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The Gut Microbiota in Camellia Weevils Are Influenced by Plant Secondary Metabolites and Contribute to Saponin Degradation

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论文题目: The Gut Microbiota in Camellia Weevils Are Influenced by Plant Secondary Metabolites and Contribute to Saponin Degradation

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论文摘要:

The camellia weevil (CW [*Curculio chinensis*]) is a notorious host-specific predator of the seeds of Camellia species in China, causing seed losses of up to 60%. The weevil is capable of overcoming host tree chemical defenses, while the mechanisms of how these beetles contend with the toxic compounds are still unknown. Here, we examined the interaction between the gut microbes of CW and camellia seed chemistry and found that beetle-associated bacterial symbionts mediate tea saponin degradation. We demonstrate that the gut microbial community profile of CW was significantly plant associated, and the gut bacterial community associated with CW feeding on *Camellia oleifera* seeds is enriched with genes involved in tea saponin degradation compared with those feeding on *Camellia sinensis* and *Camellia reticulata* seeds. Twenty-seven bacteria from the genera *Enterobacter*, *Serratia*, *Acinetobacter*, and *Micrococcus* subsisted on tea saponin as a sole source of carbon and nitrogen, and *Acinetobacter* species are identified as being involved in the degradation of tea saponin. Our results provide the first metagenome of gut bacterial communities associated with a specialist insect pest of Camellia trees, and the results are consistent with a potential microbial contribution to the detoxification of tree-defensive chemicals.

论文链接: <https://msystems.asm.org/content/5/2/e00692-19>

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