

# FURTHER INFORMATION ON THE GENETIC STRUCTURE OF PLUM POX VIRUS STRAIN M

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## Introduction

Plum pox virus (PPV) shows high genetic diversity, as nine viral strains, M, D, EA, C, Rec, T, W, AM, CR, have been identified so far (3). PPV strain M (PPV-M) has been characterised as a threat to the Mediterranean stone fruit industry (1). A previous study on the genetic diversity of PPV-M described the existence of two phylogenetic clades formed by isolates of similar geographical origin, from either the Mediterranean countries or the Central and Eastern European countries, respectively (2). A large scale survey conducted during 2013-2015 indicated that PPV-M is the prevalent viral strain in Greece and also widespread throughout the country. The purpose of this study was to shed light on the phylogenetic relationships of the Greek PPV-M isolates with those originating from other European countries.

## Materials and Methods

Phylogenetic analysis was performed using a 5'-terminal fragment of the CP gene from 14 Greek isolates, which were sequenced in the course of this study, as well as 27 PPV-M isolates of European origin and isolates from C, D, EA, T and W strains, retrieved from the databases.

## Results and Discussion

Two geographical groups (Ma, Mb) were formed, as previously described by Dallot et al (2011). The majority of Greek isolates clustered with PPV-M isolates of Mediterranean origin (Ma group). One appears to follow an intermediate evolutionary route, between the two geographical groups, while another isolate grouped with Central and Eastern European isolates (Mb group). The former Greek isolate also shares two out of the three point mutations in the N-terminal of the CP gene, described as conserved amongst Mb isolates by Dallot et al (2011). This is only the second molecular study on the intrastrain genetic diversity of PPV-M. Sequencing of more isolates from Greece and abroad is needed to establish geographical differentiation as well as to trace the strain's evolutionary history.

## References

1. Capote et al., 2006. *Phytopathology* 96: 320-325.
2. Dallot et al., 2011. *Archives of Virology* 156: 539-542.
3. James et al., 2013. *Canadian Journal of Plant Pathology* 35: 431-441.