

# PhD School on Agriculture, Environment and Bioenergy

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(XXXVIII cycle, 2022-25)

## Project draft

### 1. Field of interest

*AGR/12 – Plant Pathology*

### 2. Project title

Exploring the genomic variability and the molecular mechanisms underlying the pathogenesis of phytoplasmas

### 3. Tutor: Fabio Quaglino

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**4. Relevance of the topic and state of the art:** Phytoplasmas are phloem-limited, obligate parasitic bacteria of plants naturally transmitted by insect vectors. They are associated with numerous economically significant plant diseases worldwide. Many phytoplasma diseases affecting important crops, such as the grapevine bois noir (BN) and flavescence dorée (FD), are already epidemic in Italy and represent a key threat in some regions. Some others, such as the almond witches'-broom (AlmWB) epidemic in the Middle East and recently reported in South Italy, are worrying for their possible impact on the EC countries [1-3]. '*Candidatus Phytoplasma solani*' (BNp), 16SrV-phytoplasma (FDp) and '*Ca. P. phoenicium*', associated with BN, FD and AlmWB, respectively, have an extremely complex ecology including multiple insect vectors and host plants [4-6]. Briefly, '*Ca. P. solani*' is associated with diseases of solanaceous plants, maize and lavender; '*Ca. P. phoenicium*' is associated with important peach and apricot diseases. Recently, draft genomes of '*Ca. P. solani*', FDp, and '*Ca. P. phoenicium*' have been sequenced opening new possibilities in finding potential virulence factors, effectors, and other mechanisms by which phytoplasmas achieve their pathogenicity and successfully manipulate plant hosts and insects [6-8]. To acquire information useful as bases for developing new efficient and sustainable control strategies, it is necessary to (i) investigate accurately BN, FD and AlmWB epidemiology through a multidisciplinary approach, (ii) study differences in the virulence of phytoplasma strains and in the susceptibility in crop varieties, (iii) identify new molecular markers and the effector pools of '*Ca. P. solani*', 16SrV-phytoplasmas and '*Ca. P. phoenicium*' by comparative genomics.

### 5. Layout of the project (draft)

#### 5.1. Materials & Methods:

**WP1 (Molecular epidemiology).** FDp, BNp, and '*Ca. P. phoenicium*' strains, identified in host plants and insects in different agroecosystems, will be characterized through a multilocus sequence typing approach, based on known (*stamp*, *map*, *tufB*, *secY*, *vmp*) and newly proposed genes. Genes putatively involved in the phytoplasma-host interaction identified in WP2, will be analyzed within phytoplasma strain populations. Nucleotide sequence analyses and phylogenetic relationships will unveil intra-species diversity among phytoplasma strains, allowing to clarify the complex epidemiological patterns of FDp, BNp, and '*Ca. P. phoenicium*'.



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- [3] Bertaccini A, Duduk B, Paltrinieri S et al. (2014) Phytoplasmas and phytoplasma diseases: a severe threat to agriculture. *Am J Plant Sci* 5: 1763-88.
- [4] Pierro R, Panattoni A, Passera A et al. (2020) Proposal of a new Bois Noir epidemiological pattern related to '*Candidatus* Phytoplasma solani' strains characterized by a possible moderate virulence in Tuscany. *Pathogens* 9: 268.
- [5] Davis RE, Dally EL, Zhao Y et al. (2018) Genotyping points to divergent evolution of '*Candidatus* Phytoplasma asteris' causing North America Grapevine Yellows and strains causing Aster Yellows. *Plant Dis* 102: 1696-702.
- [6] Quaglino F, Kube M, Jawhari M et al. (2015) '*Candidatus* Phytoplasma phoenicium' associated with almond witches'-broom disease: from draft genome to genetic diversity among strain populations. *BMC Microbiol* 15: 148.
- [7] Seruga Music M, Samarzija I, Hogenhout SA et al. (2019) The genome of '*Candidatus* Phytoplasma solani' strain SA-1 is highly dynamic and prone to adopting foreign sequences. *Syst Appl Microbiol* 42: 117-27.
- [8] Mitrovic J, Siewert C, Duduk B et al. (2014) Generation and analysis of draft sequences of 'stolbur' phytoplasma from multiple displacement amplification templates. *J Mol Microbiol Biotech* 24: 1-11.