Special Issue

Population Genetics of Honeybees

Message from the Guest Editor

Honeybee is an important bioresource and model organism for eusociality. With the recent development of genome sequencing technology, the use of large-scale genetic information is becoming the mainstream of diversity studies. Approaches using mitochondrial genomes are increasing, and this leads to reexaminations of phylogenetic classification at the inter-specific level. In intra-specific level analyses, whole-genome SNPs provide insight into population history and adaptation mechanisms mainly in the western honeybee (*A. mellifera*) and eastern honeybee (*A. cerana*). Honeybee has wide-range distributions on a global scale, and the knowledge of local populations is essential for the development of the related research fields. Especially, research on the honeybee from Asian countries is lacking compared to that of the western honeybee, *A. mellifera*. We hence welcome submissions of articles focusing on the population genetics of honeybee species from Asia using complete mitochondrial genome sequences, whole-genome SNPs (e.g., RAD, MIG-seq or Re-seq), and multiplex microsatellite markers (more than eight locus).

Guest Editor

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