



Genetic diversity of the Arctic fox using SRAP markers

M. Zhang¹ and X.J. Bai²

¹College of Animal Husbandry and Veterinary Medicine,
Liaoning Medical University, Jinzhou, China

²College of Animal Science and Technology, Northeast Agricultural University,
Harbin, China

Corresponding author: M. Zhang
E-mail: zhangmin5266@163.com

Genet. Mol. Res. 12 (4): 6176-6183 (2013)

Received October 29, 2012

Accepted April 10, 2013

Published December 4, 2013

DOI <http://dx.doi.org/10.4238/2013.December.4.4>

ABSTRACT. Sequence-related amplified polymorphism (SRAP) is a recently developed molecular marker technique that is stable, simple, reliable, and achieves moderate to high numbers of codominant markers. This study is the first to apply SRAP markers in a mammal, namely the Arctic fox. In order to investigate the genetic diversity of the Arctic fox and to provide a reference for use of its germplasm, we analyzed 7 populations of Arctic fox by SRAP. The genetic similarity coefficient, genetic distance, proportion of polymorphic loci, total genetic diversity (Ht), genetic diversity within populations (Hs), and genetic differentiation (Gst) were calculated using the Popgene software package. The results indicated abundant genetic diversity among the different populations of Arctic fox studied in China. The genetic similarity coefficient ranged from 0.1694 to 0.0417, genetic distance ranged from 0.8442 to 0.9592, and the proportion of polymorphic loci was smallest in the TS group. Genetic diversity ranged from 0.2535 to 0.3791, Ht was 0.3770, Hs was 0.3158, Gst was 0.1624, and gene flow (Nm) was estimated at 2.5790. Thus, a high level of genetic diversity and many genetic relationships were found in the populations of Arctic fox evaluated in this study.

Key words: Arctic fox; SRAP marker; Genetic diversity; Germplasm