first time, to sequence from a vector the seven housekeeping loci that are used for Xf typing in plants.

However, this method is not sensitive enough to i) sequence all loci when the number of bacteria lower than 50 and ii) detect the few plant cells ingested by vectors. Thus, we developed a new approach based on the target enrichment of gene regions through hybrid capture by RNA probes. Probes were designed i) from the 7 loci of the MLST scheme and ii) from ca 30K sequences of rbcL, the most represented marker in international databases to target European plant species.

We recently succeeded in isolating the DNA of *Cistus monspeliensis*, the preferred feeding plant of *P. spumarius* in Corsica, from specimens sampled in the field when pollen was absent. Likewise, we identified *Vitis* and *Quercus* DNA from American vectors sampled in California. We will present the results of a larger experiment still in progress.

Our results show that the capture of Xf genes (and flanking regions) and rbcL from insects is effective, which opens up new avenues for the reconstruction of networks of interaction for vector-borne plant diseases.

Mark-Recapture Experiments to estimate the dispersal capacity of *Philaenus spumarius*

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Abstract: The spread of the vectors is a key point in understanding the epidemiology of *Xylella fastidiosa* and in assessing vector control strategies. In Europe, the transmission of the bacterium is mainly due to spittlebugs. In particular, in the Apulia region (Italy) *Philaenus spumarius* has been proved to play the major role in transmitting *X. fastidiosa* subspecies pauca. Despite its importance, little information is available on the dispersal capacity of *P. spumarius*. To fill this knowledge gap mark-release-recapture experiments on *P. spumarius* adults were carried out in two agroecosystems: an olive grove and in a grass meadow, in the Apulia and the Piedmont regions (Italy), respectively. Dispersal capabilities of the vector were analysed in experiments performed from May to October in 2016 and 2017. Adults of *P. spumarius* of both sexes were captured in natural grassland habitats, marked with an aqueous solution of albumin and then released at a single point in the centre of the experimental area. The dispersal capacity was described estimating the probability density function describing the distribution of the end locations of insects relative to the source point (i.e. the dispersal kernel). Under the hypothesis of a random walk and applying a Gaussian kernel, diffusion rates in the two agroecosystems were estimated. Results showed a high variability in the estimated daily median distance from the release point, ranging from 19 to 51 metres. Considering that marked insects could disperse over an area wider than the experimental field, a correction for the truncated sampling bias has been included into the dispersal kernel, leading to a significant increase in the estimated daily median distances.

Phenology and host-plant association of spittlebugs in Mediterranean olive groves

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