

Identification and worldwide populational distribution of personality-related candidate genes in goat (*Capra Hircus*) using a translational approach

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Abstract. Biodiversity of farm animals is a highly valuable resource for sustainable development of humanity especially when faced environmental and economic changes. Intensification of farm industry destabilizes animal's genetic diversity. Farm animals' behaviour shaped during the long period of domestication might be of the specific risk being poorly investigated due to the difficulties in measuring behavioural traits. Here we use translational approach by identifying goat orthologues of human personality-related genes as in the recent study of Tamu Yokomori et al. (2023) that dealt with racing horses' personality. We extended this approach by using a huge dataset covering goat populations through all the World, that allowed to investigate populational distribution of alleles in personality related genes. We identified 41 SPN in 18 genes that were previously shown to be polymorphic both in human and horses in the study of Yokomori et al. Many of them showed highly asymmetric distribution that suggest an important role for these genes in goat evolution and domestication.

1 Introduction

Sustainable development aims at meeting current human needs while preserving the environment for the future generations. Farm animals provide opportunities for economic development, better nutrition, and dietary diversity, especially for infants and children, as well as for greater social inclusion and equity through rural development and job creation (FAO). However, rapid industrialization carries risks to the genetic resources of farm animals reducing their potential to face environmental and economic changes. Of particular significance is the complex behaviour as an evolutionarily conditioned way of animals' adaptation to human-created conditions. This behaviour rarely becomes an object of selection in intensive livestock systems; therefore, the underlying genetic diversity can be destabilized. The conservation of complex behaviour is fundamentally important for organic farming. However, the data on genetics of farm animal behaviour is quite limited, mainly due to the difficulties in measuring behavioural traits. Another, translational approach is identifying candidate genes for behavioural traits. We focused on goat as the most influential farm animal

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in developing countries. We used an approach suggested by Tamu Yokomori et al. (2023) who identified orthologues of personality-related candidate genes in horse using functionally-annotated human genes. Using NCBI gene database the authors identified 18 orthologues of human personality-related genes with polymorphic alleles in whole genome database of 101 Thoroughbred horses.

Here, we aimed to identify goat orthologues of these 18 personality-related genes described in human and horse, using a large dataset containing whole-genome SNP data of 5176 animals of 188 populations distributed worldwide, with a final goal to examine populational distribution of the polymorphic alleles.

2 Methods

2.1 The working dataset

We used the working dataset from our previous work (Mukhina et al., 2022) Briefly, it includes (1) the data from the AdaptMap project described in the paper by Colli et al. that contained goat population data from all over the world; the (2) data from the study by Deniskova et al. presenting seven goat breeds from Russia; the data from six populations from five (2) Chinese regions described by Berihulay et al.; and (4) the data from five Mongolian goat populations genotyped in our study. Genotyping was performed with Goat 50K BeadChip (Illumina Inc., San Diego, CA, USA). This combined dataset, contained 38,276 SNPs from 5176 animals of 188 populations (Table S1).

2.2 Search for DNA variants in goat personality-related candidate gene

PLINK 1.9 was used to search for single nucleotide polymorphisms (SNPs) in the orthologues of 18 human personality-related gene also identified in horse by Yokomori et al. (2023) within chromosomal coordinates obtained from the goat genome annotation in Ensembl. Minor allele frequencies were calculated for the identified SNP markers. Frequency of the sane alleles were further calculated for each animal population containing at least 10 animals thar were from 158 populations with the mean number of animals of 50 ± 2.2 ($M \pm SEM$).

2.3 Distribution of DNA variants

Proportion of the minor allele (MAF) was calculated for 158 goat populations. Table 1 shows Mean values, Skewness and Kurtosis numbers to characterize the MASs statistical distribution. The populational distribution of the six most asymmetrical MAFs was visualized by histograms with MAF plotted at X-axis and Y-axis representing the number of goat populations.

3 Results

Overall, 41 SNPs were found in 17 genes (Table 1). All of them contained 1-2 SNPs except for cadherin 13 that contained 15 SNPs. Figure 1 shows Mean and Skewness for MAFs off all SNPs. Corresponding numbers are Kurtosis are listed in Table 1. It shows that distribution of many alleles in highly asymmetric. The most asymmetrically distributed alleles can be found in the bottom of Table A2 sorted by Skewness.

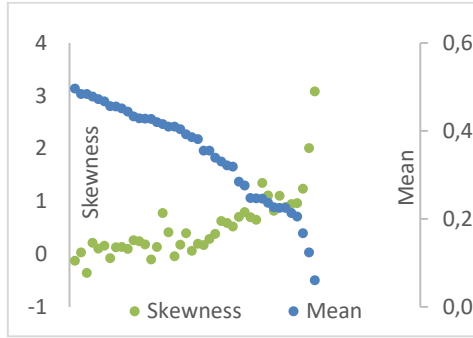


Fig. 1. Mean and Skewness populational minor allele frequencies for each SNP.

The distribution of the six most asymmetric SNPs is shown in Figure 2.

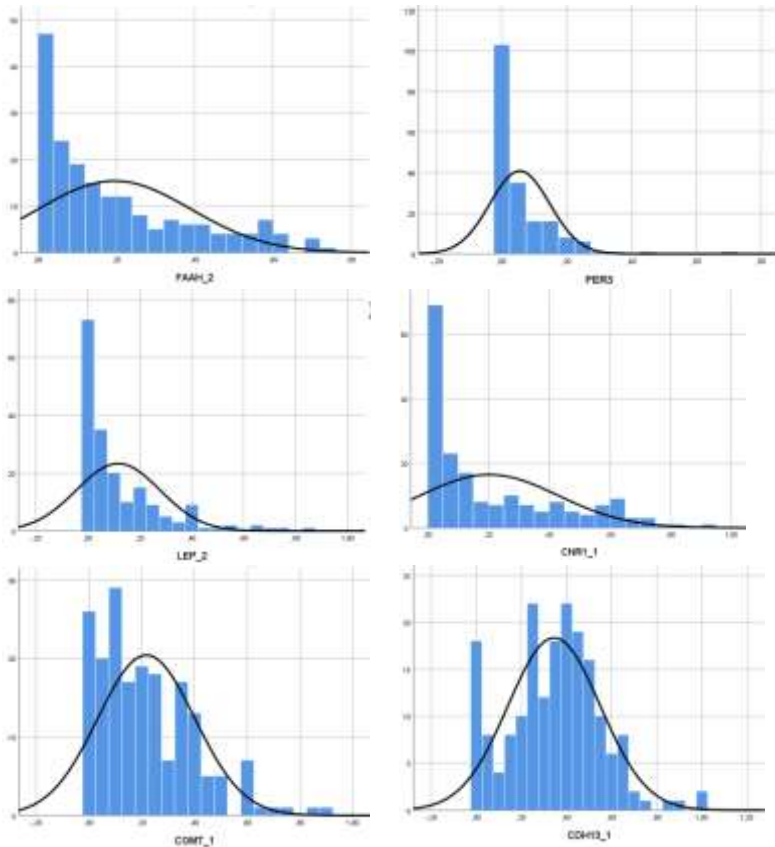


Fig. 2. Distribution of the minor alleles frequencies of LEP, PER3, CDH13, COMT, FAAH and CNR1 in the worldwide populations of domestic goat.

4 Discussions

Personality is mostly referred to time-stable individual differences in behaviour that provide adaptation to environment including exploration and social communications. Domestic animals including farm animals possess personality as shown by many In recent evolution of

domestic animals and animals, a general pattern of morphological, behavioural, and observable changes has been observed, termed the "domestication syndrome", such as increased docility, slow sexual development, reduced sexual dimorphism, smaller brain size (Wilkins et al., 2014). These changes lead to reducing aggression, choosing emotionally more stable partners, improving social and learning skills (Thomas, 2014; Wilkins et al., 2014). Goat orthologues of human-personality related genes exhibited great polymorphism. The polymorphic variants are suggested to be expressed in individual differences in behaviour making a basis for evolutionary selection. Among six more asymmetrically distribution alleles were the ones in PER3, LEP, CNR1 and FAAH genes, that showed a clear tendency to fixation of homozygous major allele in most populations, and in COMT, and CDH13 genes. In human PER3 and CNR1 is associated with Extraversion, CDH13 is associated with Agreeableness. COMT is associated with all personality traits with the highest loads on Neuroticism, as well as FAAH, and LEP – with Conscientiousness.

5 Conclusions

Data showed that goat homologues of human personality-related genes are polymorphic. Distribution of many alleles in goat populations was far from normal, implying their significance for evolution. These data provide preliminary associations of these genes with goat behavior, and future studies implying behavioral measurements are needed to further explore this relationship.

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Appendix

Table 1. List of SNPs in goat orthologues of human personality- related genes and distribution of the minor alleles in worldwide goat populations.

Gene	Protein	Position (Chr: bp range)	Mean	Skewness	Kurtosis
<i>FAAH</i>	fatty acid amide hydrolase	3: 21,026,588-21,047,140	• 0,43	0,18	-0,90
			• 0,21	0,96	-0,14
<i>PER3</i>	period circadian regulator 3	16: 44,082,685-44,149,046	• 0,06	3,08	14,00
<i>CDH13*</i>	cadherin 13	18: 10,713,157-11,547,248	• 0,21	0,95	1,49
(shown 3 of 15)			• 0,24	1,11	1,17
			• 0,25	0,65	-0,01
<i>NPY</i>	neuropeptide Y	4: 48,587,984-48,618,665	• 0,46	-0,08	-0,45
<i>LEP</i>	leptin	4: 27,665,917-27,682,282	• 0,39	0,40	0,18
			• 0,12	2,01	4,27
<i>HSD11B1</i>	hydroxysteroid 11-beta dehydrogenase 1	16:72192303-72232521	• 0,48	-0,36	-0,54
			• 0,36	0,17	-1,00
<i>ANKK1</i>	ankyrin repeat and kinase domain containing 1	15:58404829-58418257	• 0,25	0,70	-0,08
<i>DRD2</i>	dopamine receptor D2	15:58322506-58393525	• 0,43	0,24	-0,23
<i>BDNF</i>	brain derived neurotrophic factor	15:24503417-24569735	• 0,17	1,23	1,79
<i>COMT</i>	catechol-O-methyltransferase	1:547660-553624	• 0,23	1,10	1,27
			• 0,43	0,26	-0,98
<i>P2RX7</i>	purinergic receptor P2X 7	17:17203049-17255098	• 0,23	0,82	-0,12
			• 0,41	-0,04	-0,05
<i>APOE</i>	apolipoprotein E	18:58979223-58984704	• 0,38	0,19	-0,68
			• 0,32	0,52	0,11

Continuation of Table 1.

Gene	Protein	Position (Chr: bp range)	• Mean	Skewness	Kurtosis
<i>CNRI</i>	cannabinoid receptor 1	9:49082848-49084266	• 0,22	0,89	-0,40
			• 0,33	0,63	-0,07
<i>SLC6A4</i>	solute carrier family 6 member 4	19:21107560-21127442	• 0,34	0,38	0,61
<i>GABRA6</i>	gamma-aminobutyric acid type A receptor subunit alpha6	7:37186194-37207432	• 0,44	0,10	-0,99
			• 0,43	-0,10	0,49
<i>HTR2A</i>	5-hydroxytryptamine receptor 2A	12:69719711-69785162	• 0,45	0,13	-0,73
<i>DGKH</i>	diacylglycerol kinase eta	12:74178634-74373984	• 0,39	0,06	-0,48
			• 0,47	0,10	-0,82
			• 0,48	0,21	-0,17