Genome sequencing of *Ca.* Liberibacter solanacearum infecting carrots in Finland

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Why to sequence?

- Are there differences between *Ca.* L. solanacearum haplotypes infecting carrot and potato?
- If yes, how big are the differences?
- Can they be used to predict the risk of spreading from carrots to potato?

Genome sequencing

- Sequencing the genomic DNA isolated from carrot psyllid from the field
  - Proportion of Liberibacter DNA amount compared to psyllid DNA in 26 psyllids with PCR, 10 positive
  - Real-time PCR , the highest chosen for sequencing
- Sequencing at Biomedicum Functional Genomics Unit at University of Helsinki
  - Illumina, 101 nt long reads
  - Several hundred contigs

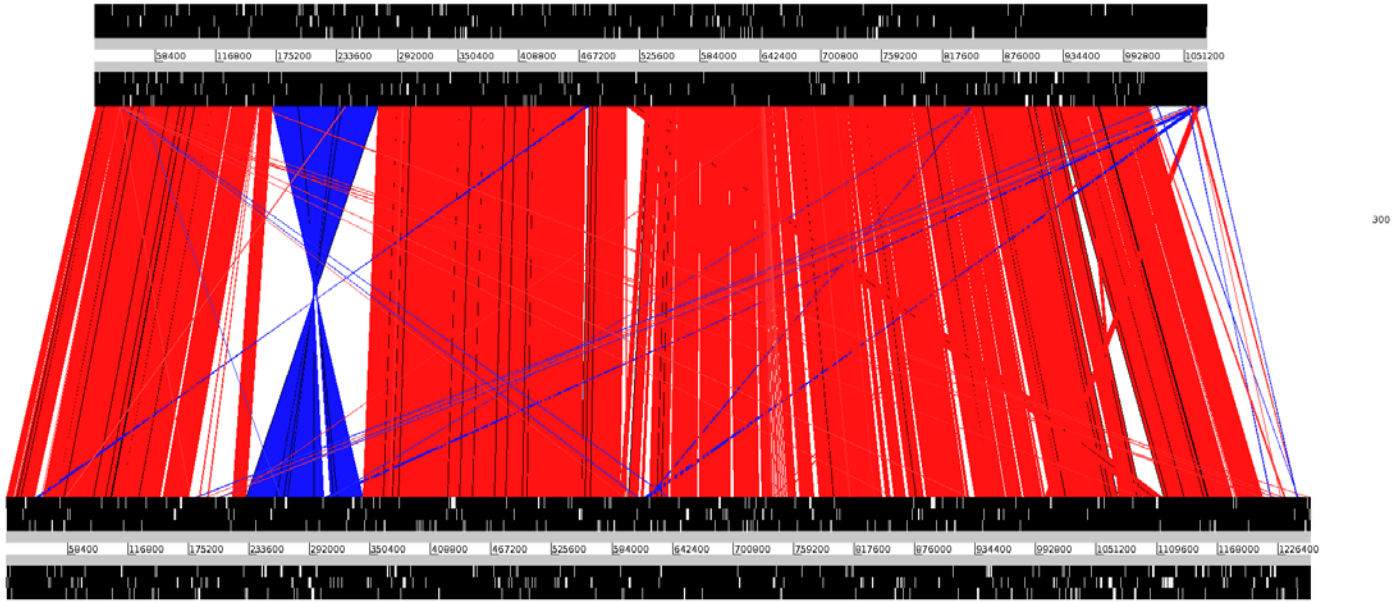
http://www.biology.lu.se/

Sequencing continued as collaboration with NZ

- Grant Smith at Plant and Food Research in New Zealand sequences *Ca.* Liberibacter solanacearum
- New samples have been sent twice to NZ
  - 20 X higher proportion of Liberibacter DNA if compared to earlier samples
- About 8% of the sequence is from Liberibacter
  - Majority of the sequence is from the psyllid
  - Sequence also from two psyllid symbionts

Results

- 1.1 Mb Liberibacter sequence in 27 contigs
- Assembled based on homology to sequenced *Ca.* L. solanacearum ZC1 from potato
- The average nucleotide identity 96-97% => carrot Liberibacter belongs to same species as ZC1



Prophage sequences

- Prophage sequences pose a problem
  - Higher differences in the sequence compared to ZC1
  - How many prophages?
  - In which location?
  - Potentially very important

- Ca. L. asiaticus prophage sequences
  - Contain hypervariable ORFs and make new combinations *in planta* (Zhou et al. 2013, PlosOne)
  - Excise from the bacterial chromosome as plasmid and lytic phages *in planta* (Zhang et al. 2011, MPMI)
  - Are related to virulence and insect transmission

Conclusions

- Carrot *Ca.* Liberibacter solanacearum belongs to the same species as the haplotype causing zebra chip
- Bigger differences between the haplotypes in the prophage sequences than between their core genomes
- Prophage sequences may contain new virulence determinants and explain host specificity
- Need to be assembled *de novo*
- Need to be cloned with PCR and sequenced from the clone

Thanks to...

- Jinhui Wang, UH
- Minna Haapalainen, UH
- Anne Nissinen, Agrifood Research
- Matti Kankainen, Functional Genomics unit, UH
- Grant Smith, Plant and Food Research, NZ
- Sarah Thompson, Plant and Food Research, NZ
- Thomas Schott

Thank you!