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Symbiont diversity of Myzus persicae complex

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phids are herbivorous insects widely distributed around the world, many species of aphids are agricultural pests causing significant economical loses due to direct damages by feeding and indirect damages by transmitting phytoviruses and contributing to fungus proliferation. Aphids live in association with endosymbiont bacteria classified as obligate or primary endosymbionts (without them the aphid does not survive) and facultative or secondary endosymbionts (the aphid can survive without them, but owning them can modify their ecological and physiological features). Among the most relevant aphid pests the peach-potato aphid, Myzus persicae (Sulzer), is a polyphagous insect able to utilize a wide range of weeds and crops, and possess a subsepecies particularly well adapted to tobacco (Nicotiana tabacum) named Myzus persicae nicotianae. Know the endosymbionts of this aphid is fundamental to understand aspects related to the evolution, ecology and control of this pest; however, the technology required for this was, until recently, insufficient. Here, a metagenomic approach was used to identify all the bacterial species present in this aphids, for which a samples were collected from different hosts, in a north south transect of 1800 km in Chile. After the massive sequencing and bioinformatic analysis, different bacteria were identified, that include some belonging different families, as the Oxalobacteraceae (related to host plants use); Comamonadaceae and Pseudomonadaceae that are plants and human pathogens; Enterobacteriaceae including the obligatory endosymbiont (Buchnera aphidicola) and facultative endosymbionts involved in the defense against natural enemies and other bacteria species that are human pathogens. These results open a new research line aimed at understanding the role of bacteria on evolutionary, ecological and physiological traits of this pest.

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