



## Selecting representative microsatellite loci for genetic monitoring and analyzing genetic structure of an outbred population of orange tabby cats in China

X.Y. Du<sup>1\*</sup>, S. Yi<sup>2\*</sup>, X.Y. Huo<sup>1</sup>, C. Wang<sup>1</sup>, D.F. Liu<sup>2</sup>, W.Z. Ren<sup>2</sup> and Z.W. Chen<sup>1</sup>

<sup>1</sup>Department of Laboratory Animal Science, Capital Medical University, Beijing, China

<sup>2</sup>Laboratory Animal Center, Jilin University, Changchun, China

\*These authors contributed equally to this study.

Corresponding authors: Z.W. Chen / D.F. Liu

E-mail: czwen@ccmu.edu.cn / ccldf@163.com

Genet. Mol. Res. 14 (1): 1788-1797 (2015)

Received February 27, 2014

Accepted August 27, 2014

Published March 13, 2015

DOI <http://dx.doi.org/10.4238/2015.March.13.6>

**ABSTRACT.** We optimized a panel of microsatellite markers from cat and tiger genetic data for efficient genetic monitoring and used it to analyze the genetic structure of an outbred cat stock in China. We selected a set of rich polymorphic microsatellite loci from 131 cat microsatellite loci and 3 Sumatran tiger microsatellite loci using agarose gel electrophoresis. Next, the set of optimized genetic markers was used to analyze the genetic variation in an outbred population of orange tabby cats in China by simple-tandem repeat scanning. Thirty-one loci rich in polymorphisms were selected and the highest allele number in a single locus was 8. Analysis of the orange tabby cat population illustrated that the average observed number of alleles, mean effective allele number, mean Shannon's information index, mean expected heterozygosity, and observed heterozygosity were 3.8387,

2.4027, 0.9787, 0.5565, and 0.5528, respectively. The 31 microsatellite markers used were polymorphic and suitable for analyzing the genetic structure of cats. The population of orange tabby cats was confirmed to be a well-outbred stock.

**Key words:** Domestic cat; Genetic structure; Microsatellite, Orange tabby cats