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# GENETIC DIVERSITY AND RELATIONSHIP OF DOMESTIC BACTRIAN CAMELS (*Camelus bactrianus*) IN CHINA AND MONGOLIA

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## ABSTRACT

The number of domestic Bactrian camels has been decreasing rapidly in recent years in Central Asia, whereas very little is known about their genetic diversity and relationship. Most of these animals are found today in China and Mongolia. Here, we used 12 microsatellite DNA markers to characterise 140 domestic Bactrian camels from 4 populations of China (n = 84) and 2 populations of Mongolia (n = 56). Genetic diversity, expressed as mean number of alleles and expected heterozygosity (He), were similar in all populations. Genetic distances ($D_S$ and $D_A$) indicate closer genetic relationships between populations within each country than between the Chinese and Mongolian populations. Significant differentiation indices (Fst) were obtained for all between-country comparisons ($P < 0.01$). However, within countries the Fst value between the two Mongolian populations and between four of the six pair-wise comparisons between Chinese populations were not significant ($P > 0.05$). The lack of genetic differentiation among the Chinese populations is possibly a historical legacy of trading along the Silk Road which favoured gene flow between populations. For Mongolia, it is possibly the result of interbreeding between populations following transhumance. Our results indicate that the domestic Bactrian camels from China and Mongolia should be considered as distinct populations in conservation and breeding programs.

**Key words :** Domestic bactrian camel, genetic diversity and relationship, microsatellite DNA marker

Domestic bactrian camels are found in the desert steppes of Central Asian countries, including Afghanistan, India, Iran, Kazakhstan, Kyrgyzstan and Pakistan, where their distributions overlap to some extent with dromedary camels, and in southern Russia, western parts of China and Mongolia (Jianlin, 2000). The development of a special subsistence-based economic system in the vast desert steppe areas of these countries would not have been possible without the Bactrian camels (Xueshi, 1990). Moreover, the camels played an essential role in providing transport for the ancient Silk Road trade between China and Europe (Olsen, 1988) and still play an important role as a beast of burden and as a riding animal in the desert steppes of Central Asia, although it has lost its dominant status since World War II (Lenscht, 1996). A rapid and dramatic reduction of number of the domestic Bactrian camels in China, from 475,000 in 1990 down to 279,000 in 2002, and in Mongolia, from 558,300 in 1990 to 352,000 in 2002, has been observed (FAO, 2002). The Bactrian camels are losing as draught and packing animals and several populations are now endangered. Eleven breeds of domestic Bactrian camels have been included into the FAO DAD-IS database (http://www.fao.org/dad-is/). There is, however, no genetic information about their genetic relationship and differentiation. The aim of this study was to carry out genetic characterisation of 140 domestic Bactrian camels from a total of six populations from China and Mongolia using microsatellite DNA markers.

## Materials and Methods

### Samples

Eighty-four samples of Chinese domestic Bactrian camels from Anxi and Wuwei counties of Gansu province, Balikun county in Xinjiang province and Alashan You county in Inner Mongolia province were collected (Table 1). Fifty-six Mongolian Bactrian camels from South Govi and Govi Altay provinces were also sampled. Additionally, a population of 32 Pakistani dromedary camels, sampled in Kenya.

**DNA extraction :** DNAs were extracted from blood as described previously by Mburu *et al* (2003).

**Primers and genotyping :** Twelve microsatellite markers isolated and characterised previously in Old

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**Table 1.** Observed (Ho), expected heterozygosities (He) across the 12 loci and mean number of alleles (MNA) per locus for the six domestic Bactrian camel populations.

| Populations | Country | No. | *Ho* ± SD | *He* ± SD | MNA ± SD all animals | MNA ± SD[1] 14 animals |
|---|---|---|---|---|---|---|
| Govi Altay | Mongolia | 17 | 0.453 ± 0.037 | 0.526 ± 0.038 | 3.58 ± 1.44 | 3.43 ± 1.38 |
| South Govi | Mongolia | 39 | 0.521 ± 0.024 | 0.545 ± 0.045 | 4.58 ± 2.23 | 3.75 ± 1.55 |
| Wuwei | China | 25 | 0.526 ± 0.029 | 0.561. ± 0.061 | 4.33 ± 1.61 | 3.89 ± 1.54 |
| Balikun | China | 16 | 0.595 ± 0.036 | 0.547 ± 0.058 | 4.25 ± 1.91 | 4.12 ± 1.83 |
| Anxi | China | 14 | 0.494 ± 0.039 | 0.577 ± 0.049 | 3.67 ± 1.23 | 3.67 ± 1.23 |
| Alashan You | China | 29 | 0.541 ± 0.027 | 0.602 ± 0.045 | 4.75 ± 2.34 | 4.05 ± 1.68 |

[1] Mean value after 250 resampling.

**Table 2.** Nei's $D_A$ (Nei *et al*, 1983) genetic distances (below the diagonal) and Fst values (above the diagonal) between populations.

| Populations | Govi Altay | South Govi | Wuwei | Balikun | Anxi | Alashan You |
|---|---|---|---|---|---|---|
| Govi Altay | | $0.029^{NS}$ | 0.048** | 0.067** | 0.057** | 0.037** |
| South Govi | 0.064 | | 0.052** | 0.057** | 0.039** | 0.032** |
| Wuwei | 0.120 | 0.103 | | $0.003^{NS}$ | $0.011^{NS}$ | 0.006** |
| Balikun | 0.137 | 0.120 | 0.055 | | $0.022^{NS}$ | 0.033** |
| Anxi | 0.133 | 0.100 | 0.059 | 0.073 | | $0.012^{NS}$ |
| Alashan You | 0.116 | 0.084 | 0.058 | 0.091 | 0.068 | |

Note : NS - Non significant (P > 0.05) and ** - significant at p < 0.01.

World Camelidae (*CVRL*2, 5, 6 and 7) (Mariasegaram *et al*, 2002) and in New World Camelidae (*LCA*66; VOLP-08, 10, and 32; *YWLL*08, 29, 38 and 44) (Jianlin *et al*, 2000) were used. PCR conditions and data collection procedures are provided (Jianlin *et al*, 2000).

**Data analysis :** Hardy-Weinberg (HW) and linkage equilibrium expectations were tested using GENEPOP 3.3 (Raymond and Rousset, 1995). Observed (*Ho*) and expected (*He*) heterozygosity values and mean number of alleles (MNA) across the 12 loci for the six populations were calculated with MICROSATELLITE TOOLKIT (Park, 2001) (Table 1). An adjusted MNA estimate based on sample size was carried out using 250 replicates of resampling of 14 individuals with replacement for all populations (Mburu *et al*, 2003) but the Anxi population, which had only 14 individuals.

**Genetic distance and phylogenetic reconstruction:** Nei's $D_S$ (Nei, 1972) and $D_A$ (Nei *et al*, 1983) genetic distances between pairs of populations were calculated using the program DISPAN (Ota, 1993) (Table 2). Pairwise tests of differentiation among the six popu-lations were examined using the program FSTAT 2.9.3 (Goudet, 2001). HW equilibrium within population was not assumed and *P*-values were obtained after 15,000 permutations.

## Results and Discussion

A total of 80 different alleles were identified. Allele number per locus ranges from three (YWLL29 and CVRL7) to 14 (VOLP-08). Only a few locus-population combinations gave P-values (P < 0.05) indicating deviation HW expectations and there is no global deviation of one locus in all populations. No linkage disequilibrium for the same pair of loci across all six populations was observed.

**Genetic diversity :** The Balikun Bactrian camel population has the highest genetic diversity among all the six populations studied with observed and expected heterozygosities of 0.595 and 0.547, respectively, and a MNA of 4.14 (Table 1). In contrast, the Anxi population with the smallest number of samples shows the lowest diversity.

**Genetic relationship :** Both Nei's $D_S$ (Nei, 1972; data not shown) and $D_A$ (Nei *et al*, 1983) genetic distances indicate close genetic relationship between the four Chinese Bactrian camel populations, with an average $D_A$ of 0.067, and between the two Mongolian Bactrian camel populations, with a $D_A$ of 0.064. The average $D_A$ genetic distance between the Chinese and Mongolian Bactrian camels is much higher (average being 0.114). Pairwise Fst tests indicate that genetic differentiation between the Chinese and Mongolian camels are significant (P < 0.01). There is no genetic differentiation between the two Mongolian populations, between the Anxi population and the other Chinese populations, and between the Wuwei and Balikun populations (P > 0.05). The lack of genetic differentiation among the Chinese populations is possibly a historical legacy of trading along the Silk Road which favoured gene flow between populations. Indeed, the Balikun, Anxi and Wuwei populations were collected from sites along this ancient trading road. The Alashan You population shows a relatively close genetic relationship with the Wuwei population (Table 2). This population did not originate from an ancient silk route location, but traditional exchanges

of breeding animals between the two populations have been reported (Xueshi, 1990). Interestingly mitochondrial DNA study also indicates a close genetic relationship between the Alashan You, Anxi and Balikun populations (Jiexia *et al*, 2000). The lack of genetic differentiation between the two Mongolian populations is likely the result of interbreeding between populations following transhumance. Our results indicate that the domestic Bactrian camels from China and Mongolia should be considered as distinct populations in conservation and breeding programs.

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## References

FAO (2002). FAO year book. Cited from http:\\www.fao.org.

Goudet J (2001). FSTAT, a program to estimate and test gene diversities and fixation indices (version 2.9.3). Available from http://www.unil.ch/izea/softwares/fstat.html. Updated from Goudet (1995).

Jianlin H (2000). Origin, evolution and genetic diversity of Old World genus of Camelus. Doctoral Dissertation of Lanzhou University, Lanzhou, China.

Jianlin H, Mburu DN, Ochieng JW, Kaufmann B, Rege JEO and Hanotte O (2000). Application of New World Camelidae microsatellite primers for amplification of polymorphic loci in Old World camelids. Animal Genetics 31:404-406.

Jiexia Q, Yaping Zh, Jianlin H and Zhenming M (2000). Genetic diversity of mtDNA of domestic camels (*C. bactrianus*) in China. Acta Genetica Sinica 27:383-390.

Lenscht J (1996). The two-humped camel (*Camelus bactrianus*). A review. Der Praktische-Tierarzt 77:1107-1118.

Mariasegaram M, Pullenayegum S, Jahabar Ali M, Shah RS, Penedo MCF, Wernery U and Sasse J (2002). Isolation and characterisation of eight microsatellite markers in *Camelus dromedarius* and cross-species amplification in *C. bactrianus* and *Lama pacos*. Animal Genetics 33: 385-387.

Mburu DN, Ochieng JW, Kuria SG, Jianlin H, Kaufmann B, Rege JEO and Hanotte O (2003). Genetic diversity and relationships of indigenous Kenyan camel (*Camelus dromedarius*) populations: implications for their classification. Animal Genetics 34:26-32.

Nei M (1972). Genetic distances between populations. American Naturalist 106:283-292.

Nei M, Tajima F and Tateno Y (1983). Accuracy of estimated phylogenetic trees from molecular data. Journal of Molecular Evolution 19:153-170.

Olsen S (1988). The Camel in Ancient China and Osteology of the Camel. Proceedings of the Academy of Natural Sciences of Philadelphia 140:18-58.

Ota T (1993). DISPAN (Pennsylvanian State University, TX, USA).

Park S (2001). Microsatellite Toolkit. Available from http://oscar.gen.tcd.ie/~sdepark/ms-toolkit/index.html.

Raymond M and Rousset R (1995). GENEPOP (version 1.2): population genetic software for exact tests and ecumenicism. Journal of Heredity 86:248-249.

Xueshi S (1990). Camel Production (Textbook, 2nd edition). Agricultural Press, Beijing, China.

**Renal diseases in camels**

**I. A. Fouad**

A survey of the prevalence and types of renal lesions was carried out on 480 Sudanese camels obtained frm Cairo abattoirs in Egypt for 2 years. Microscopic, histopathological and bacteriological examinations of the kidneys were performed. The incidence of total renal lesions was 4.375%, classified into four groups including mesangioproliferative glomerulonephritis (GN, 1.458%), endocapillary proliferative GN (0.416%), esmbolic GN (0.416%) and interstitial nephritis (2.083%). Different types of bacterial isolates were obtained in some cases, including *Escherichia coli*, *Arcanobacterium pyogenes* and *Proteus mirabilis*.

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