Selected representative microsatellite loci for genetic monitoring and population structure analysis of miniature swine

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ABSTRACT. To optimize the combination of microsatellite loci for genetic control of outbred swine stocks, 32 of 100 loci distributed among almost all chromosomes (except 12) were screened out by 1.5% agarose, 8% polyacrylamide gel and capillary electrophoresis scanning among 3 miniature swine outbred stocks, namely Bama (BM), Guizhou (GZ) and Tibeta (TB). The mean total and effective allele numbers among these stocks were 12.1 and 5.9, respectively. The mean heterozygosity for these breeds was 0.5428, 0.6978 and 0.7646, and polymorphism information content was 0.5469, 0.7296 and 0.7663, respectively. Accordingly, hereditary variation from low to high was BM < GZ < TB. This showed that the genetic relationship between BM and GZ pigs was closer, and both were distant from TB. Additionally, the effectiveness of the 32-locus combination for evaluation of genetic quality was demonstrated in Changchun-junmo-1 (CJ-1), a standard

outbred Chinese pig stock, in which the mean total and effective allele numbers and mean heterozygosity were 6.1613, 3.8483 and 0.6903, respectively. Since our results were consistent with the breeding pedigrees, the 32 loci could be used for both genetic monitoring within the individual outbred miniature swine stocks and population structure analysis between them.

Key words: Genetic monitor; Microsatellite DNA; Miniature swine; Population genetic structure