

Sec*-dependent protein export in Phytoplasmas and *Acholeplasma laidlawii

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1. INTRODUCTION

Phytoplasmas are obligate bacterial parasites of plants. The closest known relatives are the acholeplasmas, which do not contain primary pathogens. Species of this genus are characterized by a saprophytic lifestyle. Type strains were isolated from the environment including the surface of plants but also from several animals.

Phytoplasmas are suggested to export proteins via the *Sec*-dependent system (Kakizawa *et al.*, 2001) and are known to manipulate the phenotype of their host plants to their benefit by the secretion of effector proteins. For example, *tengu* encodes an effector of ‘*Ca. P. asteris*’ strain OY-M (Hoshi *et al.*, 2009). Its expression causes witches’-broom formation and dwarfism. Other effectors were identified for ‘*Ca. P. asteris*’ strain AY-WB. SAP11 causes crinkled leaves and witches’-broom formations and SAP54 is responsible for the formation of leaf-like flowers (Sugio *et al.*, 2011). Here we present a comparative analysis of the genetic repertoire of the *Sec*-dependent system and the prediction of exported proteins of the complete genomes of ‘*Ca. P. asteris*’, ‘*Ca. P. australiense*’, ‘*Ca. P. mali*’ and *A. laidlawii*.

2. MATERIALS AND METHODS

Protein data of the four phytoplasma genomes (CP000061.1, CP000061.2, CP000062.1, CP000063.1, CP000064.1, CP000065.1, AP006628.1, AM422018.1, CU469464.1) and *A. laidlawii* (CP000896.1) were used to reconstruct the *Sec*-dependent system and to obtain deduced peptide sequences. Annotation of proteins was validated by InterPro and BlastP analysis. Proteins carrying a signal peptide but lacking a transmembrane region were predicted by Phobius (Käll *et al.*, 2004) and compared by BlastP. Putative exported proteins were compared by BlastP.

3. RESULTS AND DISCUSSION

Both genera probably use the *Sec*-dependent system for protein export. All five analysed genomes encode *ffh*, *ftsY*, *secA*, *secE* and *secY*. *A. laidlawii* differs by encoding *secG* in addition. SecY, SecE and SecG are known to form the membrane complex. One may speculate, if phytoplasmas lost *secG* during genome condensation. This protein is essential for survival below 20 °C in *Escherichia coli* (Nishiyama *et al.*, 1994). Phytoplasmas are protected from strong temperature shifts due to the colonization of plant sieve cells. In contrast, SecG may increase the fitness of the ubiquitous distributed *A. laidlawii*, which is frequently exposed to temperature variations.

Furthermore, all five genomes encode the YidC protein, which acts separately or together with the *Sec*-dependent system. This protein is involved in secretion and processing of immature membrane proteins (Dalbey *et al.*, 2004).

The prediction of secreted proteins shows no shared protein content between the genera. This might be interpreted with respect to the different function of these proteins taking part in manipulation of host/vector for phytoplasmas or degradation of biomass for *A. laidlawii*.

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