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### Abstract

Molecular tools such as polymerase chain reaction (PCR)-based techniques have been widely used to analyze the genetic diversity of many social insects. Since their society has a very complicated and hierarchical structure, honeybees (*Apis*) will become a good model to study the evolution of social insects. In this report, we demonstrated a simple PCR-restriction fragment length polymorphism (PCR-RFLP) to distinguish different *Apis* species. In brief, mitochondrial DNA (mtDNA) was separately isolated from workers of five major honeybee species, *Apis mellifera* (Western honeybee), *A. cerana* (Eastern honeybee), *A. dorsata* (Giant honeybee), *A. laboriosa* (Himalayan giant honeybee), and *A. florea* (Dwarf honeybee), obtained from different geographical regions. Western and Eastern honeybees, *A. dorsata* and *A. laboriosa*, and *A. florea* were collected from Japan, Nepal, and India, respectively. The PCR technique was performed to amplify a 528-bp DNA fragment of the NADH dehydrogenase subunit 4 (ND4 according to *A. mellifera*'s mtDNA sequence). Following digestion of the individual PCR products with two restriction endonucleases, *Nde*I and *Mbo*I, the digested DNA fragments were separated with agarose gel electrophoresis, stained with ethidium bromide, and visualized over UV light. The results clearly indicated that this PCR-RFLP procedure was simple but sensitive and reproducible for the identification of the genetic variability among *Apis* species. Therefore, this procedure will be useful to confirm other techniques for the identification of honeybees.

Keywords: *Apis*, mtDNA, PCR-RFLP