

Molecular genotyping of ‘*Candidatus Phytoplasma solani*’ strains identified in different crops in Jordan

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INTRODUCTION

Recent surveys on phytoplasma-associated diseases in Jordan highlighted that ‘*Candidatus Phytoplasma solani*’ (CaPsoL) is the prevalent phytoplasma throughout the Country. It was largely reported in several crops exhibiting different symptoms, in wild plants (CaPsoL plant hosts), and putative insect vectors (Abu Alloush et al., 2023a,b, 2024). To improve the knowledge of CaPsoL ecology, this study investigated the genetic diversity within CaPsoL strain population identified in multiple crops in Jordan.

MATERIALS AND METHODS

DNA extracts from 51 CaPsoL-infected plants of 8 crops, selected from previous studies (Abu Alloush et al., 2023a,b, 2024) (Table 1), were used as templates in direct and nested PCRs for the amplification of *tufB*, *stamp*, and *vmpI* genes, carried out as previously described (Aryan et al., 2014; Fabre et al., 2011). To genotype CaPsoL strains identified in Jordan, nucleotide sequences of obtained PCR products were compared with those of representative CaPsoL strains previously described (Pierro et al., 2018; Jamshidi et al., 2022).

Table 1. CaPsoL strains infecting different crops in Jordan selected for molecular typing

Host	Symptoms	No. ‘ <i>Ca. P. solani</i> strains’
Almond	witches’-broom, yellowing, dieback	10
Cherry	yellowing	7
Grapevine	leaf reddening/yellowing and rolling	17
Peach	witches’-broom, yellowing	4
Pear	leaf reddening	1
Persimmon	leaf scorch and rolling	2
Plum	witches’-broom, yellowing	6
Pomegranate	yellowing, witches'-broom, little leaf	4

RESULTS AND DISCUSSION

Expected amplicons of *tufB*, *stamp*, and *vmpI* genes were obtained from all the 51 CaPsoL-infected plants analyzed. Surprisingly, considering the high genetic diversity generally present within CaPsoL strain populations in a specific geographic area (Quaglino et al., 2021; Jamshidi et al., 2022), nucleotide sequence analyses revealed that all 51 CaPsoL strains share identical *tufB*, *stamp*, and *vmpI* gene sequences, highlighting there is no genetic variability in CaPsoL strain populations in Jordan. Comparison with previously described CaPsoL genotypes revealed that Jordanian CaPsoL strains share sequences identical to genotypes *tuf b-1* (strain CrHo12_601, Acc. No. KJ469708), St15 (strain P7, Acc. No. FN813258), and Vm53 (strain P7, Acc. No. AM992100), previously identified in Lebanon and Georgia (Caucasus region) and associated with bindweed-related pathosystem (Quaglino et al., 2016; Pierro et al., 2018). Further studies will investigate the diffusion of CaPsoL genotype *tuf b-*

1/St15/Vm53 in additional plant hosts and putative insect vectors to study the epidemiological patterns of CaPsoI-associated diseases in Jordan.

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