



**Grapevine yellows in Jordan: associated phytoplasmas,  
putative insect vectors and reservoir plants**

Journal:	<i>Plant Pathology</i>
Manuscript ID	PP-23-041.R1
Manuscript Type:	Original Article
Date Submitted by the Author:	n/a
Complete List of Authors:	Abu Alloush, Asem; Università degli Studi di Milano, Dipartimento di Scienze Agrarie e Ambientali - Produzione, Territorio, Agroenergia (DiSAA); National Agricultural Research Center (NARC) Bianco, Piero; Università degli Studi di Milano, Dipartimento di Scienze agrarie e ambientali - Produzione, Territorio, Agroenergia (DiSAA) Busato, Enrico; Università degli Studi di Torino, Dipartimento di Scienze Agrarie, Forestali e Alimentari (DISAFA) Alkhawaldeh, Yousef; National Agricultural Research Center (NARC) Alma, Alberto; Università degli Studi di Torino, Dipartimento di Scienze Agrarie, Forestali e Alimentari (DISAFA) Tedeschi, Rosemarie; Università degli Studi di Torino, Dipartimento di Scienze Agrarie, Forestali e Alimentari (DISAFA) Quaglino, Fabio; Università degli Studi di Milano, Dipartimento di Scienze agrarie e ambientali - Produzione, Territorio, Agroenergia (DiSAA)
Topics:	aetiology, epidemiology
Organisms:	phytoplasmas & relatives
Other Keywords:	' <i>Candidatus</i> Phytoplasma solani', ' <i>Candidatus</i> Phytoplasma omanense', ' <i>Candidatus</i> Phytoplasma asteris', ' <i>Candidatus</i> Phytoplasma aurantifolia', <i>Orosius cellulosus</i>

SCHOLARONE™  
Manuscripts

1 **Grapevine yellows in Jordan: associated phytoplasmas, putative**  
2 **insect vectors, and reservoir plants**

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4 Asem Habes Abu Alloush<sup>1,2</sup>, Piero Attilio Bianco<sup>1</sup>, Enrico Busato<sup>3</sup>, Yousef Alkhaldeh<sup>2</sup>,  
5 Alberto Alma<sup>3</sup>, Rosemarie Tedeschi<sup>3</sup>, Fabio Quaglino<sup>1</sup>

6

7 <sup>1</sup>Dipartimento di Scienze Agrarie e Ambientali, Università degli Studi di Milano, Italy;

8 <sup>2</sup>National Agricultural Research Center (NARC), Amman, Jordan;

9 <sup>3</sup>Dipartimento di Scienze Agrarie, Forestali e Alimentari, Università degli Studi di Torino, Italy

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11 **Correspondence to:** Fabio Quaglino (fabio.quaglino@unimi.it)

## 12 Abstract

13 During field surveys conducted from June to October 2020 in 13 locations belonging to five  
14 governorates in North and South Jordan, typical grapevine yellows symptoms, including leaf  
15 reddening/yellowing and rolling, were observed in wine and table grape cultivar vineyards.

16 ~~Disease incidence in the investigated vineyards~~ Percentage of symptomatic vines ranged from  
17 10 to 55%. Nested PCR-based amplification of 16S rRNA gene detected phytoplasmas in 22%  
18 and 15.7% of the analyzed symptomatic wine and table grape cultivar plants, respectively.

19 Amplicon nucleotide sequence analyses allowed attributing the detected phytoplasmas to  
20 ‘*Candidatus Phytoplasma solani*’ (taxonomic subgroup 16SrXII-A), ‘*Ca. P. omanense*’  
21 (16SrXXIX-A and -B), ‘*Ca. P. aurantifolia*’ (16SrII-C), and ‘*Ca. P. asteris*’ (16SrI-R) in 72.4%,  
22 17.2%, 6.9%, 3.4% of infected plants, respectively. Such phytoplasmas were found  
23 differentially distributed in wine and table grape cultivar vineyards in the considered locations.

24 Further investigation allowed identifying ‘*Ca. P. solani*’ in the putative insect vectors *Orosius*  
25 *cellulosus* (firstly reported in Jordan), *Euscelidius mundus*, *Laodelphax striatellus*, and  
26 *Circulifer* sp., and in bindweed ~~*Convolvulus arvensis*~~; ‘*Ca. P. aurantifolia*’ in the insect *O.*  
27 *cellulosus* and in bindweed; ‘*Ca. P. omanense*’ in the insect *Psammotettix striatus*; ‘*Ca. P.*  
28 *asteris*’ in the insects *Arboridia adanae*, *Cicadulina bipunctata*, *Circulifer* sp., *L. striatellus*,  
29 *Hyalesthes obsoletus*, and *P. striatus*. Based on this preliminary data, ecological cycles of such  
30 phytoplasmas are discussed. Obtained results suggest that grapevine yellows phytoplasma  
31 diversity and ecology in Jordan are more complex than previously known, leading to a potential  
32 risk of disease outbreaks.

33

34 **Key words:** ‘*Candidatus Phytoplasma solani*’; ‘*Candidatus Phytoplasma omanense*’;  
35 ‘*Candidatus Phytoplasma asteris*’; ‘*Candidatus Phytoplasma aurantifolia*’; *Orosius cellulosus*

## 36 1. INTRODUCTION

37 Grapevine yellows (GY) are a complex of diseases associated with genetically distinct  
38 phytoplasmas causing undistinguishable symptoms on *Vitis vinifera* L., including desiccation  
39 of inflorescences, berry shrivel, leaf discolorations, reduction of growth, and irregular ripening  
40 of wood (Belli et al., 2010). Phytoplasmas are cell wall-less plant pathogenic bacteria localized  
41 in the phloem sieve elements, transmitted by phloem-feeding insects, and classified into 49  
42 species and 37 taxonomic [ribosomal](#) groups based on molecular analysis of the gene 16S rRNA,  
43 as well as other conserved genes (Bertaccini et al., 2022). The main GY diseases are: (i)  
44 Flavescence dorée (FD), present mainly in Europe, associated ~~with~~ [with 16SrV-C and -D](#)  
45 phytoplasmas [belonging to ribosomal subgroups 16SrV-C and -D](#) and ~~vine-to-vine~~ transmitted  
46 ~~mainly~~ by the vector *Scaphoideus titanus* Ball (Malembic-Maher et al., 2020); (ii) Bois noir  
47 (BN), widespread throughout Europe, Asia, South America, and South Africa, associated with  
48 ‘*Candidatus* Phytoplasma solani’ ([ribosomal subgroup 16SrXII-A](#)) and transmitted ~~to vine~~  
49 ~~mainly~~ by *Hyalesthes obsoletus* Signoret and *Reptalus panzeri* Loew (Quaglino et al., 2013);  
50 (iii) Palatinate grapevine yellows (PGY), present in Germany and in other European countries,  
51 associated with ~~16SrV-C~~ phytoplasmas [belonging to subgroup 16SrV-C](#) and transmitted ~~to~~  
52 ~~vine~~ by *Oncopsis alni* Schrank (Angelini et al., 2001); (iv) Australian grapevine yellows  
53 (AGY), present in Australia ~~and New Zealand~~ and, associated with ‘*Ca. P. australiense*’  
54 ([subgroup 16SrXII-B](#)), ~~transmitted by *Oliarus atkinsoni* Meyers~~ (Liefing et al., 1997); (v)  
55 North America grapevine yellows (NAGY), associated with ‘*Ca. P. pruni*’ ([subgroup 16SrIII-](#)  
56 [A](#)) and, transmitted ~~to vine~~ by *Jikradia olitoria* Say, and ‘*Ca. P. asteris*’ ([subgroup 16SrI-A](#))  
57 (Lenzi et al., 2019); (vi) South Africa grapevine yellows, associated with ‘*Ca. P. asteris*’  
58 ([subgroup 16SrI-B](#)) and transmitted ~~to vine~~ by *Mgenia fuscovaria* Stål (Pietersen et al., 2018).  
59 In MENA (North Africa and Middle East) region, ~~grapevine is very commonly cultivated, with~~  
60 ~~an ancient history back to 6,000 years and still possesses very rich potential of both wild (*Vitis*~~

61 ~~vinifera ssp. sylvestris) and cultivated (Vitis vinifera ssp. sativa) germplasm (Bayram et al.,~~  
62 ~~2014). Different studies reported the presence of GY diseases in MENA countries. In detail,~~  
63 ~~BN ('Ca. P. solani') was found in Lebanon, Turkey, Syria, and Iran (Pierro et al., 2019;~~  
64 ~~Hemmati et al., 2021). Moreover, GY were reported in Iran, Lebanon, Syria, and Turkey in~~  
65 ~~association found associated with 'Ca. P. solani' (16SrXII-A), 'Ca. P. trifolii' (16SrVI), 'Ca.~~  
66 ~~P. asteris' (16SrI-B), 'Ca. P. phoenicium' (16SrIX-C), 'Ca. P. aurantifolia' (16SrII-B), 'Ca. P.~~  
67 ~~fraxini' (16SrVII-A), and 'Ca. P. omanense' (16SrXXIX-A) in Syria, Turkey, Lebanon, and~~  
68 ~~Iran (Pierro et al., 2019; Hemmati et al., 2021).~~

69 Noteworthy, most GY studies were focused on wine grape cultivars, and a poor knowledge is  
70 available for table grape cultivars. Up to now, studies on these latter cultivars reported  
71 infections by 'Ca. P. solani' in Chile and Syria, and by 'Ca. P. asteris', 'Ca. P. phoenicium',  
72 'Ca. P. fraxini', 'Ca. P. aurantifolia', and 'Ca. P. trifolii' in Iran (Gajardo et al., 2009; Hemmati  
73 et al., 2021). In Jordan, grapevine (both wine and table grape cultivars) is a key commercial  
74 fruit crop with two farming styles: family and commercial farms. More cultivated in more than  
75 8,960 ha and a are cultivated with total production estimated by 56,000 ton in 2019 (MAO  
76 STAT, 2021). Table grape cultivars, very popular and cultivated in the whole Country, are  
77 characterized by a long harvesting season extending from May (for the early seedless cultivar  
78 growing in Jordan valley) to October. Concerning GY in Jordan, BN associated with 'Ca. P.  
79 solani' (16SrXII-A) was reported in wine grape cultivars and bindweed in one vineyard in  
80 North Padia (Salem et al., 2013). No further studies were conducted in the Country.

81 GY epidemiology is still poorly understood in MENA region; therefore, further studies  
82 concerning the identification of GY phytoplasma insect vectors and non-crop plant hosts are  
83 crucial steps in forecasting GY outbreaks and designing efficient control measures. Following  
84 the first report of BN and based on the recent observation of phytoplasma-like symptoms in  
85 several viticultural areas in Jordan, the present study aimed to survey the diffusion of GY

86 symptoms throughout the Country focusing on both table grape and wine grape cultivars, detect  
87 and identify the GY-associated phytoplasmas in grapevines, potential insect vectors, and  
88 reservoir plants.

89

## 90 **2. MATERIALS AND METHODS**

### 91 **2.1 Field surveys, plant sampling, and insect collection**

92 Field surveys on grapevine yellows-like symptoms were conducted from June to October 2020  
93 in 13 locations belonging to five governorates in North (12) and South (1) Jordan, including  
94 vineyards with table grape cultivars (11 locations) and wine grape cultivars (2 locations)  
95 (Figure 1). In each location, ~~phytoplasma-like disease incidence was calculated as the~~  
96 percentage of symptomatic trees out of the observed ones was calculated. Leaf samples were  
97 collected from 50 plants of wine grape cultivars, and 102 plants of table grape cultivars  
98 exhibiting ~~grapevine yellows~~GY-like symptoms, and from 25 symptomless plants (five from  
99 wine grape cultivars; 20 from table grape cultivars). Moreover, leaf samples were collected  
100 from 22 ~~symptomatic and 8 symptomless~~ bindweed (*Convolvulus arvensis* L.) plants showing  
101 phytoplasma-like symptoms and from 8 symptomless bindweed plants observed within and  
102 around the surveyed vineyards (Table 1). Leaf samples were maintained at 4°C at National  
103 Agricultural Research Center (NARC), Baqaâ, Jordan, until total nucleic acids extraction.  
104 Insects collected by entomological sweeping net within the examined vineyards were observed  
105 by stereomicroscope for preliminary selection of phloem feeders at NARC. The selected  
106 phloem feeders, maintained in 99% ethanol, were recognized at genus/species level by  
107 stereomicroscope observation of phenotypic characters and male genitalia, conducted after  
108 body dissection and clarification in a 10% potassium hydroxide solution, at the Department of  
109 Agriculture, Forest, and Food Science (DISAFA), University of Turin, Italy. Insects were kept  
110 in 99% ethanol at -20°C until total nucleic acids extraction.

111

## 112 **2.2 Phytoplasma detection**

113 Total nucleic acids (TNA) were extracted from the collected plant and insect samples as  
114 previously described by Angelini et al. (2001) and Marzachi et al. (1998), respectively.  
115 Concerning plant samples, leaf midribs and petioles (0.5 g) were grounded in 3 ml of  
116 prewarmed 2.5% CTAB-based buffer in sterile mortars. Concerning insects, single or pooled  
117 (2 to 5) individuals were crashed by sterile pestles in a 1.5 ml tube containing sand and 0.5 ml  
118 of prewarmed 2% CTAB-based buffer. Extracted TNA were dissolved in 40 (insects) or 100  
119 (plants) µl of TE-based buffer, measured for quantity and quality by Nanodrop system, and  
120 stored at -20°C until molecular analyses.

121 TNA extracted from plants and insects were used as templates in nested PCR reactions to detect  
122 the presence of phytoplasmas. Nested PCRs were carried out to amplify the 16S rRNA gene  
123 using the primer pairs P1/P7 and R16F1/R16R0. Reaction mixtures, including GoTaq® G2  
124 DNA Polymerase (Promega, Italy), and conditions were as previously described (Lee et al.,  
125 1995). No positive controls (TNA extracted from phytoplasma-infected plants) were utilized  
126 to avoid reaction contamination. Reaction mixtures devoid of TNA were used as negative  
127 controls. PCR products (6 µl) were electrophorized on 1% (w/v) agarose gels in 1X TBE buffer,  
128 stained with Midori Green, and visualized on UV transilluminator. Phytoplasma infection rate  
129 was estimated as the percentage of infected plants/insects out of the examined ones.

130

## 131 **2.3 Phytoplasma identification**

132 For each sample (plant and insect) found infected by phytoplasmas, three Nnested PCR  
133 products (F1/R0 fragment) were sequenced in both strands (3X coverage per base position) by  
134 a commercial service (Eurofins Genomics, Germany), ~~Nucleotide sequences were~~  
135 by the Contig Assembling Program, and trimmed to the annealing sites of the primers R16F1

136 and R16R0, ~~and aligned to obtain a consensus sequence using the Contig Assembling Program~~  
137 in the software BioEdit, version 7.1.3.0 (Hall, 1999). ~~Trimmed-nucleotide~~Obtained consensus  
138 sequences were aligned using the ClustalW Multiple Alignment program and analyzed by  
139 Sequence Identity Matrix in the software BioEdit to estimate their genetic diversity. For  
140 attribution to ‘*Ca. Phytoplasma*’ species, 16S rDNA nucleotide sequences, representative of  
141 the phytoplasma populations detected in this study, were aligned with those of representative  
142 strains of the 49 ‘*Ca. Phytoplasma*’ species described in literature (Bertaccini et al., 2022) and  
143 checked for their sequence identity in the software ~~Bioedit~~BioEdit. Species attribution was  
144 confirmed searching the species-specific signatures within the 16S rDNA nucleotide  
145 sequences. Group/subgroup attribution was determined by *in silico* RFLP analysis of 16S  
146 rDNA nucleotide sequences using the online tool *iPhyClassifier* (Zhao et al., 2009).  
147 Nucleotide sequences of 16S rRNA gene of phytoplasmas, identified in the present study, and  
148 reference strains of ‘*Ca. Phytoplasma*’ species were employed for phylogenetic analyses. The  
149 Minimum-Evolution method was employed using the Neighbor-Joining algorithm and  
150 bootstrap replicated 1,000 times with the software MEGAX to obtain a phylogenetic tree  
151 (Kumar et al., 2018). *Acholeplasma palmae* (GenBank Acc. No. L33734) was used for rooting  
152 the tree.

153

### 154 **3. RESULTS**

#### 155 **3.1 Grapevine yellows symptoms observed in vineyards**

156 During field surveys, undistinguishable leaf reddening/yellowing and rolling symptoms  
157 (Figure 2 A, B, C), typical of grapevine yellows (GY) disease complex, were observed in wine  
158 and table grape cultivars in vineyards localized in all the 13 considered locations. The ~~disease~~  
159 ~~incidence~~ (percentage of symptomatic trees out of the observed ones) was ranging from 10 to  
160 55%. The highest ~~incidence-percentage~~ (55%) was observed in wine grape cultivar vineyards



161 in Alsalhieh, followed by table grape cultivar vineyards in Jaber Alsarhan (25%), both in  
162 Almafraq governorate. The lowest ~~incidence percentage~~ (10%) was reported in table grape  
163 cultivar vineyards situated in Aldisi (Aqaba governorate) and in the three locations of Ajloun  
164 governorate. The remnant seven locations had a ~~disease incidencepercentage~~ ranging from 12  
165 to 15%. Within and around surveyed vineyards, 22 bindweed plants ~~exhibited-exhibiting~~ little  
166 leaf and reddening ~~were observed and collected~~ (Figure 2 D).

167

### 168 **3.2 Molecular detection and identification of phytoplasmas in plants**

169 According to results of universal nested PCR-based amplification, phytoplasmas were detected  
170 in 29 out of 152 symptomatic grapevines (infection rate 19.1%), and 12 out of 22 symptomatic  
171 bindweeds (infection rate 54.5%). In detail, F1/R0 amplicons of the expected size (around 1370  
172 bp) were obtained in 16 out of 102 symptomatic table grape cultivars (15.7%), and in 11 out of  
173 50 symptomatic wine grape cultivars (22%). No amplification was obtained in symptomless  
174 wine and table grape cultivars, in symptomless bindweed (Table 1), and in negative controls.  
175 Concerning wine grape cultivars, infection rate ranged from 20 to 27.5% in SamaAlSarhan and  
176 Alsalhieh locations, respectively. Concerning table grape cultivars, the highest infection rates  
177 were reported in plant samples collected in vineyards located in Jaber AlSarhan (AlMafraq  
178 governorate) (33%) and UmAlyanabee (Ajloun) (30%). Samples from Alfuhaisnad (AlBalqa)  
179 and Alboedah (Irbid) shared the same infection rate (20%). The lowest infection rate (8.3%)  
180 was found in Kufranjeh (Ajloun). No phytoplasma-infected table grape samples were identified  
181 in Ain Jana, Alkom Alahmar, and Thagrat AlJob. Regarding *C. arvensis*, the infection rates  
182 were 45% (9 plants out of 20) in AlSalhieh, 40% (2 plants of 5) in Sama AlSarhan and Aldisi  
183 (Table 1).

184 Based on 16S rDNA sequence identity versus the reference strains of ‘*Ca. Phytoplasma*’  
185 species and on the presence of species-specific signature sequences, the phytoplasma strains

186 detected in the present study in 29 symptomatic grapevine plants were attributed to the species  
187 '*Ca. P. solani*' (72.4%; 21 strains out of 29), '*Ca. P. omanense*' (17.2%; 5 out of 29), '*Ca. P.*  
188 *aurantifolia*' (6.9%; 2 out of 29), and '*Ca. P. asteris*' (3.4%; 1 out of 29) (Table 2). '*Ca. P.*  
189 *solani*' and '*Ca. P. aurantifolia*' strains were found in both table and wine grape cultivars, while  
190 '*Ca. P. omanense*' and '*Ca. P. asteris*' were detected exclusively in table and wine grape  
191 cultivars, respectively. In detail, '*Ca. P. solani*' strains have identical 16S rDNA nucleotide  
192 sequence (GenBank Acc. No. OL873119), distinct from the reference strain STOL by four  
193 single nucleotide polymorphisms (SNPs) at positions 504 (T/A), 595 (A/G), 888 (C/T), and  
194 1084 (T/C) from the annealing site of the primer R16F1. '*Ca. P. aurantifolia*' strains have  
195 identical 16S rDNA nucleotide sequence (GenBank Acc. No. OL873116), distinct from the  
196 reference strain WBDL by six SNPs at positions 62 (T/A), 83 (G/A), 285 (C/T), 559 (-/G), 793  
197 (-/C), and 1032 (T/C) from the annealing site of the primer R16F1. '*Ca. P. asteris*' strain VV112  
198 (GenBank Acc. No. OL873120) is distinct from the reference strain OAY by seven [323 (G/-  
199 ), 346 (G/-), 488 (C/T), 539 (C/T), 698 (C/T), 984 (A/G), 1122 (G/A)] SNPs. Within '*Ca. P.*  
200 *omanense*', the identified strains have diverse 16S rDNA nucleotide sequences. Sequences of  
201 strains VV95, VV103, VV1007, and VV1034 identical between them (GenBank Acc. No.  
202 OL873118) are distinct from the reference strain IM-1 by SNPs at positions 152 (G/A), 274  
203 (T/C), 331 (C/T), 344 (G/A), and 712 (G/A), while the sequence of strain VV1259 (GenBank  
204 Acc. No. OL873117) is identical to the reference strain IM-1. Based on similarity coefficient  
205 obtained by comparison of virtual RFLP patterns, '*Ca. P. solani*' strains were attributed to  
206 taxonomic subgroup 16SrXII-A, '*Ca. P. aurantifolia*' strains VV162 and VV632 to a variant  
207 of subgroup 16SrII-C, '*Ca. P. omanense*' strain VV1259 to subgroup 16SrXXIX-A and strains  
208 VV95, VV103, VV1007, and VV1034 to subgroup 16SrXXIX-B, and '*Ca. P. asteris*' strain  
209 VV112 to a variant of subgroup 16SrI-R (Figure 3). Phytoplasma clustering in phylogenetic  
210 tree confirmed the attribution to phytoplasma species and taxonomic subgroups (Figure 4).

211 Concerning the phytoplasma distribution, '*Ca. P. solani*' was found in table grape cultivars (10  
212 out of 16 plants: 62.5%) from 5 out of 11 considered locations, and in wine grape cultivars (11  
213 out of 13 plants: 84.6%) from both AlSalhieh and SamaAlSarahn. '*Ca. P. omanense*' was found  
214 exclusively in table grape cultivars (5 out of 16 plants: 31.3%) from Kufranjeh (subgroup  
215 16SrXXIX-A), UmAlYanabee and Aldisi (subgroup 16SrXXIX-B). '*Ca. P. aurantifolia*' was  
216 found in both table grape (1 out of 16 plants: 6.3%) and wine grape (1 out of 13 plants: 7.7%)  
217 cultivars from Javer AlSarahn and AlSalhieh, respectively. '*Ca. P. asteris*' was found only in  
218 one wine grape cultivar plant (1 out of 13 plants: 7.7%) from AlSalhieh.

219 Regarding the non-crop weeds, the phytoplasma strains detected in the present study in 12  
220 symptomatic bindweed plants were attributed to the species '*Ca. P. solani*' (83.3%; 10 strains  
221 out of 12 identified in SamaAlSarahn and AlSalhieh), and '*Ca. P. aurantifolia*' (16.7%; 2 out  
222 of 12 identified in Aldisi) (Table 2). '*Ca. P. solani* (16SrXII-A) and '*Ca. P. aurantifolia*'  
223 (variant of 16SrII-C) strains, found in bindweed, shared identical 16S rDNA sequence with  
224 strains of the same species found in *V. vinifera* plants.

225

### 226 **3.3 Molecular detection and identification of phytoplasmas in insects**

227 During the field survey carried out in the localities AlSalhieh, Alkom AlAhmar, Sabha  
228 (AlMafrag governorate), Kufranjeh and Aain Jana (Ajloun governorate) in August, September  
229 and November 2020, 1173 Auchenorrhyncha adult insects (557 and 616 from wine and table  
230 grape cultivar vineyards, respectively) were collected and distinguished, based on  
231 stereomicroscope analyses, in 11 taxonomic groups defined at species (8) and genus (3) level.  
232 Most of such insects belong to the family Cicadellidae (1133 specimens), while the remnant  
233 40 collected specimens belong to the families Delphacidae (33) and Cixiidae (7). Within  
234 Cicadellidae, the more abundant insect taxa were *Cicadulina bipunctata* (Melichar), (393  
235 specimens), *Empoasca* sp. (350 specimens), *Arboridia adanae* (Dlabola) (271 specimens),

236 *Circulifer* sp. (49 specimens), and *Orosius cellulosus* (Lindberg) (28 specimens) (firstly  
237 reported in Jordan). *C. bipunctata*, *Laodelphax striatellus* (Fallén), and *Psammotettix striatus*  
238 (Linnaeus) were the only species captured in both wine and table grape vineyards. *Empoasca*  
239 sp., *Balclutha* sp., *O. cellulosus*, *Toya propinqua* Fieber, *Circulifer* sp., and *Euscelidius*  
240 *mundus* (Haupt) were collected exclusively in wine grape vineyards in AlSalhieh, while  
241 *Hyalesthes obsoletus* Signoret and *A. adanae* exclusively in table grape vineyards in Sabha and  
242 Ain Jana (Table 3). Molecular analyses for phytoplasma detection and identification were  
243 conducted on 112 insect pools (54 from wine grape vineyards located in AlSalhieh; 58 from  
244 table grape vineyards located in Alkom AlAhmar, Sabha, Kufranjeh, and Ain Jana)  
245 representative of the observed diversity. Nested PCR allowed detecting phytoplasmas in 34  
246 insect pools (infection rate 34.8%), belonging to 10 different insect taxa. Infection rate in insect  
247 pools from wine and table grape vineyards was 38.9% (21 out of 54 pools) and 22.4% (13 out  
248 of 58 pools), respectively. No positive insect pools were found in *Balclutha* sp. and *T.*  
249 *propinqua*. Among insects captured in wine grape vineyards, infection rates were 100% in  
250 *E. mundus*, 83.3% in *P. striatus*, 50% in *Circulifer* sp., 40% in *O. cellulosus*, 33.3% in *C.*  
251 *bipunctata*, and 11.1% in *Empoasca* sp. Concerning the insects captured in table grape  
252 vineyards, infection rates were 100% in *P. striatus*, 60% in *L. striatellus*, 50% in *H.*  
253 *obsoletus*, 19% in *C. bipunctata*, and 10.7% in *A. adanae* (Table 3).

254 Analyses of 16S rDNA nucleotide sequences allowed attributing the phytoplasma strains  
255 detected in insects to the species ‘*Ca. P. asteris*’ (23 pools out of 34), ‘*Ca. P. solani*’ (8 pools),  
256 ‘*Ca. P. aurantifolia*’, ‘*Ca. P. omanense*’, and ‘*Ca. P. pyri*’ each in one pool (Table 4).

257 In detail, 22 out of 23 ‘*Ca. P. asteris*’ strains were found in *P. striatus* and *C. bipunctata* in  
258 both wine and table grape vineyards, in *Circulifer* sp. in wine grape vineyards, in *L. striatellus*,  
259 *H. obsoletus*, and *A. adanae* in table grape vineyards. Such strains share identical 16S rDNA  
260 nucleotide sequence with the wine grape-infecting strain VV112, attributed to a variant of

261 taxonomic subgroup 16SrI-R. The ‘*Ca. P. asteris*’ strain SUF5-4, identified in one pool of *P.*  
262 *striatus* from table grape vineyard in Alkom AlAhmar, is distinct from the reference strain  
263 OAY by three [323 (G/-), 346 (G/-), 539 (C/T)] SNPs. This strain was attributed to taxonomic  
264 subgroup 16SrI-B. Concerning ‘*Ca. P. solani*’, its strains were identified in *O. cellulosus* (three  
265 strains), *E. mundus* (three strains), and *Circulifer* sp. (one strain) from wine grape vineyards,  
266 and in *L. striatellus* (one strain) from table grape vineyard in Alkom AlAhmar. Such strains  
267 share identical 16S rDNA nucleotide sequence with the ones infecting wine and table grape  
268 cultivars and bindweed, attributed to taxonomic subgroup 16SrXII-A. ‘*Ca. P. aurantifolia*’  
269 strain MH8-16 and ‘*Ca. P. omanense*’ strain MH5-11, found respectively in *O. cellulosus* and  
270 *P. striatus* in wine grape vineyards, share identical 16S rDNA sequences respectively with ‘*Ca.*  
271 *P. aurantifolia*’ (variant of 16SrII-C) strains identified in grapevine and bindweed and ‘*Ca. P.*  
272 *omanense*’ (16SrXXIX-A) strain identified in grapevine. Moreover, a ‘*Ca. P. pyri*’ strain,  
273 sharing identical 16S rDNA sequence with the reference strain PD1 (subgroup 16SrX-C), was  
274 found in one *Empoasca* sp. pool in AlSalhieh. Phytoplasma clustering in phylogenetic tree  
275 confirmed the attribution to phytoplasma species and taxonomic subgroups (Figure 4).

276

#### 277 4. DISCUSSION

278 This study provided new insights on GY diffusion, associated phytoplasmas and their putative  
279 vectors and reservoir plants in Jordan. Obtained results confirmed the large diffusion of Bois  
280 noir (BN), associated with ‘*Ca. P. solani*’ (16SrXII-A), in wine grape cultivars, as previously  
281 reported by Salem and colleagues (2013). Moreover, ‘*Ca. P. asteris*’ (variant of 16SrI-R) and  
282 ‘*Ca. P. aurantifolia*’ (variant of 16SrII-C) were firstly reported in the Country in association  
283 with GY-affected wine grape cultivars. In previous studies, ‘*Ca. P. asteris*’- and ‘*Ca. P.*  
284 *aurantifolia*’-related strains were found in association with peach and potato diseases,  
285 respectively, [in Jordan](#) (Anfoka & Fatash, 2004; Salem et al., 2019). In MENA region, ‘*Ca. P.*

286 asteris' (16SrI-B) and '*Ca. P. aurantifolia*' (16SrII-B) were reported in GY affected grapevines  
287 (Hemmati et al., 2021). Thus, this is the first report in MENA region of '*Ca. P. asteris*' (variant  
288 of 16SrI-R) and '*Ca. P. aurantifolia*' (variant of 16SrII-C) in association with GY. Moreover,  
289 '*Ca. P. solani*' (16SrXII-A) was found as prevalent also in table grape cultivars in different  
290 locations, confirming its [previous](#) identification in table grapes in Chile and Syria (Gajardo et  
291 al., 2009; Hemmati et al., 2021). Also '*Ca. P. aurantifolia*' (variant of 16SrII-C) was found in  
292 table grape, as previously reported in Iran (subgroup 16SrII-B) (Hemmati et al., 2021).  
293 Furthermore, '*Ca. P. omanense*' subgroup 16SrXXIX-A, previously reported in association  
294 with wine grape cultivars in Lebanon (Foissac et al., 2019), and subgroup 16SrXXIX-B,  
295 recently reported in almond in Jordan (Abu Alloush et al., 2023), were found for the first time  
296 in association with GY-affected table grape cultivars in Jordan.

297 Although the high incidence of phytoplasma-like symptoms in the examined vineyards, only  
298 19.1% of samples collected from symptomatic wine and table grapes were found infected by  
299 phytoplasmas. This result can be explained by different hypotheses: (i) the phytoplasmas are  
300 unevenly distributed in phloem tissues of infected plants (Constable et al., 2003); (ii) the  
301 phytoplasma concentration in plant tissues in the different sampling periods (from July to  
302 November) can be extremely low (Martini et al., 2011); (iii) the persons involved in the surveys  
303 could have not enough expertise to clearly distinguish symptoms associated with phytoplasmas  
304 from those caused by other etiological agents or nutritional disorders ~~could be associated with~~  
305 ~~the observed symptoms;~~ (iv) ~~PCR inhibitors could be present in the extracted TNAs~~. Moreover,  
306 it should be considered that surveys and sample collection were carried out during a limited  
307 period throughout the season.

308 Interestingly, obtained results evidenced the presence of '*Ca. P. solani*' and '*Ca. P.*  
309 *aurantifolia*' strains, undistinguishable from those found in wine and table grape cultivars, in  
310 the putative insect vector *Orosius cellulosus* (firstly reported in Jordan) and in symptomatic

311 bindweed, a non-crop plant known for its epidemiological role in BN diffusion (Quaglino et  
312 al., 2021). No studies are available about *O. cellulolus* and its vectoring activity of  
313 phytoplasmas, but other *Orosius* species, such as *O. albicinctus* and *O. orientalis*, living on  
314 different plant hosts (Rao et al., 2018), were reported as vectors of phytoplasmas belonging to  
315 groups 16SrIX and 16SrII in Turkey and Iran (Ikten et al., 2014; Salehi et al., 2017). Based on  
316 this evidence, it is reasonable to hypothesize that diffusion of ‘*Ca. P. solani*’ and ‘*Ca. P.*  
317 *aurantifolia*’ in Jordan ~~could~~ involve *O. cellulolus* and bindweed.

318 Moreover, ‘*Ca. P. solani*’ strains, undistinguishable from those found in wine and table grape  
319 cultivars, were found also in ~~*Euscelidius- mundus*~~, ~~*Laodelphax- striatellus*~~, and *Circulifer* sp.  
320 ~~*E. uscelidius mundus*~~ was reported as putative vector of ‘*Ca. P. phoenicium*’ in Lebanon  
321 (Dakhil et al., 2011), but other species of the genus *Euscelidius*, such as *E. variegatus*, are  
322 known as vector of ‘*Ca. P. solani*’ to grapevine (Quaglino et al., 2019). ~~*L. aodelphax striatellus*~~  
323 has typically grasses as primary hosts to which it transmits virus of great economic importance  
324 (Achon et al., 2013), anyhow it was found positive to grapevine phytoplasmas (16SrI, 16SrXII-  
325 A) (Orságova et al., 2011) and reported as a vector of ‘*Ca. P. solani*’ to grapevine (Quaglino et  
326 al., 2019). In light of these evidence and our results, certainly new investigations are needed to  
327 understand the actual interactions between *L. striatellus*, grasses or weeds (located ~~within or~~  
328 ~~surrounding around~~ vineyards) and grapevine in ~~the GY~~ epidemiology ~~of phytoplasmosis~~.  
329 Concerning *Circulifer* sp., different species, such as *C. tenellus* and *C. haematoceps*, were  
330 described as vectors of phytoplasmas belonging to taxonomic groups 16SrI, 16SrII, 16SrVI,  
331 and 16SrIX (Salehi et al., 2017; Aslam et al., 2021). Thus, ‘*Ca. P. solani*’ transmission to  
332 grapevine in Jordan could involve also *Circulifer* sp., *E. mundus*, and *L. striatellus*. Further  
333 investigation should be carried out in Jordan to investigate more accurately the spread and  
334 epidemiological role of *Hyalesthes- obsoletus*, the main vector of ‘*Ca. P. solani*’ to grapevine  
335 in Europe (Maixner et al., 1994).

336 Concerning ‘*Ca. P. omanense*’ (subgroup 16SrXXIX-A), found exclusively in table grape  
337 cultivars, it was identified (subgroup 16SrXXIX-A) also in *Psammotettix striatus*, known as  
338 vector of ‘*Ca. P. tritici*’ (16SrI) (Wu et al., 2010). No insects were found infected by  
339 16SrXXIX-B phytoplasma strains. Recent studies reported *H. obsoletus* as putative vector of  
340 ‘*Ca. P. omanense*’ in Lebanon (Foissac et al., 2019), but in the present work it was found not  
341 infected by this phytoplasma. Due to the association of the subgroup 16SrXXIX-B to almond  
342 (Abou Alloush et al., 2023) and grapevine (this study) diseases in Jordan, it will be useful to  
343 focus further studies on improving the knowledge on its epidemiology throughout the Country,  
344 in different agroecosystems.

345 ‘*Ca. P. asteris*’ (variant of subgroup 16SrI-R), identified only in one plant of wine grape  
346 cultivar, was prevalent in the examined insects-vectors. It was found in *Circulifer* sp., *P.*  
347 *striatus*, *Cicadulina bipunctata*, *L. striatellus*, *H. obsoletus*, and *Arboridia adanae*. As  
348 reported above, *Circulifer* sp. and *P. striatus* are known as vectors of 16SrI phytoplasmas, and  
349 *L. striatellus* as vector of 16SrXII phytoplasmas. *C. bipunctata* is a potential vector of ‘*Ca. P.*  
350 *asteris*’-related strain to date palm (Alhudaib et al., 2007); *H. obsoletus* is known as ‘*Ca. P.*  
351 *solani*’ vector and putative vector of ‘*Ca. P. asteris*’ (Maixner et al., 1994; Zambon et al., 2018).

352 *Arboridia A. adanae*, a typical mesophyll-feeder as most of Typhlocibinae, is considered a  
353 serious pest of grapevine in Eastern Mediterranean Regions and Europe (Yigit and Erckle 1992;  
354 Olivier et al., 2012) emptying mesophyll cell content or by cell rupture feeding. Anyhow, we  
355 detected few phytoplasma-positive individuals collected in vineyards as similarly reported for  
356 the very close mesophyll-feeder genus *Erytroneura* (Olivier et al., 2014). Although  
357 phytoplasmas usually reside in the phloem sieve elements, they have been occasionally  
358 observed in parenchyma cells (Siller et al., 1987), intercellular spaces of bundle sheath cells  
359 (Fontaniella et al., 2003), and companion cells (Sears & Klomparens, 1989). That could explain  
360 why phytoplasmas are occasionally found in mesophyll-feeders and in our case in *A. adanae*



361 that may have ingested cell fluids infested by phytoplasmas transmitted by other leafhopper  
362 species.

363 Based on these findings, it is reasonable to suggest that diffusion of ‘*Ca. P. asteris*’ subgroup  
364 16SrI-R to grapevine in Jordan ~~could~~ involve multiple insect species. Upscaling the surveyed  
365 vineyards and surroundings could provide better insights on the ‘*Ca. P asteris*’ diffusion in  
366 grapevine.

367 The epidemiology of phytoplasma-associated diseases is determined by the interactions  
368 between host plants, pathogen, and environmental conditions (Rotter et al., 2018). Further  
369 studies in terms of transmission trials and upscaling the surveying orchards and non-crop plant  
370 hosts will be crucial to profound the knowledge about GY etiology and epidemiology in Jordan.  
371 Outbreak of GY epidemics could be a concrete risk in the vineyard agroecosystems in all  
372 viticultural areas. Monitoring and control strategies against GY are essential to prevent  
373 epidemic phytoplasma spread (Pierro et al., 2019).

374 Most phytoplasmas identified in *Vitis vinifera* in this study were detected also in almond and  
375 pomegranate in different areas of the Country, suggesting that phytoplasma diversity and  
376 distribution in Jordan are more complex than previously known, leading to a potential risk of  
377 disease outbreaks. Studies and knowledge about the insect vectors including their  
378 identification, distribution, and population dynamics are essential for proper management  
379 measures and mitigation of the risk of disease outbreaks. Considering the preliminary results,  
380 obtained in the present study, about the GY epidemiology in Jordan, further studies covering  
381 more areas throughout the full vegetative season of grapevine and non-crop reservoir plants are  
382 essential and will provide comprehensive insights about the GY phytoplasma diversity,  
383 ecological complexity, and epidemiology.

384

385 **ACKNOWLEDGMENTS**

386 We thank Wafaa Abu Hammour for technical assistance in preparing map of GY surveys in  
387 Jordan, Dr. Jafar AlWidyan, Eng. Nizar Obeidat and Sadeer Amashah for their assistance  
388 during insect collection and lab activities, and Jordanian farmers met during field surveys.

389

#### 390 **CONFLICT OF INTEREST STATEMENT**

391 The authors declare that they have no known competing financial interests or personal  
392 relationships that could have appeared to influence the work reported in this paper.

393

#### 394 **DATA AVAILABILITY STATEMENT**

395 The data that support the findings of this study are available from the corresponding author  
396 upon reasonable request.

397

#### 398 **REFERENCES**

- 399 Abu Alloush, A.H., Bianco, P.A., Busato, E., AlMahasneh, A., Alma, A., Tedeschi, R., et al.  
400 (2023) Association of seven ‘*Candidatus* Phytoplasma’ species to an almond disease  
401 complex in Jordan, and preliminary information on their putative insect vectors. *Crop*  
402 *Protection*, 164, 106147.
- 403 Achon, M. A., Subira, J. & Sin, E. (2013) Seasonal occurrence of *Laodelphax striatellus* in  
404 Spain: effect on the incidence of Maize rough dwarf virus. *Crop Protection*, 47, 1–5.
- 405 Alhudaib, K., Arocha, Y., Wilson, M. & Jones, P. (2007) Identification and molecular  
406 characterization of a phytoplasma associated with Al-Wijam disease of date palm in  
407 Saudi Arabia. *Arab Journal of Plant Protection*, 25, 116–122.
- 408 Anfoka, G.H. & Fattash, I. (2004) Detection and identification of aster yellows (16Srl)  
409 phytoplasma in peach trees in Jordan by RFLP analysis of PCR-amplified products (16S  
410 rDNAs). *Journal of Phytopathology*, 152, 210–214.

- 411 Angelini, E., Clair, M., Borgo, A., Bertaccini, A. & Boudon-Padieu, E. (2001) “Flavescence  
412 dorée” in France and Italy: occurrence of closely related phytoplasma isolates and their  
413 near relationships to palatinate grapevine yellows and an alder yellows phytoplasma.  
414 *Vitis*, 40, 79–86.
- 415 Aslam, M., Tanwir, S., Akhtar, Z.R. & Ahmad, J.N. (2021) First report of 16SrII-D phylloxy  
416 phytoplasma and associated insect vectors infecting multi-flower inbred lines of  
417 sunflower (*Helianthus annuus* L.) in Faisalabad, Pakistan. *Pakistan Journal of*  
418 *Agricultural Sciences*, 58, 985–992.
- 419 ~~Bayram, S., Zeybekoglu, U., Soylemezoglu, G., Canik, D., Karavin, M., Cakir, A. et al. (2014)~~  
420 ~~Presence of putative insect vectors of grapevine yellows phytoplasmas in Turkey.~~  
421 ~~*Phytopathogenic Mollicutes*, 4, 22–26.~~
- 422 Belli, G., Bianco, P.A. & Conti, M. (2010) Grapevine yellows: past, present and future. *Journal*  
423 *of Plant Pathology*, 92, 303–326.
- 424 Bertaccini, A., Arocha-Rosete, Y., Contaldo, N., Duduk, B., Fiore, N., Montano, H.G. et al.  
425 (2022). Revision of the 'Candidatus Phytoplasma' species description guidelines.  
426 *International Journal of Systematic and Evolutionary Microbiology*, 72, 005353.
- 427 Constable, F.E., Gibb, K.S. & Symons, R.H. (2003) Seasonal distribution of phytoplasmas in  
428 Australian grapevines. *Plant Pathology*, 52, 267–276.
- 429 Dakhil, H.A., Hammad, E.A., El-Mohtar, C. & Abou-Jawdah, Y. (2011) Survey of leafhopper  
430 species in almond orchards infected with almond witches'-broom phytoplasma in  
431 Lebanon. *Journal of Insect Science*, 11, 60.
- 432 Foissac, X., Jreijiri, F., Salar, P., Wakim, S., Danet, J.L. & Choueiri, E. (2019). A 'Candidatus  
433 Phytoplasma omanense'-related strain detected in yellowing grapevine, stunted  
434 bindweed and Cixiidae planthoppers in Lebanon. *European Journal of Plant Pathology*,  
435 153, 265–272.

- 436 Fontaniella, B., Vicente, C., Legaz, M.E., de Armas, R., Rodriguez, C.W., Martínez, M. et al.  
437 (2003). Yellow leaf syndrome modifies the composition of sugarcane juices in  
438 polysaccharides, phenols and polyamines. *Plant Physiology and Biochemistry*, 41,  
439 1027–1036.
- 440 Gajardo, A., Fiore, N., Prodan, S., Paltrinieri, S., Botti, S., Pino, A.M. et al. (2009)  
441 Phytoplasmas associated with grapevine yellows disease in Chile. *Plant Disease*, 93,  
442 789–796.
- 443 Hall, T.A. (1999) Bio Edit: a user-friendly biological sequence alignment editor and analysis  
444 program for Windows 95/98/NT. *Nucleic Acids Symposium Series*, 41, 95–98.
- 445 Hemmati, C., Nikooei, M., Al-Subhi, A.M. & Al-Sadi, A.M. (2021) History and Current Status  
446 of Phytoplasma Diseases in the Middle East. *Biology*, 10, 226.
- 447 Ikten, C., Catal, M., Yol, E., Ustun, R., Furat, S., Toker, C. et al. (2014) Molecular  
448 identification, characterization, and transmission of phytoplasmas associated with  
449 sesame phyllody in turkey. *European Journal of Plant Pathology*, 139, 217–229.
- 450 Kumar, S., Stecher, G., Li, M., Knyaz, C. & Tamura, K. (2018). MEGA X: molecular  
451 evolutionary genetics analysis across computing platforms. *Molecular Biology and*  
452 *Evolution*, 35, 1547–1549.
- 453 Lee, I.-M., Bertaccini, A., Vibio, M. & Gundersen, D.E. (1995) Detection of multiple  
454 phytoplasmas in perennial fruit trees with decline symptoms in Italy. *Phytopathologia*  
455 *PhytopathologyMediterranea*, 85, 728–735.
- 456 Lenzi, P., Stoepler, T.M., McHenry, D.J., Davis, R.E. & Wolf, T.K. (2019) *Jikradia olitoria*  
457 ([Hemiptera] [Cicadellidae]) transmits the sequevar NAGYIIIβ phytoplasma strain  
458 associated with north american grapevine yellows in artificial feeding assays. *Journal*  
459 *of Insect Science*, 19, 1.

- 460 Liefiting, L.W., Beever, R.E., Winks, C.J., Pearson, M.N. & Forster, R.L.S. (1997) Planthopper  
461 transmission of Phormium yellow leaf phytoplasma. *Australasian Plant Pathology*, 26,  
462 148–154.
- 463 Maixner, M. (1994) Transmission of German grapevine yellows (Vergilbungskrankheit) by the  
464 planthopper *Hyalesthes obsoletus* (Auchenorrhyncha: Cixiidae). *Vitis*, 33, 103–104.
- 465 Malembic-Maher, S., Desqué, D., Khalil, D., Salar, P., Bergey, B., Danet, J.-L. et al. (2020)  
466 When a palearctic bacterium meets a nearctic insect vector: genetic and ecological  
467 insights into the emergence of the grapevine flavescence dorée epidemics in Europe.  
468 *PLoS Pathogens*, 16, e1007967.
- 469 Martini, M., Ermacora, P., Magris, G., Ferrini, F. & Loi, N. (2011) Symptom expression and  
470 ‘*Candidatus* Phytoplasma prunorum’ concentration in different *Prunus* species.  
471 *Bulletin of Insectology*, 64, S171–S172.
- 472 Marzachi, C., Veratti, F. & Bosco, D. (2008) Direct PCR detection of phytoplasmas in  
473 experimentally infected insects. *Annals of Applied Biology*, 133, 45–54.
- 474 Ministry of Agriculture (MOA) in Jordan (2021) Annual statistical year. Available at:  
475 <http://www.moa.gov.jo/AR/> [Accessed December 5, 2021].
- 476 Olivier, C., Vincent, C., Saguez, J., Galka, B., Weintraub, P.G. & Maixner, M. (2012)  
477 Leafhoppers and planthoppers: their bionomics, pathogen transmission and  
478 management in vineyards. In: *Arthropod Management in Vineyards*. Dordrecht:  
479 Springer, pp. 253–270.
- 480 Olivier, C., Saguez, J., Stobbs, L., Lowery, T., Galka, B., Whybourne, K. et al. (2014).  
481 Occurrence of phytoplasmas in leafhoppers and cultivated grapevines in Canada.  
482 *Agriculture, Ecosystems & Environment*, 195, 91–97.
- 483 Orságová, H., Březíková, M. & Schlesingerova, G. (2011) Presence of phytoplasmas in  
484 hemipterans in Czech vineyards. *Bulletin of Insectology*, 64, S119–S120.

- 485 Pierro, R., Semeraro, T., Luvisi, A., Garg, H., Vergine, M., De Bellis, L. et al. (2019) The  
486 distribution of phytoplasmas in south and east Asia: an emerging threat to grapevine  
487 cultivation. *Frontiers in Plant Science*, 10, 1108.
- 488 Pietersen, G., Pietersen, G., Pietersen, I. & Stiller, M. (2018) Identification of *Mgenia*  
489 *fuscovaria* (Stål) (Hemiptera: Cicadellidae), a vector of aster yellows disease on  
490 grapevines in South Africa, and differentiation from *Mgenia angusta* (Theron) by  
491 nucleotide sequences of the mitochondrial cytochrome oxidase I (cox1) gene. *South*  
492 *African Journal of Enology and Viticulture*, 39, 176–179.
- 493 Quaglino, F., Passera, A., Faccincani, M., Moussa, A., Pozzebon, A., Sanna, F. et al. (2021)  
494 Molecular and spatial analyses reveal new insights on bois noir epidemiology in  
495 Franciacorta vineyards. *Annals of Applied Biology*, 179, 151–168.
- 496 Quaglino, F., Sanna, F., Moussa, A., Faccincani, M., Passera, A., Casati, P. et al. (2019)  
497 Identification and ecology of alternative insect vectors of ‘*Candidatus Phytoplasma*  
498 *solani*’ to grapevine. *Scientific Reports*, 9, 19522.
- 499 Quaglino, F., Zhao, Y., Casati, P., Bulgari, D., Bianco, P.A., Wei, W. et al. (2013) ‘*Candidatus*  
500 *Phytoplasma solani*’, a novel taxon associated with stolbur- and bois noir-related  
501 diseases of plants. *International Journal of Systematic and Evolutionary Microbiology*,  
502 63, 2879–2894.
- 503 Rao, G.P., Fiore, N., Bertaccini, A. & Liefting, L.W. (2018) *Phytoplasmas: Plant pathogenic*  
504 *bacteria - I: Characterisation and epidemiology of phytoplasma - associated diseases.*  
505 Singapore: Springer Nature.
- 506 Rotter, A., Nikolić, P., Turnšek, N., Kogovšek, P., Blejec, A., Gruden, K. et al. (2018)  
507 Statistical modeling of long-term grapevine response to ‘*Candidatus phytoplasma*  
508 *solani*’ infection in the field. *European Journal of Plant Pathology*, 150, 653–668.

- 509 Salehi, M., Esmailzadeh Hosseini, S. A., Salehi, E. & Bertaccini, A. (2017) Genetic diversity  
510 and vector transmission of phytoplasmas associated with sesame phyllody in Iran. *Folia*  
511 *Microbiologica*, 62, 99–109.
- 512 Salehi, M., Izadpanah, K. & Siampour, M. (2011). Occurrence, molecular characterization and  
513 vector transmission of a phytoplasma associated with rapeseed phyllody in Iran.  
514 *Journal of Phytopathology*, 159, 100–105.
- 515 Salem, N.M., Quaglino, F., Abdeen, A., Casati, P., Bulgari, D., Alma, A. et al. (2013) First  
516 report of ‘*Candidatus* Phytoplasma solani’ strains associated with grapevine bois noir  
517 in Jordan. *Plant Disease*, 97, 1505.
- 518 Salem, N.M., Tahzima, R., Abdeen, A.O., Bianco, P.A., Massart, S., Goedefroit, T. et al. (2019)  
519 First report of ‘*Candidatus* Phytoplasma aurantifolia’-related strains infecting potato  
520 (*Solanum tuberosum*) in Jordan. *Plant Disease*, 103, 1406.
- 521 Sears, B.B. & Klomparens, K.L. (1989) Leaf tip cultures of the evening primrose allow stable,  
522 aseptic culture of mycoplasma-like organism. *Canadian Journal of Plant Pathology*, 11,  
523 343–348.
- 524 Siller, W., Kuhbandner, B., Marwitz, R., Petzold, H. & Seemuller, E. (1987) Occurrence of  
525 Mycoplasma-like organisms in parenchyma cells of *Cuscuta odorata* (Ruiz et Pav.).  
526 *Journal of Phytopathology*, 119, 147–159.
- 527 Wu, Y., Hao, X., Li, Z., Gu, P., An, F., Xiang, J. et al. (2010) Identification of the phytoplasma  
528 associated with wheat blue dwarf disease in China. *Plant Disease*, 94, 977–985.
- 529 Yigit, A. & Erckle, L. (1992) Studies on bio-ecology and control of grape leafhopper  
530 (*Arboridia* (= *Erythroneura*) *adanae* Dlab.) (Homoptera: Cicadellidae) in southern  
531 Anatolia region. *Zirai Mücadele Arastirma Yilligi*, 22, 25–28.

532 Zambon, Y., Canel, A., Bertaccini, A. & Contaldo, N. (2018) Molecular diversity of  
533 phytoplasmas associated with grapevine yellows disease in north-eastern Italy.  
534 *Phytopathology*, 108, 206–214.

535 Zhao, Y., Wei, W., Lee, I.-M., Shao, J., Suo, X. & Davis, R.E. (2009) Construction of an  
536 interactive online phytoplasma classification tool, *iPhyClassifier*, and its application in  
537 analysis of the peach X-disease phytoplasma group (16SrIII). *International Journal of*  
538 *Systematic and Evolutionary Microbiology*, 59, 2582–2593.

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#### 540 **Figure Legends**

541 **Figure 1.** Maps of governorates and locations in Jordan where the surveys on GY diseases in  
542 vineyards were conducted.

543 **Figure 2.** Phytoplasma-like symptoms observed in *Vitis vinifera* L. [and \*Convolvulus arvensis\*](#)  
544 [L.](#) in Jordan. Leaf yellowing and rolling in wine grape cultivar (A); leaf reddening and rolling  
545 in wine grape cultivar (B); leaf yellowing and rolling in table grape cultivar (C); [little leaf and](#)  
546 [reddening in bindweed \(D\).](#)

547 **Figure 3.** Virtual RFLP profiles of 16S rDNA nucleotide sequences of phytoplasma strains  
548 identified in *Vitis vinifera* and insects in Jordan. One strain among those sharing identical 16S  
549 rDNA sequence (Tables 2 and 4) was selected as representative strain for *iPhyClassifier*  
550 analyses.

551 **Figure 4.** Phylogenetic tree based on the alignment of 16S rDNA nucleotide sequences of  
552 representative phytoplasma strains identified in *Vitis vinifera* L., putative insect vectors, and  
553 reservoir plants in Jordan (bold characters), and reference strains of previously described  
554 ‘*Candidatus Phytoplasma*’ species. Regarding phytoplasmas identified in this study, one strain  
555 among those sharing identical 16S rDNA sequence (Tables 2 and 4) was selected as  
556 representative strain for phylogenetic analysis. The evolutionary history was inferred using the



557 Minimum Evolution method. The optimal tree with the sum of branch length = 0.91088584 is  
558 shown. The percentage of replicate trees in which the associated taxa clustered together in the  
559 bootstrap test (1000 replicates) are shown next to the branches. The tree is drawn to scale, with  
560 branch lengths in the same units as those of the evolutionary distances used to infer the  
561 phylogenetic tree. The evolutionary distances were computed using the Maximum Composite  
562 Likelihood method and are in the units of the number of base substitutions per site. The ME  
563 tree was searched using the Close-Neighbor-Interchange (CNI) algorithm at a search level of  
564 1. The Neighbor-joining algorithm was used to generate the initial tree. This analysis involved  
565 52 nucleotide sequences. All ambiguous positions were removed for each sequence pair. There  
566 were a total of 1424 positions in the final dataset.

1 **Table 1.** Collected and phytoplasma-infected plant samples from surveyed locations in Jordan.

2

Governorate	Location	Plant	No. of collected samples	No. of phytoplasma-infected samples
Almafraq	AlSalhieh	Symptomatic wine grape	40	11
		Asymptomatic wine grape	3	0
		<i>Convolvulus arvensis</i> L.	20	9
	Sama-AlSarhan	Symptomatic wine grape	10	2
		Asymptomatic wine grape	2	0
		<i>Convolvulus arvensis</i> L.	5	1
	Sabha	Symptomatic table grape	10	1
		Asymptomatic table grape	2	0
	Thagrat Aljob	Symptomatic table grape	7	0
		Asymptomatic table grape	2	0
	Alkom AlAhmar	Symptomatic table grape	5	0
		Asymptomatic table grape	2	0
Jaber Alsarhan	Symptomatic table grape	15	5	
	Asymptomatic table grape	2	0	
Irbid	Hofa	Symptomatic table grape	4	0
		Asymptomatic table grape	1	0
	Bouida	Symptomatic table grape	5	1
		Asymptomatic table grape	2	0
Ajloun	Kufranjeh	Symptomatic table grape	12	1
		Asymptomatic table grape	2	0
	Ain Jana	Symptomatic table grape	5	0
		Asymptomatic table grape	2	0
	UmALyanabee	Symptomatic table grape	10	3
		Asymptomatic table grape	1	0
Aqaba	Aldisi	Symptomatic table grape	14	2
		Asymptomatic table grape	2	0
	Alfuhais	<i>Convolvulus arvensis</i> L.	5	2
		Symptomatic table grape	15	3
AlBalga	Alfuhais	Symptomatic table grape	15	3
		Asymptomatic table grape	2	0
Overall			207	41

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**Table 2.** Attribution to species and taxonomic subgroups of phytoplasmas detected in plants (part I)

Strain	Plant host	Grapevine cultivar	Location	Phytoplasma species	% id vs ref strain	16Sr subgroup	Acc. No.
VV1259	<i>Vitis vinifera</i>	table grape	Kufranjeh	' <i>Ca. P. omanense</i> '	100	XXIX-A (1.00)	OL873117 (b)
VV1003	<i>Vitis vinifera</i>	table grape	UmAlYanabee	' <i>Ca. P. omanense</i> '	99.6	XXIX-B (1.00new)	c
VV1007	<i>Vitis vinifera</i>	table grape	UmAlYanabee	' <i>Ca. P. omanense</i> '	99.6	XXIX-B (1.00new)	c
VV1034	<i>Vitis vinifera</i>	table grape	UmAlYanabee	' <i>Ca. P. omanense</i> '	99.6	XXIX-B (1.00new)	c
VV95	<i>Vitis vinifera</i>	table grape	Aldisi	' <i>Ca. P. omanense</i> '	99.6	XXIX-B (1.00new)	OL873118 (c)
VV37	<i>Vitis vinifera</i>	table grape	Aldisi	' <i>Ca. P. solani</i> '	99.7	XII-A (1.00)	d
VV1395	<i>Vitis vinifera</i>	table grape	AlFuhais	' <i>Ca. P. solani</i> '	99.7	XII-A (1.00)	OL873119 (d)
VV1398	<i>Vitis vinifera</i>	table grape	AlFuhais	' <i>Ca. P. solani</i> '	99.7	XII-A (1.00)	d
VV1399	<i>Vitis vinifera</i>	table grape	AlFuhais	' <i>Ca. P. solani</i> '	99.7	XII-A (1.00)	d
VV636	<i>Vitis vinifera</i>	table grape	Bouida	' <i>Ca. P. solani</i> '	99.7	XII-A (1.00)	d
VV1005	<i>Vitis vinifera</i>	table grape	UmAlYanabee	' <i>Ca. P. solani</i> '	99.7	XII-A (1.00)	d
VV635	<i>Vitis vinifera</i>	table grape	Jaber AlSarahan	' <i>Ca. P. solani</i> '	99.7	XII-A (1.00)	d
VV629	<i>Vitis vinifera</i>	table grape	Jaber AlSarahan	' <i>Ca. P. solani</i> '	99.7	XII-A (1.00)	d
VV633	<i>Vitis vinifera</i>	table grape	Jaber AlSarahan	' <i>Ca. P. solani</i> '	99.7	XII-A (1.00)	d
VV634	<i>Vitis vinifera</i>	table grape	Jaber AlSarahan	' <i>Ca. P. solani</i> '	99.7	XII-A (1.00)	d
VV632	<i>Vitis vinifera</i>	table grape	Jaber AlSarahan	' <i>Ca. P. aurantifolia</i> '	99.7	II-C* (0.99)	a
VV162	<i>Vitis vinifera</i>	wine grape	AlSalhie	' <i>Ca. P. aurantifolia</i> '	99.7	II-C* (0.99)	OL873116 (a)
VV112	<i>Vitis vinifera</i>	wine grape	AlSalhie	' <i>Ca. P. asteris</i> '	99.6	I-R* (0.98)	OL873120 (e)
VV134	<i>Vitis vinifera</i>	wine grape	AlSalhie	' <i>Ca. P. solani</i> '	99.7	XII-A (1.00)	d
VV131	<i>Vitis vinifera</i>	wine grape	AlSalhie	' <i>Ca. P. solani</i> '	99.7	XII-A (1.00)	d
VV110	<i>Vitis vinifera</i>	wine grape	AlSalhie	' <i>Ca. P. solani</i> '	99.7	XII-A (1.00)	d
VV157	<i>Vitis vinifera</i>	wine grape	AlSalhie	' <i>Ca. P. solani</i> '	99.7	XII-A (1.00)	d
VV158	<i>Vitis vinifera</i>	wine grape	AlSalhie	' <i>Ca. P. solani</i> '	99.7	XII-A (1.00)	d
VV159	<i>Vitis vinifera</i>	wine grape	AlSalhie	' <i>Ca. P. solani</i> '	99.7	XII-A (1.00)	d
VV163	<i>Vitis vinifera</i>	wine grape	AlSalhie	' <i>Ca. P. solani</i> '	99.7	XII-A (1.00)	d
VV1	<i>Vitis vinifera</i>	wine grape	AlSalhie	' <i>Ca. P. solani</i> '	99.7	XII-A (1.00)	d
VV2	<i>Vitis vinifera</i>	wine grape	AlSalhie	' <i>Ca. P. solani</i> '	99.7	XII-A (1.00)	d
VV3	<i>Vitis vinifera</i>	wine grape	SamaAlSarahn	' <i>Ca. P. solani</i> '	99.7	XII-A (1.00)	d
VV4	<i>Vitis vinifera</i>	wine grape	SamaAlSarahn	' <i>Ca. P. solani</i> '	99.7	XII-A (1.00)	d

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**Table 2.** Attribution to species and taxonomic subgroups of phytoplasmas detected in plants (part II)

Strain	Plant host	Location	Phytoplasma species	% id vs ref strain	16Sr subgroup	Acc. No.
CAR25	<i>Convolvulus arvensis</i>	Aldisi	' <i>Ca. P. aurantifolia</i> '	99.7	II-C* (0.99)	a
CAR26	<i>Convolvulus arvensis</i>	Aldisi	' <i>Ca. P. aurantifolia</i> '	99.7	II-C* (0.99)	a
CAR6	<i>Convolvulus arvensis</i>	SamaAlSarahn	' <i>Ca. P. solani</i> '	99.7	XII-A (1.00)	d
CAR108	<i>Convolvulus arvensis</i>	AlSalhie	' <i>Ca. P. solani</i> '	99.7	XII-A (1.00)	d
CAR5	<i>Convolvulus arvensis</i>	AlSalhie	' <i>Ca. P. solani</i> '	99.7	XII-A (1.00)	d
CAR65	<i>Convolvulus arvensis</i>	AlSalhie	' <i>Ca. P. solani</i> '	99.7	XII-A (1.00)	d
CAR153	<i>Convolvulus arvensis</i>	AlSalhie	' <i>Ca. P. solani</i> '	99.7	XII-A (1.00)	d
CAR165	<i>Convolvulus arvensis</i>	AlSalhie	' <i>Ca. P. solani</i> '	99.7	XII-A (1.00)	d
CAR168	<i>Convolvulus arvensis</i>	AlSalhie	' <i>Ca. P. solani</i> '	99.7	XII-A (1.00)	d
CAR360	<i>Convolvulus arvensis</i>	AlSalhie	' <i>Ca. P. solani</i> '	99.7	XII-A (1.00)	d
CAR109	<i>Convolvulus arvensis</i>	AlSalhie	' <i>Ca. P. solani</i> '	99.7	XII-A (1.00)	d
CAR112	<i>Convolvulus arvensis</i>	AlSalhie	' <i>Ca. P. solani</i> '	99.7	XII-A (1.00)	d

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**Table 3.** Collected and phytoplasma-infected insects from surveyed locations in northern Jordan.

Governorate	Location	Grapevine cultivar	Insect code	Family	Species	Collection date	No. of collected insects	No. of pools	No. of positive pools	Infection rate (%)
AlMafrq	AlSalhieh	wine grape	MH2	Cicadellidae	<i>Empoasca</i> sp.	Aug	350	9	1	11.1
AlMafrq	AlSalhieh	wine grape	MH3b	Cicadellidae	<i>Balclutha</i> sp.	Aug	12	1	0	0
AlMafrq	AlSalhieh	wine grape	MH5	Cicadellidae	<i>Psammotettix striatus</i>	Aug	15	6	5	83.3
AlMafrq	AlSalhieh	wine grape	MH7	Cicadellidae	<i>Cicadulina bipunctata</i>	Aug	65	9	3	33.3
AlMafrq	AlSalhieh	wine grape	MH8	Cicadellidae	<i>Orosius cellulosus</i>	Aug	28	10	4	40
AlMafrq	AlSalhieh	wine grape	MH11	Delphacidae	<i>Toya propinqua</i>	Aug	23	4	0	0
AlMafrq	AlSalhieh	wine grape	MH12	Delphacidae	<i>Laodelphax striatellus</i>	Aug	5	2	0	0
AlMafrq	AlSalhieh	wine grape	MH18	Cicadellidae	<i>Circulifer</i> sp.	Nov	49	10	5	50
AlMafrq	AlSalhieh	wine grape	MH19	Cicadellidae	<i>Euscelidius mundus</i>	Nov	10	3	3	100
AlMafrq	Alkom AlAhmar	table grape	SUF1	Cicadellidae	<i>Cicadulina bipunctata</i>	Aug	88	7	2	28.6
AlMafrq	Alkom AlAhmar	table grape	SUF3	Delphacidae	<i>Laodelphax striatellus</i>	Aug	5	5	3	60
AlMafrq	Alkom AlAhmar	table grape	SUF5	Cicadellidae	<i>Psammotettix striatus</i>	Aug	5	2	2	100
AlMafrq	Sabha	table grape	YM2	Cixiidae	<i>Hyalesthes obsoletus</i>	Aug	7	2	1	50
AlMafrq	Sabha	table grape	YM3	Cicadellidae	<i>Cicadulina bipunctata</i>	Aug	135	6	1	16.7
Ajloun	Kufranjeh	table grape	Z1	Cicadellidae	<i>Cicadulina bipunctata</i>	Sep	105	8	1	12.5
Ajloun	Ain Jana	table grape	G61	Cicadellidae	<i>Arboridia adanae</i>	Sep	271	28	3	10.7
Overall							1173	112	34	34.8

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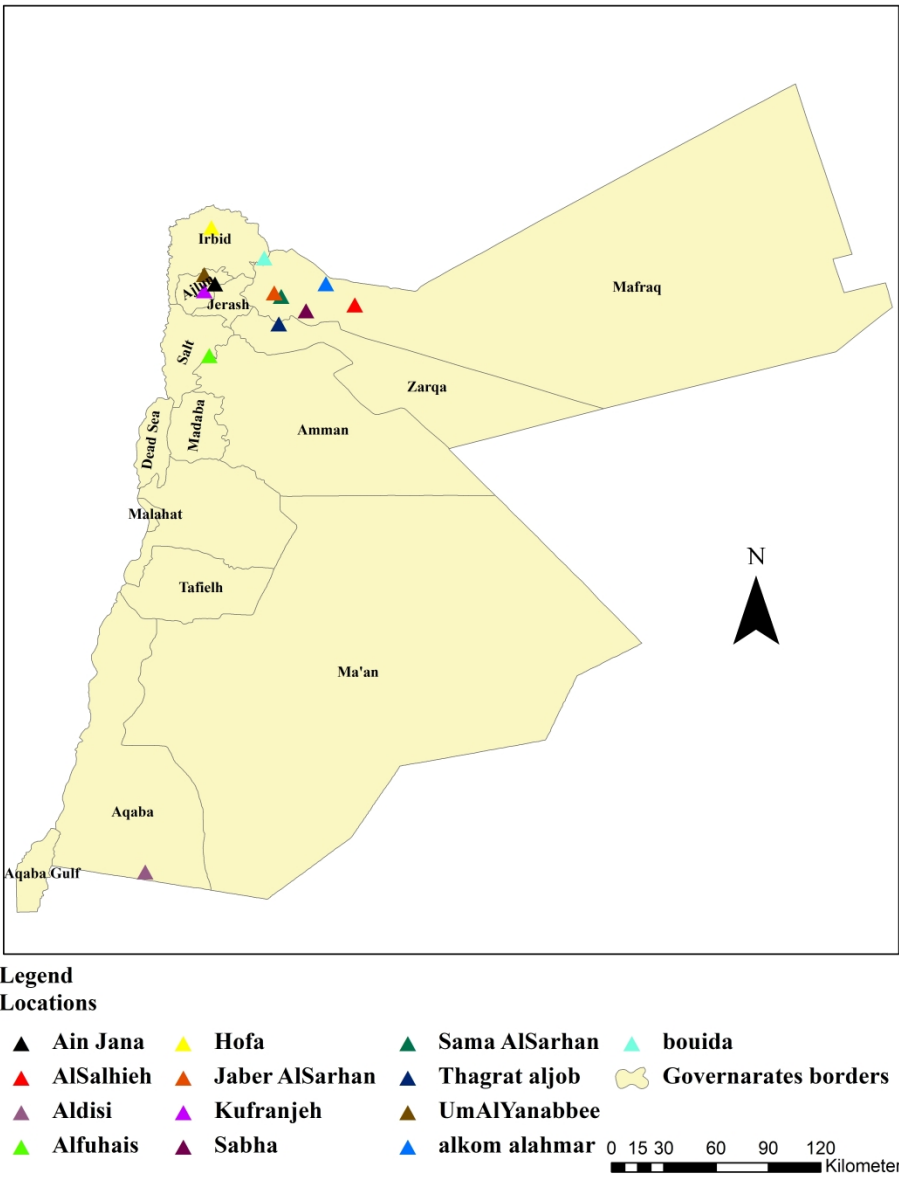
1 **Table 4.** Attribution to species and taxonomic subgroups of phytoplasmas detected in insects.

Strain	Species	Region	Phytoplasma species	% id vs ref strain	16Sr subgroup	Acc. No.
MH2-1	<i>Empoasca</i> sp.	AlSalhieh	' <i>Ca. P. pyri</i> '	100	X-C (1.00)	OL873122
MH18-3	<i>Circulifer</i> sp.	AlSalhieh	' <i>Ca. P. asteris</i> '	99.6	I-R* (0.98)	e
MH18-4	<i>Circulifer</i> sp.	AlSalhieh	' <i>Ca. P. asteris</i> '	99.6	I-R* (0.98)	e
MH18-5	<i>Circulifer</i> sp.	AlSalhieh	' <i>Ca. P. asteris</i> '	99.6	I-R* (0.98)	e
MH18-6	<i>Circulifer</i> sp.	AlSalhieh	' <i>Ca. P. asteris</i> '	99.6	I-R* (0.98)	e
MH18-23	<i>Circulifer</i> sp.	AlSalhieh	' <i>Ca. P. solani</i> '	99.7	XII-A (1.00)	d
MH5-7	<i>Psammotettix striatus</i>	AlSalhieh	' <i>Ca. P. asteris</i> '	99.6	I-R* (0.98)	e
MH5-8	<i>Psammotettix striatus</i>	AlSalhieh	' <i>Ca. P. asteris</i> '	99.6	I-R* (0.98)	e
MH5-9	<i>Psammotettix striatus</i>	AlSalhieh	' <i>Ca. P. asteris</i> '	99.6	I-R* (0.98)	e
MH5-10	<i>Psammotettix striatus</i>	AlSalhieh	' <i>Ca. P. asteris</i> '	99.6	I-R* (0.98)	e
MH5-11	<i>Psammotettix striatus</i>	AlSalhieh	' <i>Ca. P. omanense</i> '	100	XXIX-A (1.00)	b
MH7-12	<i>Cicadulina bipunctata</i>	AlSalhieh	' <i>Ca. P. asteris</i> '	99.6	I-R* (0.98)	e
MH7-13	<i>Cicadulina bipunctata</i>	AlSalhieh	' <i>Ca. P. asteris</i> '	99.6	I-R* (0.98)	e
MH7-14	<i>Cicadulina bipunctata</i>	AlSalhieh	' <i>Ca. P. asteris</i> '	99.6	I-R* (0.98)	e
MH8-16	<i>Orosius cellulosus</i>	AlSalhieh	' <i>Ca. P. aurantifolia</i> '	99.7	II-C* (0.99)	a
MH8-17	<i>Orosius cellulosus</i>	AlSalhieh	' <i>Ca. P. solani</i> '	99.7	XII-A (1.00)	d
MH8-18	<i>Orosius cellulosus</i>	AlSalhieh	' <i>Ca. P. solani</i> '	99.7	XII-A (1.00)	d
MH8-21	<i>Orosius cellulosus</i>	AlSalhieh	' <i>Ca. P. solani</i> '	99.7	XII-A (1.00)	d
MH19-24	<i>Euscelidius mundus</i>	AlSalhieh	' <i>Ca. P. solani</i> '	99.7	XII-A (1.00)	d
MH19-25	<i>Euscelidius mundus</i>	AlSalhieh	' <i>Ca. P. solani</i> '	99.7	XII-A (1.00)	d
MH19-26	<i>Euscelidius mundus</i>	AlSalhieh	' <i>Ca. P. solani</i> '	99.7	XII-A (1.00)	d
SUF3-1	<i>Laodelphax striatellus</i>	Alkom AlAhmar	' <i>Ca. P. asteris</i> '	99.6	I-R* (0.98)	e
SUF3-2	<i>Laodelphax striatellus</i>	Alkom AlAhmar	' <i>Ca. P. solani</i> '	99.7	XII-A (1.00)	d
SUF3-3	<i>Laodelphax striatellus</i>	Alkom AlAhmar	' <i>Ca. P. asteris</i> '	99.6	I-R* (0.98)	e
SUF5-4	<i>Psammotettix striatus</i>	Alkom AlAhmar	' <i>Ca. P. asteris</i> '	99.9	I-B (1.00)	OL873121
SUF5-5	<i>Psammotettix striatus</i>	Alkom AlAhmar	' <i>Ca. P. asteris</i> '	99.6	I-R* (0.98)	e
SUF1-6	<i>Cicadulina bipunctata</i>	Alkom AlAhmar	' <i>Ca. P. asteris</i> '	99.6	I-R* (0.98)	e
SUF1-7	<i>Cicadulina bipunctata</i>	Alkom AlAhmar	' <i>Ca. P. asteris</i> '	99.6	I-R* (0.98)	e
YM2-9	<i>Hyalesthes obsoletus</i>	Sabha	' <i>Ca. P. asteris</i> '	99.6	I-R* (0.98)	e
Z1-20	<i>Cicadulina bipunctata</i>	Kufranjeh	' <i>Ca. P. asteris</i> '	99.6	I-R* (0.98)	e
Z1-40	<i>Cicadulina bipunctata</i>	Kufranjeh	' <i>Ca. P. asteris</i> '	99.6	I-R* (0.98)	e
G61-1	<i>Arboridia adanae</i>	Ain Jana	' <i>Ca. P. asteris</i> '	99.6	I-R* (0.98)	e
G61-2	<i>Arboridia adanae</i>	Ain Jana	' <i>Ca. P. asteris</i> '	99.6	I-R* (0.98)	e
G61-3	<i>Arboridia adanae</i>	Ain Jana	' <i>Ca. P. asteris</i> '	99.6	I-R* (0.98)	e

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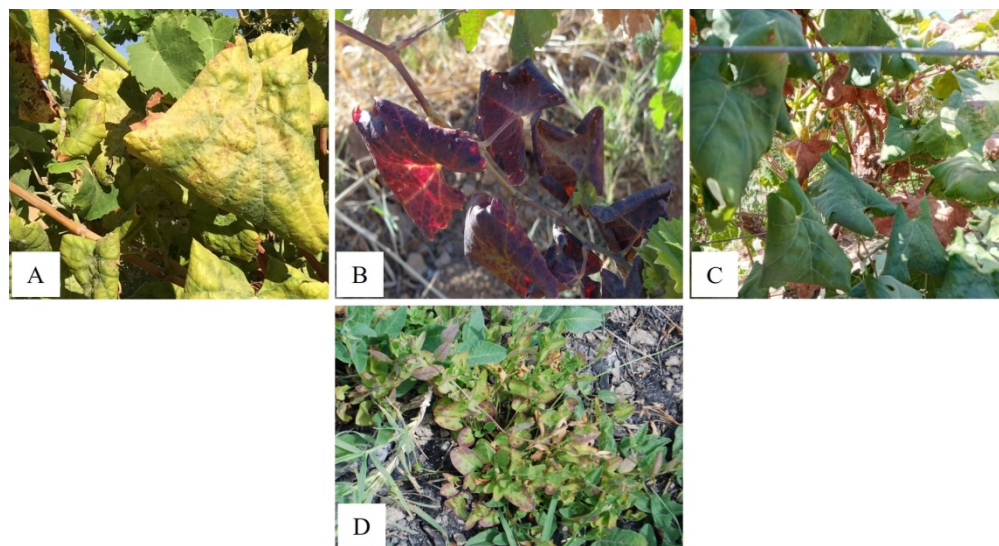
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**Figure 1.** Maps of governorates and locations in Jordan where the surveys on GY diseases in vineyards were conducted.

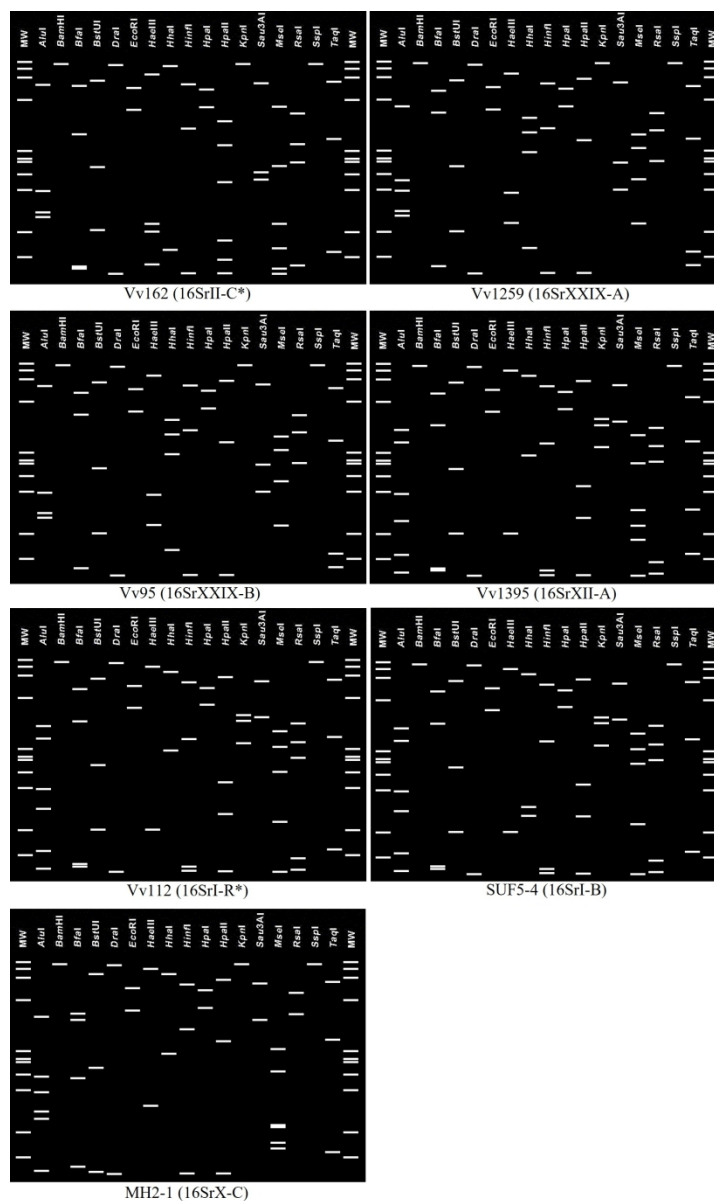
215x279mm (500 x 500 DPI)



**Figure 2.** Phytoplasma-like symptoms observed in *Vitis vinifera* L. and *Convolvulus arvensis* L. in Jordan. Leaf yellowing and rolling in wine grape cultivar (A); leaf reddening and rolling in wine grape cultivar (B); leaf yellowing and rolling in table grape cultivar (C); little leaf and reddening in bindweed (D).

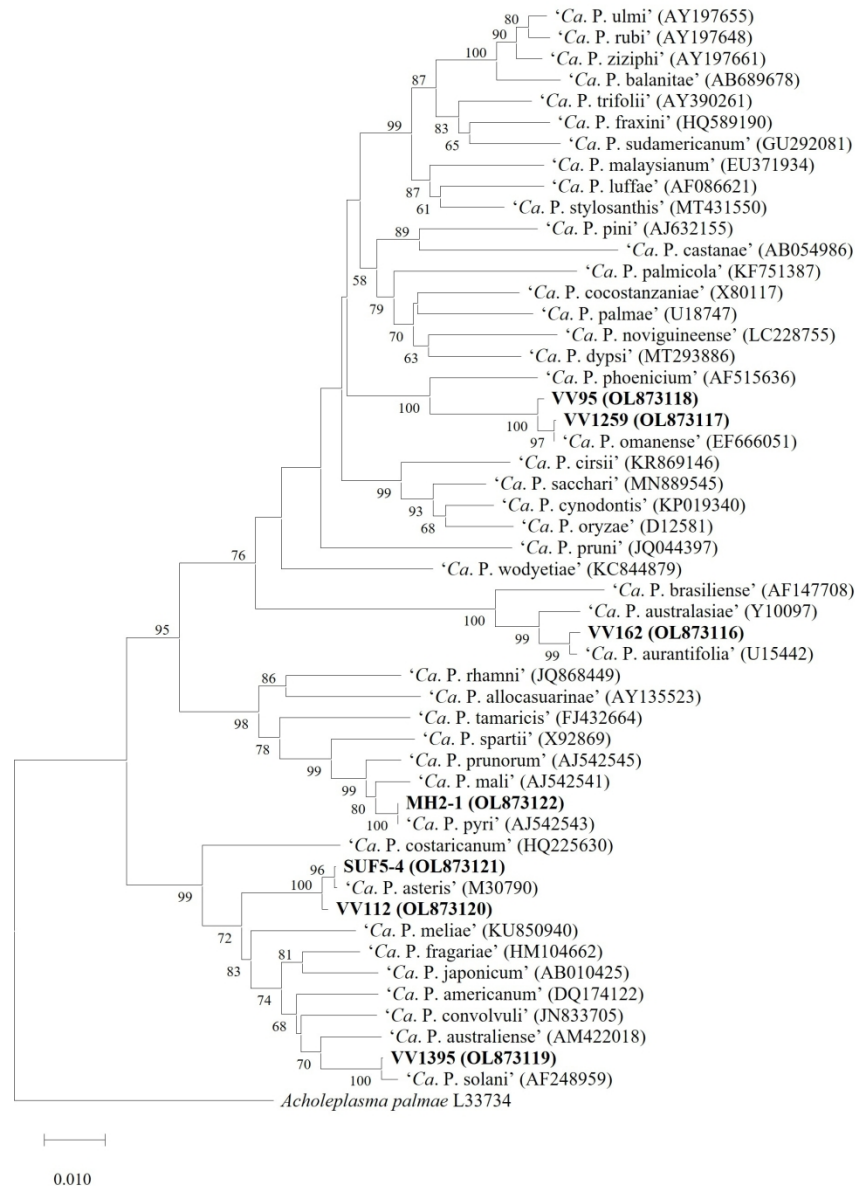
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**Figure 3.** Virtual RFLP profiles of 16S rDNA nucleotide sequences of phytoplasma strains identified in *Vitis vinifera* and insects in Jordan. One strain among those sharing identical 16S rDNA sequence (Tables 2 and 4) was selected as representative strain for *iPhyClassifier* analyses.

153x256mm (330 x 330 DPI)



**Figure 4.** Phylogenetic tree based on the alignment of 16S rDNA nucleotide sequences of representative phytoplasma strains identified in *Vitis vinifera* L., putative insect vectors, and reservoir plants in Jordan (bold characters), and reference strains of previously described 'Candidatus Phytoplasma' species. Regarding phytoplasmas identified in this study, one strain among those sharing identical 16S rDNA sequence (Tables 2 and 4) was selected as representative strain for phylogenetic analysis. The evolutionary history was inferred using the Minimum Evolution method. The optimal tree with the sum of branch length = 0.91088584 is shown. The percentage of replicate trees in which the associated taxa clustered together in the bootstrap test (1000 replicates) are shown next to the branches. The tree is drawn to scale, with branch lengths in the same units as those of the evolutionary distances used to infer the phylogenetic tree. The evolutionary distances were computed using the Maximum Composite Likelihood method and are in the units of the number of base substitutions per site. The ME tree was searched using the Close-Neighbor-Interchange (CNI) algorithm at a search level of 1. The Neighbor-joining algorithm was used to generate the initial tree. This analysis involved 52 nucleotide sequences. All ambiguous positions were removed for each sequence pair. There were a total of 1424 positions in the final dataset.

143x202mm (330 x 330 DPI)