

Population genomics of the insect biocontrol fungus *Beauveria bassiana*

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ABSTRACT:

Entomopathogenic fungi are one of the key regulators of insect populations in nature. Some species such as *Beauveria bassiana* with a wide host range have been developed as promising alternatives to chemical insecticides for the biocontrol of insect pests. However, the long-term persistence of the released strains, the effect on non-target hosts and local fungal populations remains elusive, but they are considerable concerns with respect to environmental safety. After strain collections and genome re-sequencing, we report the temporal features of the *Beauveria* population genomics and evolution over 20 years after releasing exotic strains to control pine caterpillar pests. We found that the isolates within the biocontrol site were mostly of clonal origins. The released strains could persist in the environment for a long time but with low recovery rates. Similar to the reoccurrence of host jumping by local isolates, the infection of non-target insects by the released strains was evident to endemically occur in association with host seasonality. No obvious dilution effect on local population structure was evident by the releases. However, the population was largely replaced by genetically divergent isolates once per decade but evolved with a pattern of balancing selection and towards expansion through adaptation, non-random outcrossing, and isolate migration. This study not only unveils the real-time features of entomopathogenic fungal population genomics and evolution but also provides added values to alleviate the concerns of environmental safety regarding the biocontrol application of mycoinsecticides.

KEYWORDS:

Population genomics; clonal reproduction; host jumping; population replacement; balancing selection; gene flow; biosafety