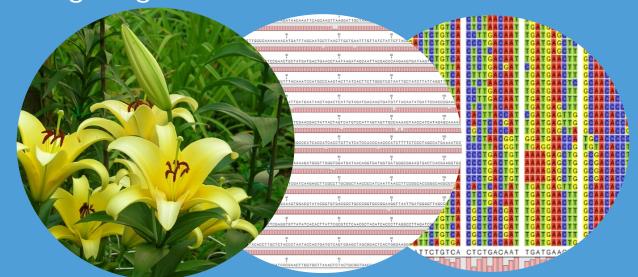
# NGS applications in plant pathogen diagnostics

#### Annette Dullemans,

Els Verstappen, Ilse Houwers, Martin Verbeek, Theo van der Lee, René van der Vlugt and Peter Bonants

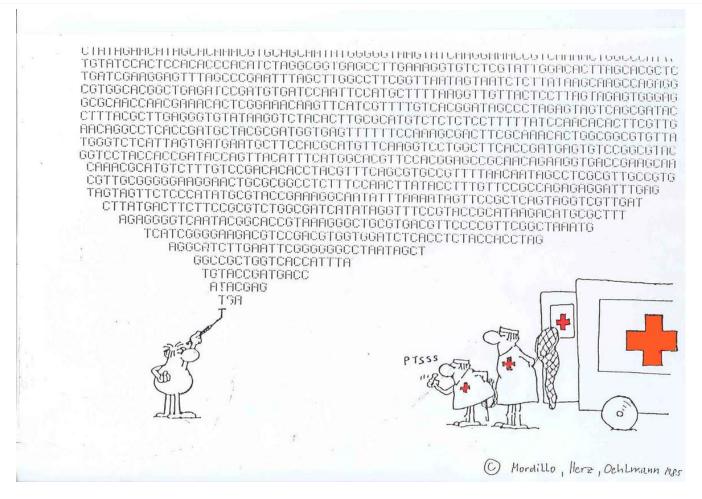
EPPO-TESTA meeting Angers, 2 December 2015





## Plant Virology Indicator plants Virus purification RNA isolation Total RNA isolation cDNA synthesis/ Sanger sequencing NGS Virus sequence Primer design Virus purification WAGENINGEN UR Koch's postulates For quality of life

## a DNA sequence in itself is useless





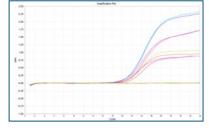
## Plant Virology

- Applications for NGS:
  - Identification of (new) viruses
  - Quality control of virus collection material
  - Study of diagnostic samples (presence: yes/no & sequence variation)
    - Developing primers for detection strategies:
      - (Real time)-(RT)-PCR
      - Luminex: xTAG
      - On-site: LAMP











## Strawberry Latent Ringspot Virus (SLRSV)

- Unassigned species in the family Secoviridae
- Worldwide distribution
- Many hosts: Strawberry, Raspberry, Blackberry, Impatiens, Anemone, Tibouchina, Bean, Pepino, Mint, Rose, Prunus Robinia, Quinoa, Lily,....
- 1 full length sequence: Golden Ginger Mint
- 2 RNA segments: 7.5 + 3.8 kb





## SLRSV in Lily

- Symptomless
- Screening bulbs for export



- Antiserum available:
  - Bioreba & Prime Diagnostics
- Different reaction with different isolates

- RT-PCR (Tang et al, 2012)
  - Not in accordance with ELISA results





#### Procedure

- Total RNA isolated
  - collection material (indicator plants)
  - Lily bulbs
- DNase treatment
- RiboZero TrueSeq Illumina HiSeq library preparation
  - MiD labeling, maximum 24 samples/lane
  - Paired-end reads, 125 nts

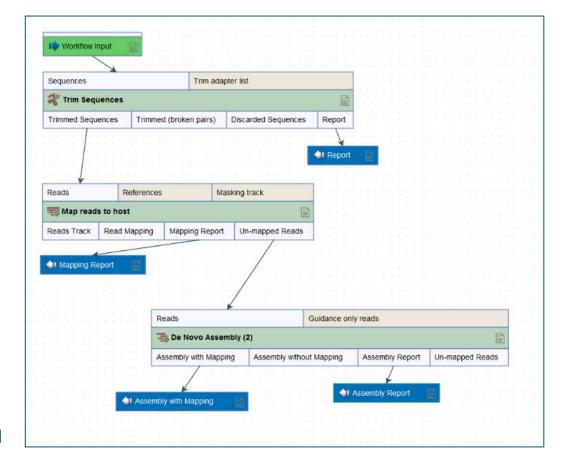




## Data analysis



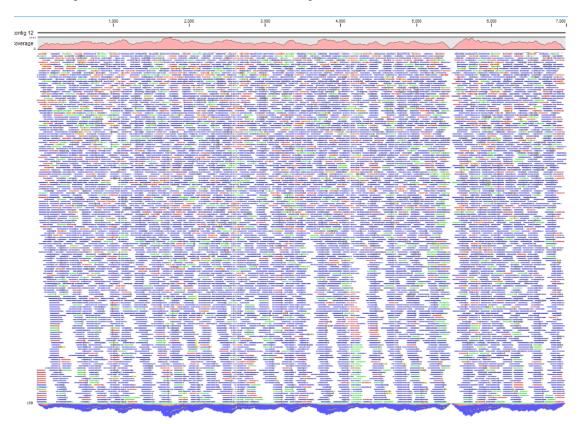
- CLC Genomics Workbench
- In workflow
- In batch





#### Results

- Contig list
- Select virus contigs by Blast analysis
  - Expected & unexpected virus sequences
- Near full length sequences

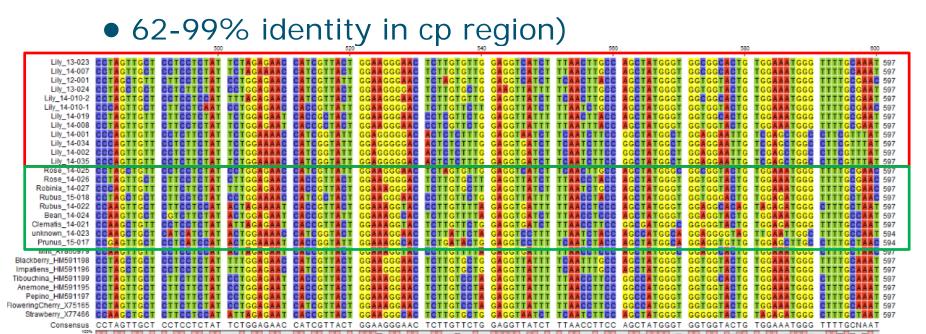




#### Results

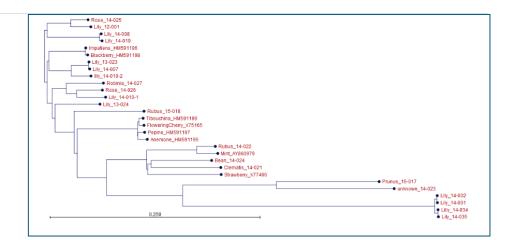
#### 21 new SLRSV sequences

- 12 from Lily
- 9 from virus collection
  - Very variable nt-sequences





Conservation

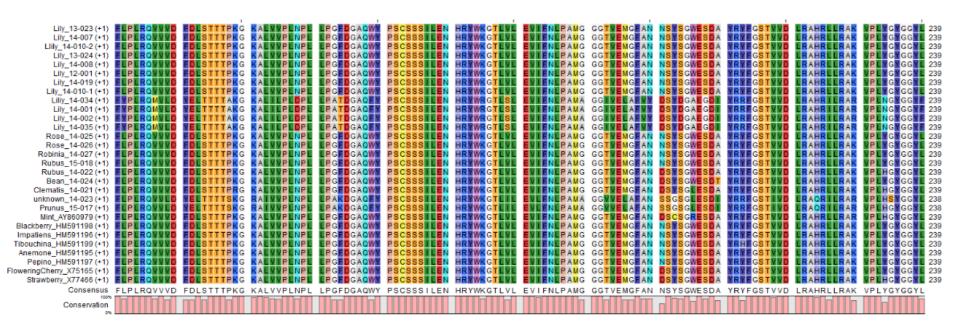


#### Results

#### aa alignment

- Much higher identity
  - 2 groups

- Impatiens\_HM591196 (+1) Blackberry\_HM591198 (+1) Lily\_12-001 (+1) Lily\_14-008 (+1) Rose\_14-025 (+1) Lily\_14-019 (+1) lilv 14-010-2 (+1) Lily\_14-007 (+1) Lily\_13-023 (+1) Lily\_13-024 (+1) Lily\_14-010-1 (+1) Robinia\_14-027 (+1) Rose\_14-026 (+1) Rubus\_15-018 (+1) Tibouchina\_HM591199 (+1) FloweringCherry\_X75165 (+1) Pepino HM591197 (+1) Anemone\_HM591195 (+1) Bean 14-024 (+1) Clematis\_14-021 (+1) Rubus\_14-022 (+1) Mint\_AY860979 (+1) Strawberry\_X77466 (+1) unknown\_14-023 (+1) Prunus 15-017 (+1) Lily\_14-002 (+1) Lily\_14-001 (+1) Lily\_14-035 (+1) Liliy\_14-034 (+1)
- >93 & 63-72% identity





## Next step

- Develop specific (real time-)RT-PCR test for routine screening by the Dutch Flower Bulb Inspection Service (BKD)
  - Select the best region
  - Cover all known sequences



## Advantages of NGS in Virology

- Fast
  - Virus sequence
    - Help to develop purification strategy
    - Virus identification
    - Insight in population variance
    - Epidemiology studies
    - Disease management
- Result: (PCR) detection based on several isolate sequences



## Acknowledgements

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  - Marleen Botermans
  - Marcel Westerberg



NL funding: PPS diagnostics

