ABSTRACT BOOK AND PROGRAM

2nd Joint Conference of the
International Working Groups on Legume (IWGLV)
and
Vegetable Viruses (IWGVV)

April 10-14, 2005

Fort Lauderdale, Florida USA

UNIVERSITY OF FLORIDA
IFAS

Project #0501
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Program Agenda

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1140–1200  A New Species of Begomovirus Infecting Capsicum annuum grossum (Bell Pepper) and Prevalence of Tomato Leaf Curl New Delhi Virus in Momordica charantia and Eclipta prostrata under Natural Conditions of Pakistan – M. S. Haider and M. Tahir; School of Biological Sciences, University of the Punjab, Lahore, Pakistan ................................................................. (p. 12)

1200–1220  History of Potyviruses - E. Hiebert; University of Florida, FL, USA

1220–1330  Lunch on Own

1330 –1500  SESSION II – DETECTION AND MOLECULAR/GENOMICS. [HIMMARSHEE ROOM]

Moderator: Scott Adkins

1330–1340  Opening Remarks and Session Overview by Moderator

1340–1400  Physalis Mottle Virus Infection of Tomato in Nebraska, USA – J. Th. J. Verhoeven¹, J. W. Roenhorst¹, D. E. Lesemann² and R. Koenig²; ¹Plant Protection Service, Wageningen, the Netherlands; ²BBA Institut für Pflanzenvirologie, Mikrobiologie und Biologische Sicherheit, Braunschweig, Germany ................................................................. (Abstract withhold at Authors' request)

1400–1420  Effects of Beet Western Yellows Virus, Cauliflower Mosaic Virus and Turnip Mosaic Virus on Stored White Cabbage and Their Involvement in the Occurrence of Internal Disorders – P. J. Hunter, J. E. Jones and J. A. Walsh; Warwick HRI, Wellesbourne, Warwick, UK ............................................. (p. 40)

1420–1440  Increasing Yields and Quality of the Illinois Horseradish Crop Using In Vitro Disease Elimination – M. Uchanski, M.A. Norton and R.M. Skirvin; University of Illinois at Urbana-Champaign, IL, USA ................................................. (p. 33)

1440–1500  Functional Genomics in Pea by Virus Induced Gene Silencing (VIGS) – Ole S. Lund¹, Gabriela D. Constantin¹, Britta N. Krath¹, Stuart A. MacFarlane², Mogens Nicolaisen³ and I. Elisabeth Johansen¹; ¹Biotechnology group, Danish Institute of Agricultural Sciences, Denmark; ²Scottish Crop Research Institute, Invergowrie, Dundee, Scotland; ³Department of Crop Protection, Danish Institute of Agricultural Sciences, Denmark ................................................................. (Abstract withhold at Authors' request)

1500–1700  Formal Poster Session and Refreshment Break .............................................[NEW RIVER B]
(Poster presenters to be stationed at displays)

1800–2300  Jungle Queen Dinner Cruise
**Tuesday, April 12, 2005**

0730–1700  **Registration Open** .......................................................................................... [8TH FLOOR FOYER]

0730–0830  **Early Morning Refreshments** ........................................................................ [HIMMARSHEE ROOM]

0730–1700  **Posters on Display** ....................................................................................... [NEW RIVER B]

0830–1000  **SESSION III – MOLECULAR AND NEW/EMERGING** .................. [HIMMARSHEE ROOM]

**Moderator: William Wintermantel**

0830–0840  **Opening Remarks and Session Overview by Moderator**

0840–0900  **Investigations on the Genomics of Plant-Virus Co-Evolution in Wild Brassica Species – C. Obermeier**\(^1\), J. Reeves\(^2\), D. Pallett\(^2\), H. Wang\(^2\), J. I. Cooper\(^3\), R. Machado\(^3\), Z. Luo\(^3\), A. Sharpe\(^4\), D. Lydiate\(^4\), P. J. Hunter\(^1\), K. Ohshima\(^5\), M. Kearsey\(^3\) and J. A. Walsh\(^1\); \(^1\)Warwick HRI, Wellesbourne, Warwick, UK; \(^2\)Centre for Ecology and Hydrology, Oxford, UK; \(^3\)School of Biosciences, The University of Birmingham, Birmingham, UK; \(^4\)Agriculture & Agri-Food Canada, Saskatoon Research Centre, Saskatoon, Canada; \(^5\)Laboratory of Plant Virology, Saga University, Japan....................................................... (p. 25)

0900–0920  **Complete Sequence and Capsid Protein Variability of Chickpea chlorotic stunt virus, a New Polerovirus Infecting Cool Season Legume Crops – A. D. Abraham**\(^1,2\), W. Menzel\(^1\) and H. J. Vetten\(^1\); \(^1\)Federal Research Center for Agric. & Forestry, Institute for Plant Virology, Microbiology & Biosafety, Braunschweig, Germany; \(^2\)Ethiopian Agric. Res. Organization, National Plant Protection Research Center, Ambo, Ethiopia ................................................................................... (p. 4)

0920–0940  **Viral Involvement in Vine Decline of Watermelon in Florida – Scott Adkins**\(^1\), Carlye A. Baker\(^2\), Diann Achor\(^3\), Pamela D. Roberts\(^4\), Ivanka Kamenova\(^1\), Rosa M. Muchovej\(^4\), Phyllis Gilreath\(^5\) and Gene McAvoy\(^6\); \(^1\)USDA-ARS, Fort Pierce, FL, USA; \(^2\)FDACS-DPI, Gainesville, FL, USA; \(^3\)University of Florida, Lake Alfred, FL, USA; \(^4\)University of Florida, Immokalee, FL, USA; \(^5\)Florida Cooperative Extension Service, Palmetto, FL, USA; \(^6\)Florida Cooperative Extension Service, LaBelle, FL, USA ....................... (p. 5)

0940–1000  **Squash Leaf Curl Virus (SLCV) and Watermelon Chlorotic Stunt Virus (WmCSV), Newly Emerging Begomoviruses in Israel – Y. Antignus, O. Lachman and M. Pearlsman; Department of Virology, ARO, The Volcani Center, Bet Dagan, Israel................................................................. (p. 6)

1000–1030  **Refreshment Break and Networking** .......................................................... [8TH FLOOR PATIO]
Tuesday, April 12, 2005 (continued)

1030–1200 SESSION IV – NEW/EMERGING I ......................................................... [HIMMARSHEE ROOM]

Moderator: Joe Vetten

1030–1040 Opening Remarks and Session Overview by Moderator

1040–1100 Watermelon Mosaic Virus (WMV, Potyvirus): How Interspecific Recombination Between Two Legume-Infecting Potyviruses Yields a Vegetable-Infecting Virus – Cecile Desbiez, C. Costa, M. Girard, C. Rys and H. Lecoq; INRA, Station de Pathologie Végétale, Domaine Saint Maurice, Montfavet, France ................................................................. (p. 19)

1100–1120 Naturally Occurring Partial Diploid Strains of Bean Pod Mottle Virus Induce Exceptionally Severe Symptoms on Soybean – S. A. Ghabrial, H. Gu, C. Zhang and A. Kritzman; University of Kentucky, Plant Pathology, Lexington, KY, USA ................................................................................. (p. 11)

1120–1140 Characterization of Snake Melon Asteroid Mosaic Virus, a Tentative New Sobemovirus Infecting Cucurbits – H. Lecoq1, G. Dafalla2, C. Desbiez1, B. Delécolle1, C. Wipf-Scheibel1 and M. Girard1; 1INRA, Station de Pathologie Végétale, Montfavet, France; 2Plant Pathology Center, University of the Gezira, Wad Medani, Sudan ........................................................................ (p. 18)

1140–1200 High Sequence Homology between Pepino Mosaic Virus Isolates from Chile and the USA – Kai-shu Ling; USDA-ARS, U. S. Vegetable Laboratory, Charleston, SC, USA ................................................................................. (p. 20)

1200–1330 Group Lunch ............................................................................................ [NEW RIVER A]

1330–1500 SESSION V – RESISTANCE I ................................................................. [HIMMARSHEE ROOM]

Moderator: Jane Polson

1330–1340 Opening Remarks and Session Overview by Moderator

1340–1400 Recent Progress over Natural Virus Resistance in Lupinus spp. – Roger A. C. Jones1,2, L. J. Smith2 and G. M. Burchell1; 1Department of Agriculture, South Perth, Western Australia; 2Centre for Legumes in Mediterranean Agriculture, University of Western Australia ................. (p. 14)

1400–1420 Identification of Cucurbita Sources of Resistance to the Czech Strain of Zucchini Yellow Mosaic Virus – J. Svoboda and J. Polák; Research Institute of Crop Production, Division of Plant Medicine, Prague - Ruzyně, Czech Republic ................................................................................. (p. 28)

1420–1440 Translocation of Genetically Engineered Resistance to Tomato Yellow Leaf Curl Virus across a Graft – J. E. Polston1, M. Lapidot2, R. W. England1 and E. Hiebert1; 1Department of Plant Pathology, University of Florida, Gainesville, FL, USA; 2Department of Virology, Volcani Center, Agricultural Research Organization, Bet Dagan, Israel ................................................................................. (p. 29)
Tuesday, April 12, 2005 (continued)

1440–1500  *Mirafiori Lettuce Virus* (MiLV) and *Lettuce Big Vein Virus* (LBVV) Sequence Diversity and Frequency in California and Arizona Lettuce, and Analysis of Big Vein Resistance – *William M. Wintermantel, Ryan J. Hayes, Patricia A. Nicely* and *Edward J. Ryder*; USDA-ARS, Salinas, CA, USA.......................................................... (p. 44)

1500–1730  Formal Poster Session and Refreshment Break....................... [NEW RIVER B]

1730–1800  Poster Removal

EVENING  Dinner on Own

Wednesday, April 13, 2005

0645–0715  Registration Open.......................................................... [8TH FLOOR FOYER]

0645–0715  Early Morning Refreshments ..............................................[8TH FLOOR FOYER]

0730–1700  Field Trip

Thursday, April 14, 2005

0730–1200  Registration Open............................................................ [8TH FLOOR FOYER]

0730–0830  Early Morning Refreshments ..............................................[HIMMARSHEE ROOM]

0830–1000  SESSION VI – NEW/EMERGING II ........................................[HIMMARSHEE ROOM]

**Moderator: Roger Jones**

0830–0840  Session Overview and Introduction

0840–09:00  *Recently Detected Viruses on Pepper in the Czech Republic* – *J. Svoboda¹, G. Červená², J. Rodová²* and *M. Ducháčová¹*; ¹Research Institute of Crop Production, Division of Phytomedicine, Prague, Czech Republic; ²State Phytosanitary Office of the Czech Republic.....(Abstract withhold at Authors' request)

0900–0920  *A New Strain of Cowpea Mild Mottle Virus Infects French Bean in Spain and Morocco – J. Th. J. Verhoeven¹, J. W. Roenhorst¹, C. C. C. Jansen¹, R. Miglino², A. R. van Schadewijk², E. Segundo³, I. M. Cuadrado³ and D. Janssen³;* ¹Plant Protection Service, Wageningen, the Netherlands; ²Bulb Inspection Service, Lisse, the Netherlands; ³Dirección General de Investigación y Formación Agraria, El Ejido, Spain...........(Abstract withhold at Authors' request)

0920–0940  Identification and Detection of a Closterovirus from Carrot in Germany – *W. Menzel, D. E. Lesemann* and *H. J. Vetten*; Federal Research Center for Agriculture and Forestry (BBA), Institute of Plant Virology, Microbiology and Biosafety, Braunschweig, Germany................................. (p. 38)
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0940–1000 Serological and Molecular Evidence for the Occurrence of Nanovirus Species other than Faba Bean Necrotic Yellows Virus in Morocco and Ethiopia – A. D. Abraham\textsuperscript{1,2}, B. Bencharki\textsuperscript{3}, V. A. Torok\textsuperscript{1}, L. Katul\textsuperscript{1} and H. J. Vetten\textsuperscript{1}; \textsuperscript{1}Federal Research Center for Agriculture and Forestry (BBA), Institute of Plant Virology, Microbiology and Biosafety, Braunschweig, Germany; \textsuperscript{2}Ethiopian Agricultural Research Organization, Ambo, Ethiopia; \textsuperscript{3}Université Hassan 1er; Faculté des Sciences et Techniques, Settat, Morocco ......................................................................................................................... (p. 39)

1000–1030 Refreshment Break & Networking ................................................................................................................. [8\textsuperscript{th} Floor Patio]

1030–1130 SESSION VII – RESISTANCE II ................................................................................................................. [Himmarshee Room]

\textbf{Moderator: Gail Wisler}


1050–1110 Mapping Resistance Genes to Turnip Mosaic Virus in the Brassica Genome and Identifying the Viral Determinants of Virulence – J. A. Walsh\textsuperscript{1}, C. E. Jenner\textsuperscript{1}, S. L Hughes\textsuperscript{1}, P. J. Hunter\textsuperscript{1}, A. G. Sharpe\textsuperscript{2}, D. J. Lydiate\textsuperscript{2}, F. Ponz\textsuperscript{3}, K. Tomimura\textsuperscript{4}, K. Ohshima\textsuperscript{4} and X. Wang\textsuperscript{1,3,5}; \textsuperscript{1}Horticulture Research International, Wellesbourne, Warwick, UK; \textsuperscript{2}Agriculture & Agri-Food Canada, Saskatoon, Saskatchewan, Canada; \textsuperscript{3}Dpto de Biotecnologia, INIA, Madrid, Spain; \textsuperscript{4}Laboratory of Plant Virology, Faculty of Agriculture, Saga University, Saga, Japan; \textsuperscript{5}Institute of Vegetables and Flowers, CAAS, Beijing, China......................................................................................................................... (p. 42)

1110–1130 History of Internal Working Group IWGLV – Roger A. C. Jones; Department of Agriculture, South Perth, Western Australia

1130–1300 Conference Recap and Closing Business Meeting
Poster Session Directory

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1........Detection and Identification of *Potato Virus Y* by RT-PCR and IC-RT-PCR – C. Abdmishani¹, S. Gholami¹ and M. Koohi Habibi²; ¹Dep. of Biotechnology, College of Agriculture, Tehran University, Karaj, Iran; ²Dep. of Plant Protection, College of Agriculture, Tehran University, Karaj, Iran

2........Characterization of Karyopherin α1 Gene Expression in IAA Over-Producing Tomatoes – K. Assa¹, I. Kobrinsky², D. Dabush², Y. Levi², R. Aloni¹ and Y. Gafni²; ¹Tel Aviv University, Department of Plant Sciences, Tel Aviv, Israel; ²Volcani Center, A.R.O., Department of Plant Genetics, Bet Dagan, Israel ........................................... (p. 7)

3........Management of Virus Diseases of Legume Crops in Uganda – Flavia Atugonza¹, J. Mukasa² and S. Bukunya³; ¹International Institute of Tropical Agriculture, Eastern and Southern Africa Regional Centre, Kampala, Uganda; ²Namulongo Agricultural and Animal Production Research Institute, Kampala, Uganda; ³Makerere University, Kampala, Uganda ............................................................................................................................... (p. 8)

4........Multipurpose Inoculation Machines for Small and Large Scale Applications – Herve Huet, Aviv Cahana, Itai Maoz, Yarden Dloomy, Nitzan Paldi, Gal Yarden and Rony Hemo; Bio-Oz Biotechnologies Ltd., Yad Mordechai, Hof-Ashkelon, Israel.............................. (p. 13)

5........Seed-transmitted Viruses of Important Grain Legumes in India: Prevalence and Management Through Quality Control of Seeds – R. K. Khetarpal¹, V. Celia Chalam¹, H. S. Prakash² and A. Mishra³; ¹National Bureau of Plant Genetic Resources, New Delhi, India; ²University of Mysore, Mysore, India; ³Gujarat Agricultural University, Anand, India............................................................................................................................... (p. 15)

6........Improvement of Resistance to *Turnip Mosaic Virus* in Cabbage (*Brassica oleracea* L.) – R. Krämer¹, F. Marthe¹, E. Klocke¹, U. Ryschka¹, G. Schumann¹, F. Rabenstein² and J. Schubert²; ¹Federal Centre for Breeding Research on Cultivated Plants, Institute of Horticultural Crops, Quedlinburg, Germany; ²Federal Centre for Breeding Research on Cultivated Plants, Institute of Resistance Research and Pathogen Diagnostics, Aschersleben, Germany........................................................................................................... (p. 16)

7........Prevalence and Incidence of Potato Carlavirus S (PVS) and *Potato Potexvirus X* (PVX) in Tasmanian Seed Potato Crops – S. Lambert¹, F. Hay¹, I. Kirkwood², S. Pethybridge¹, P. Cross³ and C. Wilson⁴; ¹Tasmanian Institute of Agricultural Research (TIAR), University of Tasmania Cradle Coast Campus, Burnie, Tasmania, Australia; ²Department of Primary Industries Water and Environment (DPIWE), Stoney Rise Government Centre, Devonport, Tasmania, Australia; ³DPIWE, New Town Research Laboratories, Hobart, Tasmania, Australia; ⁴TIAR, New Town Research Laboratories, Hobart, Tasmania, Australia...........................................(Abstract withhold at Authors' request)
8. **Non Transmissibility of Radish Mosaic Comovirus (RaMV) European Strain Through Seed of Wild Turnip Rape (Brassica campestris L.) – Dj. Mamula¹, E. Djermic², Z. Stafa³, B. Cvjetkovic², M. Pospisil³, Z. Liber¹ and T. Milicevic²;¹University of Zagreb, Faculty of Science, Department of Botany, Zagreb, Croatia; ²University of Zagreb, Faculty of Agriculture, Department of Plant Pathology, Zagreb, Croatia; ³University of Zagreb, Faculty of Agriculture, Department of Field Crop Production, Zagreb, Croatia...........................................................................................................(p. 22)

9. **Dolichos Yellow Mosaic Virus Belonging to a Distinct Phylogenetic Cluster Causes Yellow Mosaic Disease of Dolichos in the Indian Sub-Continent – M. N. Maruthi¹, B. Manjunatha¹, A. R. Rekha², M. R. Govindappa², J. Colvin¹ and V. Muniyappa²;¹Plant, Animal and Human Health Group, Natural Resources Institute, University of Greenwich, Central Avenue, Chatham Maritime, Kent, UK; ²Department of Plant Pathology, University of Agricultural Sciences, GKVK, Bangalore, India........................................(p. 23)

10. **Molecular Diversity of Begomoviruses Causing Tomato Leaf Curl Disease in Bangladesh – M. N. Maruthi¹, S. N. Alam², K. A. Kader², A. R. Rekha¹, A. Cork¹ and J. Colvin¹;¹Natural Resources Institute, University of Greenwich, Central Avenue, Chatham Maritime, Kent, UK; ²Bangladesh Agricultural Research Institute, Joydebpur, Gazipur, Bangladesh.................................................................................................................................(p. 24)

11. **Plastic Mulches for Increasing Yields and Delaying Symptoms of Whitefly-Borne Viruses in Cucurbits – H. S. Paris¹, M. Edelstein¹, F. Baumkoler¹, A. Porat¹, U. Saar¹, A. Hanan¹, Y. Burger¹ and Y. Antignus²;¹Agricultural Research Organization, Newe Ya’ar Research Center, Ramat Yishay, Israel; ²Agricultural Research Organization, Volcani Center, Bet Dagan, Israel ......................................................................................................................(p. 26)

12. **Radish Mosaic Virus Phylogenetic Relationships in the Genus Comovirus – K. Petrzík¹, M. Holá¹² and J. Špak¹;¹Institute of Plant Molecular Biology, Academy of Sciences of the Czech Republic, České Budějovice, Czech Republic; ²Faculty of Biological Sciences, University of South Bohemia, České Budějovice, Czech Republic...................................................................................................................(p. 27)

13. **Preliminary Study on the Spherical Virus Transmitted by Greenhouse Whitefly (Trialeurodes vaporariorum) – Henryk Pospieszny; Institute of Plant Protection, Dept of Virology and Bacteriology, Miczurina, Poznań, Poland..(Abstract withheld at Authors' request)

14. **Detection of Low Concentration of Tomato Mosaic Virus (ToMV) in Water Samples Using Real-time PCR – M. Ravnikar¹, J. Boben¹, Peterka², P. Kramberger², N. Petrović¹ and A. Štrancar²;¹National Institute of Biology, Ljubljana, Slovenia; ²BIA Separations, d.o.o., Ljubljana, Slovenia...........................................................................................(p. 31)

15. **Epidemiological Developments in Potato virus Y – M. Verbeek, R. A. A. van der Vlugt, C. Cuperus and P. G. M. Piron; Plant Research International, Wageningen, the Netherlands.................................................................................................................................(p. 35)
16.......Investigating the Molecular Mechanisms Involved in Cross-Protection by *Turnip Mosaic Virus* – J. A. Walsh, G. A. Turnbull and C. E. Jenner; Warwick HRI, Wellesbourne, Warwick, UK.............................................................. (p. 41)

17.......Integrated Production Technology in Chickpea – S. S. Yadav, Division of Genetics, Indian Agricultural Research Institute, New Delhi, India............................... (p. 45)
Abstracts

Listed alphabetically by presenting author. Presenting authors appear in **bold**.
Complete Sequence and Capsid Protein Variability of Chickpea chlorotic stunt virus, a New Polerovirus Infecting Cool Season Legume Crops

A. D. Abraham\textsuperscript{1,2}, W. Menzel\textsuperscript{1} and H. J. Vetten\textsuperscript{1}

\textsuperscript{1}Federal Research Center for Agric. & Forestry, Institute for Plant Virology, Microbiology & Biosafety, Braunschweig, Germany

\textsuperscript{2}Ethiopian Agric. Res. Organization, National Plant Protection Research Center, Ambo, Ethiopia

When samples collected from faba bean, chickpea, grass pea and fenugreek plants showing yellowing and stunting symptoms in Ethiopia were serologically tested in 2002, many samples reacted with a broad-spectrum monoclonal antibody for luteoviruses but not with antibodies to known luteo- and poleroviruses. This suggested the occurrence of a previously unrecognized virus. In attempts to further characterize this virus, a pair of degenerate primers permitted PCR amplification of closely related coat protein (CP) sequences from legume samples from Ethiopia and other countries. These sequences were most closely related to, but distinct from, the CP sequence of Groundnut rosette assistor virus (GRAV). Since they have nucleotide and deduced amino acid sequence identities of only about 76% and 78%, respectively, with the GRAV CP, we propose that this previously unrecognized polerovirus is named Chickpea chlorotic stunt virus (CpCSV). Phylogenetic analysis of the CP sequences of 18 isolates originating from five countries separated the isolates into two distinct strain groups differing by about 9%. One group is represented by isolates from Ethiopia and the Sudan and the other by those from Egypt, Morocco and Syria.

The complete genome of an Ethiopian isolate of CpCSV was sequenced and shown to consist of 5900 nucleotides and contain six major ORFs that are organised in a fashion characteristic of members of the genus Polerovirus. Among the luteoviruses for which complete genome sequences are available, CpCSV is most closely related (identity of 56%) to Cucurbit aphid-borne yellows virus, with which it also shares special features in genomic organisation. Biological studies indicated that the host range of the virus is limited to cool season food legumes and that the virus is transmitted persistently by Aphis craccivora but not by Myzus persicae, Acyrthosiphon pisum or Aphis fabae. Polyclonal and monoclonal antibodies were produced to permit serological diagnosis of CpCSV.

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Viral Involvement in Vine Decline of Watermelon in Florida

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A severe watermelon vine decline occurred just before or soon after the first harvest in spring 2003 and 2004 in southwest Florida and in fall 2003 in west central Florida. Slight yellowing to scorched and brown leaves, wilting of the vines, defoliation, and rapid mature vine collapse were characteristic symptoms. Frequently, the interior fruit rind appeared greasy and discolored (brown) and fruit were not marketable. Disease progress was very rapid. In some fields, vine decline incidence increased from 10% to greater than 80% within a week. Entire fields were lost. Some growers experienced losses in excess of 50% of their crop.

Possible environmental and biological causes of this vine decline were explored including nutrient analyses of soil and plant tissue, grower cultural practices and pathogens. Various fungi and bacteria were recovered from symptomatic crown, root, foliar, and fruit tissue. Several fungal isolates caused watermelon seedling death following inoculation in the laboratory but their role as primary factors or opportunistic secondary factors in vine decline remains under investigation.

Watermelons with decline symptoms were also examined for the presence of viruses and virus-like agents. Crude extracts of plant sap from these symptomatic watermelons were filtered to remove fungi and bacteria and used to inoculate greenhouse grown watermelon plants. The inoculated plants developed decline symptoms similar to those observed in the field and died. Other tests indicated the presence of a potyvirus in the declining plants. This potyvirus was identified as Papaya ringspot virus type W (PRSV-W), a pathogen commonly observed in Florida watermelon fields. PRSV-W was purified and used to inoculate additional watermelon plants. However, the purified PRSV-W alone did not lead to the same symptoms of vine decline. This and other evidence suggest the presence of a second virus or virus-like agent that may be involved in vine decline. Research is ongoing to identify this other virus or virus-like agent and determine the role it may play in vine decline.

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**Squash Leaf Curl Virus (SLCV) and Watermelon Chlorotic Stunt Virus (WmCSV), Newly Emerging Begomoviruses in Israel**

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A severe epidemic of leaf curling was observed during autumn of 2002 in squash crops in all growing areas of Israel. The vegetative growth of affected plants was significantly retarded and the fruits in some varieties were distorted and showed blisters and green depressions. In most cases the incidence of affected plants was near 100% and the phenomenon was always associated with the presence of large populations of the whitefly *Bemisia tabaci*. Transmission tests revealed that the disease is transmitted by *B. tabaci* to a wide host range in the *Cucurbitaceae* including squash (*Cucurbita pepo*), pumpkin (*Cucurbita maxima*), melon (*Cucumis melo*), watermelon (*Citrullus vulgaris*) and cucumber (*Cucumis sativus*). The disease could be transmitted also to beans (*Phaseolus vulgaris*) and *Nicotiana benthamiana*. The causal agent was detected in squirting cucumber (*Ecballium elaterium*) and in *Malva nicaeensis* that are known as common weeds in Israel. The viral nature of the disease was confirmed by ELISA tests showing a specific reaction with antiserum against *Squash leaf curl virus* (SLCV) a member of the genus *Begomovirus* of the *Geminiviridae*. The coat protein gene of the virus was cloned and sequenced showing 98% identity with the published sequence of SLCV-E. This is the first report of an epidemic caused by SLCV in the Eastern hemisphere.

Another geminivirus was identified in the same year in watermelon crops grown in autumn. Symptoms included bright yellow mosaic, vein clearing and leaf distortion. In most cases the fruits were not affected externally, but their internal tissue was severely affected showing discoloration and browning that make them unmarketable. The virus was easily transmitted by *B. tabaci* to a relatively narrow host range. Watermelon and melon were found as susceptible symptomatic hosts, while squirting cucumber (*Ecballium elaterium*) is a symptomless host of the virus. The coat protein of the virus was cloned and its nucleotide sequence had 95% identity with the Yemen isolate of *Watermelon chlorotic stunt virus*.

Mixed infection of both viruses in watermelon resulted in synergistic interaction as reflected by a dramatic amplification of symptoms and viral DNA synthesis of both viruses.

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Characterization of Karyopherin α 1 Gene Expression in IAA Over-Producing Tomatoes

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The tomato yellow leaf curl virus (TYLCV), a member of the Geminiviruses family, causes severe damage to tomato (Lycopersicon esculentum M.) yield world-wide. Viruses in this family share a similar capsule structure of fused icosahedra that forms a twinned (geminate) structure. TYLCV genome is a closed circular ssDNA that replicates in the plant host cell nucleus via dsDNA. The nuclear import of the virus is an open question and the mechanism is yet unclear. Recently accumulated evidence suggests that the coat protein (CP) is more than just a structural protein participating in capsule forming. It is also assumed to have function in shuttling the viral genome into the host plant cell nucleus.

The transport of macromolecules into the nucleus is supported by cytoplasmic proteins, namely karyopherins. A karyopherin α gene from a tomato was isolated and characterized (LeKAPα1, Accession No. AF012752). It was demonstrated in a yeast two hybrid system that LeKAPα1 interacts directly with TYLCV CP, thus indicating that the CP’s nuclear import is a karyopherin α-dependent mechanism.

Analysis of LeKAPα1 expression pattern, detected by LeKAPα1 promoter fused to GUS, has revealed that it is developmental and tissue specific. It is expressed in the leaves: initially in the primordium tip, then along the leaf margins and ends sporadically inside the leaf. The expression is also typically found in the root tip. This expression pattern is similar to that of DR5, a promoter which is known to be active in the presence of IAA. Accordingly, we suggest that IAA is involved in the regulation of the LeKAPα1 gene.

In order to study the effect of IAA on LeKAPα1 activity, tomato plants were transformed with the iaaM gene from Agrobacterium tumefaciens. Plants showing high IAA levels were re-transformed with the LeKAPα1 promoter fused to GUS.

IAA over-producing plants were shown to have higher GUS activity, thus indicating possible IAA involvement in LeKAPα1 induction.

Further studies are in progress.

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Complete Genome Sequence, Experimental Host Range, Phylogenetic Relationships, and Heterologous Reassortment for Five Begomoviruses in the Squash Leaf Curl Virus Clade

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Four species of begomovirus (genus: Begomovirus; family: Geminiviridae), which are now recognized as members of the New World Squash leaf curl virus clade, and which naturally infect species of the Cucurbitaceae and common bean Phaseolus vulgaris (L.), were characterized with respect to experimental host range, symptom phenotype, and phylogenetic relationships. The bipartite genome for each virus was cloned and the DNA sequence was determined. Phylogenetic analysis was carried out, and the % shared nucleotide identity was estimated for the DNA-A and DNA-B components, respectively, in relation to their closest begomovirus relatives (Table 1). Results collectively indicated that these viruses comprise a tight subcluster of distinct species within the larger SLCV clade. These four species are: Cucurbit leaf curl (CLCuV), and Melon chlorotic leaf curl (MCLCV) (also, 90% identical to the Costa Rican strain, Squash yellow mild mottle; NC003865), Squash mild leaf curl (SMLCV), and Squash leaf curl (SLCV) viruses. The closest relatives of the cucurbit virus cluster also are classified in the SLCV clade, and include Bean calico mosaic virus (BCaMV), Cabbage leaf curl virus (CaLCV), Cotton leaf crumple virus (CLCrV), and the Pepper golden mosaic virus complex (PepGMV), all viruses that are extant to North and/or Central America. Interestingly, there was little evidence for intermolecular recombination (using GenConV & RDP) between the components of the four cucurbit-infecting species, even though they share a number of hosts in common and several are sympatric where they are endemic. Infectious clones (1.5-mer or dimer) were constructed for each pair of cognate viral components, and used to demonstrate infectivity, and to determine the experimental host range using key and discriminating test species. Each DNA-A and DNA-B component was examined for the potential to yield a viable reassortant in combination with all non-cognate components, respectively. That reassortants might be equally or more fit than parental viruses was considered of interest in predicting the potential for outbreaks of new and emerging begomoviruses.

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Naturally Occurring Partial Diploid Strains of *Bean Pod Mottle Virus* Induce Exceptionally Severe Symptoms on Soybean

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*Bean pod mottle virus* (BPMV) is a member of the genus *Comovirus* in the family *Comoviridae*. It has a bipartite positive-strand RNA genome consisting of RNA1 and RNA2, which are separately encapsidated in isometric particles 28 nm in diameter. BPMV is widespread in the major soybean-growing areas in many of the southern and southeastern states. A recent severe outbreak in BPMV incidence in the north central and northern Great Plains states is currently the cause of serious concerns to the soybean industry in this region. Concomitant with the increased incidence of BPMV has been an augmentation in disease symptom severity and the emergence of apparently new and unusual severe strains. Molecular characterization of such severe BPMV isolates revealed that they are reassortants/recombinants between two distinct subgroups of strains. Characterization of some of the most severe isolates, which were collected from various locations in the United States, indicated that they are partial diploid reassortants containing two distinct types of RNA1 and one type of RNA2. The partial diploids appeared to be stable and of frequent occurrence in the natural populations of BPMV. The very severe symptoms induced by these strains can be mimicked by inoculation of plants with a mixture of RNA1 transcripts from two distinct strain subgroups and RNA2 transcript from either subgroup. Plants inoculated with a mixture of RNA1 transcripts derived from strains in the same subgroup did not produce very severe symptoms. Although the mechanism underlying the enhancement of symptom severity induced by the partial diploids is unknown, the interaction between two distinct RNA1s is required.

The availability in our laboratory of full-length cDNA clones of genetically distinct strains that differ in symptom severity allowed us to generate the appropriate chimeric constructs needed for mapping the determinants of symptom severity. We established that symptom severity maps to the coding regions of the protease co-factor (Co-pro) and the C-terminal half of the putative helicase (Hel). Although augmentation of symptom severity correlated well with higher accumulation of viral RNA, we were not able to demonstrate that either the Co-pro or Hel protein is a suppressor of RNA silencing.

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A New Species of Begomovirus Infecting Capsicum annuum grossum (Bell Pepper) and Prevalence of Tomato Leaf Curl New Delhi Virus in Momordica charantia and Eclipta prostrata under Natural Conditions of Pakistan

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Begomoviruses (family Geminiviridae) are single-stranded DNA viruses that infect dicotyledonous plants, and transmitted by whitefly [Bemisia tabaci (Gennadius)]. The characteristic symptoms include, leaf curling, yellow leaf curling, vein yellowing, vein thickening, and in some cases, mosaics, yellow blotching and stunting. Young symptomatic leaves of Capsicum annuum grossum (leaf curling), Momordica charantia (yellow blotching) and Eclipta prostrata (yellow veining) were collected from vegetable fields around Lahore. Total DNA was extracted by CTAB method. The presence of begomoviruses infection was confirmed by PCR amplification using a pair of degenerate primers based on the conserved regions of coat proteins of begomoviruses from the Old World. A DNA fragment of the expected size approximately 750 bp was amplified from infected samples only whereas healthy samples did not yield the fragment. The PCR amplified DNA fragment was cloned, sequenced and analyzed. The DNA sequence obtained from C. annuum grossum showed the highest level of sequence homology to Cucurbita maxima yellow mosaic virus coat protein (83% identity over a stretch of 457 nucleotides in the virion sense). The sequence obtained from M. charantia and E. prostrata had the highest level of sequence identity (95% and 98%, respectively) to Tomato leaf curl New Delhi Virus (ToLCNDV). The presence of DNA β was identified from C. annuum grossum and M. charantia. A full length DNA β of expected size (1.3 kb) was obtained from C. annuum grossum and a possibly defective DNA β of 0.6 kb from M. charantia using universal DNA β primers. The results indicate the presence of a new begomovirus species infecting Bell pepper and ToLCNDV infecting M. charantia and E. prostrata in Pakistan under natural conditions.

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Multipurpose Inoculation Machines for Small and Large Scale Applications

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Bio-Oz Biotechnologies Ltd. has commercialized the use of cross-protection against zucchini yellow mosaic virus (ZYMV) for several years. One of the key elements for successful application has been the development of machinery for the inoculation on a large scale. Thus, several machines have been designed primarily for plant virus inoculation. These machines have been called "BIM" (Bio-Oz Inoculation Machine). They have been designed either for laboratory, for field and for small or large scale nursery inoculation. However, it has been demonstrated that other solutions could be delivered into plant tissue, such as RNA or DNA, bacterial extracts, or Agrobacterium culture. Besides, the target tissue, are certainly not limited to plants. Results illustrating this versatility will be presented, as well as the latest development of the BIM series.

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Recent Progress over Natural Virus Resistance in *Lupinus* spp.

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Western Australia is the world’s largest producer of *Lupinus* spp. (lupin). The seed is mainly sold for stockfeed and exported overseas. Current breeding efforts focus mostly on *L. angustifolius* (narrow-leafed lupin) and *L. luteus* (yellow lupin), but *L. mutabilis* (pearl lupin) was recently also included. All three species suffer from damaging diseases caused by *Bean yellow mosaic virus* (BYMV) and *Cucumber mosaic virus* (CMV). Selection for BYMV resistance in *L. angustifolius* and *L. luteus* relies on partial ‘infection resistance’ but *L. angustifolius* also develops a strain specific, systemic hypersensitive response present in all cultivars. Breeding for CMV resistance relies on selection for low inherent seed transmission rates in *L. angustifolius* and incorporation of hypersensitivity gene *Ncm-1* in *L. luteus*.

In *L. angustifolius*, segregation for the systemic hypersensitive response to infection with necrotic isolate MI of BYMV was studied in progeny plants from six crosses involving four parents. The parents were two cultivars that develop necrosis when infected with isolate MI (Danja and Merrit) and two genotypes that MI infects without necrosis (90L423-07-13 and P26697). In the four combinations of crosses between the different necrotic and non-necrotically reacting genotypes, segregation for the necrotic response in F<sub>2</sub> progeny plants always fitted a 3:1 ratio (necrotic: non-necrotic). All F<sub>2</sub> progeny plants from the cross between the two non-cultivar genotypes became infected without necrosis while those from the cross between the two cultivars developed necrosis. These results indicate that the hypersensitive response to infection is controlled by a single dominant hypersensitivity gene for which the name *Nbm-1* is proposed. In *L. mutabilis*, accession P26956 remained uninfected with CMV when exposed to infection in the field and after repeated sap inoculations with six isolates. In contrast, plants of P26961 were readily infected with CMV in the field and by sap inoculation with three legume isolates. Three other CMV isolates infected most or all plants of P26961 only after repeated sap inoculations. Several other accessions became infected readily by a legume isolate in field screening. When CMV-infected scions were grafted onto P26956, necrosis developed in shoots just below the graft union whilst other axillary shoots grew vigorously with no virus being detected. P26956 therefore has ‘extreme resistance’ to CMV.

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Seed-transmitted Viruses of Important Grain Legumes in India: Prevalence and Management Through Quality Control of Seeds

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Seed-transmitted viruses are one of the most important yield-reducing factors in grain legumes throughout India. Quality control of seeds thus assumes great importance in their management and to achieve this, a realistic assessment of prevalence of these viruses at national level became a prerequisite. Studies were thus recently undertaken on important seed-transmitted viruses viz., Bean common mosaic virus (BCMV) of mungbean and urdbean, urdbean leaf crinkle disease (ULCD) of urdbean and mungbean, Black-eye cowpea mosaic virus (BICMV) and Cowpea aphid-borne mosaic virus (CABMV) of cowpea, Soybean mosaic virus (SMV) of soybean and Pea seed-borne mosaic virus (PSbMV) of pea. The detection and identification of the viruses both in leaves and seeds were done by deploying a combination of growing-on test, infectivity assays, electron microscopy, ELISA and RT-PCR. The extensive surveys carried out for three years in nine major legume-growing States of the country revealed that the disease incidence varied with the location and the crop variety. A total of 972 seed samples collected from public sector seed producing agencies, research institutes and farmers’ fields throughout the country were tested in the laboratory, of which 463 samples showed the presence of viruses. Based on the results of field surveys complemented by seed testing, a national map on prevalence of seed-transmitted viruses of grain legumes was prepared. The seed transmission rate of viruses was assessed by growing-on test and ELISA and in most of the cases, a high rate of seed transmission was observed. Epidemiological studies carried out in cases of BICMV/ cowpea, CABMV/ cowpea, PSbMV/ pea and SMV/ soybean revealed a correlation in viral disease incidence with aphid vector population, and appreciable losses in seed yield in these cases were demonstrated. Based on virus spread using a known level of initial seed/ seedling infection, the seed standards for certification against both BICMV of cowpea and SMV of soybean were proposed to be 0.5%. Antisera to BICMV and SMV were produced in bulk and immunodiagnostic kits were prepared. Group testing of embryos using ELISA was standardized for quality control of seeds. It is expected that the results would be optimally utilized at national level for seed certification of grain legumes.

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Improvement of Resistance to Turnip Mosaic Virus in Cabbage (Brassica oleracea L.)

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Turnip mosaic virus (TuMV) is one of the economically most important pathogens in Brassica vegetables. Establishment of resistance to TuMV in white cabbage (Brassica oleracea var. capitata L.) is an effective way to control this disease.

Sources of genetic resistance to TuMV have been identified in a white cabbage land race, in cabbage primitive forms (B. oleracea var. ramosa DC.) and in radish (Raphanus sativus L.). In the cabbage land race four homozygous lines (I8 generation) with resistance to high virulent TuMV isolate 2 (pathotype 4, typed by Jenner and Walsh, HRI Wellesbourne, UK) were developed through successive selection after self-pollination. From two primitive forms seven homozygous lines (I7) were established with resistance to mixture 1 comprising five TuMV isolates (pathotypes 1, 4, 6). The stability of the resistance in these lines could be confirmed after exposure to viruliferous aphids in the field. Resistance to TuMV mixture 1 in lines of the primitive forms was transferred into domesticated white cabbage by sexual crossings. Uniform reactions of F1 plants (no systemic symptoms, ELISA negative) show the dominant nature of resistance. First results of segregation analysis in F2 plants suggested that more than one gene is involved in TuMV resistance.

Intergeneric somatic hybridization between B. oleracea and R. sativus was used for transferring TuMV resistance into Raphanobrassica hybrids (Ryschka et al. 1999). In seven different combinations of somatic hybrids between 11.1% and 100% of plants revealed resistance to TuMV isolate 2. In progenies (F5) of combination PF 137, 82.4% of plants had also expressed resistance to this isolate. According to Hughes et al. 2002, we could classify different resistance types in hybrid PF 137. In resistant plants virus movement was restricted to inoculated leaves (resistance type R, 81% of plants) or was not detectable in the whole plant with ELISA (resistance type 0, 14.3%). In contrast, in susceptible plants (susceptibility S, 4.7%) TuMV was spread systemically throughout the plant.

The results demonstrate that it was possible to generate and characterize new donors with durable resistance to different TuMV pathotypes in the Brassica vegetables.

References:

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Characterization of *Snake Melon Asteroid Mosaic Virus*, a Tentative New Sobemovirus Infecting Cucurbits

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Cucurbits are important vegetable crops in Sudan and are severely affected by several viruses inducing yellowing or mosaic diseases which cause important yield losses. A 10-years survey has shown that the most common cucurbit viruses were *Cucurbit aphid borne yellows virus* (CABYV, Polerovirus), *Zucchini yellow mosaic virus* (ZYMV, Potyvirus), *Watermelon chlorotic stunt virus* (WmCSV, Begomovirus), *Moroccan watermelon mosaic virus* (MWMV, Potyvirus) and *Squash mosaic virus* (SqMV, Comovirus). In addition, a virus was isolated from a naturally infected snake melon (*Cucumis melo* var *flexuosus*) plant collected in Eastern Sudan presenting severe mosaic and leaf deformation symptoms. This unknown virus was tentatively named *Snake melon asteroid mosaic virus* (SMAMV) because of the star-like shape of the chlorotic areas of the mosaic. SMAMV is mechanically transmissible and has a host range mostly limited to a few cucurbit species. Isometric virus particles circa 30 nm in diameter were consistently observed in leaf dip preparations from symptomatic plants. Observations in ultrathin sections of infected tissue revealed numerous virus particles scattered in the cytoplasm, sometimes forming crystals, but no specific cellular alteration. SMAMV is not transmitted by aphids but is seed-transmitted at a low rate (0.1%). A polyclonal antiserum has been produced which permitted us to search for this virus in frozen extracts from the samples collected during our previous survey. This showed that SMAMV was present in 10.6% of the 558 samples tested and occurred in most regions surveyed. SMAMV properties could relate it to members of Genus *Sobemovirus*. Search for generic primers for sobemoviruses was conducted by aligning sequences available in GenBank and a set of degenerate primers was designed within the polymerase gene. These primers allowed amplifying a fragment of the expected size of 384 base pairs, either from purified SMAMV preparation or from infected tissue extracts. The amplified fragments were sequenced and the most closely related sequence (71% amino acids identity) was that of a strain of *Rice yellow mottle virus* (RYMV), a member of Genus *Sobemovirus*. No sobemovirus has been reported so far as infecting naturally cucurbits. So, the biological, cytological and molecular characteristics of SMAMV suggest that this virus should be considered as a tentative new member of the Genus *Sobemovirus*.

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**Watermelon Mosaic Virus (WMV, Potyvirus): How Interspecific Recombination Between Two Legume-Infecting Potyviruses Yields a Vegetable-Infecting Virus**

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*Watermelon mosaic virus* (WMV) is a potyvirus with a broad host range, that infects cucurbit crops worldwide, as well as pea, orchids, and numerous weeds that can host the virus during intercrops. However, molecular data on this virus remain limited. Partial sequence data had previously shown that WMV is closely related to the legume-infecting potyvirus *Soybean mosaic virus* (SMV), belonging to the “*Bean common mosaic virus*” (BCMV) cluster, and could almost be considered as a strain of SMV, although it presents different biological properties. Establishing the full-length sequence of WMV has revealed that WMV is closely related to SMV in most of its genome, except for the N-terminal half of the P1 coding region, that is 84% identical to BCMV. The putative recombination spot was determined by sequence analysis. The P1 protein of different WMV isolates was partially sequenced, and all sequences so far presented the same putative recombination spot, indicating that the recombination event probably occurred ancestrally during the evolution of WMV, and could be involved in the evolution of the virus towards a broader host range.

The molecular variability of several regions of the genome of WMV isolates from different geographic origins was also studied. Sequence analysis revealed the presence of three major molecular groups of WMV, with a very limited relation to the biological or serological properties of the isolates, or their geographic origins. Besides, several independent intraspecific recombinations were detected within WMV populations, with recombination sites located in different regions of the genome. The biological consequences of these recombinations are not yet determined.

In order to understand the variability of WMV, and to determine the cause for the recent emergence of severe isolates in the last years in France, a molecular epidemiology survey was performed for 4 years (2001-2004) in an experimental plot. This has revealed a very high variability of the virus, with strains belonging to two of the 3 major phylogenetic groups based on the CP-coding region. The high frequency of mixed infections (100% of the plot within 8 weeks in 2002 and 2003) could be explained by the lack of cross-protection between strains of different CP groups, revealed in experimental conditions. These characteristics of WMV may favour frequent recombinations and/or the emergence of severe stains.

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High Sequence Homology between *Pepino Mosaic Virus* Isolates from Chile and the USA

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*Pepino mosaic virus* (PepMV), a Potexvirus, was first observed to infect greenhouse tomatoes in the Netherlands and the U. K. in 1999. In recent years, it has spread throughout Europe and the Americas. In general, Potexviruses are not regarded as seed borne. However, our preliminary study indicated that PepMV is seed borne in tomato. Most of the PepMV European isolates share high genome sequence similarity, while two recently sequenced U.S. isolates (US-1 and US-2) (GenBank accessions AY509926 and AY509927) are more divergent (from each other and from European isolates). This suggests that the U.S. isolates did not originate in Europe. Using commercial seed that was originally produced in Chile as inoculum, several tomato plants were mechanically inoculated with PepMV. The PepMV-infected plants were maintained in a growth chamber for isolation and containment. A genome sequencing project was initiated using tissues collected from a single PepMV-infected plant. The sequencing strategy was based on RT-PCR with consensus sequence primers flanking the coat protein gene and subsequently with specific primers extending towards the 5’ and 3’ directions of the virus genome. The RT-PCR products were cloned into pCR4-TOPO (Invitrogen) for sequencing. The 5’ terminal sequence was determined with RT-PCR using primers against polyadenylated dsRNA. The sequencing data were generated with a dye-terminator cycle sequencing on a Beckman-Coulter CEQ8000 sequencer. The sequencing data indicated the presence of two distinct variants of genome sequence. One isolate (Chile-1) has high nucleotide sequence homology (~98%) to that of US-1 while the other isolate (Chile-2) has a similar high sequence homology to US-2. Like the US isolates, the Chilean isolates are divergent from each other (~83% nucleotide sequence homology). This strong similarity in genome sequences between the two US and Chilean isolates suggests that they might share a common source of origin. Genome sequencing data of these two Chilean isolates and their phylogenetic relationship will be presented.

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Non Transmissibility of Radish Mosaic Comovirus (RaMV) European Strain Through Seed of Wild Turnip Rape (Brassica campestris L.)


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RaMV and about 14 other viruses in Comovirus genus, together with 30-35 viruses in Nepovirus (the majority of them) and Fabavirus genus, belong to family Comoviridae, a group of viruses with isometric particles of 28-30 nm diameter and bipartite ssRNA genomes. In most Comovirus members natural hosts are from one family, in RaMV from Brassicaceae. Aside from leaf beetle (Chrysomelidae) vectors, some 6 viruses of the genus are seed-transmitted. European (including Moroccan isolate) and neotype (type Californian, Japanese and Russian Far East isolates) strains differ in natural hosts and serology. The European strains, depending on the isolate, is deleterious or harmful to Brassica species and varieties, especially to turnip, also Eruca sativa L. under cultivation and Sinapis arvensis L., then to Chinese cabbage, hybrid Perko PVH and somewhat less to perennial kale, cauliflower, swede varieties. The neotype strain is damaging to Raphanus sativus L. varieties: radish, daikon, Chinese radish.

Seed for investigation was taken in late October/November 2004 from wild (weed) plants of wild turnip rape (Brassica campestris L.; synonyms: B. rapa L. subsp. campestris L./Clapham/; etc) - some varieties of it were bred for forage, green manure, etc., which were spontaneously infected with RaMV European strain/Croatian HZ isolate (proved serologically). In three fields located several kilometers apart from each other in Zagreb region (central Croatia), cca 15% to 30% specimens of the plant (here found as a new natural host of RaMV) were infected. Testing of seeds was conducted using 'Kranjska' turnip as assay plant (necrotic local lesions followed by systemic infection). About 2000 seeds were assessed when starting the experiments. Only those of normal appearance but smaller than with healthy plants, about 20% of them, were fertile, other 80%, quite dwarved, were not. Samples of about 100 fertile seeds, not washed (two samples) or washed with tap water were ground with 3 ml of 1/15 M, pH 7.0 Sörensen's phosphate, carborundum inoculated (in a glasshouse during October to December) onto 10 leaves (3 or 4 plants) and after 2-3 min washed with distilled water. A similar sample was inoculated as above after being left for two days to germinate. In the experiments with altogether about 400 fertile seeds no virus symptoms were detected; consequently no virus transmission through wild turnip rape seed occurred. Similarly, no virus transmission was found with neotype strain (Californian and Japanese isolates) in seed of infected radish plants.

Experiments which include more seeds and respective seedlings are continued.

References:

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Dolichos Yellow Mosaic Virus Belonging to a Distinct Phylogenetic Cluster Causes Yellow Mosaic Disease of Dolichos in the Indian Sub-Continent

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Dolichos yellow mosaic disease (DYMD) has been affecting the cultivation of dolichos, Lablab purpureus (L.) in India since the 1950s. Diseased plants produce characteristic bright yellow coloured mosaic patches on leaves. Early infection causes stunting, small leaves and reduction in yield. An isolate of Dolichos yellow mosaic virus (DYMV), from Mysore (DYMV-[Mys]), Karnataka, South India, was sequenced in this study. DYMV was transmitted by grafting and by the whitefly, Bemisia tabaci (Gennadius). Putative virus was detected in diseased plants by polymerase chain reaction (PCR) using a set of degenerate primers. Sequences obtained from these PCR products were used to obtain full-length DNA-A sequences of DYMV-[Mys], which were most similar to the corresponding sequences (EMBL Accession No. AY271891) of an undescribed begomovirus infecting dolichos in Bangladesh at 95% nucleotide (nt) identities. Phylogenetic analyses of DNA-A sequences indicated that the isolates of DYMV formed a sister clade to Mungbean yellow mosaic virus and Mungbean yellow mosaic India virus and clustered separately from viruses infecting other host-plants (cassava, cotton, cucurbits, okra, tobacco, tomato etc) in the Indian sub-continent. DYMV shared only 62.9-63.8% nt identities with the mungbean-infecting viruses and was equally dissimilar to all other begomoviruses sharing only 61.0-63.9% nt identities. These results indicate the infection of dolichos by a distinct begomovirus that may have had different evolutionary pathways. The number and arrangement of open reading frames, however, were similar to those of Old World begomoviruses of the genus Begomovirus, family Geminiviridae. Further studies are being carried out in order to obtain the sequences of the DNA-B component and for better understanding of the genetic diversity of DYMV.

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Molecular Diversity of Begomoviruses Causing Tomato Leaf Curl Disease in Bangladesh

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Genetic diversity was analysed of tomato leaf curl viruses (ToLCVs) collected in September 2003 from the two main tomato growing areas of Jessore and Joydebpur in Bangladesh. Putative viral DNA was amplified from tomato plants exhibiting mild or severe symptoms by polymerase chain reaction (PCR) and the complete genomes of ToLCVs were sequenced. An isolate of the bipartite Tomato leaf curl New Delhi virus (ToLCNDV) was associated with the severe symptom phenotype from Jessore (ToLCNDV-[Jes]) while a previously undescribed monopartite virus, designated Tomato leaf curl Joydebpur virus (ToLCJV), was sequenced from plants showing mild symptoms. ToLCNDV-[Jes] was closest to ToLCNDV-[Lucknow] (EMBL Accession No. Y16421) at 95.7% and Tomato leaf curl Gujarat virus-[Varanasi] (AY190291) at 90.6% nucleotide (nt) identities based on DNA-A and -B component sequences, respectively. ToLCJV was similar to Pepper leaf curl Bangladesh virus at 87.1% DNA-A nt identity. Less than 89% nt identities of ToLCJV allowed it to be classified as a new species. Identification of ToLCNDV-[Jes] and ToLCJV was in addition to the previously described Tomato leaf curl Bangladesh virus (AF314531) with which they shared 73.2% and 86.0% DNA-A nt identities thus confirming the infection of tomato in Bangladesh by at least three distinct viruses belonging to both mono- and bipartite groups. Nucleotide identities and their placement in phylogenetic trees suggested that the viruses may have had different evolutionary pathways. The whitefly vector Bemisia tabaci can transmit all three viruses equally efficiently. The virus diversity and potential mixed infections pose a challenge for tomato leaf curl virus disease management in Bangladesh.

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Investigations on the Genomics of Plant-Virus Co-Evolution in Wild 
Brassica species

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The extent of plant-virus co-evolution in wild forms of two diploid Brassica species, the 
perennial B. oleracea and the annual/biennial B. rapa, is being studied. We are investigating 
whether genetic variation within and among these plant species in their interaction with Turnip 
mosaic virus (TuMV) is a response to genetic variation in the pathogen. Plants grown from 
seed collected from two TuMV-infected wild B. oleracea plants one in Wales and the other in 
Dorset and the two genetically diverse TuMV isolates (GBR 83 and GBR 98) recovered from 
these original plants were used to test for genetic adaptation of TuMV isolates and their native 
hosts. Competition experiments involving mechanical co-inoculation of native and non-native 
TuMV isolates to wild B. oleracea plants from Wales and Dorset were performed. Up to 5 
rounds of consecutive transmission were carried out to test the relative fitness (adaptation) of 
virus isolates in terms of their ability to replicate and move efficiently within different host 
plants. The adaptation of these TuMV isolates and their wild B. oleracea hosts will be further 
investigated in hybridisation experiments comparing plant RNA expression profiles following 
challenge with their native or non-native TuMV genotypes. This will identify plant genes 
differentially up-, or down-regulated. For this purpose 15,000 oligonucleotides derived from 
expressed sequence tags (ESTs) from the B. napus (a natural hybrid of B. rapa and B. 
oleracea) genome have been produced and used to generate microarrays for hybridisation 
analysis.

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Plastic Mulches for Increasing Yields and Delaying Symptoms of Whitefly-Borne Viruses in Cucurbits


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Viruses borne by whiteflies (*Bemisia* spp.) are becoming increasingly problematic for cucurbit production during the late summer and autumn in Israel. During the past three years, two whitefly-borne viruses newly identified in Israel were observed to inflict severe damage to crops of squash and pumpkin (*Cucurbita pepo* L., *C. moschata* Duchesne) and watermelon (*Citrullus lanatus* (Thunb.) Matsum. & Nakai), these being the geminiviruses *Squash leaf curl virus* (SLCV) and *Watermelon chlorotic stunt virus* (WmCSV), respectively. This is in addition to the relatively mild damage inflicted over many years to melon (*Cucumis melo* L.) crops in Israel by the whitefly-borne closterovirus, *Cucurbit yellow stunting disorder virus* (CYSDV). Whitefly populations during the second half of the summer and through the autumn are enormous and difficult or impossible to control with chemicals, and therefore other means are necessary to delay plant infection by the whitefly-borne viruses. One of these means is the use of polyethylene mulches. Use of silver polyethylene mulch has proven effective over many years against the spread and damage caused by aphid-borne viruses of cucurbits in the field. However, severe damage has been inflicted on cucurbit crops grown on this now standard silver mulch by the whitefly-borne viruses. Our objective was to determine if another polyethylene mulch or mulches might prove more effective against the damage inflicted by the whitefly-borne viruses. We chose to compare the standard silver mulch (24% reflectively), with metallized silver mulch (82% reflectivity), and yellow mulch (averages 32% reflectivity in the range of photosynthetically active radiation). The yellow mulch was the most effective in delaying virus infection. The metallized silver mulch hastened plant development. The highest yields of watermelons and melons were obtained with the metallized silver mulch. Higher yields of squash were obtained with the metallized silver and yellow mulches than with the standard silver mulch.

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Radish Mosaic Virus Phylogenetic Relationships in the Genus Comovirus

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Radish mosaic virus (RaMV) is one of fifteen definitive members of the genus Comovirus, family Comoviridae, which includes nonenveloped, icosahedral, beetle-transmitted plant viruses, with a genome comprised of two positive-sense RNA segments. RaMV was described in California by Tompkins (1939). Much later it was found in Japan (1968) and Europe (1972). Comoviruses in general have a narrow host range restricted to a few plant species. RaMV is the only comovirus capable to infect brassicas, whereas the majority of comoviruses infect legumes.

In serological and biological tests, the Japanese and the American isolates proved to be identical (Campbell & Tochihara, 1969), whereas the latter, when compared with the Yugoslav (European) isolate HZ revealed differences both in spur tests and plant reactions (Štefanac & Mamula, 1972). Originally, European isolates were considered as serologically uniform, but our recent study (Špak & Kubelková, 2000) revealed a reasonable serological variability among them.

A comparison of the RNA polymerase gene encoding on the RNA-1 genomic segment of the Czech isolate RaMV 1 revealed about 57% aminoacid identity with the Red clover mottle virus, lower with the Cowpea mosaic virus, Cowpea severe mosaic virus, Squash mosaic virus, Bean pod mottle virus and only 50% with the Andean potato mottle virus, the comoviruses sequenced so far. Phylogenetic analysis based on the RNA polymerase gene did not solve unambiguously the relationships in the genus Comovirus. It classified RaMV closely to the Andean potato mottle virus, although RaMV is known to be serologically related to the Bean pod mottle, Squash mosaic (Campbell, 1964) Red clover mosaic and Cowpea mosaic viruses (Bruening, 1978).

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Identification of Cucurbita Sources of Resistance to the Czech Strain of Zucchini Yellow Mosaic Virus

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Several Cucurbita cultivars reported as resistant or tolerant to the Zucchini yellow mosaic virus (ZYMV) were evaluated for resistance to the highly pathogenic Czech isolate of ZYMV (ZYMV-H). Plants of tested cultivars Cucurbita pepo L. were inoculated with ZYMV-H mechanically. Highly susceptible plants of squash cultivar Zelená were used as a control. The degree of resistance of tested cultivars was assessed by visual inspection of virus symptoms in leaves and fruits and by determination of relative concentration of virus protein in leaves by ELISA. Two independent trials were performed. Cucurbita moschata Duch., cv. ´Menina 15´ was proved to be immune to ZYMV-H. C. moschata is immune to both, mechanical and by aphids infection of ZYMV-H. C. pepo, cv. ´Cougar´ and cv. ´Jaguar´ were evaluated as medium resistant, and cv. Hurakan as medium susceptible to ZYMV-H. C. moschata cv. ´Menina 15´ and C. pepo, cvs. ´Cougar´ and ´Jaguar´ were selected for investigation of molecular markers of resistance to ZYMV-H and research on inheritance of Cucurbita resistance to ZYMV-H. C. pepo cv. ´Zelená´, highly susceptible to ZYMV-H is proposed to be used as the donor of susceptibility to ZYMV. This work was supported by Project MZe 0002700603 of the Ministry of Agriculture, Czech Republic.

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Translocation of Genetically Engineered Resistance to *Tomato Yellow Leaf Curl Virus* across a Graft

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Resistance to *Tomato yellow leaf curl virus* (TYLCV) in tomato (*Lycopersicon esculentum*) was demonstrated previously by transforming tomato with a truncated version of the TYLCV *Rep* gene (2/5Rep). TYLCV resistance was readily apparent under both greenhouse and field conditions and the resistant plants had a normal phenotype. Inoculation of resistant 2/5Rep plants does not produce any symptoms of infection and viral DNA is not detected in upper leaves (Yang et al 2004). Cuttings from susceptible plants (scions) were grafted onto inoculated but resistant transformed plants to determine if transformed plants were immune. No symptoms were present and no DNA was detected in the scions 4 weeks after the graft was established. Susceptible scions grafted onto non-transformed inoculated plants showed symptoms within 2-3 wks.

This work demonstrates that the 2/5 TYLCV *Rep* transgene can provide non-host resistance in independent transformation events in tomato. Based on these and other data, the mechanism of resistance appears to be some form of gene silencing.

Studies were conducted to determine if the resistance had a mobile signal that could be used to generate virus resistant non-transgenic scions. Inoculation of grafted plants composed of transgenic stocks with non-transgenic scions showed that resistance could be generated in the scions. The presumed signal was found to move more effectively from transgenic stocks to non-transgenic scions rather than from transgenic scions to non-transgenic stocks, which suggests that the signal is moving primarily in the phloem. It was also found that established infections in susceptible plants could be suppressed after grafting onto transgenic stocks.

Grafted tomatoes are widely used in the commercial production of tomatoes in protected agriculture in many parts of the world. These studies suggest that the use of transgenic rootstocks could be a new approach to obtaining virus resistance without having to transform the genotypes used in the scion. This would be a more cost-effective approach to virus resistance since it would require the transformation of fewer genotypes and would allow the production of non-transgenic fruit while still having the benefits of genetically-engineered non-host resistance.


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Detection of Low Concentration of *Tomato Mosaic Virus* (ToMV) in Water Samples Using Real-time PCR

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Water used for irrigation can serve as a source of viruses which can in concentration below limit of conventional detection methods infect host plants through root system and cause the development of disease symptoms. This has already been shown using ToMV and *Nicotiana glutinosa* (Krambergar et al). 2004 On the other hand plant viruses may be released from the roots of infected plants into drainage water (Koenig, 1986). Therefore, the laboratory testing of irrigation water for the presence of harmful viruses, especially in greenhouse plant production, is essential (Koenig and Lesemann, 1985; Horvath et al., 1999; Tomlinson et al., 1983).

To solve the problem we developed Real time PCR for detection of ToMV as a model virus in plant tissue, soil and water samples. In addition concentration of viruses using CIM Convective Interaction Media disk monolithic columns has been applied to ToMV concentration. It has been demonstrated that ToMV, which had been diluted way below the sensitivity of Real time PCR, was concentrated by several orders of magnitude in the one-step procedure.

The virus was concentrated using a strong anion exchanger, CIM QA disk monolithic column. A high salt concentration was used to elute the concentrated virus from the columns. The procedure could be applied to the analysis of other highly diluted plant viruses. In addition, CIM disks are being applied for the concentration of viruses for antiserum production.

Using only Real time PCR limit of detection is $10^{-9}$ mg/ml of ToMV in irrigation water. If CIM column is used for virus concentration prior detection, extremely low concentration of viruses could be followed. In comparison with methods described for concentrating plant viruses from irrigation water, the above procedure may provide a much faster and more efficient way to concentrate highly diluted plant viruses.

References:


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Increasing Yields and Quality of the Illinois Horseradish Crop Using In Vitro Disease Elimination

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Illinois is the nation’s leading producer of horseradish (Armoracia rusticana) (USDA website, 2001). However, production in the state has decreased recently due to complications caused by discoloration and internal rotting of the root tissue. Growers and University of Illinois researchers believe the problem results from a combination of pests and cultural problems including viral and fungal infestations. These factors express themselves as a disease complex that weakens the plants. The most detrimental viral pathogen is thought to be Turnip mosaic virus (TuMV-Marmor brassicae H.). Using tissue culture techniques and meristemming, three different cultivars of horseradish were freed of TuMV and propagated asexually for field testing. The polymerase chain reaction (PCR) can be an effective and accurate way to assay for plant viruses by multiplying the DNA copied from plant virus RNA sequences (Langeveld, 1991). Using this system, it is possible to detect even the smallest number of viral particles, increasing the chances of detecting of recently infected plants or those with low viral loads. Field testing of these TuMV-free plantlets in the summer of 2003 and 2004 indicate substantial yield increases over infected controls. “Dirty”, disease-infected roots produced only half the yields of “clean”, disease-free roots (0.27 and 0.55 kg/plant, respectively). However, quality of the roots (discoloration) was improved only slightly. Illinois horseradish growers can combine modified cultural practices with this disease-free plant material to produce higher quality roots.

References:
United States Department of Agriculture Website: Crop Profiles.

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Epidemiological Developments in *Potato virus Y*

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*Potato virus Y* (PVY) is still responsible for important losses in ware potato production and seed potato quality. In the Netherlands a control system is in place that is based on monitoring virus infections in the field and flight data of a selected group of aphids. From these data, foliage destruction dates are determined in order to prevent tuber infection. In the Netherlands, three PVY strains are known: PVYO (old), PVYC (common) and PVYN (new). PVYN is considered to predominate. Recent research revealed that PVYO and PVYC are more common than generally assumed. The idea that PVYN predominates has led to resistance tests of new potato cultivars in which only PVYN is included. This in contrast to research on new potato cultivars conducted before 1980, in which primary and secondary symptoms of the three PVY-strains were described. Nowadays for many cultivars, the symptoms of and resistance levels to PVYC and PVYO are not known.

The green peach aphid (*Myzus persicae*) is considered as the most important vector of PVY. During the last few years, the population of *M. persicae* decreased substantially in the Netherlands; however, problems with (primary) PVY infections persist. Probably the role of other aphid species is underestimated.

We will report on new insights into the occurrence of different PVY strains in the field as determined by biological, serological and molecular biological methods, differences in symptom expression in potato cultivars of different PVY strains and the vector efficiency of different field isolates of *M. persicae* for these strains.

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Identification and Detection of a Closterovirus from Carrot in Germany

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Following dsRNA isolation from a stunted and chlorotic carrot plant growing in a seed propagation plot near Bingenheim, Hessen, Germany, a complex pattern of dsRNA bands was obtained. Since one of the dsRNAs had a notably high molecular weight, it was used as starting material for random RT-PCR, cloning and sequencing. Several clones were obtained which shared sequence similarity with viruses of the genus *Closterovirus*. A stretch of about 12,000 nucleotides comprising the complete 3’ half of the genome of the carrot closterovirus (CCV) was sequenced and analysed. Based on the *hsp70h* gene, which is commonly used for illustrating relationships in the family *Closteroviridae*, CCV is most closely related to *Beet yellow stunt virus* and *Beet yellows virus*, with which it shares *hsp70h* amino acid sequence similarities of 49% and 48%, respectively. Moreover, CCV has a genomic organisation characteristic of the genus *Closterovirus* and, thus, can be confidently assigned to the genus *Closterovirus* of the family *Closteroviridae*.

In attempts to develop a serological detection method for CCV, the major coat protein (CP) gene of CCV was expressed in *E. coli* and the resulting protein preparation was used for polyclonal antibody (PAb) production in a rabbit. When these PAbs were used for immunoelectron microscopy (IEM), the number of closterovirus-like particles that could be visualized on PAb-coated grids was considerably increased as compared to non-treated grids. CCV particles had a normal length of 1600 nm and a width of 12 nm. In IEM decoration, all particles were densely decorated. However, one end (c. 100 nm) of the CCV particle was not decorated by the CP-specific PAbs, indicating that CCV virions also have a bipolar particle structure. In Western-blot experiments, the PAbs reacted with a protein band of about 25 kDa (and two of its degradation products) which was only present in CCV-infected but not in non-infected carrot plants. PAbs also permitted sensitive detection of CCV in field carrot samples in double antibody sandwich ELISA. A reference sample of *Carrot yellow leaf virus* (CYLV) from the Netherlands also gave a strong Western-blot reaction with the PAbs to CCV CP (but failed to yield closterovirus-like particles in IEM and CCV-like sequences by RT-PCR). Therefore, we regard CCV as a German isolate of CYLV, the only known closterovirus infecting Apiaceae.

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Serological and Molecular Evidence for the Occurrence of Nanovirus Species other than Faba Bean Necrotic Yellows Virus in Morocco and Ethiopia

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The three members of the genus Nanovirus (family Nanoviridae) differ clearly in geographic distribution. Milk vetch dwarf virus (MDV) and Subterranean clover stunt virus have been reported only from Japan and Australia, respectively. In contrast, results of serological surveys suggest that Faba bean necrotic yellows virus (FBNYV) occurs not only in West Asian and North African countries but also in Ethiopia, Sudan, and Spain. However, there is evidence that a nanovirus isolate (Eth1) from Holetta, Ethiopia, differs remarkably in serology and phylogeny from the type strain of FBNYV from Egypt (Eg). When universal FBNYV as well as Eth1- and Eg-specific monoclonal antibodies were used for the analysis of faba bean samples from Morocco and Ethiopia, obvious serological differences were observed among some isolates from each country. Sequence analysis of each of the eight genomic DNA components of two representative Moroccan isolates differing in epitope profiles showed that both Eth1- and Eg-like isolates occur in Morocco. Serological analysis of faba bean samples from Ethiopia indicated that Eth1 is the predominant nanovirus in this country. However, sequence analysis of two other Ethiopian isolates with contrasting serological reaction patterns distinct from those of Eth1, provided evidence for the occurrence of two further nanovirus types in the southern part of the country. Here not only Eg-like isolates (e.g. Eth218) but also another very distinct nanovirus isolate (Eth231) were additionally identified. These observations suggested that the nanovirus isolates infecting faba bean in Ethiopia and Morocco are extremely variable in their coding sequences. Since the amino acid sequences of the predicted gene products of Eth1, Eth231 and Eg differ as much (>15%) from one another as those of Eg (= FBNYV) from MDV (Japan), this may warrant their classification as distinct nanovirus species.

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Effects of *Beet Western Yellows Virus*, *Cauliflower Mosaic Virus* and *Turnip Mosaic Virus* on Stored White Cabbage and Their Involvement in the Occurrence of Internal Disorders

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Warwick HRI, Wellesbourne, Warwick, UK

Experiments over two growing seasons clearly showed that *Turnip mosaic virus* (TuMV) infection was associated with internal necrosis (sunken necrotic spots 5 to 10 mm in diameter) and *Beet western yellows virus* (BWYV) infection was associated with collapse of leaf tissue at the margins (tipburn) in heads of stored white cabbage (*Brassica oleracea* var. *capitata*). Virtually no tipburn was seen in the cv. Polinius, whereas the cv. Impala was affected severely. Internal necrotic spots were seen in both cultivars. BWYV appeared to interact with TuMV. Plants infected with both viruses showed a lower incidence of external symptoms and had less internal necrosis than plants infected with TuMV alone.

*Cauliflower mosaic virus* (CaMV) did not induce significant amounts of internal necrosis or tipburn, but did in most cases exacerbate symptoms caused by TuMV and BWYV.

BWYV-induced tipburn worsened significantly during storage. Post-transplanting inoculation with TuMV induced more internal necrosis than pre-transplant inoculation. There was a significant association between detection of TuMV just prior to harvest and subsequent development of internal necrotic spots.

Individually, all three viruses significantly reduced the yield of cv. Polinius, whereas only BWYV and CaMV treatments reduced the yield of cv. Impala.

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Investigating the Molecular Mechanisms Involved in Cross-Protection by Turnip Mosaic Virus

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Cross-protection offers a biological control strategy for plant viruses and has been used successfully in commercial production of zucchini, citrus and papaya. However, the spectrum of efficacy has to be determined for each viral species, and the mode of action is still unclear, which prevents the registration of cross-protection for use in organic and integrated crop systems.

We are trying to elucidate the molecular mechanisms involved in the protection of plants by mild strains of Turnip mosaic virus (TuMV) against infection by severe strains. Molecular techniques (RT-PCR and restriction digest analysis) have been developed to differentiate the mild and severe strains in the same leaf sample in cross-protection experiments. Initial work in Arabidopsis thaliana and Nicotiana benthamiana clearly demonstrated that the severe strain could not be detected in plants pre-inoculated with the mild strain, but was present in all mock-inoculated plants that were subsequently challenged with the severe strain. Current research is investigating this interaction in commercial cultivars of Brassica oleracea in order to evaluate the durability and sustainability of TuMV cross-protection as a viable control strategy.

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Mapping Resistance Genes to *Turnip Mosaic Virus* in the *Brassica* Genome and Identifying the Viral Determinants of Virulence

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*Turnip mosaic virus* (TuMV) is an important pathogen worldwide of various crops, particularly brassicas. To date TuMV is the only potyvirus known to infect brassicas. It has the broadest known host range in terms of plant genera and families of any potyvirus. It is probably the potyvirus that is best adapted to *Arabidopsis*.

We are studying the compatible and incompatible interactions between TuMV and brassicas with a view to developing durable resistance to TuMV and have identified and characterised a range of resistance sources to TuMV in *Brassica* species. We have been mapping the genes involved in these resistances in the *Brassica* genomes and identifying the regions of the TuMV genome determining virulence / avirulence to the plant genes. To date, 8 TuMV resistance genes have been mapped in the *Brassica* genome and the TuMV determinants of virulence for 6 *Brassica* resistance genes have been identified.

A new source of resistance to the pathotype 4 isolate of TuMV, CDN 1, identified in *Brassica napus* (oilseed rape) will be used as an example to illustrate how the resistance genes have been mapped and how the avirulence determinants have been identified.

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Mapping of Tombusvirus Resistance in Lettuce and the Influence of Soil Salinity on Lettuce Dieback Disease Development

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Lettuce dieback is responsible for losses in Romaine and leaf lettuce production California and Arizona. Losses vary, ranging from severe in some years to mild in others, and the disease is tightly linked to fields with poorly drained soils. Characteristic symptoms include severe stunting, necrosis and death of lettuce plants. Field isolates from lettuce have been identified and characterized as the tombusviruses, Lettuce necrotic stunt virus (LNSV), and Tomato bushy stunt virus (TBSV). To identify factors contributing to variability in infection, soil analyses were conducted on adjacent lettuce fields with similar soil type, but differing in the presence or absence of LNSV infected lettuce. These studies, coupled with subsequent greenhouse and growth chamber studies demonstrated that high salt, as measured by elevated electrical conductivity levels in soil, rather than soil moisture, lead to increased LNSV infection and increased incidence of lettuce dieback in two different soils. The inheritance of tombusvirus resistance was studied for Salinas, a modern iceberg cultivar, and PI 491224, the progenitor of recently released romaine germplasm with resistance to lettuce dieback. Resistance was conferred by a dominant allele at a single locus in both genotypes. The tombusvirus resistance locus from Salinas, Tvr1, was mapped in an intraspecific Lactuca sativa population to a location that corresponds to linkage group 2 on the consensus map of Lactuca. To our knowledge, Tvr1 is the first tombusvirus resistance gene identified for any plant host. Although this gene is highly effective in preventing symptom development, the mechanism of resistance is not known, and ELISA results suggest that not all symptom-free plants are completely immune to viral infection.

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Mirafiori Lettuce Virus (MiLV) and Lettuce Big Vein Virus (LBVV) Sequence Diversity and Frequency in California and Arizona Lettuce, and Analysis of Big Vein Resistance

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Lettuce plants with varying severity of lettuce big vein disease symptoms were collected from fields throughout the Salinas Valley (CA), Yuma Valley (AZ), and adjacent lettuce producing areas. Symptom severity was determined based on a disease scale, and total nucleic acids were extracted from leaf tissue and analyzed by RT-PCR for the presence of MiLV and LBVV, and for genetic similarity to these viruses from other parts of the world. All symptomatic plants were infected with MiLV, and 83% were also co-infected with LBVV. Twenty-five percent of non-symptomatic plants were infected with MiLV and 69% were infected with LBVV. Sequence analysis of RT-PCR amplicons from each of 4 MiLV RNAs and from the LBVV coat protein region was used to determine the genetic diversity of these viruses in western lettuce growing regions and their similarity with samples from other parts or the world. Amplicons from each of the MiLV RNAs were at least 95 percent identical to one another and to sequenced isolates deposited in databases, with RNAs 3 and 4 having the highest conservation. The LBVV amplicon shared at least 93% identity among western isolates. Growth of plants in infested soil under conditions facilitating disease induction in the greenhouse resulted in variable symptom production on susceptible and tolerant lettuce cultivars, but no symptoms on the L. virosa accession IVT 280. RT-PCR was used to confirm the presence or absence of MiLV and LBVV in symptomatic and asymptomatic plants. RT-PCR results confirmed that both susceptible and tolerant varieties accumulate virus, but that IVT 280 appears to be immune to both viruses. RT-PCR analysis for the presence of MiLV is an effective and valuable tool for germplasm improvement.

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**Integrated Production Technology in Chickpea**

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Chickpeas are favoured crop of dry areas globally and in India approximately 80 percent cultivation is under rainfed environments. Thus, chickpeas are mostly depending at the mercy of climatic stresses because some time there are good rains and some time no rain at all. Likewise some time temperature rise above normal and some time below normal during cropping season. These fluctuations influence crop growth adversely. Farmers do not apply proper management technologies in crop production. Inputs application like weedicides, insecticides, quality seed, irrigation and proper fertilizer do not find any place. Under these conditions chickpea cultivation is always at risk, productivity is always low, market is uncertain and there is no profitability in chickpea cultivation.

In order to minimize the adverse effects of these factors and to mitigate the impact of drought on crop production it is essential to implement the integrated crop production technology in chickpea growing area for a sustainable production system. With out application of a good management and advance crop planning it is not possible to have a good harvest in any farming system. It is imperative to *chake* out a strategy for a profitable cultivation of any crop especially of rainfed environments.

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