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Correction

Correction: Gorris et al. Detection and Diagnosis of *Xylella fastidiosa* by Specific Monoclonal Antibodies. *Agronomy* 2021, *11*, 48

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Missing Citations and Errors in Tables

In the original publication [1], the explanation of Table 3 in Section 3, Section 3.4, and the title of that table were not correct. In addition, the information in Tables 4 and 5 was not complete and a sentence was missing. In Table 6, there were minor calculation mistakes; the diagnostic parameters of Cohen's Kappa indices have been recalculated, and Reference [39] has been included; a related sentence and Reference [35] have been added to the Materials and Methods section. Finally, Reference [31] was not complete. All of this information has been corrected as follows.

A correction has been made to Section 3.4, and it should read:

Out of the 233 samples, all were analyzed with real-time PCR by Harper et al. [31], 231 were analyzed with real-time PCR by Francis et al. [32], and 218 were analyzed by using DAS-ELISA with MAb2 G1/PPD (developed in this study). The total number of positive (and negative) samples for each technique out of the 233 that were analyzed (Table 3) is shown in the contingency Tables 4 and 5: In Table 4, DAS-ELISA is compared with Harper's PCR; in Table 5, DAS-ELISA is compared with Francis' PCR.

The corrected captions of Tables 3–5 read as follows.

Table 3. Number of plant samples for the detection of *Xylella fastidiosa* with DAS-ELISA MAb 2G1/PPD, real-time PCR by Harper et al. [31], and real-time PCR by Francis et al. [32]. The number of samples analyzed with each technique with respect to the total number of samples.

Table 4. Contingency table comparing MAb2G1/PPD DAS-ELISA with real-time PCR by Harper et al. [31] for *Xylella fastidiosa* detection in samples of naturally infected and healthy plants. The upper part shows the positive and negative results for each technique. The diagnostic parameters corresponding to these results are shown in the lower part. The positive samples correspond to almond trees.

Table 5. Contingency table comparing MAb2G1/PPD DAS-ELISA with real-time PCR by Francis et al. [32] for *Xylella fastidiosa* detection in samples of naturally infected and healthy plants. The upper part shows the positive and negative results for each technique. The diagnostic parameters corresponding to these results are shown in the lower part. The positive samples correspond to almond trees.

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The corrected version of Table 6 reads as follows.

Table 6. Agreement between MAb2G1/PPD DAS-ELISA and real-time PCR by Harper et al. [31] or Francis et al. [32] for the detection of *X. fastidiosa* in 233 tree samples from the demarcated area for *X. fastidiosa* in Alicante (Spain) [39].

	MAb2G1/PPD DAS-ELISA vs. Harper's Real-Time PCR	**MAb2G1/PPD DAS-ELISA vs. Francis' Real-Time PCR**
Agreement	0.93	0.94
Cohen's Kappa (95% CI)	0.87 (0.81–1.0)	0.89 (0.81–1.0)
McNemar's test; *p*-value	12; *p*-value < 0.0005	10; *p*-value < 0.001

Concerning the information in Table 6, a sentence has been added to Section 2, Section 2.8, so this subsection should read:

Aliquots from naturally infected plant samples processed as described above were analyzed in parallel by using DAS-ELISA Mab and two standard protocols for real-time PCR according to EPPO [6]: those of Harper et al. [31] and Francis et al. [32], with previous DNA extraction by using the CTAB method [6]. In order to compare the results of the different methods employed and evaluate the use of DAS-ELISA MAb as a new diagnostic tool, contingency tables were calculated. The diagnostic specificity, diagnostic sensitivity, false positive and negative ratings, and relative accuracy were calculated according to Olmos et al. [33] and the EPPO standard [6]. The agreement between techniques was evaluated with Cohen's Kappa index [34], which indicates the proportion of agreement beyond that expected by chance, by using the R platform package epi-R (https://cran.r-project.org, accessed on 24 May 2023) while following the approach reported by Altman et al. [35]. The benchmarks of Landis and Koch [36] were used to categorize Cohen's Kappa index, where <0.00 indicates poor agreement, 0 to 0.2 indicates slight agreement, 0.21 to 0.40 indicates fair agreement, 0.41 to 0.60 indicates moderate agreement, 0.61 to 0.80 indicates substantial agreement, and 0.81 to 1.00 indicates almost perfect agreement. All data were also subjected to the McNemar 2 test [37] to detect bias effects, which would affect the results of Cohen's Kappa index [38].

Reference Corrections

31. Harper, S.J.; Ward, L.I.; Clover, G.R.G. Development of LAMP and real-time PCR methods for the rapid detection of *Xylella fastidiosa* for quarantine and field applications. *Phytopathology* **2010**, *100*, 1282–1288; Erratum in *Phytopathology* **2013**, *103*, 762.
35. Altman, D.G.; Machin, D.; Bryant, T.N.; Gardner, M.J. *Statistics with Confidence*, 2nd ed.; British Medical Journal: London, UK, 2000; pp. 116–118.
39. Marco-Noales, E.; Barbé, S.; Monterde, A.; Navarro-Herrero, I.; Ferrer, A.; Dalmau, V.; Aure, C.M.; Domingo-Calap, M.L.; Landa, B.B.; Roselló, M. Evidence that *Xylella fastidiosa* is the Causal Agent of Almond Leaf Scorch Disease in Alicante, Mainland Spain (Iberian Peninsula). *Plant Dis.* **2021**, *105*, 3349–3352. https://doi.org/10.1094/PDIS-03-21-0625-SC.

With this correction, the order of some references has been adjusted accordingly. The authors state that the scientific conclusions are unaffected. This correction was approved by the Academic Editor. The original publication has also been updated.

Reference

1. Gorris, M.T.; Sanz, A.; Peñalver, J.; López, M.M.; Colomer, M.; Marco-Noales, E. Detection and Diagnosis of *Xylella fastidiosa* by Specific Monoclonal Antibodies. *Agronomy* **2021**, *11*, 48. [CrossRef]