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Finding answers to a global problem

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BOOK OF ABSTRACTS













Sevilla and Mallorca. *P. spumarius* were almost absent in regions with conventional tillage such as the "Campiña" of Jaén and Córdoba. Furthermore, we collected another xylem feeder, namely *Neophilaenus campestris* mainly on grasses in Madrid, Córdoba and Mallorca. Data gathered on the population dynamics of *X. fastidiosa* vectors will be analyzed in relation to climatic variables, as the first step to develop a risk assessment model applicable to the sampled regions. Moreover, our data on the spatial distribution on aggregated behavior of the spittlebug species will be useful to develop an environmentally sustainable *X. fastidiosa*-disease mediated control strategy.

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5.8 DNA barcoding to identify vectors of *X. fastidiosa* in the Balearic Islands

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Abstract: *X. fastidiosa* has recently being detected in the Balearic Islands. Although three of the current varieties of this bacteria has been recorded, there is not yet definitive information on the vectors that transmit this disease in the Balearic archipelago. The DNA-barcoding region is located in the cytochrome oxidase 1 gene (CO1). This has shown efficient to differentiate animal species and it has been widely used in the identification of disease vectors. We propose to standardize the methodology and the selection of the fragment to be amplified to homogenize results obtained by different groups.

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Paredes-Esquivel et al. Molecular Phylogenetics and Evolution. 2009

5.9 Predatory potential of two functional groups of spiders on *Philaenus* spumarius

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Abstract: There is an urgent need of increasing the knowledge about natural enemies of *Philaenus spumarius* and finding strategies to limit the spread of *X. fastidiosa*. Generalist predators, such as spiders, can arise as potential natural control agents. Determining the functional response is crucial for understanding the potentiality of a predator as biological control agent. In this work, the functional response of two widespread palearctic spider species belonging to two different functional groups was assessed. The ambusher spider *Synema globosum* and the orb-weaver *Araniella cucurbitina* were used as model species and *P. spumarius* as prey under laboratory conditions. In parallel, *Ceratitis capitata* was also used as prey in order to compare the spiders' predatory potential between a non-flying insect (*P. spumarius*) and a flying one (*C. capitata*). *A. cucurbitina* and *S. globosum* showed a type II and type I functional response respectively when fed with *P. spumarius* and a type II response when fed with *C. capitata*. Both the handling time and attack rate were significantly different between spider species when fed with *P. spumarius* (p<0.01) and between prey types for each spider functional group (p<0.01). The results suggest that *S. globosum* was more efficient capturing spittlebugs one by one than *A. cucurbitina*. On the contrary, *A. cucurbitina* was more efficient killing flies in webs than *S. globosum*.

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5.10 Investigations on dispersal capability of Philaenus spumarius by mark-release-recapture method

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Abstract: Philaenus spumarius is the vector of the CoDiRO strain (subsp. pauca) of X. fastidiosa in the Apulian olive orchards (Saponari et al. 2014). Dispersal capability of the vector is of capital importance to predict future spreading of the pathogen, thus representing a research priority (EFSA 2016). Mark-release-recapture (MRR) is the method of choice to study movement of vector insects, including Homalodisca vitripennis, the main vector of X. fastidiosa in South California (Northfield et al. 2009, Blackmer et al. 2006). Although few information on the flight distance covered by *P. spumarius* are available (Halkka et al. 1971, Putman 1953, Weaver and King 1954), none have been obtained with a scientifically sound experimental plan. An experiment was conducted in Piedmont Region, with 650 adult insects marked by a solution of albumin, and released in a single point in a meadow. Spittlebugs were recaptured by sweeping net in 8 directions radiating from the release point up to 200 m, for a total of 92 collection points. Recaptures were conducted up to 15 days after the release. Marked insects were identified via an indirect ELISA. Twenty marked individuals were found within a maximum distance of 60 m. Two similar experiments were conducted in an olive orchard in the Apulia Region, with a total of 2500 marked insects released. Insects were then collected up to 30 days after, by sweeping net on the canopy of olive trees around the point of release up to 120 m in 170 collection points. Five marked insects were recaptured, with the most distant specimen at 100 m. Studies are ongoing during 2017.

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