Accepted Manuscript

Title: Evaluation of the genetic diversity and population structure of *Gasterophilus pecorum* in Xinjiang Province, China, using fluorescent microsatellites (SSR) markers

Authors: Liu Shan-Hui, Cheng Fang, Fan XiaoZe, Li Kai, Hu DeFu, Ma YuHui, Li Hai, Bayinchahan Gailike

PII: S0304-4017(18)30294-2
DOI: https://doi.org/10.1016/j.vetpar.2018.08.005
Reference: VETPAR 8730

To appear in: *Veterinary Parasitology*

Received date: 10-4-2018
Revised date: 5-8-2018
Accepted date: 8-8-2018

Please cite this article as: Liu S-Hui, Cheng F, Fan X, Li K, Hu D, Ma Y, Li H, Bayinchahan G, Evaluation of the genetic diversity and population structure of *Gasterophilus pecorum* in Xinjiang Province, China, using fluorescent microsatellites (SSR) markers, *Veterinary Parasitology* (2018), https://doi.org/10.1016/j.vetpar.2018.08.005

Evaluation of the genetic diversity and population structure of *Gasterophilus pecorum* in Xinjiang Province, China, using fluorescent microsatellites (SSR) markers

Liu Shan-Hui[a,b,c]┼ , Cheng Fang[a]┼, Fan XiaoZe[d], Li Kai[a*], Hu DeFu[a], Ma YuHui[e], Li Hai[f], Bayinchahan Gailike[b]*

a. Beijing Forestry University, Institute of Nature Reserve，Beijing 100083，China.

b. Xinjiang Agricultural University, Institute of Animal Medicine，Urumqi 830052, China.

c. Beijing Language and Culture University, Office of Educational Administration，Beijing 100083，China.

d. Chinese Association of Zoological Gardens, Beijing 100037，China.

e. College of Veterinary Medicine, Northeast Agricultural, Heilongjiang, Harbin,150030,China.

f. Animal Husbandry and Veterinary Station of Zhaosu , Xinjiang, Zhaosu, 835600,China.

┼These authors contributed equally to this study.

*Corresponding author: Kai Li, Email: liuhuidaofeng@163.com and Likai_sino@sina.com.

Bayinchahan Gailike, Email: 2514062881@qq.com

Highlights

- The genetic variation was mainly distributed within the *G. pecorum* populations.
- The narrow range of *G. pecorum* may be not the main reason for its rarity.
- The *G. pecorum* possess higher genetic diversity and frequent gene exchange.

Abstract: The genetic diversity of *Gasterophilus pecorum* populations consisting of 192 individuals sampled from Przewalski’s horses (*Equus ferus przewalskii*) in Xinjiang Province, China, was evaluated using 12 microsatellite loci. The genetic variability within populations and genetic differentiation among populations were estimated. A total of 163 alleles were detected and the average value of observed number of alleles at each locus ranged from 7 to 19 (average 13.5625). The expected heterozygosity (He) varied from 0.5933 (GP361) to 0.9208 (GP253) and averaged 0.8426. The effective number of alleles (Ne) of the simple sequence repeat (SSR) markers was 7.1756, and it ranged from 2.4430 to 11.5214. The polymorphism information content (PIC) ranged from 0.5643 (GP361) to 0.9053