

# Ovine Domestication and Diversity

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## Abstract

Sheep are a highly versatile and adaptable domestic species. Dissection of the genetics responsible for the ovine domestic phenotype relies on an understanding of the genetic variability that resides within and between breeds and also knowledge regarding both the maternal and paternal origins of sheep. Mitochondrial DNA was investigated in the search for novel *Ovis aries* matriline and the complete mitogenome sequenced from a subset of domestic and wild sheep to resolve the phylogenetic relationships between these groups. A fifth domestic lineage was identified in sheep from the Near East, a proposed centre of domestication. Mitogenome analysis revealed no wild sheep introgression in the five *O. aries* groups. To contrast this maternal picture, variation in the male-specific region of the ovine Y chromosome was investigated. Seven novel single nucleotide polymorphisms and a previously uncharacterised microsatellite from the ovine sex determining gene region were used to generate 17 paternal haplotypes. Analysis of these markers across wild and domestic sheep again failed to identify signatures of wild *Ovis* introgression in modern sheep. The emerging picture of male mediated domestication suggested that there are at least two patriline present within *O. aries*. One of these has a possible European origin and the other, a less restricted distribution. Genetic diversity and linkage disequilibrium (LD) was characterised using autosomal microsatellites. Five domestic populations were investigated, with the result that in genetically diverse breeds, LD extended for only short distances, whilst more homogeneous populations displayed extensive patterns of LD. This clearly illustrated the impact of population history on the extent LD and will inform subsequent gene mapping studies in sheep. The three classes of genetic variation investigated (autosomal, paternal and maternal), each reveal aspects of the genetic architecture present within domestic sheep and only by assaying each of these, will the true picture of ovine domestic and diversity be revealed.

Keywords: diversity, domestication, sheep, linkage disequilibrium, Y chromosome, mitochondria

I certify that the substance of this thesis has not already been submitted for any degree and is not currently being submitted for any other degree or qualification.

I certify that any help received in preparing this thesis, and all sources used, have been acknowledged in this thesis.



Signature

## Abbreviations

bp	base pair
cM	centimorgan
DNA	deoxyribonucleic acid
kb	kilobase
LD	linkage disequilibrium
Mb	megabase
MSY	male specific region of the Y chromosome
mt	mitochondria
mtDNA	mitochondrial DNA
OAR	ovine chromosome
<i>oY</i>	SNP located to the ovine MSY
PAR	pseudoautosomal region of the Y chromosome
SNP	single nucleotide polymorphism

## Glossary

List of scientific and common names used for *Ovis* species throughout this thesis

<i>Ovis aries</i>	Domestic sheep
<i>O. canadensis</i>	Bighorn sheep
<i>O. dalli dalli</i>	Dall sheep
<i>O. dalli stonei</i>	Stone sheep
<i>O. nivicola</i>	Siberian snow sheep
<i>O. ammon</i>	Argali sheep
<i>O. vignei</i>	Urial sheep
<i>O. musimon</i>	European mouflon
<i>O. orientalis</i>	Asiatic mouflon

### List of Original Manuscripts

The thesis is based on the following five original manuscripts. These papers are organised according to subject matter. The candidate's contribution to each manuscript is indicated in bracketed text.

- I Meadows JRS, Cemal I, Karaca O, Gootwine E, Kijas JW. 2007. Five ovine mitochondrial lineages identified from sheep breeds of the Near East. *Genetics* .**175**: 1371-1379.  
*[JRSM contribution as percentage of whole, 75%]*
- II Meadows JRS, Hiendleder S, Kijas JW. 2008. Complete ovine mitochondrial genomes resolve domestic haplogroup relationships. *Manuscript*.  
*[JRSM contribution as percentage of whole, 95%]*
- III Meadows JRS, Hanotte O, Drögemüller C, Calvo J, Godfrey R, Coltman D, Maddox JF, Marzanov N, Kantanen J, Kijas JW. 2006. Globally dispersed Y chromosomal haplotypes in wild and domestic sheep. *Anim Genet*. **37**: 444-453.  
*[JRSM contribution as percentage of whole, 70%]*
- IV Meadows JRS, Kijas JW. 2008. Re-sequencing regions of the ovine Y chromosome in domestic and wild sheep reveals novel paternal haplotypes. *Anim Genet*. Nov 11.  
[Epub ahead of print].  
*[JRSM contribution as percentage of whole, 75%]*
- V Meadows JRS, Chan EKF, Kijas, JW. 2008. Linkage disequilibrium compared between five populations of domestic sheep. *BMC Genet*. **9**: 61.  
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