

Comparative genome analysis of *Acholeplasma brassicae*, *A. palmae*, *A. laidlawii* and *Candidatus Phytoplasma* species highlights limits in shared genetic content

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The *Acholeplasmataceae* comprises the genera *Acholeplasma* and ‘*Candidatus Phytoplasma*’. Members of the first genus are characterized by a saprophytic lifestyle and do not contain primary pathogens. The pathogenic phytoplasmas can be separated as insect vector spread obligate parasites colonising the sieve cells of the plant phloem.

Sequencing of the plant-derived *Acholeplasma brassicae* strain O502 and *A. palmae* strain J233 resulted in determination of circular chromosomes with 1,9 Mb and 1,6 Mb in size and a G + C content of 36% and 29%, respectively. Genomes encode above 1,690 and 1,439 proteins respectively. Comparative analysis of these and recently published genomes of *A. laidlawii*, ‘*Ca. P. asteris*’ strains, ‘*Ca. P. australiense*’ and ‘*Ca. P. mali*’ highlights a limited shared basic genetic repertoire of acholeplasmas and phytoplasmas. *Acholeplasma* chromosomes are characterized by a lower genetic instability. Rare exceptions are the unusual duplication of rRNA-

operons and independently introduced gene copies in both genera. Furthermore, acholeplasmas differ e.g. by encoding a wide variety of ABC transporters, the F_0F_1 ATP synthase, the *Rnf*-complex, an additional gene of the *Sec*-dependent secretion system, a rich equipment for carbohydrate, fatty acid, isoprenoid and partial amino acid metabolism. Important proteins of phytoplasmas such as several transporters, proteins involved in metabolism as well as host-interaction and virulence-associated effectors were not identified in acholeplasmas indicating an early evolutionary split of both genera.