



Diets shape the bacterial communities of three predatory mites in Phytoseiidae*

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Microbial communities can affect host ecology and evolution by host deterministic selection or stochastic processes from diets. Host deterministic selection is generally considered as a strong force in shaping the microbial structures, while host diets basically define the major sources of microbial colonizers. To explore how feeding habits and diet sources respectively affect the deterministic and stochastic processes of host microbial communities, we selected specialized predators of *Tetranychus* mite (*Phytoseiulus persimilis*), selective predators of tetranychid mites (*Neoseiulus californicus*) and generalist predators (*Amblyseius swirskii*; *Neoseiulus barkeri* and *Amblyseius orientalis*) feeding on two types of diets, natural prey (*Tetranychus urticae*) and alternative prey (*Carpoglyphus lactis*) to investigate the bacterial community composition by high-throughput sequencing of the 16S rRNA gene. We found that core microbiota of *P. persimilis* was significantly different from those of three generalist predatory mites even feeding on the same prey of *T. urticae*. Meanwhile, *P. persimilis* and *N. californicus* had similar network structure of microbiota compared with three generalist predatory mites, because more than 65 common operational taxonomic units (OTU) were shared between two strict feeding predatory mites. These results suggested a deterministic process to microbial community by predatory mites with different feeding habits. Additionally, prey change could also modify the microbial composition and network complexity in polyphagous predators, although prey effect on host microbiota was closely related to the predator species. *T. urticae* and *C. lactis* provided 74% and 18% microbes to predator *A. orientalis*, respectively. Conversely, 56% bacteria of *A. swirskii* came from the prey *C. lactis*, while only 10% was passed on by the original *A. swirskii*, suggesting that bacteria changed more rapidly in *A. swirskii*. Additionally, diet change led to significant changes in composition and content of bacterial communities, including variable abundance elevations of major microbes belonging to the orders of Micrococcales, Selenomonadales, Mycobacteriales, Sphingomonadales, Mycobacteriales, Verrucomicrobiales, Rhodospirillales and etc. In short, our results confirmed the expectation that host-imposed selection shaped the microbiota, and highlighted key influence of diets on the stochastic process of host microbiome.

Keywords: microbiota, feeding habit, prey-predator interaction, 16S rRNA sequencing, microbial composition, network complexity