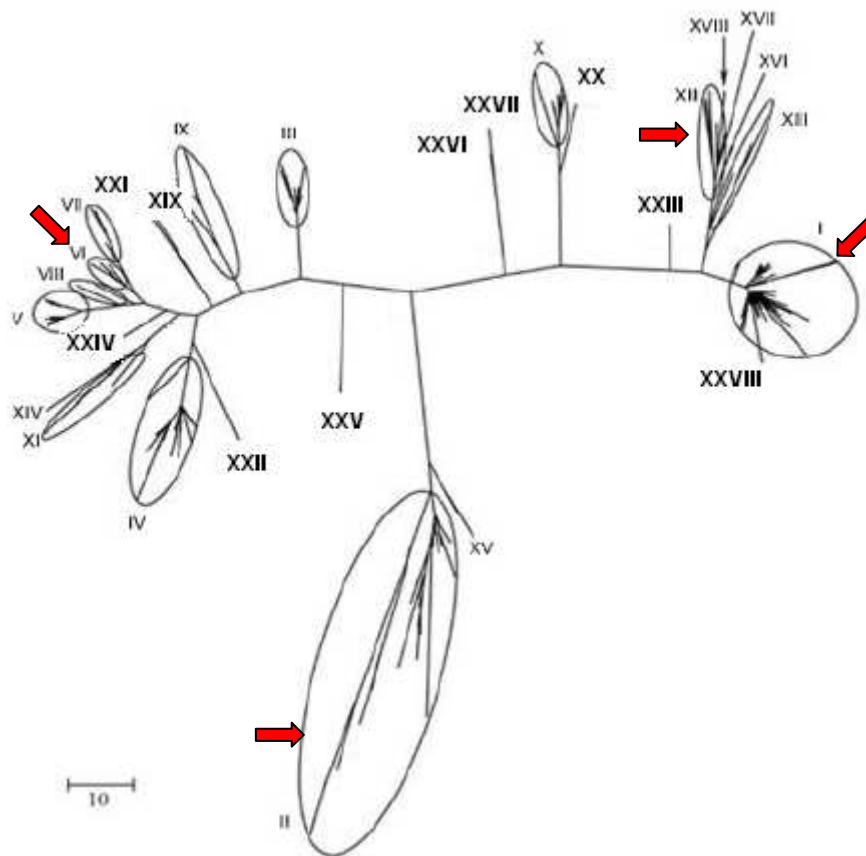**Phytoplasma plasmids**

Phytoplasmas are cell-wall-less, non-helical prokaryotes associated with diseases in more than a thousand plant species. They are phloem-limited and uncultivable on artificial media plant pathogens.

Phylogenetic analyses indicate that the *Mollicutes* arose monophyletically from a gram-positive, low G+C content *Eubacteria*. But, phytoplasmas are more diverse than originally thought and are not distributed uniformly over all continents.

There are about 40 '*Candidatus Phytoplasma* species' (or I-XXX 16S rRNA restriction groups) of phytoplasma.

Plasmids were found predominantly in *Ca.Phytoplasma asteris* (16Sr I), *Ca.P. australiense* (16Sr XII), *Ca.P.trifolii* (16Sr VI), and *Ca.P.aurantifolia* (16Sr II).

The size of plasmid was from 2.587 to 10.785 nt and genome content from 2 to 11 genes.

Clusters of isolates where plasmids are known (arrows). Picture redraw with modification from: Wei et al. 2007, *J.Sys. Evol. Microbiol*. 57: 1855-1867

We have found plasmids in Czech isolates of phytoplasmas from restriction groups I, II, and X. We suppose that other isolates (all ???) also contain various kinds of plasmids...

We are looking for isolates from another restriction groups, not detected in the Czech Republic, especially that from restriction groups III, IV, V, X, XI. Cooperation in plasmid study is welcome!
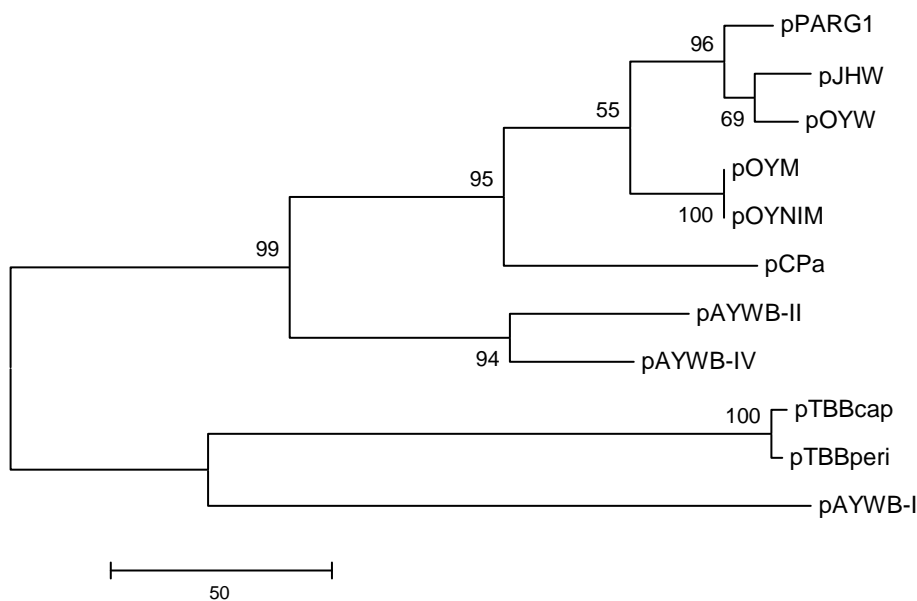
Contact: petrzik@umbr.cas.cz
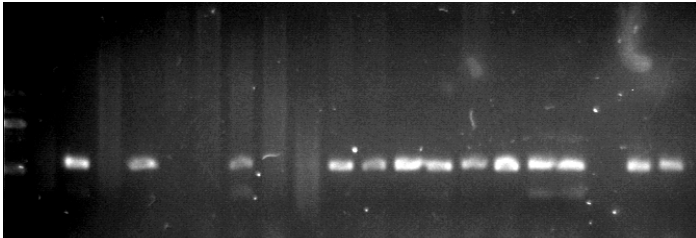
Plasmid gene PCR-detected in phytoplasma isolates from fruit trees and small fruit trees.

In phylogeny based on the plasmid *rep* gene, there are several branches of plasmids, not reflecting the phytoplasma classification!

Phylogenetic tree for the rep protein. The bootstrap consensus tree using the Maximum Parsimony method from 100 replicates was taken to represent the evolutionary history of the analyzed taxa. Branches corresponding to partitions reproduced in less than 50% bootstrap replicates were collapsed. *In silico* translated ORFs were blastp compared with sequences in GenBank. The phylogenetic relationships of the Rep protein were computed with the maximum parsimony algorithm in MEGA (Tamura et al., 2007).