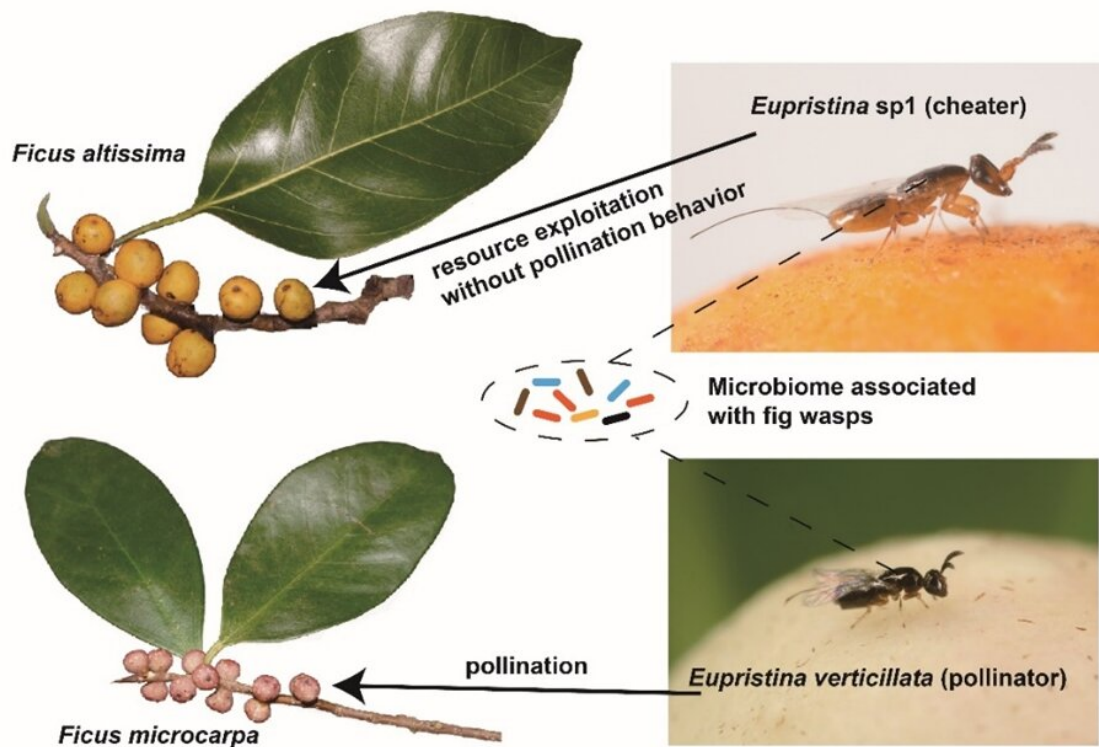


Study provides insights into how microbiome community and metabolic functions may couple with fig-wasp mutualism

November 23 2022, by Zhang Nannan



Figs and fig wasps. Credit: DONG Yiyi

Microorganisms play an important role in regulating plant-herbivore

interactions. However, research has mainly focused on the crops and generalist insects. In the obligate pollinating systems, the cheater visitors are rare, and the role of microorganism in this system remains unknown.

In a study published in *Frontiers in Microbiology*, researchers from the Xishuangbanna Tropical Botanical Garden (XTBG) of the Chinese Academy of Sciences explored the [microbial diversity](#) and potential metabolic functions in fig-wasp mutualism, which is a classic example of coevolution and obligatory pollinator system.

The researchers performed [whole genome](#) resequencing (WGS) on 48 individual fig wasps (*Eupristina* spp.) from Yunnan, China, to reveal the phylogenetic relationship and genetic divergence between pollinator and congeneric cheater wasps associated with the *Ficus* trees.

They then extracted metagenomic sequences to explore the compositions, network structures, and functional capabilities of microbial communities associated with these wasps.

According to the researchers, the cheater and pollinator wasps are highly divergent genetic lineages. And their association microbial groups are extremely diverse, which may play essential roles in maintaining nutrient, health, and speciation of fig wasps.

Besides, fig species dominate over the fig wasp genotype in shaping the microbial communities, which may help cheater to coexist with pollinators in figs.

"Our results provide novel insights into how microbiome community and metabolic functions may couple with the fig-wasp mutualistic systems," said Peng Yanqiong of XTBG.

More information: Yiyi Dong et al, Diversity and metabolic potentials

of microbial communities associated with pollinator and cheater fig wasps in fig-fig wasp mutualism system, *Frontiers in Microbiology* (2022). [DOI: 10.3389/fmicb.2022.1009919](https://doi.org/10.3389/fmicb.2022.1009919)

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