We are what we eat, so do aphids

Many studies are currently done on the human microbiota, mainly because its relevance to medicine. Characterization of the human and mice microbiota diversity and their responses to stress conditions and association with a range of illnesses are under deep investigation. Diet is one the factors affecting the human's microbiota diversity. In our research, we showed that it is not different for aphids. Host plant impacts the aphid's microbiota diversity, which may impact several of the aphid's bioecological traits. Aphids are well known for their association with endosymbiont bacteria.

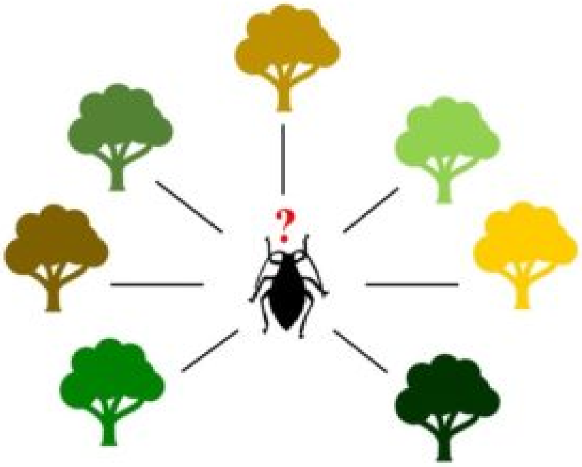

Fig. 1.

Almost all aphids harbor *Buchnera aphidicola* as an obligate symbiont and several other bacteria as facultative symbionts. Associations of facultative symbionts and aphids are quite variable in terms of diversity and prevalence across aphid species. Facultative symbionts can have a major impact on aphid fitness. A number of factors shape the outcome of the facultative symbiont-aphid association, including aphid genotype, bacterial genotype, geography, and host plant association. The effects of host plant on aphid-facultative symbiont associations are the least understood. We sequenced the 16S -V4 region of aphids using Illumina MiSeq platform. Field populations of the oligophagous aphid *Aphis citricidus* were collected from seven different *Citrus* plants based on their chloroplast types, which it is used to define *Citrus* phylogeny. We demonstrated that *A. citricidus* harbors very low symbiont diversity as compared to polyphagous aphids, and that host plant suitability and phylogeny influence the diversity and abundance of primary and secondary symbionts of *A. citricidus.* A comparison of the microbial diversity data we generated with the existing data on *A. citricidus* fitness based on *Citrus* chloroplast type strongly suggests that the microbial community of *A. citricidus* may respond to host plant suitability, with a decrease in the relative abundance of *Buchnera* as host suitability decreases. Curiously, the association with an unclassified *Enterobacteriaceae* determined as Cluster B showed the opposite pattern. Therefore, we suggest that the Cluster B symbiont may play key roles in helping *A. citricidus* to exploit less suitable host plants by complementing the contribution provided by *Buchnera*. Our work is one of the few to focus on oligophagous aphid species, and our data highlight the importance of considering models other than polyphagous, nearctic or palearctic aphid species in investigations of the microbiome diversity and functions.

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