



Isolation and characterization of 16 novel microsatellite loci in two inbred strains of the Chinese hamster (*Cricetulus griseus*)

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ABSTRACT. The Shanyi inbred A and E strains of the Chinese hamster are widely used in biomedical research, but detailed genetic characterization has been lacking. We developed microsatellite markers that could be used for genetic diversity analysis and linkage map construction. We isolated and characterized 16 novel microsatellite loci from a microsatellite-enriched genomic DNA library. These loci were genotyped in 48 animals from the two strains, and the polymorphic information content was determined. In the Shanyi A and E populations, 14 and 15 loci were found to be polymorphic, respectively, with polymorphic information content ranging from 0.1393 to 0.8082 and from 0.1109 to 0.7397, respectively. A total of 115 alleles were found for the 16 microsatellite loci in the two populations; the mean observed heterozygosity (H_o) was 0.5191 and 0.4333 for the A and E populations, respectively, indicating marked genetic variation within the two populations. Correspondingly, the F_{ST} values ranged from 0.002 to 0.9253, with an overall mean of 0.1935, indicating significant genetic

difference between the two strains. The population differentiation levels were substantiated by Nei's genetic distance and full Bayesian analyses computed with STRUCTURE. Despite the genetic diversity and differentiation within and between the two inbred populations, the 48 individuals were correctly allocated into their original populations with high statistical confidence based on these 16 microsatellite loci. These novel microsatellite loci should be useful genetic markers for these two Chinese hamster inbred strains.

Key words: Chinese hamster; Enriched library; Microsatellite marker; Genetic differentiation