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# Characterization of novel microsatellite markers for a dominant parasitoid

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## ABOUT THE STUDY

Biological pest control is an important pest control strategy in agriculture, as more information is avail-able and less tolerated by the general public about the use of pesticides that can harm humans and the environment. In the tea plantation, the leafhopper Em-poasca onukii is the main pest, losing 15-50% of the annual yield. Currently E. Onukii's control strategies are primarily based on the use of synthetic pesticides, and efficient biological control strategies are still lack-ing. Field research has shown that *Stethynium em-poasca*, the only egg-parasitoid wasp, is E's most common natural enemy. A high parasitism rate (up to 30%). As a parasitoid of eggs, S. Unlike most larval parasitoids, which normally keep their hosts alive to prolong nutrient uptake, *empoasca* tends to provide more effective biological control as it can immediately prevent further herbivores. Therefore, *S. empoasca* is the most promising candidate for supplemental bio-control and may also be the subject of conservative biocontrol. However, little is currently known about its biology, ecology, and genetics. Knowledge of the bio-logical characteristics, ecological preferences, genet-ic variation, and gene flow of parasitoid populations enhances acceptance and success as biological con-trol agents and is an effective habitat for parasitoid protection. Needed to facilitate the development of management strategies.

The lack of research on S. empoasca may be due primarily to the fact that it is small and traditional ob-servation methods can face challenges when studying such small parasites. Alternatively, molecular mark-ers can detect trace amounts of parasitoid DNA. In-deed, molecular marker-based techniques have been widely used to assess the genetic diversity and phy-logenetic relationships of natural enemy populations, including ecological studies on small parasites (eg, population dynamics and distribution). It is increasingly recognized as a valuable tool to promote. Among the available markers, microsatellites are widely used for a variety of desirable properties, such as high muta-genesis, polymorphisms, codominant inheritance, and genome-wide distribution, and are highly reproducible when used in analysis.

The traditional approach to microsatellite development with enhanced libraries is time consuming and labor in-tensive. Therefore, a high-throughput sequence-based approach can be a good alternative. The advantage of this technology is that it streamlines the development of new microsatellite markers and, most importantly, enables the study and characterization of microsatel-lites at the genome-wide level.

Linkage disequilibrium between each pair of loci in each population and Hardy-Weinberg equilibrium in each locus in each population were tested with GE-NEPOP 4.7.0. The null allele frequency was estimat-ed for each locus within each population using Free-NA's expected value maximization algorithm with 1000 bootstrap replications. The genetic diversity index of the population, such as the total number of alleles and expected unbiased heterozygotes, was estimated at GENCLONE 2.0, and the observed heterozygotes and polymorphisms (PIC) are macro microsatellites. Con-sidering the effect of sample size on diversity statistics, the standardized number of conflicts for the minimum sample size of the nine diploid individuals of GEN-CLONE was calculated using a dilution approach. Al-lele abundance and private allele abundance were also calculated from the minimum sample size of nine dip-loid individuals using the HPRARE 1.1 dilution method.