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Insights into the spatio-temporal spread of *Xylella fastidiosa* in south-eastern Italy

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Abstract: *X. fastidiosa* causes serious diseases in a broad range of woody plants (EFSA 2015). The pathogen is xylem-limited and vectored by insects. Several subspecies have been described, differing in their host range, aggressiveness, and vectors. The movement of infected plants and vectors are considered the main pathways of introduction. In 2013, olive quick decline, caused by *X. fastidiosa* subsp. *pauca*, was first reported in Apulia in south-eastern Italy (Martelli *et al.* 2016) and *Philaenus spumarius* was confirmed as the main vector. Spatio-temporal analysis can inform about the epidemiological factors driving disease distribution and may assist to limit further spread. A mechanistic model was recently developed for the early stages of *X. fastidiosa* invasion in Apulia (White *et al.* 2017). In the present study, spatio-temporal models were fitted to the distribution of *X. fastidiosa* in Apulia from 2013 to 2016. Different sampling strategies were followed each year, so the analysis was focused only in the Salento peninsula where a more regular sampling was observed. Bayesian inference by INLA (Rue *et al.* 2009) was used and the geostatistical effect was implemented by the SPDE approach (Lindgren *et al.* 2011). Results confirmed the high rate of disease spread under favorable environmental conditions, absence of effective vector control, and presence of highly susceptible hosts.

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Modeling and estimating the dynamics of *Xylella fastidiosa* based on French surveillance data

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Abstract: Since the detection of *X. fastidiosa* in 2015 in Corsica, France, a rather intense surveillance of infections has been carried out and has generated a total of nearly 18000 samples, 5% of which