the presence of Phytoplasma-like diseases. After examining past literature to better know precedent situation, a survey by local specialists engaged by CIP-Tashkent was undertaken in the regions of Tashkent and Samarkand, the major potato producing areas of Uzbekistan. Results from the DAS-ELISA test on potato leaves taken from 30 fields revealed that fields in Samarkand region appeared more infected by potato virus diseases than those in Tashkent region. The mean virus distribution in the two years (2007-2009) was equivalent to 93.6 and 27.2% for PVY, 45.3 and 16.5% for PLRV and 34.1 and 52.2% for PVS in Samarkand and Tashkent regions, respectively. Consequently, infected potato fields would serve as a source for secondary spread by resident insect vectors to neighboring fields causing greater yield losses and affecting the quality of potatoes produced. Samples analyzed by radioactive NASH technique gave 3 positive results to PSTVd in Tashkent and 8 for Samarkand regions. Some samples sent to a referenced laboratory in UK to perform PCR so as to determine the presence of phytoplasmas gave negative results in all cases. Furthermore, no PMTV was detected in the spotted membranes through the test by NCM-ELISA. The following solutions would improve the situation: introducing farmer-participatory approaches to bring awareness about virus diseases and the value of selecting virus-free potato tubers for new plantings; the application of a set of practices currently considered as part of an Integrated Disease Management approach and capacity building to update background knowledge of local specialists.

PP-113: Developing banana bunchy top virus-free Planting material in Kisangani, Province oriental, DR Congo

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Bananas and plantains (*Musa* spp.) are one of the major food crops in the Democratic Republic of Congo (DRC). Banana bunchy top disease (BBTD), caused by the Banana bunchy top virus (BBTV) transmitted by the banana aphid *Pentalonia nigronervosa*, is considered a major constraint, not only to banana and plantain production, but also to banana and plantain biodiversity reduction. A pilot strategy to develop a clean *Musa* seed system focusing on reducing the spread and impact of BBTD and multiplying highly productive clones of preferred cultivars was tested in Kisangani (Oriental Province, DRC). Suckers selected from asymptomatic mats were multiplied locally using macropropagation techniques. Resulting plantlets were grown under screen house conditions for 6 months with monthly serological testing for the presence of the virus before BBTV-free plantlets could be subsequently transplanted *in situ* in BBTD hotspot conditions. TAS-ELISA based results indicate that 32% of symptomless plants collected in the field harbored the virus. Moreover, no cases of secondary infection were observed during the 12 months spanning the phases of macropropagation and growth in the screen house. BBTV-free plantlets around 50 cm in height were established in three distinct sites, varying in their location (adjacent, 100m and total isolation) to existing infected banana plots, and followed up for a period of one year. At Masako (experimental plantation located adjacently to BBTD-affected plots), the presence of the vector varied from 34.3 to 97.8% and TAS-ELISA confirmed BBTD symptoms that appeared after 3 months at the rate of 1.38% increasing to 4.2% after 12 months. In the distantly located field, the presence of the vector varied from 15.7 to 51.6% with BBTV-positive plants equally appearing 3 months after establishment at the rate of 1.4% increasing to 2.4% the fourth month. Following prompt removal of symptompatic plants in both sites, no further cases were observed. At Yangambi, monthly scouting of the 290 plants transplanted in a very isolated primary forest did not reveal the presence of the vector nor BBTD symptoms after 6 months. These results suggest the possibility of establishing a BBTV-free planting material production system in Kisangani region conditions.

PP-114: Incidence, symptom severity and distribution of tomato viral diseases in Uganda

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A survey was conducted to assess the incidence, symptom severity and distribution of viral diseases in 71 tomato fields in eight districts of Uganda including: Kasese, Mbarara, Mpigi, Luweero, Ntungamo, Rukungiri, Kamuli and Mbale during April to June 2010 and August to September 2010. In addition, 127 virus isolates were collected for further serological identification. There were significant differences (P=0.01) in disease incidence between the districts. However, disease symptom severity varied significantly (P=0.05) in season two only. Kasese had the highest disease incidence (88.2%) and severity (3.6), while Kamuli had the lowest incidence (14.0%) and severity (2.2). Variety Roma and Marglobe had the highest (77.9%) and lowest (55.6%) disease incidence, respectively. On average, variety Money maker and Heinz had the highest disease severity (3.6) and lowest severity (3.1), respectively. ELISA results detected five viruses on tomato including: *Tomato mosaic virus* (ToMV), *Tobacco mosaic virus* (TMV), *Cucumber mosaic virus* (CMV), *Tomato spotted wilt virus* (TSWV) and potyviruses using ELISA. The distribution of the tomato viruses is also discussed.

PP-115: Host range and incidence of European mountain ash ringspot-associated virus in the Czech Republic and other European countries

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European mountain ash ringspot-associated virus (EMARAV) is present in Germany, Finland, north western Russia and Austria. Typical symptoms of infection are light rings, spots or variegation on *Sorbus aucuparia* leaves. In 2010, mountain ash trees showing ringspot symptoms were found around the Czech capital Prague. RT-PCR tests were performed (Mielke et al., 2008) and products of predicted lengths were obtained from all symptomatic plant samples. The partial EMARAV putative nucleoprotein gene fragments of two Czech isolates were amplified (Kallinen et al., 2008) and sequenced in both orientations (No. FR751461 and FR751462). Comparisons of nucleotide and deduced amino acid sequences of the isolates with several sequences from GenBank showed identities ranging from 97 to 99% at the nucleotide level and 100% at the amino acid level. To our knowledge, this is the first proof of EMARAV occurrence in the Czech Republic. Successively, virus-free plants consisted of *Sorbus*, *Amelanchier*, *Crataegus*, *Malus* and *Pyrus* species and varieties were inoculated by chip budding in 2011 using buds from EMARAV infected mountain ash trees. In 2012, the 204 bp EMARAV-specific cDNA fragment was obtained from most tested species. Due to these results, the EMARAV woody host range was extended by new species and varieties of *Sorbus* and for the first time by *Malus*, *Pyrus*, *Amelanchier* and *Crataegus* species. Clear cut symptoms associated to EMARAV were exhibited by the some *Sorbus* and *Amelachier* species. Finally, a survey of infected trees was performed all over the Czech Republic. Infected trees were found in most localities checked, sometimes with a rather high prevalence (up to 70% of tree populations), suggesting that EMARAV may be rather widespread in this country. Limited survey was also done in other European countries. EMARAV was found in Slovakia and Italy.

PP-116: Incidence, symptom severity and geographic distribution of cassava mosaic disease and associated viruses in Tanzania

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Two comprehensive surveys were conducted between March-April in both 2009 and 2012 to assess the incidence, symptom severity and geographic distribution of cassava mosaic disease (CMD) and the associated cassava mosaic begomoviruses (CMBs) within 12 regions in 4 main agroecological zones: Lake Victoria Basin, Eastern zone, Western zone and Southern Highlands in Tanzania. In all 309 fields surveyed in 2009 and 2012, CMD symptoms were observed in 86.4% (267) of the surveyed fields. Overall CMD incidence averaged 50% and 27% in 2009 and 2012, respectively. CMD incidence differed significantly ($P<0.05$) between agroecological zones. It was highest in Eastern zone where it ranged between 46 and 65% in 2009 and 34.2 and 100% in 2012, and lowest in the Lake Victoria Basin with 28 to 50% and 11.7 to 29.2% incidence in 2009 and 2012, respectively. Disease severity was generally low and averaged 3.3 and 2.2, in 2009 and 2012, respectively. Of the 384 PCR-assayed leaf samples, 173 were singly infected with *East African cassava mosaic virus* (EACMV), 6 with *African cassava mosaic virus* (ACMV) and 8 dually infected by EACMV and ACMV. EACMV (24/48), ACMV (6/48) and the dual infections of ACMV+ EACMV (5/48) predominated in Kigoma region in Western zone. The Coast region in Eastern zone was affected by only EACMV, which was detected in 1 out of 9 samples. Whitefly population abundance differed significantly ($P<0.05$) between agro ecological zones. We discuss here the significance of these findings on the epidemiology and management of CMD in Tanzania.

PP-117: Two generic PCR primer sets for the detection of members of the genus *Torradovirus*

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Recently, the plant virus genus *Torradovirus* was created within the family *Secoviridae* to taxonomically position two newly described virus species: *Tomato torrado virus* (ToTV) and *Tomato marchitez virus* (ToMarV). In addition to ToTV and ToMarV, two tentative members of the genus *Torradovirus* have been described: Tomato chocolate spot virus (ToChSV) and Tomato chocolàte virus (ToChV). All torradoviruses described so far infect tomato in which they induce necrotic symptoms on leaves and, most of the time, on fruits. Torradovirus particles are spherical with a diameter of approximately 28-30 nm. The torradovirus genome is bipartite and consists of single-stranded plus-sense RNA. The first RNA (RNA1) ranges from 7.2 kb for ToMarV to 7.8 kb for ToTV and has one open reading frame (ORF), which encodes replication proteins like protease, helicase and RNA-dependent RNA polymerase (RdRp). The second RNA (RNA2) ranges from 4.9 kb for ToMarV to 5.7 kb for ToChV and has two ORFs. In comparison to other plant picorna-like viruses, the existence of the first ORF is unique for torradoviruses, but its function is still unclear. The second ORF has coding regions for a putative movement protein and the three coat proteins (~35, 26 and 23 kDa). Two degenerate primer pairs were designed for the universal detection of members of the genus *Torradovirus*. Primer pair Torrado-1F/Torrado-1R was designed to the RdRpregion located in RNA1 and primer pair Torrado-2F/Torrado-2R to a region overlapping the two first coat proteins Vp35 and Vp26 in RNA2. The primers were used in two-step and one-step RT-PCR procedures. Both primer pairs proved to be suitable for the universal RT-PCR detection of torradoviruses and can be deployed for the detection of all currently known and possibly new torradoviruses.

PP-118: Next Generation Sequencing as a quality tool for plant virus collections

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Plant virus collections often contain many old and sometimes unique specimens that have been collected over a prolonged period of time. Upon inclusion in the collection, initial identification of the particular virus was often based on typical host and indicator plant symptoms and properties like serological reactivity. Nowadays, molecular data is of increasing importance for the correct identification of (new) collection material. (RT)-PCR and real-time (RT)-PCR methods, however, rely on the availability of specific sequences and by nature are specific for a particular genus, virus, or virus strain. Therfore, if available, they have their limitations for identification of collection materials, especially in the case of 'new' virus species. With an increased emphasis on the reliability of detection tools, validation of diagnostic tests is becoming a standard. Reference material thereby plays a crucial role in development, validation as well as routine performance of these tests. This puts high demands on the correct identification of virus species and strains used, hence on those present in virus collections. We investigated the possibilities of Next Generation Sequencing using the IlluminaHiSeq platform to study the identity and purity of plant virus isolates from the Dutch National Reference Centre and other collections. This approach generated very large datasets. Deployment of a Bio-informatics pipeline involving a combination of *de novo* and reference assemblies resulted in contigs which could be successfully identified by Blastn and Blastx database searches. This approach not only positively identified particular virus isolates but also generated their near full-length sequences. It revealed impurities, like mixed infections, not encountered when using specific tests. Last but not least, sequence data were obtained of a number of 'new', previously unidentified, plant viruses.

PP-119: Sources of PVY infections in potato fields

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Potato virus Y (PVY) is still a major virus disease in potato crops worldwide both in ware and seed potatoes. It causes very significant economic damage especially by loweringthe quality of seed potatoes. In addition the extensive use of insecticides and mineral oil used to control aphids, the main vectors of PVY, have a significant negative impact on the environment. In the field spread of PVY occurs through non-persistent transmission by several aphid species of which *Myzuspersicae* (Mp) is considered the most important in terms of PVY transmission efficiency. Despite the use of clean seed stocks and extensive aphid monitoring programs PVY infections remain very difficult to control.
It is generally assumed that the main spread of the virus within a potato field occurs through in-flying aphids that acquire the virus from source plants within that field.
To investigate the possible role of external virus sources and relative importance of different aphid species in PVY spread and epidemiology in the field, funnel traps and yellow water traps were used to monitor aphid flights to and in two isolated potato fields. Numbers of 10 different aphidspecies were recorded between April and September. A TaqMan assay was developed to test the presence of PVY in individual aphids caught in these traps. In addition, plants of different common and abundant weed species were tested for PVY infections. Results indicate that the different monitoring traps show differences in the numbers of aphids caught and that a significant number of these aphids, that are likely to originate from outside the potato field, already carry PVY. Given the fact that a number of common weeds were shown to be PVY- infected, this raises questions on the most important sources of PVY infections in potato fields.

PP-120: Plant virome ecology in African farming systems: assessing food security

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Diseases are one of the major constraints to crop production for small-scale farmers in sub-Saharan Africa (SSA). The identification of emerging diseases and associated risks is paramount for improving and safeguarding African food security, especially in the face of climate change. Small farm ecosystems are a complex mix of crop and non-crop plants, insects, vectors and pathogens. The 'maize mixed' farming system, characterized by a combination of maize and other crops grown together within a single farm (e.g., potatoes, beans, banana, rice, sorghum, cassava), is among the most common in SSA. Whilst mixed cropping systems offer resilience to crop loss, they also support greater pathogen and vector diversity. Pathogens thriving in this environment are afforded significant opportunity to recombine, evolve, infect different hosts, and persist perennially, paving the way fornew diseases. This project aimsto assess the overall diversity of viruses in the'maize mixed' farming systems in Kenya. Our effort will include areas affected by Maize lethal necrosis (MLN), caused by a combination of Maize chlorotic mottle virus (MCMV) and Sugarcane mosaic virus (SMV); MLN is causing severe losses in expanding areas of Kenya, also affected by other viruses. Genomics and bioinformatics approaches will be used to gain a better understanding of the factors influencing the spread of viruses in this ecosystem. Next generation sequencing will help characterize the complex mix of hosts, vectors and viruses. A bioinformatics pipeline and aGIS-based information system for collecting, analyzing and reporting all viral data will be developed. Virome comparison, geographical distribution, epidemic establishment and spread between geographical regions will be achieved. Methods for pathogen detection and characterization will be established in the region and information will be disseminated to policy-makers, aimed at strengthening control and response strategies.

PP-121: Status of cassava brown streak in Western Kenya

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Cassava (*Manihot esculenta* Crantz) is constrained by many biotic factors which impact on its production. The most serious are cassava mosaic virus disease (CMD) and cassava brown streak disease (CBSD) which in combination may cause up to 100% yield loss. In 1990s a virulent CMD devastated all cassava landraces in Western Kenya causing a yield loss of >80%.The problem was solved with the adoption CMD resistant cassava varieties. In the recent past years it has been documented that over 50% restoration of cassava in the farmers' fields has been realized. In 2006 CBSD attacked a few cassava varieties in Western Kenya and it has been on the increase every year. The disease causes hard root rot rendering the cassava roots unfit for consumption. A study was conducted in Western Kenya in August/September 2009 to determine the extent of spread of the disease and the damage it had caused to farming communities in the region. The findings of this study indicate that symptoms of CBSD are widespread in all the 15 districts surveyed. The highest CBSD incidence of 27.8% and 44% on the young and old cassava fields were found in Busia district. It was noted that in some districts CBSD symptoms were not seen on the leaves but roots had necrosis. Fields which had high percentage of unusable roots of >3 on a core scale of 1-5 were in districts where CBSV pressure was high. This was a clear indication that some districts have varieties which are highly susceptible to the disease. Distribution of CBSD in Western Kenya is widely localized irrespective of altitude, varieties, presence of whiteflies or age of the crop. The findings provide data which indicate the extent of spread and damage of cassava brown streak disease in Western Kenya and factors which affect distribution of the disease.

PP-122: Cassava mosaic disease and associated viruses in Zambia: Occurrence and distribution

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Cassava mosaic disease (CMD) and associated viruses were assessed in a country-wide survey in seven provinces of Zambia between April and May 2009. CMD incidence was highest in Northwestern (71.2%) and lowest in Western (34.3%) provinces. Disease symptoms were severe in Eastern (3.94) and Lusaka (3.88), moderate in Central (3.54), Luapula (3.48) and Northern (3.31) and mild in Northwestern (3.01) and Western (2.50) provinces. Adult whitefly (*Bemisia tabaci*) populations were highest in Lusaka (2.12) and lowest in Central (0.02) province. Polymerase chain reaction (PCR) detected two virus species: *African cassava mosaic virus* (ACMV) and *East African cassava mosaic virus* (EACMV), that occurred as single and dual infections in 65.4% (ACMV), 25% (EACMV) and 9.6% (ACMV+EACMV) of the positive reactions. None of the samples was positive for EACMV-Ug. This is the first comprehensive report of CMD and the associated viruses infecting cassava in Zambia.

PP-123: Diagnostics in biosecuring agriculture from transboundary plant viruses: a case study of India

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About 130 viruses are transmitted through true seeds and many more infect vegetative propagules. A number of them are of great economic and quarantine significance and can be introduced through import of seeds and other planting material. This calls for stringent quarantine processing of imports. National Bureau of Plant Genetic Resources (NBPGR) is empowered for quarantine processing of germplasm including transgenic planting material imported for research purposes into India. The challenges in virus detection include availability of antisera, viral genome sequences in Genbank, detecting an unknown/ exotic virus etc. Efforts are being made to develop techniques viz., RT-PCR, multiplex RT-PCR, Real-time RT-PCR, LAMP and HDA for detecting viruses of quarantine significance for India. LAMP and HDA are isothermal DNA methods which do not require a thermal cycler and has potential application in quarantine stations dealing with bulk material imported for commercial purposes. Adopting a workable strategy such as post-entry quarantine (PEQ) growing in PEQ greenhouses/ containment facility, electron microscopy, ELISA and RT-PCR, 34 viruses have so far been intercepted in germplasm including transgenics, which includes 11 viruses not yet reported from India viz., *Barley stripe mosaic virus*, *Bean pod mottle virus*, *Broad bean stain virus, Cherry leaf roll virus*, *Cowpea mottle virus, Cowpea severe mosaic virus, Maize chlorotic mottle virus*, *Pea enation mosaic virus*, *Raspberry ringspot virus, Tomato ringspot virus* and *Wheat streak mosaic virus*. Besides, 15 viruses not known to occur on particular host(s) in India were intercepted. The infected plants were incinerated and harvest from virus-free plants was released for crop improvement programmes. The risk of introduction of 34 seed-transmitted viruses or their strains into India was thus eliminated. Adopting the appropriate technique and the right strategy for virus detection would go a long way in ensuring the biosecurity of Indian agriculture from transboundary introduction of plant viruses.

PP-124: Simultaneous detection of DNA viruses infecting sweetpoptato (*Ipomoea batatas*) by multiple PCR

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Sweet potato collusive virus (SPCV, genus *Cavemovirus*), Sweet potato vein clearing virus (SPVCV, genus *Solendovirus*) and Sweet potato leaf curl virus (SPLCV, genus *Begomovirus*) are widespread viruses with DNA genome found in sweetpotato in single or multiple infections. Identification and detection of these viruses are complicated since they frequently are symptomless and occur in low titer in sweetpotato plants. A multiple PCR (mPCR) assay was developed for simultaneous detection of SPCV, SPVCV and SPLCV (and related 'swepoviruses'). Specific forward and reverse primers unique for SPCV and SPVCV were selected and used in the assay together with the degenerate primers for begomoviruses developed by Li et al. (2004). The mPCR assay was optimized for primer concentration and cycling conditions. It was tested using graft-infected sweetpotato plants with one to three target viruses and then validated/evaluated using greenhouse-grown sweetpotato plants coming from CIP's in vitro germplasm collection. This assay showed to be reliable, sensitive and simple. The mPCR assay will be useful to quarantine programs, as a rapid and cost-effective method if a large number of samples are pre-tested before submitting the negative ones to the routine/current indexing procedure.

PP-125: First serological characterization and molecular phylogeny of *Rice yellow mottle virus* in Southern Benin

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Rice yellow mottle virus (RYMV) is the best known rice viral disease indigenous to Africa that causes severe economic losses in farmer's fields. The current study assessed variability of 11 isolates collected in southern Benin using immunological tests with monoclonal antibodies (MAbs). Two serotypes Ser1 and Ser2 were distinguished showing the existence of difference between the RYMV isolates.Sequences of the capsid protein gene were obtained from RT-PCR products and their molecular properties confirmed the serological results. These sequences were used for phylogenetic analysis of the Beninese isolates and showed that strains S1 Benin are the West-Central African lineage and are related to those from Togo and Niger while strains S2 Benin are the stumps of the West African lineage and are related to those from Mali, Burkina and Ivory Coast.Benin is the only country to harbor isolates of these two lineages, a likely consequence of the ongoing RYMV expansion in Africa. All 11 isolates were inoculated to the available 5 differential rice accessions and results obtained showed that they were all virulent on IR64 carrying the resistance allele Rymv1-1. However, none of them was able to attack accession Gigante, Tog5681 and Tog5672 carrying respectively the resistance alleles Rymv 1-2, Rymv 1-3, and Rymv 1-4 & Rymv 2. By contrast, isolates Be20, Be21 and Be27 (all being S2) were able to attack Tog5674 carrying the resistance allele Rymv 1-5.

PP-126: Stable internal reference genes for normalization of real-time RT-PCR in tobacco (*Nicotiana tabacum*) during virus infection

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Real-time RT-PCR is a powerful technique for the measurement of gene expression during infection by various microorganisms including viruses, but its accuracy depends on the stability of the internal reference gene(s) used for data normalization. Tobacco (*Nicotiana tabacum*) is a crop in a number of countries, but is also an important model in studies of plant gene expression during infection; however, reference genes, the expression of which remains stable during biotic stresses, have not been well-studied in the tobacco system. We addressed this problem by analyzing the expression stability of seven potential tobacco reference genes. Primers targeting each gene (*18S rRNA*, *EF-1α*, *Ntubc2*, *β-tubulin*, *PP2A*, *L25,* and *actin*) were developed and optimized. The expression of each gene was then measured by real-time PCR of tobacco cDNAs derived from inoculated and upper leaves of tobacco plants inoculated with *Tobacco mosaic virus*, *Cucumber mosaic virus*, *Potato virus X*, or *Potato virus Y*. The mRNAs expressed from the genes *L25* and *Ntubc2* demonstrated the highest expression stability, followed by *β-tubulin*. Measurement of expression of *L25* and *Ntubc2* was sufficient for accurate normalization in virus-infected tobacco. Stimulation of defense genes in *N* gene tobacco after infection by *Tobacco mosaic virus* was verified using these reference genes, and all techniques were optimized to enable a high-throughput approach. These results provide a foundation for the more accurate and widespread use of real-time RT-PCR for measuring quantitative changes in gene expression during infection of tobacco.

PP-127: Status of yam viruses in West Africa

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Boosting and sustaining yam production in West Africa remains key to enhancing global yam production. Due to its long storage attribute and West Africa's potentials for production, yam is an important food security crop and source of income for millions of people in West Africa. The dip in West African yam production in 2007, which consequentially lead to global dip in yam production, contributed and worsened the food price crises in the region and production has continued to fluctuate to date. Virus diseases, among other factors, are a major constraint to production, international trading and international movement of yam germplasm for research purposes. Viruses belonging to the *Potyvirus, Badnavirus, Cucumovirus, Comovirus, Potexvirus* and *Macluravirus* genera infect yam world wide. We present a chronological review of the identification and characterization of yam viruses and the current status of yam virology research in West Africa and attempt to clarify often conflicting nomenclatures. The current distribution of the more commonly encountered yam viruses across West Africa is also presented. Although viruses accumulate in yam tubers due to vegetative propagation, we found that the incidence and diversity of mixed virus infections in yam field leaf samples were higher than those detected in yam tubers. Co-infection of different virus species enhances the potential for genomic recombination and emergence of more virulent virus strains. Furthermore, synergistic interactions during co-infection often culminate in greater yield losses. Therefore, a proper analysis of the dynamics of interplaying factors contributing to the abundance of mixed virus infections in yam fields would appropriately guide resource allocation, research focuses and ultimately result in more effective virus control strategies.

PP-128: The prevalence of cassava mosaic begomoviruses in Malawi

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Cassava (*Manihot esculenta)* is one of the most important staple crops for farmers in the tropics due to its high calorie content, low production cost as well as ability to adapt to different soil types and climatic conditions. The crop is a staple food for more than 30 percent of Malawians along the central and northern lake shore areas of Lake Malawi and the Shire highlands. However, sustainable production of the crop is hampered by Cassava Mosaic Disease (CMD) which reduces tuber yield by up to 80%. CMD is caused by several species of circular single-stranded *begomoviruses*. Currently, eleven cassava mosaic *begomoviruses* (CMBs) are recognized, of which nine occur in Africa. Two comprehensive surveys were conducted in 2006-07 and 2010 to determine the distribution and diversity of CMBs in Malawi. Diseased samples of cultivated cassava varieties from southern, central and northern Malawi were collected and screened for the presence of CMD-causing viruses using species-specific diagnostic primers by PCR. Results from the analysis of 176 samples indicated that EACMV was widespread through the country; while ACMV and EACMKV were restricted to the north (Chitipa and Nkhata Bay) and south (Phalombe and Thyolo), respectively. EACMZV was absent in the central region but prevalent in the south (Machinga) and north (Chitipa, Karonga and Rumphi) regions. SACMV was diagnosed only in Machinga district.. Survey in 2010 confirmed the continuing prevalence of CMD throughout the main cassava-growing areas of Malawi with an average incidence of 23.8% and mean severity of 2.9. The disease was severe in the central lakeshore areas and southern region. The highest severity score of 4.0 was observed in Nkhotakota district. PCR-based diagnostic tests confirmed EACMV-like viruses are the most predominant CMBs in Malawi. These include EACMV, EACMMV and EACMCV. ACMV or the CMD pandemic-associated EACMV-UG was not detected in the two surveys. In view of the continued widespread occurrence of CMD-causing viruses in Malawi, greater emphasis needs to be placed on the development and deployment of control measures including promotion of resistant varieties.

PP-129: Genetic diversity of the Polish isolates of *Tomato black ring virus* (TBRV)

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Tomato black ring virus (TBRV) is a member of the genus *Nepovirus*, building group "b" with *Beet ringspot virus* (BRSV), *Grapevine chrome mosaic virus* (GCMV), *Olive latent ringspot virus* (OLRV) and *Cycas necrotic stunt virus* (CNSV) (subfamily *Comovirinae*; family *Secoviridae*). In Poland TBRV is classified as a quarantine pathogen on strawberry and raspberry. TBRV infects a wide range of economically important crops: vegetables (zucchini, cucumber, tomato and potato), berry fruits, grapevines, solanaceous and ornamental species and member of weeds. Diversity of the Polish isolates of TBRV was analyzed by the genetic characterization. Isolates were collected from naturally infected *Robinia pseudoacacia* L., *Sambucus nigra*, *Cucumis sativus*, *Solanum lycoperscium* and *Cucurbita pepo.* Primer set (1 MP4 and 3ter) was used to amplify a 1200 bp of RNA1 encoding for RNA dependent RNA polymerase (RdRp). The obtained RT-PCR products were cloned and sequenced. Sequence comparisons were performed basing on 831 nt of RNA dependent RNA polymerase. The sequence alignment was performed using ClustalW and identity matrix was established. Amino acids sequence was also deduced and compared. Analysis revealed high level of the genetic diversity between isolates ranging from 82.9%-99.6% for nucleotides and 88.8%-98.9% for amino acids, respectively.

PP-130: *Potato Virus Y* on Tomato in Poland

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Potato virus Y (PVY) is the member of the *Potyvirus* genus of the *Potyviridae* family and is one of the most widespread viruses infecting potatoes. PVY infection of potato plants results in a variety of symptoms depending on the viral strain. On tomato PVY was first reported in Poland in 2002. Symptoms on tomato vary according to PVY strain, plant age, varieties infected, and environmental conditions. General symptoms on tomato are faint mottling and slight distortion of the leaves. Severe symptoms include dark brown, dead areas in the blade of nearly mature leaflets. In 2012, a collection of several PVY isolates from tomato, originating from commercial fields and greenhouses from different region of Poland was obtained. PVY isolates were characterized by biological and molecular assays. In the RT-PCR four different strains were identified: PVY^{NTN}, PVY^{N} Wi-P, PVY^{N}Wi N242 and PVY^{O} whereas PVY^{N} Wi-P was dominated. The presence of PVY^{C} was not confirmed in any of samples tested. Interestingly, on potatoes in Poland in the majority of samples PVY^{N} Wi-P was detected. Potatoes can be a one of the source for PVY infection due to 40% of infection noticed in potato cultivars. The growing distribution of PVY indicated that the control of the presence of virus vector and avoiding of close neighborhood of tomato and potato cultivars are necessary to avoid PVY infection.

PP-131: Production and conservation of virus-free cowpea germplasm

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Cowpea (*Vigna unguiculata* (L.) Walp) is susceptibility to several economically important viruses, 17 of those have been recognized to spread through its seed. Seed-transmission has a high epidemiological significance as the virus-infected seedling serve as primary sources of virus inoculum in the fields for acquisition and further spread by the insect vectors, and also contributes to long distance spread of viruses through international exchange of germplasm and seed trade. A systematic approach has been initiated to establish virus-free cowpea germplasm held in the IITA genebank that holds world collection of 15,122 accessions of cultivated cowpea from 89 countries. Current efforts target cowpea 'core collection' that constitutes 2,062 accessions of landraces, improved varieties and wild species and also 140 accessions of elite varieties. This paper reports of the efforts to generate virus-free cowpea germplasm during 2011-12. About 20 to 40 seeds of each accession were tested for seed-transmitted viruses by growing-out test, visual examination and virus indexing by enzyme-linked immunosorbent assay (ELISA) for viruses know to be endemic in West Africa *Bean pod mottle virus*, *Blackeye cowpea mosaic virus*. *Cowpea aphid-borne mosaic virus*, *Cucumber mosaic virus*, *Cowpea mottle virus*, *Cowpea mild mottle virus*, *Cowpea yellow mosaic virus* and *Southern bean mosaic virus*. Seed-transmission was between 0 to 45%. Most of the virus positive plants were asymptomatic. Seed were harvested from only plants that have normal growth and tested negative in ELISA and they were conserved further use. High frequency of seed-transmission observed in this study underscores the need for rigorous monitoring of cowpea germplasm prior to conservation and distribution.

PP-132: Sweetpotato virus degeneration study in Lake Zone of Tanzania

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Lake zone (Mwanza, Musoma and Bukoba) is one of the major sweetpotato producing area in Tanzania. However, production is facing many problems including lack of enough clean planting during planting season. This work was conducted to study degeneration of virus on sweetpotato planting materials over time. Tissue culture plantlets for varieties Ejumula, Ukerewe, Polista, Jewel and Kabode cleaned at KEPHIS Kenya and hardened at Maruku Research Station before distributing to nine sites for mass multiplication. Field assessment and leaf samples for virus test were conducted for each season/generation before distribution of materials to farmers. Nitrocellulose membrane-ELISA (NCM-ELISA) was used to detect *Sweetpotato feathery mottle virus* (SPFMV) and *Sweetpotato chlorotic stunt virus* (SPCSV) in leaf samples. Field results shows that percent incidence was high in variety Ejumula for first and second generation and low in variety Polista for the first and third generation. The NCM-ELISA results show that SPCSV was higher than SPFMV. Also the level of infection decreased from second generation to fourth generation. The level of virus for SPFMV and SPCSV show that many samples scored positive 1 which is the lowest score of disease and the number of plants infected and scored high decreased with increasing scores. The study concluded that clean materials get infection but when there is good management practice it helps to reduce virus infection. And even if there is infection, it will be at low level.

PP-133: Impact of banana bunchy top disease in Chiawa, Zambia: need for more integrated disease control programs

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Bananas in Zambia are grown in organized farm lands. The major factor determining the expansion of banana fields in Zambia is proximity to reliable sources of water and access to market. Bananas are largely grown under irrigation in Zambia with the preferred varieties being, Cavendish Williams and Grande nain. Although banana growing is not at the same scale as maize, banana fruits are a common feature on the open market and in all chain stores. The sold bananas are on a bigger proportion locally grown by both commercial farmers and small-scale farmers. The small-scale farmers, however, lack knowledge and financial capacity to control different banana diseases especially banana bunchy top disease (BBTD). In a survey conducted in 2011, an area called Chiawa was selected as a model for assessing the importance of banana in this area and the impact of BBTD on livelihoods of banana growers in Zambia as a whole. The contribution of banana sales to the household income and the proportion that banana income contributed to the education of their children were some of the parameters measured. On average each household had 7 children. Of the households interviewed, 66% had a child in primary school, 12% in lower secondary school and only 6% indicated having children in upper secondary school. In educating these children, 42% of the households had reported banana sales as their only source of income. The remainder had had other sources of income. Among those who had other sources of income, 70% attributed a larger portion of their income to banana growing. Although BBTD has ravaged the banana fields for most households, slightly above 86% are still growing bananas. Of these, 82% reported low to high incidences of BBTD in their fields. In terms of source of planting material, 70% sourced from fellow farmers. Because of the high disease burden, yields have plummeted to below profitable levels. This situation is related more to small-scale farmers than to commercial farmers. In trying to help rebuild the fields destroyed by BBTD over the years, Zambia Agriculture Research Institute (ZARI) has established tissue culture and virus diagnostics laboratories, trained manpower in virus disease indexing and tissue culture techniques, and organized several meetings with the agriculture extension services as well as the Seed Certification and Control Institute (SCCI) as a way of preparing to put in place a reliable seed system for banana farmers in Zambia.

PP-134: Molecular detection and identification of begomoviruses and its associated satellite molecules affecting some important plants in India

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India is rich in plant diversity and has good climate conditions for agricultural and other economically important plant species which makes the ideal conditions for insect vectors and begomoviruses to perpetuate. Begomoviruses have bipartite (DNA-A and DNA-B genomic components) or monopartite having only DNA-A genome. The satellite molecules referred to as DNA-β and DNA-α have also been found to be associated with begomoviruses. The existence of begomovirus and the associated satellite molecules on various plant species grown in India are known to cause serious economically losses, therefore, study on molecular detection and identification of begomoviruses and its associated satellite molecules has been carried out. During the survey in 2008 to 2012 some economically important plants species viz. *Capsicum annuum, Gossypium hirsutum, Hibiscus rosa-sinensis,*, *Alcea rosea*, *Aster alpinus*, *Nicotiana tabacum* cv. White burely, *Parthenium hysterophorus* and Ageratum species growing at various locations in Lucknow U. P., India were found to be exhibiting begomovirus like symptoms. For detection of begomoviruses, the total DNA was isolated from naturally infected leaf samples of these plants species and PCR was performed using begomovirus and its satellite molecules (DNA-β & DNA-α) specific primers. The presence of expected size amplicons were observed by electrophoresis of PCR products in 1.0 % agarose gels. To confirm the begomovirus the obtained amplicons were sequenced and sequence data were analyzed. Further, to identify the begomovirus the complete DNA-A genome and their satellite molecules was amplified, sequenced and analyzed. The sequence analyses suggested occurrence of diverse begomovirus species and its satellite molecules on these plant species viz. *Tomato leaf curl New Delhi virus* (EU309045) and Chilli leaf curl betasatellite (DQ343289) on *C. annum; Cotton leaf curl Burewala virusand* (HM461866), Cotton leaf curl Multan betasatellite (HM140826) and Cotton leaf curl Shahdadpur alphasatellite (HQ343234) on *G. hirsutum; Cotton leaf curl Multan virus (*JN807763) and Ludwigia leaf curl distortion betasatellite (JQ408216) on *H. rosa-sinensis; Papaya leaf curl virus* (JQ954859) and Ageratum leaf curl virus betasatellite (JQ408217) on *A. alpinus*; *Tomato leaf curl Patna virus* (GU253915) on *N. tabacum; Tomato leaf curl Karnataka virus* (JX524172), and Nanovirus (JX570736) on *P. hysterophorus;* and *Ageratum enation virus* (JQ911767) and Ageratum yellow leaf curl betasatellite (JQ408218) on ornamental Ageratum species. The results obtained during the study of these begomoviruses will be presented in the conference.

PP-135: Molecular detection, identification, genetic diversity and distribution of begomoviruses causing severe mosaic disease on *Jatropha* species in India

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Jatropha curcas L. of *Euphorbiaceae* family has generated the interest of many researchers in the field of bio-energy due to many excellent characteristics. The *J. curcas* crop was introduced in Southern India in the year of 2002 for biodiesel production and now it is being cultivated in 200 districts of 19 potential states of India. Unfortunately, the cultivation of Jatropha crop is limited due to prevalence of the severe mosaic disease which has affected drastically the production of Jatropha fruits and seeds. Literature survey revealed occurrence of few begomovirus species on *J. curcas*: Jatropha mosaic virus, *Indian cassava mosaic virus* from India and *African cassava mosaic virus* from Kenya. During surveys in five subsequent years 2008-2012, severe mosaic disease like symptoms were observed on *J. curcas* and other species of Jatropha viz. *J. multifida*, *J. integerrima*, *J. podagrica* grown for their ornamental values and *J. gossypifolia* grows as weed nearby road side and along with the agricultural fields in India. To find out how many begomoviruses/species are associated with the mosaic disease of these Jatropha species in India, the surveys were conducted and the symptomatic leaf samples of Jatropha species and other were collected from various locations from India. The total DNA from all the samples were extracted and PCRs were performed using three begomovirus specific primers (PALIv 722/ PALIc 1960) and the expected size ~ 1.2kb amplicons were obtained in many samples collected from various location in India which confirmed the association of begomovirus/es with mosaic disease of Jatropha species and distribution of begomovirus in the country. For identification of the begomovirus/es and to investigate the genetic diversity among them exists if any, the full length ~2.7 Kb DNA-A genome of these begomovirus isolates were amplified by RCA followed by digestion with *Bam* HI restriction enzyme. Cloning, sequencing of RCA amplicons (~2.7 Kb) were done and sequence data were analyzed by BLAST, Genomatix DiAlignment and MEGA 4 programmes for sequence identities and phylogenetic relationships of these begomovirus isolates. The sequence analysis of RCA amplicons (~2.7 Kb) resulted identification of four begomovirus species based on completed DNA-A: *Jatropha mosaic India Virus* and *Jatropha curcas mosaic virus* on *J. curcas* and *Croton yellow vein mosaic virus* and *Jatropha yellow mosaic India virus* on *J. gossypifolia*. The sequence analysis of ~1.2 kb DNA-A amplicons also revealed presence of three begomovirus species *Sri Lankan Cassava mosaic virus* on *J. podagrica*, *Tomato leaf curl Patana virus* on *J. multifida* and *Papaya leaf curl virus* on *J. integerrima*. During phylogenetic analysis these isolates formed seven separate clusters, therefore, they were considered as seven distinct begomovirus species. These results indicated that genetic diversity exists among the begomoviruses infecting various species of *Jatropha* grown in India. The detailed findings on existence and diversity of begomoviruses on Jatropha species would be discussed in the conference.

PP-0136: Status of mungbean research and development in Bangladesh

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Mungbean *(Vigna radiata* (L) Wilczek) is the second most important pulse crop of Bangladesh in area and production. Due to its short duration nature it can be fitted as a catch crop in between the major cropping seasons. It is grown in 3 seasons a year in Bangladesh and more than 70% area belongs to the southern part of the country. Presently it is grown in 163,000 ha and the production is 150,000 metric tons, with an average of yield 920 kg/ha. Various biotic and abiotic stresses are responsible for low productivity of this crop. So far 20 diseases have been recorded of which, yellow mosaic virus disease, *Cercospora* leaf spot (CLS) and powdery mildew are the major diseases and leaf beetle, whitefly, thrips and pod borers are the major insect pests. Among the abiotic, stresses lack of moisture during sowing time and excess moisture during flowering and harvest may cause substantial yield loss. Moreover farmers do not take much care for its cultivation. Eighteen improved varieties have been developed so far and they are being gradually extended among the farmers. Cultural management packages and new cropping patterns have also been designed involving mungbean and these are also being extended among the farmers. Screening of different germplasm resulted in identification of tolerant/resistant sources to *Mungbean yellow mosaic virus* (MYMV) and CLS. The use of host resistance is the most important and useful way of management of the disease. For controlling vectors, systemic insecticides were found effective. Powdery mildew can be escape by adjusting the planting time and by effective use of chemical fungicides. Cercospora leaf spot may be controlled by foliar spray of Bavistin 50 WP and also by Daconil. Besides these, government's emphasis towards increased mungbean production and future research and development strategies has been discussed in the paper.


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