Interestingly, viral RNAs of grapevine fanleaf virus (GFLV, *Nepovirus*, *Secoviridae*) are uridylated to very high levels (>81%) with a mono-uridylation pattern. To evaluate the evolutionary conservation of GFLV 3' terminal features among *Secoviridae*, we investigated RNA uridylation patterns from nine other viruses from this family. Interestingly, only RNAs from GFLV and its closed relative, arabis mosaic virus, had in common this remarkable high percentage of mono-uridylation.
The immediate perspectives of this work are to identify which plant or viral factor catalyzes the mono-uridylation in GFLV RNAs and to determine the importance of GFLV RNA 3' terminal uridylation for viral infection using uridylated or non-uridylated GFLV viral infectious transcripts.

P1.2-036

DEVELOPMENT OF A QUANTITATIVE PEA NECROTIC YELLOW DWARF VIRUS (PNYDV) SCREENING SYSTEM FOR THE SELECTION OF RESISTANT PEA (PISUM SATIVUM L.) ACCESSIONS

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Text
Pea (*Pisum sativum* L.) is a widely grown grain legume in temperate regions and contributes largely to protein rich food and feed and biological nitrogen fixation in the crop rotation. However, many biotic stresses, such as fungal and viral pathogens and insect pests are crucial constraints of successful pea production. Pea necrotic yellow dwarf virus (PNYDV), an obligate aphid transmitted nanovirus, emerged in Central Europe only recently during the last 10-15 years. In contrast to other viral diseases of pea, PNYDV leads to substantial yield reduction or even complete loss in highly epidemic years. Control of this virus is challenging particularly in organic agriculture, where insecticidal treatment against the aphid vector is very limited or not allowed. The selection and breeding of resistant pea varieties is therefore the most promising approach. We have established a screening system for the selection of resistant lines by employing a newly developed qPCR assay for the differential assessment of the virus load between pea accessions upon inoculation with aphids carrying PNYDV. This quantitative assessment will allow the identification of breeding lines able to limit or suppress the virus multiplication. Breeding lines will be selected based on qPCR assay and validated in the field. This novel screening approach can be translated to other obligate aphid transmitted virus in different crops and become an important selection tool for breeding and genomic analysis.

P1.2-037

GRAPEVINE FANLEAF VIRUS AVIRULENCE FACTOR 2AHP (HOMING PROTEIN) INTERACTS WITH SEVERAL PROTEINS OF NICOTIANA OCCIDENTALIS INVOLVED IN PLANT IMMUNITY

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