

Development of Microsatellite Markers for Genetic Variation Analysis in House Cricket, *Acheta domesticus*

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Abstract : The house cricket, *Acheta domesticus* is one of the commonly found species of field crickets. Although it is very commonly used as food and feed, the genomic information of house cricket is still missing for genetic investigation. DNA sequencing technology has evolved over the decades, and it has also revolutionized the molecular marker development for genetic analysis. In the present study, we have sequenced the whole genome of *A. domesticus* using illumina platform based HiSeq X Ten sequencing technology for searching simple sequence repeats (SSRs) in DNA to develop polymorphic microsatellite markers for population genetic analysis. A total of 112,157 SSRs with primer pairs were identified, 91 randomly selected SSRs used to check DNA amplification, of which nine primers were polymorphic. These microsatellite markers have shown cross-amplification with other three species of crickets which are *Gryllus bimaculatus*, *Gryllus testaceus* and *Brachytrupes portentosus*. These nine polymorphic microsatellite markers were used to check genetic variation for forty-five individuals of *A. domesticus*, Phitsanulok population, Thailand. For nine loci, the number of alleles was ranging from 5 to 15. The observed heterozygosity was ranged from 0.4091 to 0.7556. These microsatellite markers will facilitate population genetic analysis for future studies of *A. domesticus* populations. Moreover, the transferability of these SSR makers would also enable researchers to conduct genetic studies for other closely related species.

Keywords : cross-amplification, microsatellite markers, observed heterozygosity, population genetic, simple sequence repeats

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