

## Poster Presentations

### Viruses

to other agents with resembling symptoms. Last but not least, human influence on the assessment result is clear. Factors affecting results of visual surveys are introduced and their role discussed.

#### P VIRUS 53

##### **Cherry leaf roll virus (CLRV) - a generalist among plant viruses infecting woody hosts**

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*Cherry leaf roll virus* (CLRV) is a worldwide occurring plant virus with an exceptional wide host range, so far comprising 33 plant genera, predominantly deciduous and stone fruit trees and shrubs. The fact that consistently new host species are detected suggests that the host range might be much larger than described so far.

Among natural hosts CLRV is most abundant in birch species (*Betula* sp.), black elderberry (*Sambucus nigra* L.), English walnut (*Juglans regia* L.) and sweet cherry (*Prunus avium* L.). The most recent first descriptions of CLRV host plants being wild potato (*Solanum acaule*) in Peru and nasturtium (*Tropaeolum majus*) from the sub-antarctic Amsterdam Island, apple (*Malus* sp.), Kiwi fruit (*Actinidia deliciosa*) and Hydrangea (*Hydrangea macrophylla*) from New Zealand and Australia, respectively.

The ecologic and economic impact of CLRV is reflected by increasing demands on CLRV monitorings in stone fruit production areas and during sanitary production of propagation material.

Consequently, there is a strong need for intensive studies on the evolution, genetic adaptability of CLRV to specific hosts, and on changes in its virulence. Moreover, the natural modes of transmission have to be elucidated, especially a putative vector transmission.

#### P VIRUS 54

##### **Occurrence of a new recombinant begomovirus species infecting tomato crops in Al Batinah region of Oman**

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Tomato (*Solanum lycopersicum*) is the most important vegetable crop and the second most important agricultural crop, after date palm, in the Sultanate of Oman. Whitefly-transmitted geminiviruses (family Geminiviridae, genus Begomovirus) causing tomato leaf curl diseases (ToLCD) are a major constraint for tomato cultivation worldwide. The aim of this study was to screen the presence of different begomoviruses and their associated satellites on tomato crops grown in commercial farms in Al Batinah region of Oman. Leaf samples were collected from nine tomato plants and total nucleic acid extracts were resuspended in sterile distilled water and stored at 20°C. PCR positive samples were subjected to rolling circle amplification (RCA) to amplify circular DNA using the Illustra TempliPhi 100 Amplification kit (GE Healthcare Bio-Sciences). The resulting linear DNA was digested with restriction endonucleases to obtain DNA fragments of 2.8 kb or 1.4 kb, which were cloned into the pUC19 vector. Clones were sequenced in both orientations using the primer walk strategy (Macrogen Inc.). Phylogenetic relationships were inferred using the neighbour joining method with bootstrapping. Recombination analysis was carried out using SIMPLOT v. 3.2 and the recombination detection program, RDP v. 3. All nine tomato samples were found to be positive for the presence of begomoviruses by PCR-mediated diagnostics and were used to amplify circular DNAs by RCA. The full-length sequences of the five putative begomovirus clones from tomato were determined to be between 2753 and 2757 nt in length. Alignment of the five sequences showed them to share >97% sequence identity. This indicates that the five tomato clones represent a single species based on the present species demarcation threshold for begomoviruses. An initial comparison of the sequences obtained here to all sequences available in the GenBank databases using BLASTN showed the highest levels of sequence identity with isolates of Tomato leaf curl Oman virus (ToLCOMV). Additional pairwise sequence comparisons showed the five sequences to have 85.8-88.6% nucleotide sequence identity with ToLCOMV, followed by 77.4-83.8% identity with Croton yellow vein virus. These results indicate that the five isolates represent a new species in the genus Begomovirus, based on the 89% species demarcation threshold for begomoviruses. The name Tomato leaf curl Barka virus (ToLCBrV) is proposed for this newly identified species. The newly identified virus, ToLCBrV, at this time occurs across a relatively narrow geographical area. The focus of future studies will be monitoring the spread of this virus in Oman and determining whether the virus evolves further. With the diversity of begomoviruses now known to occur in Oman, further recombination is a distinct possibility.