



Development of novel DNA markers for genetic analysis of grey hamsters by cross-species amplification of microsatellites

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ABSTRACT. The grey hamster has been used in biomedical research for decades. However, effective molecular methods for evaluating the genetic structure of this species are lacking, which hinders its wider usage. In this study, we employed cross-amplification of microsatellite loci of species within the same genus by polymerase chain reaction. Loci screened included 107 from the Mongolian gerbil (MG) and 60 from the Chinese hamster (CH); of these, 15 polymorphic loci were identified for the grey hamster. Of the 167 loci screened, 95 (56.9%) with clear bands on agarose gel were initially identified. After sequencing, 74 (77.9%) of these matched the criteria for microsatellite characteristics, including 41 from MG and 33 from CH. Lastly, 15 (20.3%) loci with more than two alleles for each locus were identified through capillary electrophoresis scanning. To justify the applicability of the 15 grey hamster loci, genetic indexes of grey hamsters were evaluated using 46 generations of outbred stock, established 20 years ago, from Xinjiang, China. Mean effective allele numbers and expected heterozygosity of stock were as low as, respectively, 1.2 and 0.14; these were 2.8 and 4.0 times inferior, respectively,

to wild grey hamsters. This finding suggests that the genetic structure of the stock-bred population is too weak to resist artificial and natural selection, mutation and genetic drifting. In conclusion, we have developed *de novo* microsatellite markers for genetic analysis of the grey hamster, providing data and methodology for the enrichment of a genetic library for this species.

Key words: Genetic structure; Microsatellite DNA; Grey hamster; Cross-species amplification; Biomarker