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XXI Convegno Nazionale Società Italiana di Patologia Vegetale (SIPaV)

XXI Convegno Nazionale
Società Italiana di Patologia Vegetale
(SIPaV)

*Difesa delle piante per l'alimentazione
e l'energia*

BOOK OF ABSTRACTS

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59. IDENTIFICATION OF *LYCHNIS RINGSPOT VIRUS* IN *MENTHA PIPERITA* IN ITALY BY NEXT GENERATION SEQUENCING (NGS) TECHNOLOGY.

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A sap-transmissible virus was detected since early 2013 in peppermint (*Mentha piperita*) plants growing in commercial nursery of Northwest Italy (Liguria Region). Susceptible host species were found in the family *Chenopodiaceae* (*Chenopodium amaranticolor* and *C. quinoa*), *Fabaceae* (*Pisum sativum* and *Vigna unguiculata*), *Lamiaceae* (*Ocimum basilicum* and *Salvia splendens*) and *Solanaceae* (*Nicotiana benthamiana*, *N. clevelandii*, *N. tabacum*, *Petunia hybrida*, *Solanum lycopersicum* and *Solanum melongena*), whereas species belonging to *Asteraceae* (*Zinnia elegans*), *Brassicaceae* (*Brassica rapa*) and also to *Fabaceae* (*Phaseolus vulgaris* and *Vicia faba*) did not show any symptoms. Electron microscope observations of crude-saps from peppermint leaves with bright yellow mosaic symptoms, revealed the presence of rod shaped virus particles of different lengths. In order to identify the virus, dsRNAs were extracted from inoculated *N. tabacum* and submitted to deep sequencing. Five scaffolds were reconstructed: two mapped in the RNA beta of *Lychnis ringspot virus* (LRSV, Acc. Z46351), with percentages of identity of 95.4 and 96.4% (of 410 and 1036 nts, respectively), two in the RNA alpha of LRSV (Acc. Z46630), with percentages of identity of 96.9 and 92.4% (of 357 and 392 nts, respectively), while last scaffold mapped in the RNA alpha of *Barley stripe mosaic virus* (67% identity with BSMV, Acc. KJ433977), because the corresponding sequence is not available for LRSV. LRSV was previously described in 1972 in *M. longiflora* in Hungary. By NGS technology we were able to identify the same *Hordeivirus* specie in *M. piperita*; however some differences in host symptomatology and some genomic sequence variations suggest that it should represent a new variant of LRSV.