

Identification of *Nectarine stem pitting-associated virus (NSPaV)* by Next-Generation Sequencing (NGS) in Hungary

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Introduction

- NSPaV (genus *Luteovirus*) first described in the USA in imported nectarine by NGS (Bag *et al.*, 2015)
- Later identified in peach, nectarine and *Prunus mume* (Villamor *et al.*, 2016, Lu *et al.*, 2017, Candresse *et al.*, 2017)
- Peach leaves showing severe yellowing symptoms collected from *Prunus persica* 'Baby Gold' tree from a 13-year-old organic orchard in Szob (Pest County) in May 2011 in Hungary

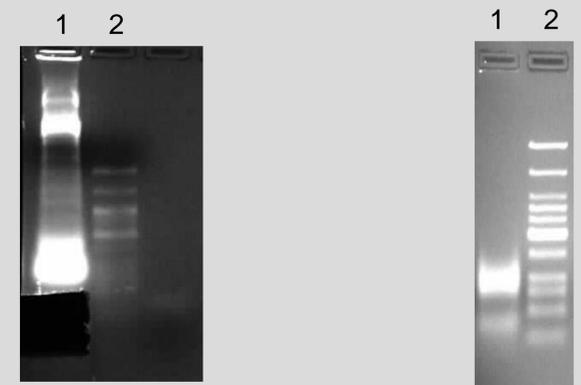


Peach tree showing strong yellowing symptoms (Szob, Hungary)

Methods

'In house' small RNA library preparation and sequencing on Ion Torrent PGM

- Total RNA extraction by TRI Reagent; run, excise and purify small RNA from 3% non-denaturing agarose gel
- Adenylation of ION P1B DNA adapter (Song *et al.*, 2015)
- Adenylylated P1B DNA adapter ligation to small RNA 3'-end
- ION RNA adapter ligation to small RNA 5'-end
- Reverse transcription and PCR amplification
- Run, excise and purify amplified library from 3% non-denaturing agarose gel
- Qubit HS library quantification
- Run emulsion PCR (Ion One Touch 2 system)
- Template Ion Sphere Particles enrichment (Ion One Touch ES system)
- Sequencing on ION 314 Chip (Ion Torrent Personal Genome Machine)
- Sequence analysis by VirusDetect pipeline (Zheng *et al.*, 2017)

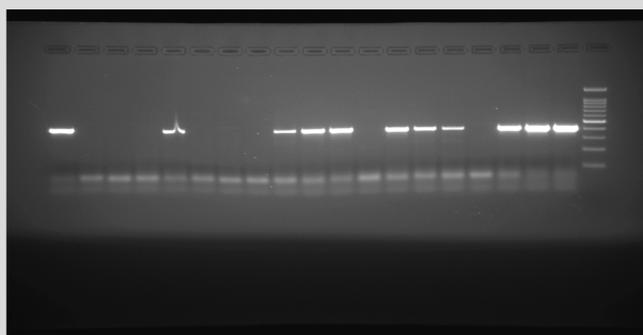


1. Total RNA extracted from infected peach leaves by TRI Reagent; excised small RNA
2. Low Molecular Weight DNA Ladder

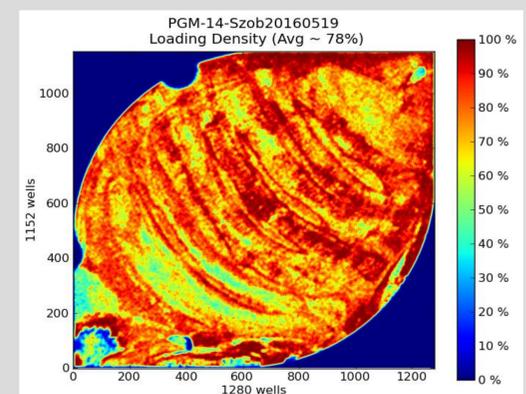
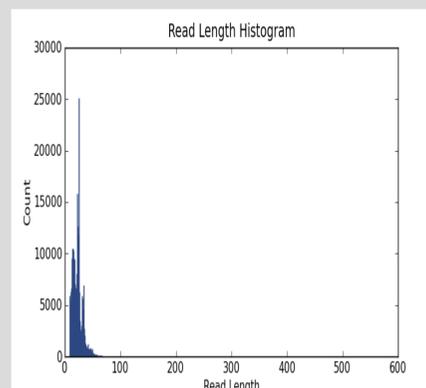
1. Amplified small RNA library by A/P1B Ion Torrent platform-specific primers
2. Low Molecular Weight DNA Ladder (25, 50, 75, 100, 150, 200, 250, 300, 350, 500, 766 bp)

Results

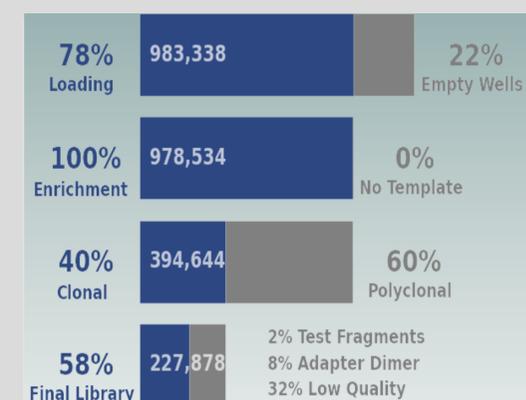
- 18 contigs were assembled from 227,878 reads showing 95 to 100% homology to NSPaV sequences in GenBank (NC_027211, KT273409 and KT273410)
- 75 contigs revealed 95 to 100% similarity to *Plum pox virus* (PPV)
- The presence of NSPaV in the sample was confirmed by specific primers based on the contig sequences and also by NSPaVF-NSPaVR primers (Bag *et al.*, 2015)
- RT-PCR products of two NSPaV isolates from the same orchard were Sanger-sequenced and deposited in GenBank (KY626337.1 and KY829024.1) that shared 96 to 98% nucleotide identity with NSPaV sequences in GenBank
- NSPaV and PPV mixed infection was detected in all the additionally tested 13 peach samples showing the same symptoms from the same place
- NSPaV and PPV mixed infection was detected in 9 peach samples from another orchard showing no typical yellowing symptoms
- NSPaV was detected also in symptomless trees (11 out of 19 samples)
- NSPaV seems to be very frequent in peach in Hungary (36 out of 46 tested samples)
- NSPaV association with the yellowing disease remains uncertain



Detection of NSPaV in symptomless peach samples by RT-PCR



Loading density of the ION 314 Chip



Wells-beadogram of the loaded ION 314 Chip

References

Bag S, Al Rwahnih M, Li A, Gonzalez A, Rowhani A, Uyemoto JK, Sudarshana R, 2015. Detection of a new luteovirus in imported nectarine trees: A case study to propose adoption of metagenomics in post-entry quarantine. *Phytopathology* 105, 840-846.

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