

## Estimation of inbreeding in Ethiopia goats using runs of homozygosity

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This study was carried out to estimate the inbreeding levels in Abergelle, Gumuz, Keffa and Woytoguji goats in Ethiopia from genomic information. A total of 161 animals (53 Abergelle, 39 Gumuz, 31 Keffa and 38 Woytoguji) were genotyped using the Illumina 50K SNP chip. Runs of homozygosity were computed at cut-offs of 1 Mb, 2 Mb, 4 Mb, 8 Mb and 16 Mb, using cgaTOH Analysis & Clustering Suite, Version 1.0.1. The estimated levels of inbreeding based on runs of homozygosity greater than 1 Mb were 0.0210, 0.0209, 0.0502 and 0.0199 for Abergelle, Gumuz, Keffa and Woytoguji, respectively. The results suggest that inbreeding levels are low in the four breeds, although relatively higher in the Keffa breed than in the other three breeds. Suitable strategies may need to be implemented for reducing inbreeding when designing breeding programmes for the Keffa goats.

**Keywords:** goats, genome, inbreeding, runs of homozygosity

### 1 Introduction

Inbreeding is one of the most important population parameters and is crucial for designing appropriate breeding programmes. In practical terms, inbreeding represents the level of diversity of a population or of the genome of an individual. An individual is inbred at a locus if the locus has alleles that are identical by descent. Traditionally, inbreeding has been computed from pedigree information, through the degree of relatedness of parents of an individual (Falconer and Mackay, 1996). However, in low-input livestock production systems, complete pedigrees are usually not available.

An alternative method of computing inbreeding levels is by checking the proportion of contiguous homozygous segments of the genome (runs of homozygosity, ROH). Such segments are likely identical by descent. Inbreeding calculated using this method has been demonstrated to be highly positively correlated with pedigree inbreeding coefficient (Ferenčaković et al., 2013, 2011; Purfield et al., 2012).

This study was carried out to estimate the levels of inbreeding in four goat populations of Ethiopia, two in the North and two in the South of the country.

### 2 Materials and methods

Data for this study were obtained from a characterisation study carried out by the African Goat Improvement Network (AGIN) in Ethiopia. Tissue samples were collected from 161 goats: 53 Abergelle and 39 Gumuz in the Northern, and 31 Keffa and 38 Woytoguji in the Southern part of the country. The goats are raised in low-input production systems in different regions in the country (Table 1).

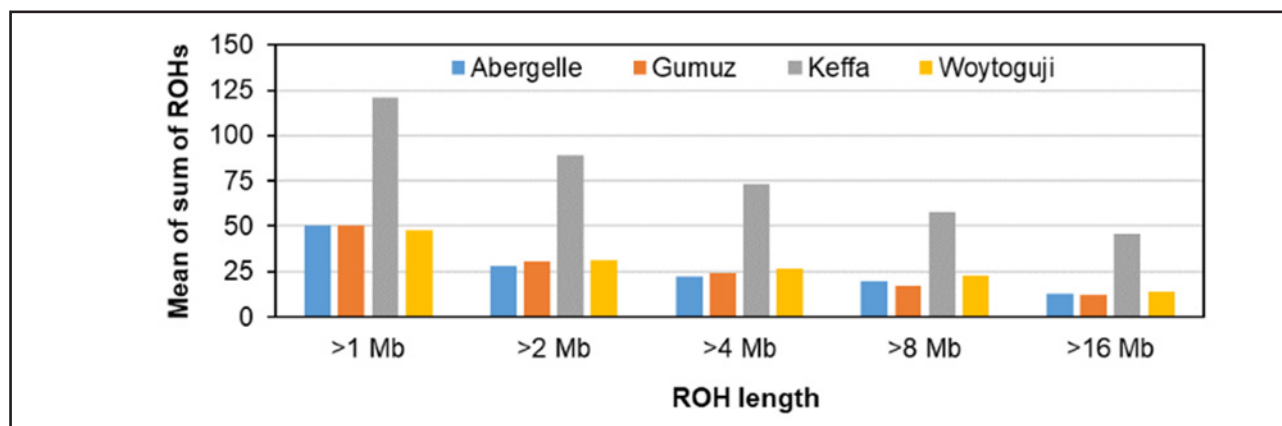
Genotyping was done using the Illumina 50K SNP chip. Data quality check of the genotype data was done using PLINK (Purcell et al., 2007). Starting with 11 males, 150 females and 49,953 SNPs, all the 161 goats and 48,925 SNPs passed filters and quality control (autosomal chromosomes, genotyping rate of 5%, missing genotype data rate of 10%, Hardy-Weinberg equilibrium of  $1e-5$ ),

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**Table 1** Description of the four Ethiopian goat breeds

Breed	Region	Estimated population	Management
Abergelle	Wollo, Tigray	200,000	Agropastoral
Keffa	Keffa	1,000,000	Sedentary
Gumuz	Gojam, Wellega, Illubabor	400,000	Pastoral
Woytoguji	Sidamo	900,000	Agropastoral

Source: Tefera (2013)



**Figure 1** Mean sums of ROHs for each breed

with a total genotyping rate of 98%. A total of 959 SNPs were removed due to missing genotypes and 69 were removed due to the Hardy-Weinberg exact test.

ROH were calculated using cgaTOH Analysis & Clustering Suite, Version 1.0.1 (Zhang et al., 2013) including segments >1 Mb, >2 Mb, >4 Mb, >8 Mb and >16 Mb. No heterozygous calls in ROH were allowed up to 16 Mb, one heterozygous call was allowed for ROH >16 Mb. The proportions of the ROH for each of the cut-offs ( $F_{ROH1}$ ,  $F_{ROH2}$  ...  $F_{ROH16}$ ) were computed using a reference map of 2,402,763.307 kb computed from the coverage of the SNPs.

### 3 Results and discussion

The number of ROHs greater than 1 Mb, 2 Mb, 4 Mb, 8 Mb and 16 Mb were 3813, 1009, 439, 232 and 103, respectively. All goats had ROHs above 1 Mb. All Keffa goats had ROHs more than 2 Mb long, and 90% had ROHs longer than 4 Mb. The longest ROH was 106.5 Mb in a Keffa goat. Overall, the minimum, median, mean and

maximum ROH >1 Mb sums for each individual were 10.5, 33.8, 63.3 and 684.3 Mb, respectively. The means of total length of ROH are given in Figure 1 for each ROH category by breed.

The means of sums of ROHs for the Abergelle, Gumuz and Woytoguji breeds were similar, while those for the Keffa goats were much higher. The estimated mean levels of inbreeding for each of the ROH size limits were higher for Keffa goats (Table 2). The most inbred individual had a ROH >1 Mb inbreeding level of 0.2848, with sums of ROH above 1 Mb and 16 Mb of 684.3 and 556.4 Mb, respectively. Occurrence of such long ROH segments points at parent-offspring or full sib mating of the parents of this individual.

The high levels of inbreeding in the Keffa goats may be occurring because the Keffa goats are geographically isolated and coffee production is the mainstay of farmers in the region. The animals are also tethered, which restricts communal mating.

**Table 2** Estimated inbreeding levels at each cut-off point of runs of homozygosity

Breed	$F_{ROH1}$	$F_{ROH2}$	$F_{ROH4}$	$F_{ROH8}$	$F_{ROH16}$
Abergelle	0.0210	0.0117	0.0092	0.0081	0.0054
Gumuz	0.0209	0.0127	0.0100	0.0073	0.0051
Keffa	0.0502	0.0372	0.0304	0.0240	0.0191
Woytoguji	0.0199	0.0129	0.0112	0.0094	0.0059

#### 4 Conclusions

The levels of inbreeding in the four Ethiopian goat breeds suggest that inbreeding in low-input goat production systems may be lower than is generally assumed. The relatively higher level of inbreeding in Keffa goats suggests that specific mating strategies may be needed for reducing inbreeding when designing sustainable breeding programmes for this breed.

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