

# Genetic polymorphism of adult reindeer coat colour in a herding cooperative in Finnish Lapland

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*Abstract:* In a random sample of 188 adult reindeer belonging to a reindeer herding cooperative in Finnish Lapland, the following coat colour mutants were identified: *A<sup>bl</sup>* at the locus *Agouti* (*A*), *kalppinokka* (*WN<sup>k</sup>*) at the locus *White Nose* (*WN*) and *white* at the locus *W* (*White*). Coefficients of coat colour phenotypic polymorphism *K* were estimated, in order to quantify this genetic polymorphism. Estimations of *K* were 12.8% for the locus *A* (*Agouti*), 5.1% for the locus *WN* (*White Nose*), and 7.5% for the locus *W* (*White*). This polymorphism results probably from a change in fitness coefficient of genotypes carrying colour mutants following domestication in a random mating context which has not yet been proved.

**Key words:** coat colour; Finland; genetic polymorphism; genetics; *Rangifer tarandus*; reindeer.

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## Introduction

Since 2006 a coat colour genetic project is run by the Reindeer Research Station in Kaamanen (RKTL) in collaboration with the Committee for Genetic Nomenclature in Sheep and Goat (COGNOSAG) (Lauvergne, 2006).

The argument is that, according to Darwin (1868), one observes a polymorphism of visible characters in every animal species after its domestication, knowing now that, in mammals, this polymorphism affects mainly coat colour loci (Searle, 1968; Lauvergne, 2010).

This polymorphism, which has already been described in the domesticated reindeer species (Skjenneberg, 1984; Eira, 1994; Delaporte,

2002), deserves to be explained in terms of Mendelian genetics (identification of loci and alleles) and Lauvergne & Nieminen (2010) have started to give a genetic interpretation of several colour phenotypes in the Finnish reindeer population according to the principle of homology between loci inducing coat colour in mammals (Searle, 1968).

The present article is devoted to the interpretation of coat colour polymorphism in terms of Mendelian genetics with an attempt to give a quantitative measurement of this polymorphism. It is based on data collected in a Finnish reindeer herding cooperative during a round up in December 2010.

Table 1. Code for coat colour phenotypes.

Phenotypic dimension	Grade	Code
Pigmentary pattern	Common wild	+
	Wild without flank stripe	+1
	Badger face	BF
	Dark	D
	Not identified	NI
White designs	Wild (no white design)	+
	White nose	WN
	Not identified	NI
Alteration of pigmentation	Wild (no alteration)	+
	Greying	G
	Full White	W
	Not identified	NI

## Material and methods

### Collecting data

The data we collected at the Ahvenjärvi corral belonging to the Herding Cooperative N°3 (Näätämö), near the village of Sevettijärvi in Inari, Lapland, cf. Fig. 1. This herding cooperative is operating on 1353 km<sup>2</sup> in northern Finland with 40 herders and around 3000 adult reindeer females, the mating ratio is about 1/10.

The collection of pictures was done on December 2, 2010 with a Nikon 50 D digital

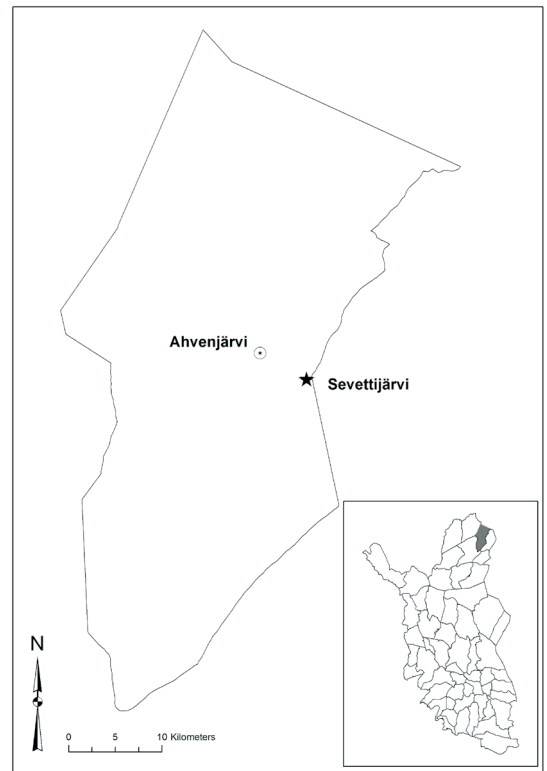


Fig. 1. The Näätämö Reindeer Herding Cooperative N°3 in the Sami reindeer herding area.

camera and a 80-200 mm objective in sections around the central circle of the corral by operating from about 15 meters away, with a flash.

Table 2. Phenotypic frequencies in 3 dimensions (pigmentary pattern, white designs, alteration of pigmentation) in the Ahvenjärvi sample.

Dimension	Phenotypes	Code	Number	Percentage
Pigmented pattern	Wild	+	137	87.3
	Wild without stripe	+1	7	4.4
	Badger face	BF	13	8.3
	Dark (non identified)	D	1	Not plotted
	Total identified		157	
White design	Wild (no white design)	+	145	94.8
	White nose	WN	8	5.2
	Total identified		153	
Alteration of pigmentation	Wild (no dilution)	+	174	92.0
	Grey	G	7	4.0
	Full white	W	7	4.0
	Total identified		188	

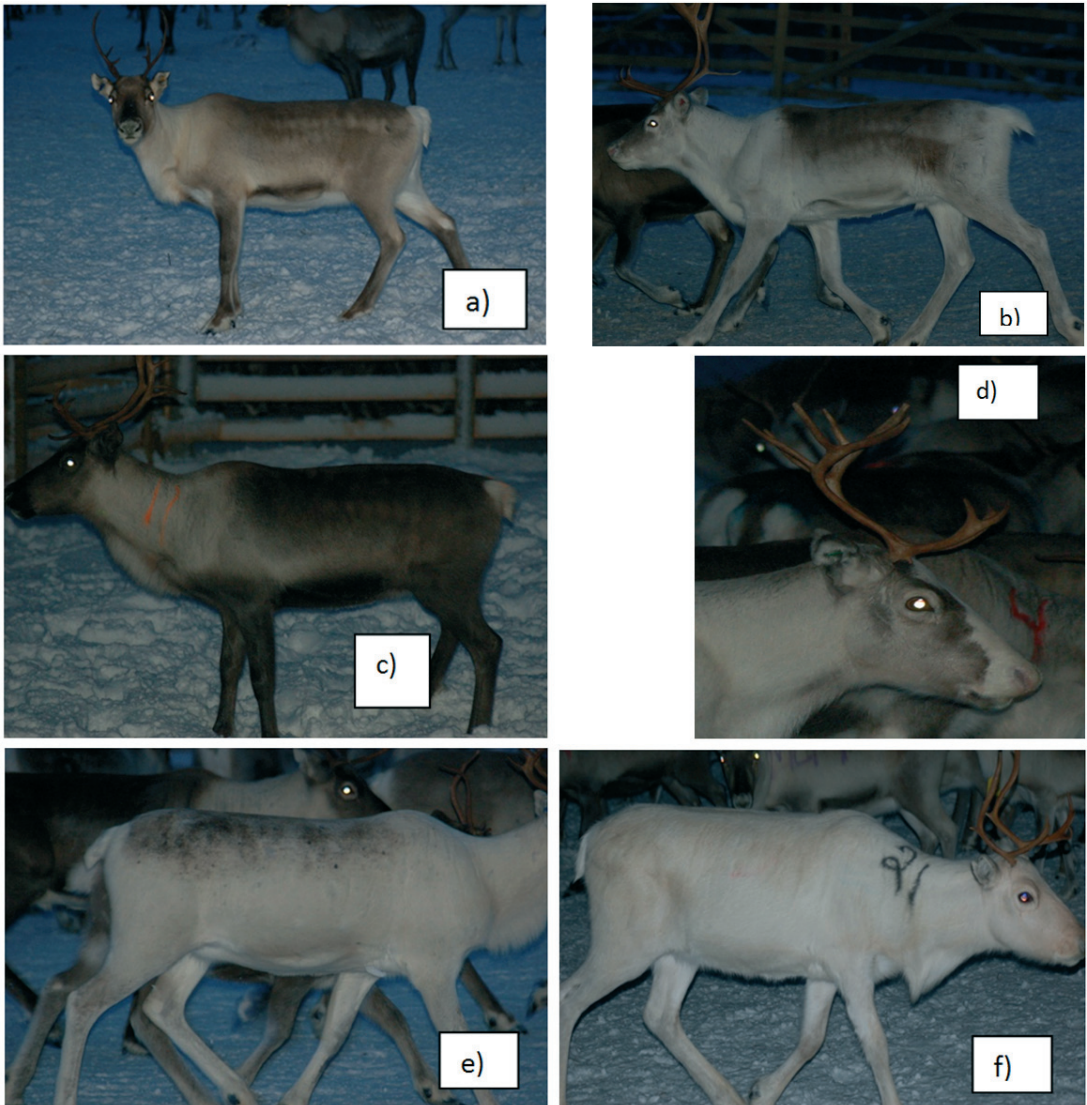


Fig. 2. Scale of reindeer phenotypic coat colour: a) Common wild pattern (wild); b) Wild without flank stripe; c) Badger face; d) White nose [*kalppinokka*]; e) Greying; f) Full white.

#### Data analysis

The examination of pictures was done on the screen of computers. Individual side photographs of a total of 188 adult animals of both sexes chosen at random were classified according to three dimensions of the phenotypic description of coat colour in mammals proposed by Lauvergne *et al.* (1991): pigmentary pattern, white design and alteration of pigmentation. The code for coat colour phenotypes is given in Table 1 and illustrated in Fig. 2.

#### Results

Phenotypic frequencies of coat colour of 188 adults are given in Table 2.

#### Analysis of results

##### *Loci in segregation*

##### Pigmented pattern

Variations of pigmented pattern suggest the presence of at least 3 alleles at the very well known mammalian *Agouti* locus (Searle, 1968):  $A^+$  (wild), Fig. 2a;  $A^{bf}$  (badger face), Fig

2c, already described by Lauvergne & Nieminen (2010) when the phenotype wild without dark flank stripe (Fig. 2b) has been assigned to the heterozygote  $A^+A^{bf}$ .

### White design

The piebaldness described by Lauvergne & Nieminen (2010) has not been observed at Ahvenjärvi but, on the other hand, a white design which happened to be rather popular among breeders has been observed: a white nose known under the Finnish name of *kalppinokka* (Fig. 2d). It has been allocated to the allele *kalppinokka* ( $k$ ) at another locus of white design called *White Nose* ( $WN$ ).

### Alteration of pigmentation

The very well known and popular full white phenotype (Fig. 2f) has been observed at Ahvenjärvi with a frequency of 4%. According to Lauvergne & Nieminen (2010) it could be given by the dominant allele *white* ( $W^w$ ) at the locus  $W$  (*White*). The  $W^+W^w$  genotype could have a variable expressivity, some carriers being only partially white with some diluted areas as seen on Fig. 2e. They were called grey. Segregations at various loci are summarized in table 3.

### Measuring phenotypic polymorphism

In order to measure this polymorphism it has been proposed to use a *coefficient of phenotypic coat colour polymorphism* named  $K$ . At every coat colour locus  $K$  may be estimated as the percentage of animals showing a phenotypic expression of mutant alleles (different from the wild one). The values of  $K$  at the loci in segre-

gation observed in the Ahvenjärvi sample are given in Table 4.

### Discussion and conclusion

The present study on a sample of adult reindeer belonging to the Näätamö cooperative confirms the field observations of Skjenneberg (1984), Eira (1994) and Delaporte (2002) to which Lauvergne & Nieminen (2010) have added a Mendelian interpretation and they give a first quantitative measurement of the genetic polymorphism with the proposed *coefficient  $K$  of phenotypic coat colour polymorphism*. But given the dominance observed at the  $WN$  locus and potential uncertainties on heterozygotes identification at the  $A$  and  $W$  loci, one cannot reliably estimate gene frequencies according to Hardy-Weinberg principles.

Now, if one considers that the frequencies of colour mutants have reached a value of equilibrium, it is necessary to admit that the value of fitness coefficients of the genotypes carrying mutant alleles allows this obtaining. This may result from single-gene overdominance arising after domestication, as proposed by Wills

Table 3. Coat colour loci segregating in the Ahvenjärvi sample.

Locus		Alleles	
Name	Symbol	Name	symbol
<i>Agouti</i>	$A$	<i>wild</i>	$A^+$
		<i>(badger face)</i>	$A^{bf}$
<i>White Nose</i>	$WN$	<i>wild</i>	$WN^+$
		<i>kalppinokka</i>	$WN^k$
<i>White</i>	$W$	<i>wild</i>	$W^+$
		<i>white</i>	$W^w$

Table 4. Coefficients  $K$  of phenotypic coat colour polymorphism at various coat colour loci in the Ahvenjärvi sample.

Locus		Number of observed animals		$K$
Name	Symbol	Total	With a mutant phenotype	
<i>Agouti</i>	$A$	156	20 (badger face or wild without flank stripe)	12.8%
<i>White Nose</i>	$WN$	153	8 (kalppinokka)	5.1%
<i>White</i>	$W$	188	14 (grey or full white)	7.5%

(1980). But this author underlines that this hypothesis calls for panmixy (random mating) which yet needs to be proved among the Näätämo reindeer population. In fact, many events in the past may have affected the observed polymorphism, such as deviation from random mating, bottleneck effect, migration, partial selection against or in favour of a given phenotype etc. Therefore, following the present estimation of polymorphism a RKTL/COGNOSAG survey is currently running in the Cooperative, in order to check if, at least during the last mating season, panmixy was enforced.

The input of the proposed rough measurement of visible genetic polymorphism may be of some practical value being easy to do in order for example to map this polymorphism among all cooperatives of northern Finland (cf. Fig. 1).

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Aikuisten porojen turkin värin perinnöllinen muuntelu yhdessä Suomen Lapin paliskunnassa

*Abstract in Finnish /Lyhennelmä:* Suomen Lapin paliskunnasta kerätystä 188 aikuisen poron satunnaisnäytteessä tunnistettiin seuraavat turkin värin mutantit:  $A^{\theta}$  lokuksessa *Agouti* (*A*), *kalppinokka* ( $WN^{\theta}$ ) lokuksessa *valkonokka* (*WN*) ja *valkoinen* lokuksessa *W* (*White*). Turkin värin fenotyypin muuntelun yleisyyskertoimet *K* arvioitiin suhteessa aina perinnöllisen muuntelun määrään. Kerroin *K* oli noin 12,8% lokukselle *A* (*Agouti*), 5,1% lokukselle *WN* (*valkonokka*) ja 7,5% lokukselle *W* (*valkoinen*). Tämä muuntelu johtuu mahdollisesti väriin liittyvien genotyypimutanttien yleisyysmuutoksista ja on seurausta satunnaisessa lisääntymisessä tapahtuneesta kesyyntymisestä, jota ei ole kuitenkaan vielä todistettu.

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