Beauveria bassiana ERL836 and JEF-007 with similar virulence show different gene expression when infecting western flower thrips, Frankniella occidentalis

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Abstract

Background: Insect-killing fungal species, Beauveria bassiana, is as an environment-friendly pest management tool, and many isolates are on the track of industrialization. However, some of B. bassiana isolates show similar morphology and virulence against insect pests, and so it is hard to differentiate them. Herein we used two patented isolates, ERL836 and JEF-007, and investigated their virulence against western flower thrips, Frankliniella occidentalis, and further analyzed genome structures and transcriptional responses when infecting the thrips to see possible differences.

Results: The two isolates showed no significant differences in fungal growth, conidial production, virulence against thrips, and they were structurally similar in genome. But, in transcription level, ERL836 appeared to infect thrips easily, while JEF-007 appeared to have more difficulty. In the GO analysis of ERL836 DEGs (differentially expressed genes), the number of up-regulated genes was much larger than that of down-regulated genes, when compared to JEF-007 DEGs (more genes down-regulated). Interestingly, in the enrichment analysis using shared DEGs between two infecting isolates, plasma membrane-mediated transporter activity and fatty acid degradation pathway including cytochrome P450 were more active in infecting ERL836.

Conclusion: The two B. bassiana isolates had similar morphology and virulence as well as genome structure, but in transcription level they differently infected western flower thrips. This comparative approach using shared DEG analysis could be easily applied to characterize the difference of the two B. bassiana isolates, JEF-007 and ERL836.

Full-text

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