A

A picture containing timeline

Description automatically generated

B

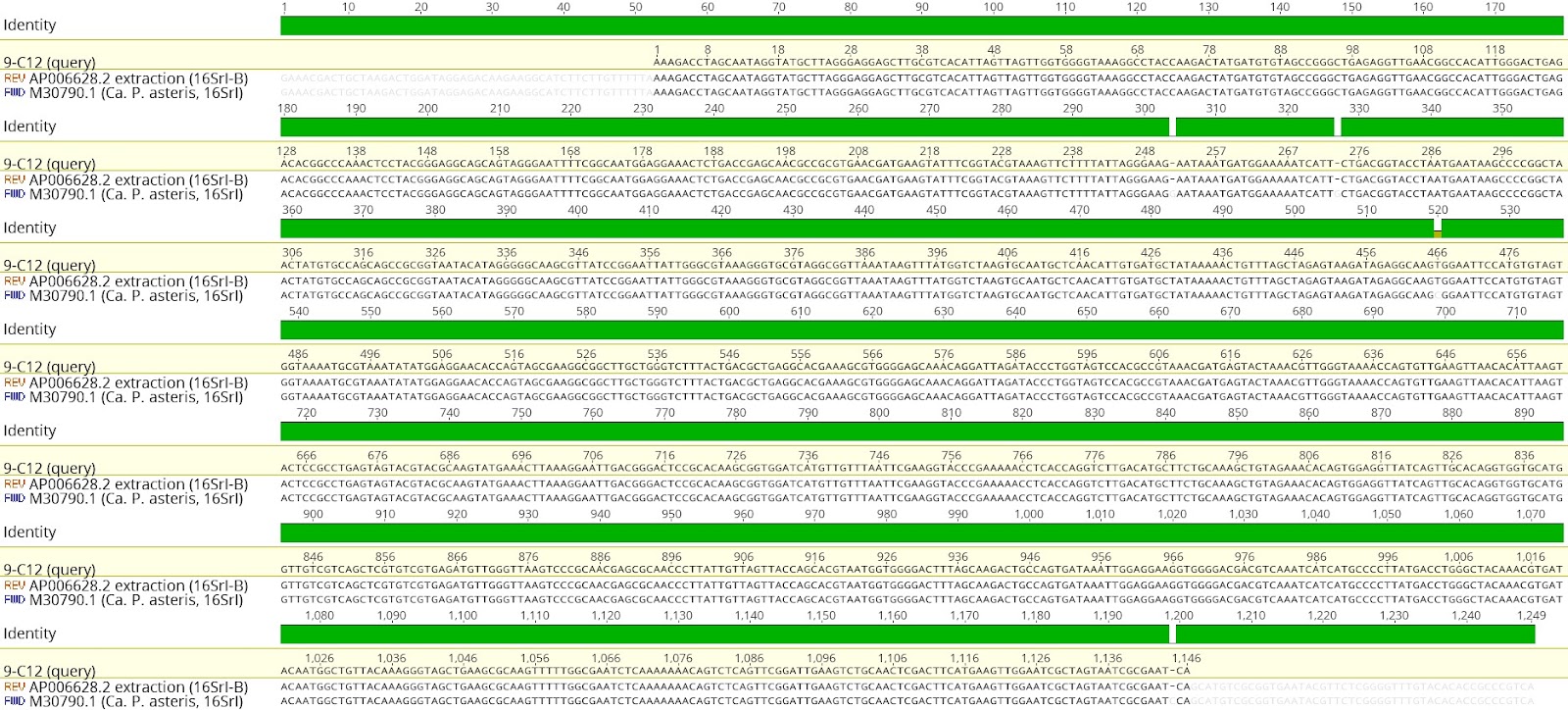


Fig. S1: Sequence alignment of a 16S rRNA gene stretch amplified in samples 1209-F5-W (9-A9) and 1396-F8-M (9-C12). The 16S rRNA gene sequence stretch relevant for the phytoplasma subgroup identification using iPhyClassifier is depicted. In this alignment the amplicon sequence (query) from the nested PCR of sample 1209-F5-W (9-A9) and 1396-F8-M (9-C12) is compared to the reference sequence from '*Ca*. P. asteris' (M30790.1). Both samples share over 99 % 16S rRNA sequence similarity to the '*Ca*. P. asteris' reference strain, belonging to the 16SrI group. The sequence from sample 1209-F5-W (9-A9) is 100 % identical to the sequence of the 16SrI-L subgroup reference strain GU223209.1 (A). The sequence of 1396-F8-M (9-C12) is 100 % identical to the 16SrI-B subgroup reference strain AP006628.2 (B). Sequence alignment was performed using the software Geneious 11.1.5 ([https://www.geneious.com](http://www.geneious.com/)).