

1 **A new resource for research and risk analysis: the updated European Food Safety**  
2 **Authority database of *Xylella* spp. host plant species**

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9 **Abstract**

10 Following a series of requests for scientific advice from the European Commission starting in  
11 2013, the European Food Safety Authority (EFSA) conducted pest risk assessment and  
12 created a comprehensive *Xylella fastidiosa* host plant database. The last update of the  
13 database, published in September 2018, includes information on host plants of both *X.*  
14 *fastidiosa* and *X. taiwanensis*, together with details on botanical classification, infection  
15 conditions, geographic location, pathogen taxonomy including information on subspecies,  
16 strain and sequence type, detection techniques and tolerant/resistant response of the plant.  
17 This updated database of host plants of *Xylella* spp. reported world-wide provides a key tool  
18 for risk management, risk assessment and research on this generalist bacterial plant  
19 pathogen.

20

## 21 Database announcement

22 *Xylella fastidiosa* is a generalist plant pathogenic bacterium (Almeida and Nunney, 2015)  
23 causing numerous plant diseases worldwide such as Pierce's disease of grapes, bacterial leaf  
24 scorch of shade trees and oleander leaf scorch in North America, and citrus variegated  
25 chlorosis in Brazil. In Taiwan, a leaf scorch disease of pear was described in association with  
26 a fastidious bacterium originally designated as a strain of *X. fastidiosa* (Leu and Su, 1993),  
27 which was later shown to be genetically distant from other *X. fastidiosa* strains and thus  
28 classified as a novel species, *X. taiwanensis* (Su *et al.*, 2016). In 2013, the identification of  
29 olive trees affected by *X. fastidiosa* in southern Italy represented the first record of an  
30 outbreak of this pathogen under field conditions in the European Union (EU) (Saponari *et*  
31 *al.*, 2013). This first report was then followed by additional outbreaks in France and Spain  
32 (Denancé *et al.*, 2017; Olmo *et al.*, 2017). The European Commission requested the  
33 European Food Safety Authority (EFSA) to provide scientific assistance on this matter. In  
34 January 2015, EFSA published a pest risk assessment of *X. fastidiosa* for the EU territory  
35 (EFSA PLH Panel, 2015) which included a list of the known host plant species of *X. fastidiosa*  
36 collected through a literature search. EFSA was then given the task to periodically update  
37 the database of *X. fastidiosa* host plants, and in 2016 an electronic version was published  
38 (EFSA, 2016). For the period 2016-2020, EFSA was requested to further update this database  
39 by taking into account the different subspecies, strains and European isolates of *X.*  
40 *fastidiosa*, together with information on tolerant/resistant plant varieties and negative  
41 results of diagnostic tests.

42 The process for updating the host plant database of *Xylella* spp., taking into account both *X.*  
43 *fastidiosa* and *X. taiwanensis*, was divided into the following steps: (1) an extensive

44 literature search to identify the relevant references; (2) the selection of the retrieved  
45 studies based on titles, abstracts and full-text; (3) the extraction of the relevant information  
46 from the selected references; (4) and data analysis and reporting.

47 The literature search was conducted in 2017 and 3595 references were obtained,  
48 supplemented by additional information provided by scientific experts and national  
49 authorities. On the whole, 853 publications were selected for data extraction and 8391 data  
50 extraction forms were filled with data covering botanical classification of the plant according  
51 to the updated taxonomy from the European and Mediterranean Plant Protection  
52 Organization (EPPO) global database (EPPO, 2018), infection conditions and location of the  
53 infected plant, geographic coordinates, isolate characterization (*Xylella* species, subspecies,  
54 disease, strain, multilocus sequence type), methods of detection, and information about the  
55 tolerant/resistant response of the plant.

56 Data reporting was designed to categorise *Xylella* host plant species based on the number  
57 and type of detection methods applied for each finding. Different combinations of detection  
58 methods were considered:

59 A. Plant species positive with at least two detection methods (out of: symptom  
60 observation on the test plant in experimental vector transmission, enzyme-linked  
61 immunosorbent assay (ELISA), other immunological techniques, polymerase chain  
62 reaction (PCR)-based methods, sequencing or culture) or positive with sequencing or  
63 culture.

64 B. The same as category A, but also including microscopy.

65 C. Plant species positive with at least one detection method (out of: symptom  
66 observation on the test plant in experimental vector transmission, ELISA, other  
67 immunological techniques, PCR-based methods, sequencing or culture).

68 D. The same as category C, but also including microscopy.

69 E. All plant species reported positive, regardless of the detection method (positive  
70 records but without the detection method specified, symptom observations,  
71 microscopy, symptom observation on the test plant in experimental vector  
72 transmission, ELISA, other immunological techniques, PCR-based methods,  
73 sequencing, or culturing).

74 An example of data reporting is presented in Table 1, in which the number of host plant  
75 species (according to categories A, B, C, D, E) reported infected by different *X. fastidiosa*  
76 subspecies in artificial, natural and unspecified conditions is shown. The complete lists of  
77 plant species are available in the database and scientific report (EFSA, 2018), both of which  
78 are open access.

79 *Xylella taiwanensis* is not included in Table 1 as up now it was reported only in naturally  
80 infected *Pyrus pyrifolia* in Taiwan.

81 A detailed genetic characterization of *Xylella* spp. (such as species, subspecies, strains and  
82 multilocus sequence type) as well as the tolerant/resistant host status of the plant species  
83 or variety are included in the current version of the database, with special categories and  
84 extensive comments.

85 This updated *Xylella* spp. host plant database was released in September 2018 together with  
86 a detailed report (EFSA, 2018). The raw data and related metadata are published in Zenodo

87 in the EFSA Knowledge Junction community: <https://doi.org/10.5281/zenodo.1339344> .

88 Interactive reports are available at the following link:

89 <https://www.efsa.europa.eu/en/microstrategy/xylella> .

90 The EFSA database of *Xylella* spp host plant species reported world-wide is a key tool for risk  
91 management, risk assessment and research on this generalist bacterial plant pathogen, and  
92 is expected to be kept up-to-date as new relevant information becomes available.

### 93 **Acknowledgments**

94 Many thanks to EFSA staff members: Andrea Baù, Ciro Gardi, Tomasz Kaluski, Olaf  
95 Mosbach–Schulz, Irene Muñoz Guajardo, Luca Pasinato and Sara Tramontini; to the external  
96 contractor Minh Ngoc Quan from BV-Tech for developing the interactive reports; and to the  
97 experts for scientific advice: Rodrigo Almeida, Claude Bragard, Thierry Candresse, Marie-  
98 Agnès Jacques, João Roberto Spotti Lopes and Leonard Nunney.

### 99 **DISCLAIMER**

100 The positions and opinions presented in this article are those of the authors alone and are  
101 not intended to represent the views or any official positions of their institutions.

### 102 **Literature Cited**

- 103 • Almeida, R. P. P. and L. Nunney (2015). "How do plant diseases caused by *Xylella*  
104 *fastidiosa* emerge?" *Plant Disease* 99(11): 1457-1467.
- 105 • Denancé, N., et al. (2017). "Several subspecies and sequence types are associated  
106 with the emergence of *Xylella fastidiosa* in natural settings in France." *Plant*  
107 *Pathology* 66(7): 1054-1064.

- 108 • EFSA PLH Panel (EFSA Panel on Plant Health) (2015). "Scientific Opinion on the risks  
109 to plant health posed by *Xylella fastidiosa* in the EU territory, with the identification  
110 and evaluation of risk reduction options". EFSA Journal 13(1):3989.
- 111 • EFSA (European Food Safety Authority) (2016). "Scientific report on the update of a  
112 database of host plants of *Xylella fastidiosa*: 20 November 2015". EFSA Journal  
113 14(2):4378.
- 114 • EFSA (European Food Safety Authority) (2018). "Scientific report on the update of  
115 the *Xylella* spp. host plant database". EFSA Journal 16(9):5408.
- 116 • EPPO (2018). EPPO Global Database (available online). <https://gd.eppo.int>
- 117 • Leu, L. S. and C. C. Su (1993). "Isolation, cultivation, and pathogenicity of *Xylella*  
118 *fastidiosa*, the causal bacterium of pear leaf scorch disease in Taiwan." Plant Disease  
119 77(6): 642-646.
- 120 • Olmo, D., et al. (2017). "First detection of *Xylella fastidiosa* infecting cherry (*Prunus*  
121 *avium*) and *Polygala myrtifolia* plants, in Mallorca Island, Spain". Plant Disease  
122 101(10): 1820-1820.
- 123 • Saponari, M., et al., (2013). "Identification of DNA sequences related to *Xylella*  
124 *fastidiosa* in oleander, almond and olive trees exhibiting leaf scorch symptoms in  
125 Apulia (Southern Italy)". Journal of Plant Pathology 95(3), 668.
- 126 • Su, C.C., et al. (2016). "*Xylella taiwanensis* sp. nov., causing pear leaf scorch disease".  
127 International Journal of Systematic and Evolutionary Microbiology, 66, 4766–4771.
- 128
- 129

130 **Table**

131 Table 1: Number of host plant species reported infected by different subspecies of *Xylella*  
 132 *fastidiosa* under artificial, natural or unspecified conditions<sup>a</sup>, according to confirmation  
 133 categories A, B, C, D, E<sup>b</sup>.

Infection method	Artificial					Natural					Unspecified				
	Category	A	B	C	D	E	A	B	C	D	E	A	B	C	D
<b><i>X. fastidiosa</i></b>															
<b>subspecies</b>															
<i>fastidiosa</i>	35	35	41	41	42	32	32	32	32	32	3	3	3	3	3
<i>fastidiosa/sandyi</i>	0	0	0	0	0	2	2	2	2	2	0	0	0	0	0
<i>morus</i>	0	0	0	0	0	4	4	4	4	4	0	0	0	0	0
<i>multiplex</i>	8	8	11	11	11	108	108	116	116	116	10	10	11	11	11
<i>pauca</i>	7	7	13	13	13	41	41	43	43	43	1	1	1	1	1
<i>sandyi</i>	3	3	3	3	3	6	6	7	7	7	0	0	0	0	0
<i>tashke</i>	0	0	1	1	1	1	1	1	1	1	0	0	0	0	0
unknown	93	96	191	195	204	144	148	326	333	338	15	15	15	15	16

134 <sup>a</sup> Artificial inoculation includes both mechanical inoculation and vector transmission; natural  
 135 infection includes all records of host plants found during survey or research activities; unspecified  
 136 infection includes all cases where no details on the type of infection methods were reported.

137 <sup>b</sup> Categories A through E represent progressively less stringent confirmation criteria as described in  
 138 detail in the text.