

1 **First Report of ‘*Candidatus Phytoplasma phoenicium*’ on almond in Southern Italy**

2

3 **Nigro F.<sup>1</sup>, Sion V.<sup>1</sup>, Antelmi I.<sup>1</sup>, Choueiri, E.<sup>2</sup>, Habib W.<sup>3</sup>, Bruno A.<sup>1</sup>, Boscia D.<sup>4</sup>.**

4

5 <sup>1</sup>Dipartimento di Scienze del Suolo, della Pianta e degli Alimenti, Università degli Studi di Bari –  
6 Aldo Moro, Bari, Italy. Email: [franco.nigro@uniba.it](mailto:franco.nigro@uniba.it) ; <sup>2</sup>Lebanese Agricultural Research Institute,  
7 Department of Plant Protection, Tal Amara, Lebanon; <sup>3</sup>Lebanese Agricultural Research Institute,  
8 Laboratory of Mycology, Department of Plant Protection, Fanar, Lebanon; <sup>4</sup>Consiglio Nazionale  
9 delle Ricerche, Istituto per la Protezione Sostenibile delle Piante, Bari, Italy.

10

11 In spring 2017, phytoplasma suspected symptoms were reported on 25% of 15-yr-old almond  
12 plants, cv Filippo Ceo and Genco grafted onto GF677, in a commercial orchard (20 ha) located at  
13 Grottaglie, Apulia (South-East Italy). Among the symptoms, development of many axillary buds  
14 with small and yellowish leaves, and witches’ brooms developing from the trunk, were the most  
15 frequent, followed by leaf rosetting, proliferation of slender shoots, tree decline, and dieback.  
16 Twenty-six leaf samples were collected in the symptomatic orchard, from both symptomatic (19)  
17 and asymptomatic (7) plants. Moreover, additional leaf samples (5) from asymptomatic almond  
18 orchards of the same varieties, located 80 km away from the infected fields at Valenzano (Province  
19 of Bari), were also collected. Leaf midribs were homogenized in extraction bags by using the  
20 Homex apparatus (Bioreba AG, Reinach, Switzerland), and total genomic DNA was extracted by  
21 using CTAB protocol (Abou-Jawdah et al. 2002). The nucleic acid pellet was washed with 70%  
22 ethanol, air-dried, suspended in 50 µl of nuclease-free water (Qiagen, Venlo, The Netherlands), and  
23 maintained at -80°C until use. Polymerase chain reaction (PCR) was carried out with phytoplasma  
24 16S rRNA universal primer pair R16mF2/R16mR1, followed by nested PCR using R16F2n/R16R2  
25 (Gundersen and Lee 1996), resulting in DNA amplicons of 1.41 and 1.23 kb, respectively.  
26 Moreover, another primer pair, groELF1/groELR1 and groELF2/groELR2, amplifying a region of

27 the *groEL* gene, and originating amplicons of 1.34 and 1.28 kb, respectively, were also used  
28 following the protocol described by Quaglino et al. (2015). Lyophilized DNA from ‘*Ca.*  
29 *Phytoplasma phoenicium*’-infected almond located in Lebanon (AF515636.1), was resuspended in  
30 nuclease free water, and used as positive control. All the symptomatic and 2 of 7 asymptomatic  
31 samples collected in the infected field located at Grottaglie, as well as the control DNA, resulted  
32 positive with all the tested primers. However, all the samples collected in Valenzano and 5  
33 asymptomatic samples from Grottaglie were tested as negative. Therefore, these results confirmed  
34 that the observed symptoms were caused by a phytoplasma. Twelve nested-PCR products for both  
35 16S rRNA and *groEL* coding region were purified, ligated into pGEM-T Easy Vector Systems  
36 (Promega, Madison WI, USA), and the plasmid DNA was sequenced (Genewiz, London, England).  
37 BLASTn analysis revealed that 16S rRNA gene sequence of Apulian phytoplasma strain shared  
38 100% sequence identity with that of the reference strain of the species ‘*Ca. P.*  
39 *phoenicium*’(AF515636.1) (Verdin et al. 2003). The affiliation to this species was also confirmed  
40 by *groEL* gene sequence identity of 100% with that of ‘*Ca. P. phoenicium*’ strain SA213  
41 (KM275493) (Quaglino et al. 2015). The sequences obtained from the 12 samples for each coding  
42 region were identical, therefore two representative sequences were deposited in GenBank, under the  
43 accession numbers [MK377252](#) and [MK377253](#) for 16S rDNA, and [MK387076](#) and [MK387077](#) for  
44 *groEL* gene. Additional analysis of the 16Sr group/subgroup classification, based on *in silico*  
45 restriction fragment length polymorphism analyses using iPhyClassifier, confirmed that the Apulian  
46 phytoplasma strain was a member of the taxonomic subgroup 16SrIX-B, which include  
47 ‘*Candidatus Phytoplasma phoenicium*’ strains (Zhao et al. 2009). ‘*Ca. P. phoenicium*’, the causal  
48 agent of the almond witches’ brooms, is a quarantine pathogen in the European Union, being  
49 included in the List A1 of the European Plant Protection Organization (EPPO) by September 2018.  
50 It may be rapidly spread to healthy stone fruits plantations, and a natural epidemic spread to peach  
51 and nectarine orchards has been reported in Lebanon (Abou-Jawdah et al. 2009). Recently, the  
52 pathogen has also been reported on apricots in Iran (Salehi et al. 2018). To the best of our

53 knowledge, this is the first report of ‘*Ca. P. phoenicium*’ on almond in Italy, and its impact on stone  
54 fruit and other hosts production can be destructive (Abou-Jawdah et al. 2009; Salehi et al. 2018).

55 This work has received funding from Regione Puglia, Progetto EPIZIXY (Ulteriori studi di  
56 epidemiologia ed eziologia di *Xylella fastidiosa* in Salento [D.G.R. n. 1410, 12/06/2015; D.D.S.A.  
57 n. 495, 14/10/2015]).

58 The present work reflects only the author's view and the Agency is not responsible for any use that  
59 may be made of the information it contains.

60

## 61 **References**

62 Abou-Jawdah et al. 2002. Plant Dis. 86:477. <https://doi.org/10.1094/PDIS.2002.86.5.477>

63 Abou-Jawdah et al. 2009. OEPP/EPPO Bulletin, 39, 94-98. <https://doi.org/10.1111/j.1365->

64 [2338.2009.02223.x](https://doi.org/10.1111/j.1365-2338.2009.02223.x)

65 Gundersen and Lee. 1996. Phytopath. Medit. 35: 144.

66 Quaglino et al. 2015. BMC Microbiology 15:148. <https://doi.org/10.1186/s12866-015-0487-4>

67 Salehi et al. 2018. Phytopath. Medit. 57: 269. [http://dx.doi.org/10.14601/Phytopathol\\_Mediterr-](http://dx.doi.org/10.14601/Phytopathol_Mediterr-)

68 [22588](http://dx.doi.org/10.14601/Phytopathol_Mediterr-22588)

69 Verdin et al. 2003. Int. J. Syst. Evol. Microbiol. 53: 833. <https://doi.org/10.1099/ijs.0.02453-0>

70 Zhao et al. 2009. Int. J. Syst. Evol. Microbiol. 59: 2582. <https://doi.org/10.1099/ijs.0.010249-0>



Potential cover image, NOT an e-Xtra

514x386mm (180 x 180 DPI)



Potential cover image, NOT an e-Xtra

514x386mm (180 x 180 DPI)