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GENETIC DIVERSITY OF COMMERCIAL CHICKENS CONSUMED IN SELANGOR, MALAYSIA

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ABSTRACT

Chickens represent the most widely consumed meat in the world. Modern breeds are generally from a narrow genetic base. The genetic diversity of chickens consumed in urban areas of Malaysia has not been previously investigated. The aim of this study was to investigate the genetic diversity of chickens available for purchase in urban areas of Selangor adjacent to Kuala
Lumpur. DNA of chickens were isolated from meats and livers. Seven microsatellite markers were selected and fluorescently labeled to allow the identification of each individual chicken from the seventeen populations based on the amplification of target DNA. A total of 52 different alleles was observed for the seven markers, giving a mean of 7.1 alleles per marker. The

cumulative power of discrimination (CPd) of the seven microsatellites used was 0.999 based upon our population study. The data showed that most of the chickens consumed in the urban areas came from a very narrow genetic base. The supply is thus vulnerable to disruption caused by outbreaks of disease. Furthermore the data obtained illustrates the potential of this system to be used in chicken lineage identification. This would help to resolve uncertainties over the origin of the chickens. This system could be used for product assurance as well as safety.

Key words: Simple Tandem Repeats (STR), Halal assurance, Genotyping, Microsatellite, Individual identification