

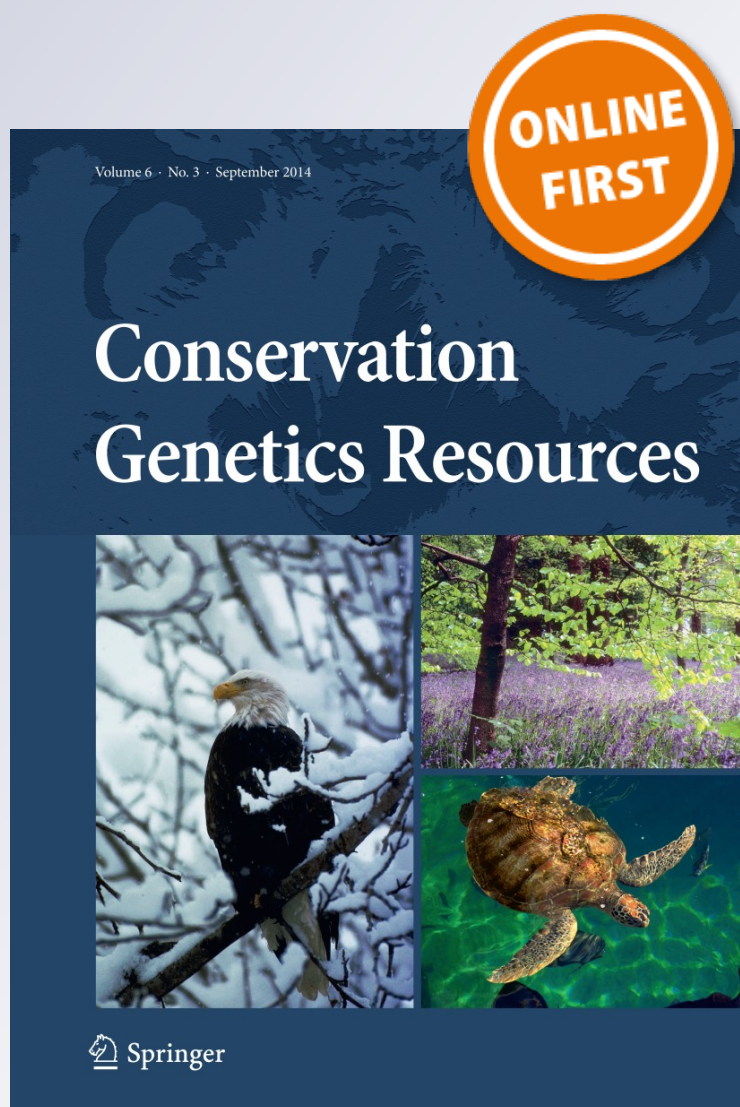
Development and characterization of nine polymorphic microsatellite markers for the blue sheep (Pseudois nayaur)

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Development and characterization of nine polymorphic microsatellite markers for the blue sheep (*Pseudois nayaur*)

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Abstract *Pseudois nayaur* is a major component of Caprini and a keystone species in Qinghai-Tibet Plateau ecosystems. Due to the excessive hunting and habitat loss, its numbers are being reduced drastically. We developed and characterized the first set of microsatellite markers in this species to investigate its population genetic diversity and structure. Nine polymorphic loci displayed an average of 5.73 alleles (range between 2 and 14) and the levels of expected heterozygosity ranged from 0.422 to 0.816. Cross-amplification within dwarf blue sheep was successful for the nine loci. The loci characterized here will be useful for detecting fine-scale spatial structuring and resolving the taxonomic status of divergent *Pseudois* populations.

Keywords *Pseudois nayaur* · Microsatellite markers · Polymorphism · Population genetics

Blue sheep (*Pseudois nayaur*), a Central Asian ungulate with restricted geographic distribution, exhibits extensive variation in morphology and phylogeographic structure (Zeng et al. 2008). The composition of species and subspecies in the genus *Pseudois* is controversial, particularly with respect to the taxonomic designation of geographically restricted populations (Tan et al. 2012). The genus *Pseudois* includes two morphologically variable taxa, blue sheep (*P. nayaur*) and dwarf blue sheep (*P. schaeferi*). Blue sheep have a wide distribution range across the entire Tibetan Plateau region, while dwarf blue sheep were only found in the gorges of the upper Yangtze River (Jinsha River) near Batang county, Sichuan province. As the body size of dwarf blue sheep is only about a half of blue sheep, its taxonomic status in the genus *Pseudois* has been argued for several decades since its discovery in 1937 (Schafer 1937). More genetic evidences from blue sheep and dwarf blue sheep are required to clarify this question.

The (AC)_n microsatellite-enriched libraries were constructed based on the protocol described by Peng et al. (2011). The primers amplifying the microsatellites were designed using the software PRIMER5. Finally, 9 primer pairs were characterized using PCRs (Table 1). The primers that were characterized successfully using PCR were labeled with fluorescence and PCR products were analyzed using an ABI PRISM377 squencer and GeneMapper version 3.2. GENETIX 4.0.5 was used to check allelic richness and expected and observed heterozygosity. Hardy-Weinberg equilibrium and Linkage disequilibrium was tested by GENEPOP v.4.1.4 and the frequency of null alleles was estimated using MICRO-CHECKER.

DNA samples from 25 blue sheep were examined for the 9 loci. Cross-amplification within dwarf blue sheep was successful for the nine loci. The observed and expected heterozygosity (H_O and H_E) ranged from 0.167 to 0.792

Min Yang and Quekun Peng have contributed equally to this work.

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Table 1 Primer sequences and characteristics of nine microsatellite loci isolated in *P. nayar*

Locus	Primer sequence(5'-3')	Repeat motif	Labeled dye	T _m (°C)	Size range (bp)	A	H _o	H _E	PIC	GenBank accession no.
PND01	F: CTACTGGACTGAGGCAAGATTTACC ^a R: ACTAATTCGATGTCATAAAGTAGGGGAG	(AC) ₁₉ AT(AC) ₆	HEX	61	144–174	4	0.792	0.562	0.487	KM272976
PND02	F: CTAATCAGTCCCTTTGCTCC ^a R: CATCTCAGGTGGGTGTCTT	(AC) ₂₂	FAM	55	190–228	9	0.542	0.715	0.666	KM272977
PND03	F: TCCAAAAGATCAGATACAAT ^a R: TAACAGGACAACCCACAGC	(AC) ₆ AT(AC) ₅ AT(AC) ₉	TAMAR	55	102–116	4	0.542	0.587	0.483	KM272978
PND04	F: CGACTGAAATGAAAGAAACGA ^a R: ACAACAAGGGGATGGTGAA	(CT) ₂₅ (CTCCCT) ₃ (CA) ₂₀	HEX	55	220–244	14	0.750	0.816	0.780	KM272979
PND05	F: CAAAAGATTGGGTACAACCTGGGTGA ^a R: GTTCCAAATGTCGGAAGCATCTAATTA	(AC) ₁₇	FAM	60	166–174	5	0.167	0.479	0.439	KM272980
PND06	F: GCCCAGGGAGGATAAGTAAAC ^a R: TCCGTGGCAAAAGATCAGC	(GT) ₄ ATCT(GT) ₇ CT (GT) ₁₅	HEX	59	183–189	3	0.625	0.536	0.424	KM272981
PND07	F: GTTCCCGCAGATGGCATTATT ^a R: GAGAAGCCCCAAGTAGCAACAAAAG	(GT) ₁₈	FAM	57	180–186	4	0.167	0.451	0.413	KM272982
PND08	F: GTGTGAAATCATTACTGTCCGA ^a R: CCACCTCTTAAATCAAGCAAAAA	(GT) ₇ GAACAT(GT) ₇	TAMAR	55	93–121	2	0.333	0.422	0.328	KM272983
PND09	F: ATAGTCAAGACGAGCAAAAGAAAAG ^a R: CTGCCTCCATAATCTGAACCTG	(AC) ₂₉	TAMAR	56	208–256	4	0.533	0.486	0.497	KM272983

T_m Annealing temperature of primer pair, A number of alleles, H_o observed heterozygosity, H_E expected heterozygosity, PIC polymorphism information content

^a Primers labeled with the fluorochrome

and 0.422 to 0.816 respectively. The average of number of alleles per locus (A), polymorphism information content, and observed and expected heterozygosity (H_O and H_E) in the blue sheep were 5.73, 0.489, 0.574, and 0.505, respectively. No significant deviations from Hardy–Weinberg equilibrium and linkage association was found among all loci. Therefore, these 9 microsatellite loci were highly polymorphic, suggesting that these markers will be valuable for studies on the genetic structure of blue sheep populations.

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References

- Peng QK, Wang GC, Tan S, Wang T, Li L, Zou FD (2011) Isolation and characterization of thirteen polymorphic tetranucleotide microsatellite markers in the Tokay gecko (*Gekko Gecko*). *Conserv Genet Resour* 3:617–619
- Schafer E (1937) On the dwarf bharal (*Pseudois spec. nov*) and the large bharal (*P. nahhor* Hodgson) of the Tibet. *Zool. Gart Leipz* 9:263–278
- Tan S, Zou DD, Tang L, Wang GC, Peng QK, Zeng B, Zhang C, Zou FD (2012) Molecular evidence for the subspecific differentiation of blue sheep (*Pseudois nayaur*) and polyphyletic origin of dwarf blue sheep (*Pseudois schaeferi*). *Genetica* 140:159–167
- Zeng B, Xu L, Yue BS, Li ZJ, Zou FD (2008) Molecular phylogeography and genetic differentiation of blue sheep *Pseudois nayaur szechuanensis* and *Pseudois schaeferi* in China. *Mol Phylogenet Evol* 48:387–395