



## Short Communication

# Correlation Analysis Between Microsatellite Marker Polymorphism and Wool Fineness of Sunite Bactrian Camel (*Camelus bactrianus*)

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## ABSTRACT

In this study, the correlation between microsatellite marker polymorphism and wool fineness of sunite bactrian camel was analyzed. The results show that, the average effective allele number, heterozygosity and polymorphism information content of 17 microsatellite markers in sunite bactrian camel were 2.8913, 0.6205 and 0.5602, respectively. The wool fineness of AB genotype of CMS36 locus was significantly higher than that of BB genotype ( $P<0.05$ ). The wool fineness of AC genotype at YWLL44 locus was significantly higher than that of BD, BE and CE genotype ( $P<0.05$ ). The wool fineness of AA and BC genotype at YWLL 29 locus was significantly higher than that of AC genotype ( $P<0.05$ ). The wool fineness of AB genotype at LCA33 locus was significantly higher than that of AC, AD and BC genotype ( $P<0.05$ ). Therefore, CMS36, YWLL 44, YWLL 29 and LCA33 microsatellite markers can be used in marker assisted selection of wool fineness of sunite bactrian camel.

### Article Information

Received 20 March 2020

Revised 18 April 2020

Accepted 23 April 2020

Available online 15 October 2021

### Authors' Contribution

JB conceived and designed the study and conducted the lab work. RW analyzed the data and wrote the article. LD helped in sampling. XT and QH helped in analysis of data.

### Key words

Sunite bactrian camel, Microsatellite markers, Wool fineness, Correlation analysis, Polymorphism information content

Microsatellite markers have been extensively applied to genetic diversity studies of cow (Ni *et al.*, 2018), sheep (Bai *et al.*, 2015) and poultry (Bai *et al.*, 2016a, b, c, 2017) by virtue of high abundance, good repeatability, co-dominance marker and selective neutrality, it is also widely used in plant genetic diversity research (Guo *et al.*, 2018; Yang *et al.*, 2013). In recent years, domestic and foreign researches regarding genetic diversity and organization structure (Ye *et al.*, 2014a, b; Wang *et al.*, 2016) of bactrian camels have achieved progress. For the epidemiological study of mastitis in camel and the serological detection of neosporia has also made some progress. Genetic diversity of microsatellite markers in the sunite bactrian camel population was analyzed in this study, association analysis of these microsatellite markers with wool fineness was conducted, protection and rational utilization of sunite bactrian camel.

### Materials and methods

Random collection of 40 sunite bactrian camels, blood was taken from jugular vein (10ml from each Bactrian

camel), ACD anticoagulant was added for anticoagulation, blood DNA was extracted using the whole-blood genomic DNA extraction kit method from Beijing Dingguo Changsheng. Seventeen microsatellite markers with high polymorphism were screened (Evdotchenko *et al.*, 2003; Sushma *et al.*, 2014), The primers were synthesized by Shanghai Shengong Bioengineering Technology Service Co., Ltd.

Pre-denaturation at 94 for 4 min, then denaturation at 94 for 40 s, annealing at 60 for 1 min, annealing at 72 for 20 seconds, denaturation, annealing and elongation were carried out for 35 cycles, then elongation at 72 and finally the reaction was completed and cooled and preserved at 4°C. 15% non denaturing polyacrylamide gels were used to detect the products, silver nitrate dyeing method is used for dyeing, mainly through fixation, oxidation, dyeing, color rendering, photography and other links. SPSS software was used to analyze the relationship between the wool fineness and microsatellite of sunite bactrian camel.

### Results and discussion

It can be seen from Table I. That the number of effective alleles, heterozygosity and polymorphism information content of CVRL101 locus are the highest, which are 4.5262, 0.7464 and 0.7437, respectively. The number of effective alleles, heterozygosity and polymorphism

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0030-9923/2021/0006-2459 \$ 9.00/0

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**Table I. Population genetic diversity of microsatellite markers in sunite bactrian camel.**

Locus	Number of effective alleles	Heterozygosity	Polymorphism information content	Locus	Number of effective alleles	Heterozygosity	Polymorphism information content
LCA33	2.3038	0.5356	0.5111	CMS36	1.9406	0.3795	0.3672
LCA37	2.0997	0.5248	0.4103	CMS104	2.4042	0.5728	0.5000
LCA63	2.9712	0.6756	0.6004	CVRL101	4.5262	0.7464	0.7437
LCA66	3.5635	0.7330	0.6680	YWLL29	1.9913	0.4025	0.4410
LCA71	2.2551	0.5727	0.4566	YWLL36	2.2099	0.5993	0.4446
LCA82	2.4390	0.6045	0.5039	YWLL44	3.2258	0.6963	0.6373
LCA90	3.7209	0.7270	0.6823	VOLP08	3.9604	0.7413	0.7003
CMS15	2.9144	0.6782	0.5938	VOLP32	3.9120	0.7298	0.6968
CMS18	2.7142	0.6292	0.5664	Mean value	2.8913	0.6205	0.5602

information content of CMS36 locus were the lowest, which were 1.9406, 0.3795 and 0.3672, respectively. The average effective allele number, heterozygosity and polymorphism information content of 17 microsatellite markers in sunite bactrian camel were 2.8913, 0.6205 and 0.5602, respectively.

The study carried out by Gao *et al.* (2009) showed that the average polymorphic information content value of microsatellite markers detected in hundreds of Bactrian camels from 13 areas of China and Mongolia was 0.5414. Tian *et al.* (2012) studied the genetic diversity of Bactrian camels from 6 places of Xinjiang by microsatellite markers, and showed that all of the used microsatellite markers presented high polymorphism, with polymorphic information content values ranging from 0.6099 to 0.6551. So the polymorphic level (PIC=0.5602) of microsatellite markers in this study was moderate, intermediate between Gao *et al.* (2009) and Tian *et al.* (2012).

The correlation between microsatellite marker polymorphism and villus fineness of sunite bactrian camel is shown in Figure 1. The wool fineness of AB genotype of CMS36 locus was significantly higher than that of BB genotype ( $P<0.05$ ). The wool fineness of AC genotype at YWLL44 locus was significantly higher than that of BD, BE and CE genotype ( $P<0.05$ ). The wool fineness of AA and BC genotype at YWLL 29 locus was significantly higher than that of AC genotype ( $P<0.05$ ). The wool fineness of AB genotype at LCA33 locus was significantly higher than that of AC, AD and BC genotype ( $P<0.05$ ). Wu *et al.* (2018) showed that the marker YWLL 29 of bactrian camel in Alxa Desert was related to body height, body length, chest circumference, tube circumference and body weight; the marker LCA33 was related to body height, chest circumference, body weight and body length; the marker CVRL101 was related to body length, body weight and chest circumference. Gu (2013) showed that

microsatellite markers BM1824, BM6506 and LSCV15 were significantly correlated with cashmere fineness. In conclusion, only CMS36, YWLL 44, YWLL 29 and LCA33 had significant correlation with wool fineness of sunite bactrian camel ( $P<0.05$ ), while the other 13 microsatellite loci had no significant correlation with wool fineness, therefore CMS36, YWLL 44, YWLL 29 and LCA33 microsatellite markers can be used in marker assisted selection of wool fineness of sunite bactrian camel.

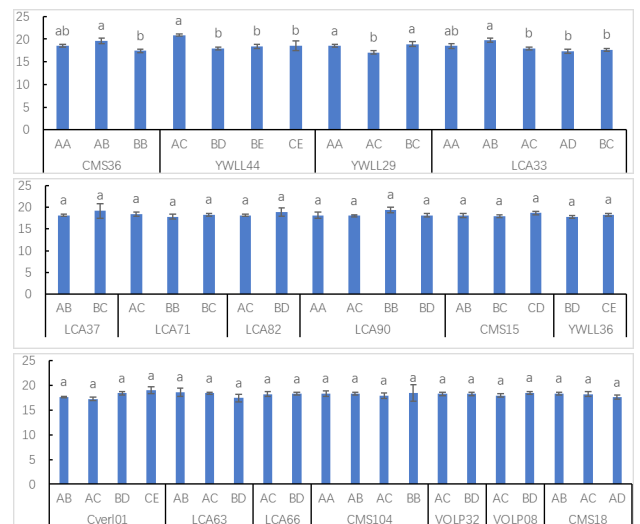


Fig. 1. Correlation between microsatellite markers and wool fineness of sunite bactrian camel.

*Acknowledgements*

Sincere gratitude goes to the sponsor of Alxa League Science and Technology Project in Inner Mongolia (2012-12).

*Statement of conflict of interest*

The authors have declared no conflict of interest.

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