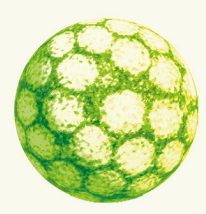




ICVG
International Council for
the Study of Virus and
Virus-Like Diseases
of the Grapevine

Proceedings of the 20th Congress of the International Council for the Study of Virus & Virus-like Diseases of the Grapevine



25-29 September 2023 Thessaloniki, Greece



The 20th Congress of the International Council for the Study of Virus and Virus-like diseases of the Grapevine (ICVG)

Porto Palace Hotel, Thessaloniki, Greece, 25-29 September 2023

Welcome

We have the honor to host and welcome you to the 20th ICVG congress in Thessaloniki, five years after the 19th ICVG meeting held in Santiago, Chile and almost 60 years after the first ICVG meeting in Changins, Switzerland. This is the second meeting held in Greece, after the 10th ICVG meeting in Volos 33 years ago. The Covid-19 pandemic delayed the present congress but now that life has regained its normal pace, we are more than happy to be able to interact in person with all of you here.

We hope that you will enjoy the meeting, during which scientists from all over the world will present their research progress in grapevine viruses, viroids and phytoplasmas. Also, you will have the chance to discover and enjoy Thessaloniki, a vibrant modern city with a long history of 2300 years. And of course, last but not least, we hope that everyone will appreciate the company of colleagues and friends.

Finally, we would like to express our gratitude to all the sponsors for their kind support, as well as to all the students of the Plant Pathology Laboratory of the Aristotle University of Thessaloniki for their help in the preparation and organization of the 20th ICVG congress.

Kind regards,

On behalf of the organizing committee

Varvara Maliogka and Nikolaos Katis

P24. Hidden genetic diversity of ‘*Candidatus Phytoplasma solani*’ strains in Istrian vineyards: how small can be rich

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INTRODUCTION

Grapevine Yellows (GY) are economically important diseases associated to phytoplasmas (genus ‘*Candidatus Phytoplasma*’), uncultivable bacteria from the class Mollicutes. In Euro-mediterranean region, GY are mainly attributed to phytoplasmas belonging to ribosomal 16SrXII-A subgroup (‘*Ca. P. solani*’; *Bois Noir* phytoplasma; BNp) and 16SrV group (*flavescence dorée* phytoplasma; FDp), with the latter one being a quarantine pathogen (Plavec et al. 2015, Quaglino et al. 2013). Although symptomatology can be similar, epidemiology of FDp and BNp is very different as they are transmitted by different insect vectors and could have different alternative hosts. In Croatia, GY diseases have been continuously monitored since 1997 with FDp appearing only in 2009 (Šeruga Musić et al. 2011). While BNp is more diverse and widespread, FDp belonging to 3 *map* phylogenetic clusters are differently distributed throughout regions. Istria is heavily affected with FDp since 2014 with only one genotype (mapFD2/M54) being attributed to great losses (Plavec et al. 2019). On the contrary, information on BNp diversity is scarce with only couple of genotypes detected so far (Plavec et al, manuscript in preparation). Therefore, the aim of this case study was to assess the diversity of BNp genotypes in a small selected area of Istria, in order to draw attention to the presence and importance of BNp as GY agent in this important Croatian viticultural region.

MATERIALS AND METHODS

The samples of asymptomatic and symptomatic grapevine (cvs. ‘Teran’ and Chardonnay’, respectively), weeds and vegetation surrounding vineyards such as *Urtica dioica* L. (nettle), *Cornus sanguinea* L. (common dogwood) and *Ulmus* sp. (elm), as well as insect vectors, were taken during late summer or early autumn in 2019 - 2022 from two selected vineyards in Vižinada area (Istria). Detection and identification of phytoplasmas was performed by triplex real-time PCR (Pelletier et al. 2009) and PCR/RFLP analyses of 16S rDNA. In order to perform multilocus sequence typing (MLST), *secY*, *stamp*, *tufB* and *vmp* gene fragments were amplified from BNp detected isolates. All obtained amplicons were sequenced (Genewiz-Azenta Life Sciences, Leipzig, Germany) and subjected to phylogenetic analysis (ClustalX, MEGA X).

RESULTS AND DISCUSSION

In one of the monitored vineyards with ‘cv. Chardonnay’ displaying strong GY symptoms, BNp infection was continuously confirmed in every year of sampling, while in the other vineyard, asymptomatic cv. ‘Teran’ vines always tested negative for phytoplasma presence. In the latter vineyard, BNp was detected in nettle as well as elm trees positioned at its edge. More over, BNp-infected *Euscelis incisus* and *E. lineolatus* specimens were also found, which were never been reported previously to be BNp-infected in Croatia. Among detected isolates, eight were subjected to MLST so far – five from grapevine, two from elm and one originating from nettle. The results of MLST analysis have revealed the presence of 4 different *secY* genotypes (S1, S4, S6 and S39), 5 *stamp* genotypes (ST19, ST22, ST29, ST46), 2 *vmp1* genotypes (V3, V14) as well as 2 *tuf* genotypes (tuf-a, tuf-b2). Altogether, six different collective genotypes were found, with one being detected in elm and nettle samples (S1/ST29/V14/tuf-b2) close to the vineyard without BN-infected grapevine, while five different collective genotypes were detected in five ‘Chardonnay’ samples from the same vineyard (Fig 1., Fig. 2). Out of six detected collective genotypes under the scope of this case study, three were previously found in Istria, while three represent newly detected genotypes for this vinegrowing region. Such a great diversity of BNp genotypes found in such a restricted and small area, especially in cv. ‘Chardonnay’ where each of the characterized isolates had a distinct collective genotype, point out that continuous surveillance of BNp presence and genotyping should not

be neglected as a tool in our attempts of controlling and preventing GY outbreaks. Moreover, presence of distinct BNP genotypes in asymptomatic vegetation in the vicinity of vineyards as well as a report of new BNP-infected insect vector species for Croatia, suggest their importance and role of these key-players in the GY epidemiology.

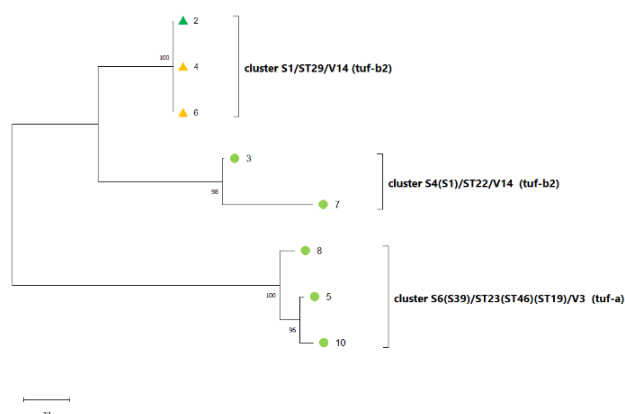


Fig 1. Unrooted phylogenetic tree depicting phylogenetic relationship of concatenated *stamp* (ST), *secY* (S) and *vmp1* (V) gene sequences, of 'Candidatus Phytoplasma solani' isolates infecting different host plants in Istria, inferred by neighbour-joining analysis (number of differences) with bootstrap values obtained after 500 repeats. Samples originating from different plant hosts are marked as follows: green dot – grapevine, green triangle – nettle, orange triangle – elm trees.

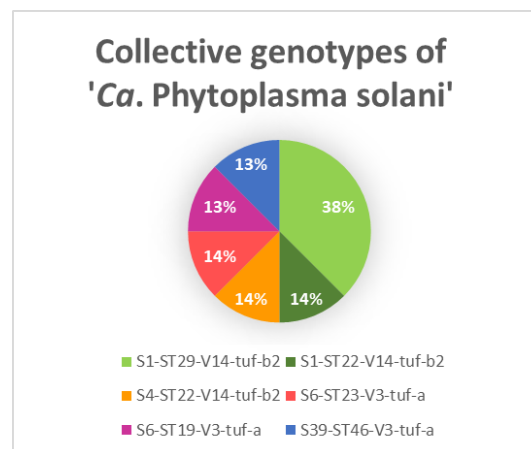


Fig 2. Distribution of collective genotypes (genes *secY*, *stamp*, *vmp1* and *tufB*) of 'Candidatus Phytoplasma solani' isolates detected in grapevine, nettle and elm from selected vineyards in Istria.

ACKNOWLEDGEMENTS

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