



# The Complete Genome of the “Flavescence Dorée” Phytoplasma Reveals Characteristics of Low Genome Plasticity

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# Phytoplasmas

- gram+ well-less bacteria.
- Obligatory parasites of the phloem.
- Transmitted by sap-sucking insects (e.g. leafhoppers).
- Cause numerous diseases:
  - Apple proliferation, European stone fruit yellow, grapevine yellows, Potato stolbur, ...



## Genome sequencing: challenges

- Impossibility to isolate and cultivate the phytoplasma.
- The genetic material of the phytoplasma is "embedded" in the genetic material of the host (plant or insect).
- Genome rich in A/T (only ~20% G/C) and "repeated" regions.

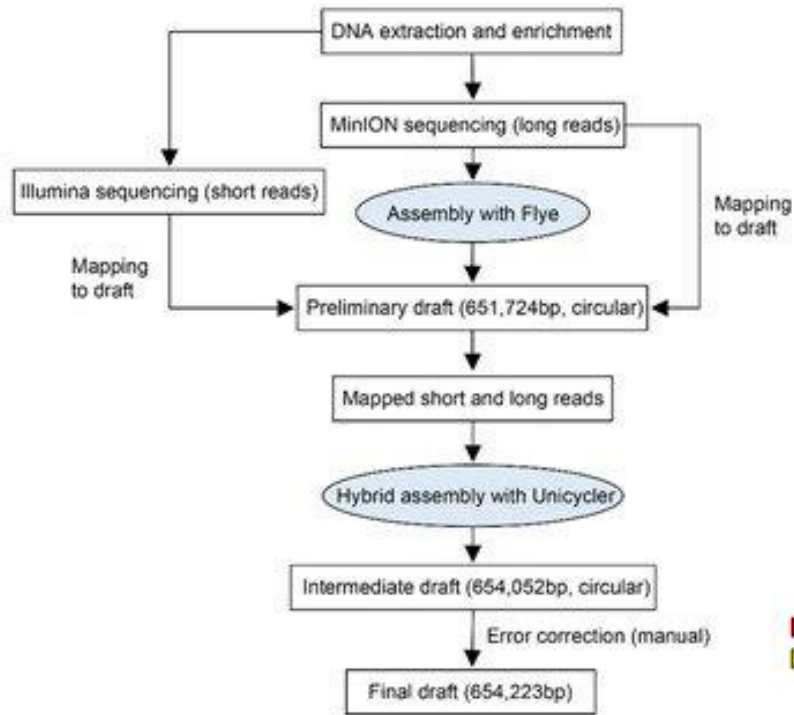
## Genome sequencing: solutions

- Choice of the genetic material source: insect rather than plant.
- Enrichment of the pathogen's genetic material (from 0.1% → ~1% of total reads).
- Combination of 2 high throughput sequencing methods: Oxford Nanopore MinION (long reads) and Illumina (short reads).

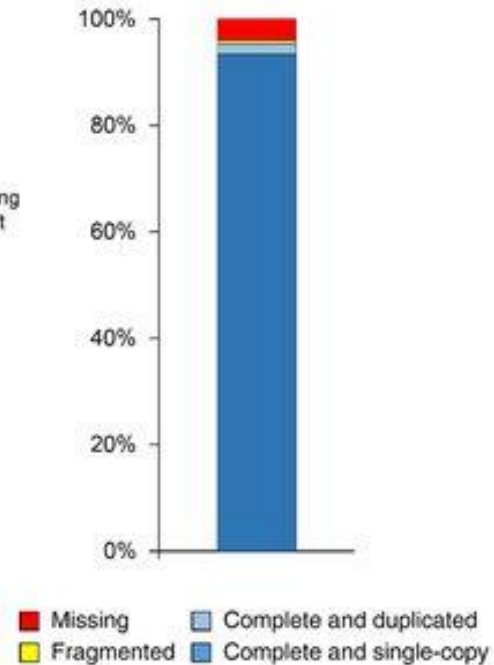


# Assembly and Quality control

A



B



151 core genes: 95% present (144/151)



# Genome annotation

Tools used:

Prokka v1.13

Go Feat

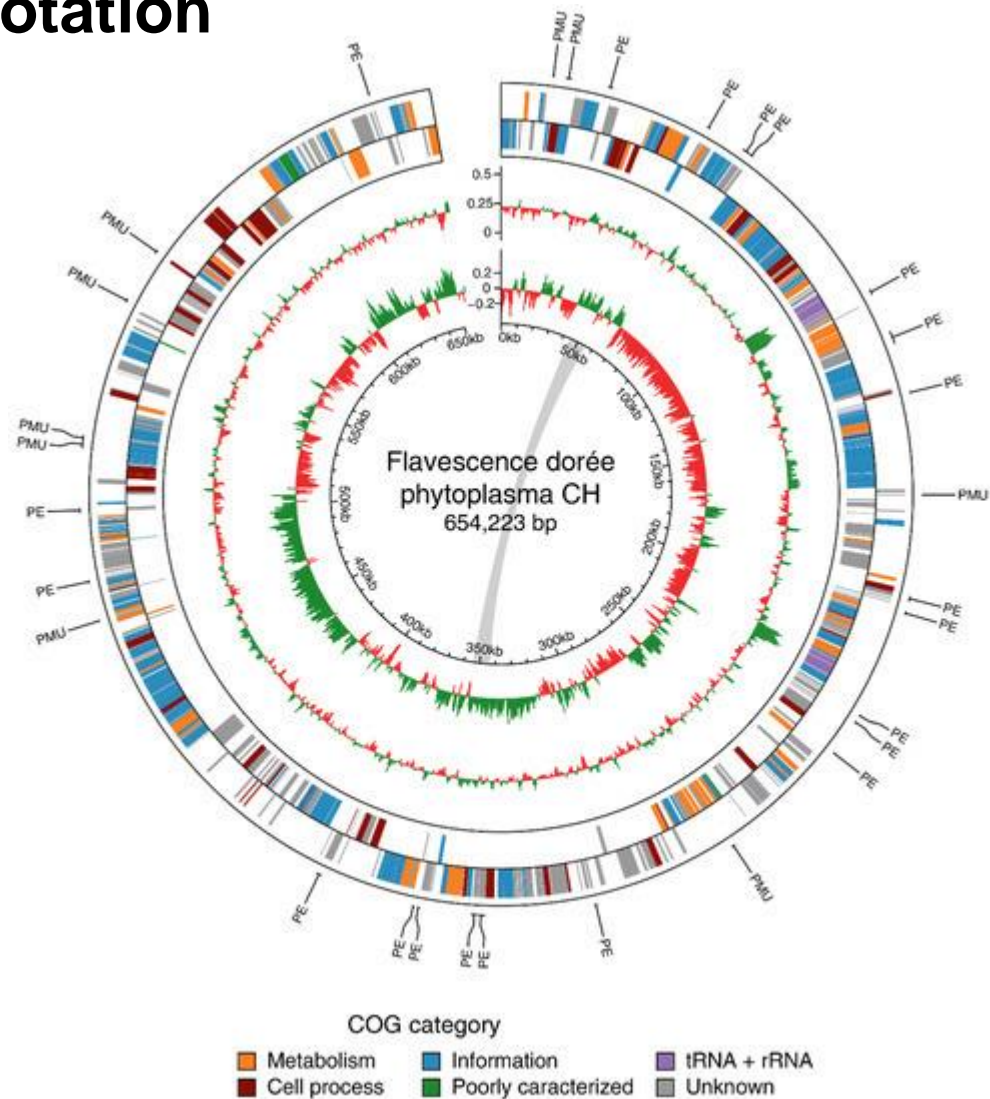
BlastKoala

OrthoVenn2

Size: 654'223 bp

21,7% G/C

506 predicted proteins







# Thank you for your attention

Cully, 2021



Photos: C. Parodi