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Large host jumps in some powdery mildew species revealed by phylogeny and cross inoculations

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Powdery mildew fungi have long been considered as highly specific pathogens, i.e. a given species can infect only a narrow range of host plants, usually in the same genus. The availability of molecular markers has dramatically improved and changed our vision on these fungi, especially that host specificity is not as simple and narrow as previously believed. For example, recent phylogenies have strongly suggested that species causing oak and mango powdery mildew are closely related. Here we analysed mango powdery mildew samples from southern Spain (6 different orchards in Malaga region) by combining multi-gene phylogeny (ITS + 4 single-copy coding genes) and cross inoculations between oak and mango. Based on genetic analyses, two *Erysiphe* species were identified in mango samples, which are the species usually associated with oak powdery mildew in Europe. *Erysiphe quercicola* was dominant with 97% positive samples, whereas *E. alphitoides* was found in only 11% of all samples, 3% alone and 8% in mixture with *E. quercicola*. Cross inoculations between oak and mango, which led to typical symptoms, further supported the conspecificity of oak and mango powdery mildew species. These results constitute the first report of mango powdery mildew in mainland Spain and mainland Europe, caused by *E. quercicola* and *E. alphitoides*. Our study confirmed the broad host range and/or host shifting ability of both *E. quercicola* and *E. alphitoides*, which may explain their invasive success. Furthermore, it opens interesting prospects to the elucidation of molecular mechanisms underlying host range since the two closely related *Erysiphe* species belong to a small clade with both generalist and specialist powdery mildews.

Keywords: powdery mildew, host range, host shift, biological invasion