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

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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 (H_e) varied from 0.5933 (GP361) to 0.9208 (GP253) and averaged 0.8426. The effective number of alleles (N_e) 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

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