

## Publication

## Small RNA-Omics for Virome Reconstruction and Antiviral Defense Characterization in Mixed Infections of Cultivated Solanum Plants

**JournalArticle (Originalarbeit in einer wissenschaftlichen Zeitschrift)****ID** 4488866**Author(s)** Turco, Silvia; Golyaev, Victor; Seguin, Jonathan; Gilli, Céline; Farinelli, Laurent; Boller, Thomas; Schumpp, Olivier; Pooggin, Mikhail M.**Author(s) at UniBasel** [Boller, Thomas](#) ;**Year** 2018**Title** Small RNA-Omics for Virome Reconstruction and Antiviral Defense Characterization in Mixed Infections of Cultivated Solanum Plants**Journal** Molecular plant-microbe interactions : MPMI**Volume** 31**Number** 7**Pages / Article-Number** 707-723

**Mesh terms** Coinfection; Genome, Viral; Plant Diseases, virology; Potexvirus, genetics, isolation & purification; Potyvirus, genetics, isolation & purification; RNA Interference; RNA, Viral; Solanum, virology In plants, RNA silencing-based antiviral defense generates viral small RNAs (sRNAs) faithfully representing the viral genomes. We employed sRNA sequencing and bioinformatics (sRNA-omics) to characterize antiviral defense and to reconstruct the full genomic sequences and their variants in the evolving viral quasispecies in cultivated solanaceous plants carrying mixed infections. In naturally infected Solanum tuberosum (potato), one case study revealed a virome comprising Potato virus Y (genus Potyvirus) and Potato virus X (genus Potexvirus), which was reconstructed by de novo-assembling separate genome-size sRNA contigs. Another case study revealed a virome comprising NTN and O strains of Potato virus Y, whose sRNAs assembled in chimeric contigs, which could be disentangled on the basis of reference genome sequences. Both viromes were stable in vegetative potato progeny. In a cross-protection trial of Solanum lycopersicum (tomato), the supposedly protective mild strain CH2 of Pepino mosaic virus (genus Potexvirus) was tested for protection against strain LP of the same virus. Reciprocal mechanical inoculations eventually resulted in co-infection of all individual plants with CH2 and LP strains, reconstructed as separate sRNA contigs. LP invasions into CH2-preinfected plants and vice versa were accompanied by alterations of consensus genome sequences in viral quasispecies, indicating a potential risk of cross-protection measures. Additionally, the study also revealed, by reconstruction from sRNAs, the presence of the mechanically nontransmissible Southern tomato virus (genus Amalgavirus) in some plants. Our in-depth analysis of sRNA sizes, 5'-nucleotide frequencies and hotspot maps revealed similarities in sRNA-generating mechanisms in potato and tomato, differential silencing responses to virome components and potential for sRNA-directed cross-targeting between viral strains which could not, however, prevent the formation of stable viromes.

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