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IDENTIFICATION OF MICROSATELLITES AND PARENTAGE TESTING DEVELOPMENT OF BACTRIAN CAMEL (*Camelus bactrianus*)

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ABSTRACT

This report is aimed to identify polymorphic microsatellites from Bactrian camel transcriptome sequences and apply microsatellite multiplex systems for parentage testing. 1,820 simple sequence repeats (SSRs) were identified from 23,624 transcriptome sequences, representing an average density of SSR/26.57 kb. The most abundant SSR, the trinucleotide repeat motif, accounts for 30% of all SSRs. Tetra-, penta-, di- and hexanucleotide repeats account for 29%, 22%, 17% and 2% of SSRs, respectively. Based on sequence redundancy and PCR amplification, we selected 14 polymorphic microsatellites for Bactrian camel parentage testing analysis in a population of 117 unrelated camels from China and Mongolia. We identified a total of 149 alleles, with 5-23 alleles per locus (10.64 ± 5.472) and an average heterozygosity (HE) of 0.676 (range: 0.380-0.888). Based on only the genotype of the offspring, a parentage exclusion probability of 0.9999 was calculated when excluding a candidate parent from parentage of an arbitrary offspring. When excluding a candidate parent from parentage of an arbitrary offspring and based on both the genotype of the offspring and the other parent, an exclusion probability of 0.9999 was calculated. We selected 15 baby camels, 20 sires and 20 dams for parentage testing. According to the parentage assignment, the microsatellite panel assigned all 15 offspring with high confidence. This core set of 14 microsatellites represent a powerful and efficient method for determining parentage in domestic Bactrian camels.

Key words: Multiplex, parentage exclusion probability genotyping, simple sequence repeats