# Characterization of linkage disequilibrium and consistency of gametic phase in Canadian goats

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## Introduction

One important parameter to evaluate aiming the implemention of genomic selection in a breeding program is the extent of linkage disequilibrium (LD) in the population. The marker density required for a successful implementation of genomic selection depends on the extent of LD across the genome (Khatkar, et al. (2008)).

The accuracy of genomic selection also depends on the number of records available to estimate marker effects. It can be increased by combining data from multi-breeds. However, the estimation of the effect of each marker across breeds requires not only high LD between the markers and the QTL in each breed, but also high persistence of gametic phase between the markers and the QTL across breeds.

## Objective

➢ Estimate genome-wide levels of LD in six Canadian goat breeds;

➢ Evaluate the persistence of gametic phase between different breeds.

## Material and Methods

➢ 976 goats from six breeds were genotyped using the Illumina goat SNP50 BeadChip.

➢ **Quality Control:** MAF: 5% (for Alpine and Saanen breeds) or 15% (for LaMancha, Nubian, Toggenburg, and Boer Breeds); animal call rate: 10%; SNP call rate: 10%, only autosomes were included.

➢ The extent of LD between markers was measured by allelic $r^2$.

➢ The consistency of gametic phase was defined as the Pearson correlation of signed r values between two breeds.

## Results and Discussion

At the average distance between adjacent SNPs (~0.06 Mb), most of the breeds exceeded or approached an useful $r^2$ value of 0.20 (Calus et al. (2008)), except for Alpine and Saanen ($r^2 \sim$ 0.12 - 0.13).

This indicates that, with a large enough training population, genomic selection could potentially be implemented with the current 50k panel within breed, but Alpine and Saanen might benefit from a denser panel.

The highest consistency of phase was found between Alpine and Saanen. However, even for these two breeds, the consistency of phase between adjacent markers was not high enough (~0.50) to support the pooling of breeds in a training population for genomic selection.

Alpine and Saanen were the breeds with the largest sample sizes (**Table 1**). The higher observed levels of LD in the other breeds could be due to sampling, but they are more likely due to smaller effective population size in those breeds.

**Table 1:** Number of animals (N), average LD ($r^2$) between adjacent SNPs by breed and average distance between adjacent SNPs (Mb).

| Breed | N | $r^2$ | Distance(Mb) |
|---|---|---|---|
| Alpine | 403 | 0.1445 | 0.05296 |
| Saanen | 318 | 0.1534 | 0.05336 |
| LaMancha | 81 | 0.1934 | 0.06181 |
| Nubian | 54 | 0.2721 | 0.07247 |
| Toggenburg | 53 | 0.2431 | 0.07132 |
| Boer | 67 | 0.2860 | 0.06701 |

**Figure 1:** Average $r^2$ values at given distances for six goat breeds

**Figure 2:** Consistency of gametic phase (Pearson correlations of signed r values) at given distances for 15 goat breed pairs

## Conclusion

With a large enough training population, genomic selection could potentially be implemented within breeds with the current 50k panel, but the Alpine and Saanen breeds might benefit from a denser panel.

The phase consistency between adjacent markers is not high enough to encourage the pooling of breeds in a single training population for genomic selection. For multi-breed genomic evaluation, a denser SNP panel seems to be required.
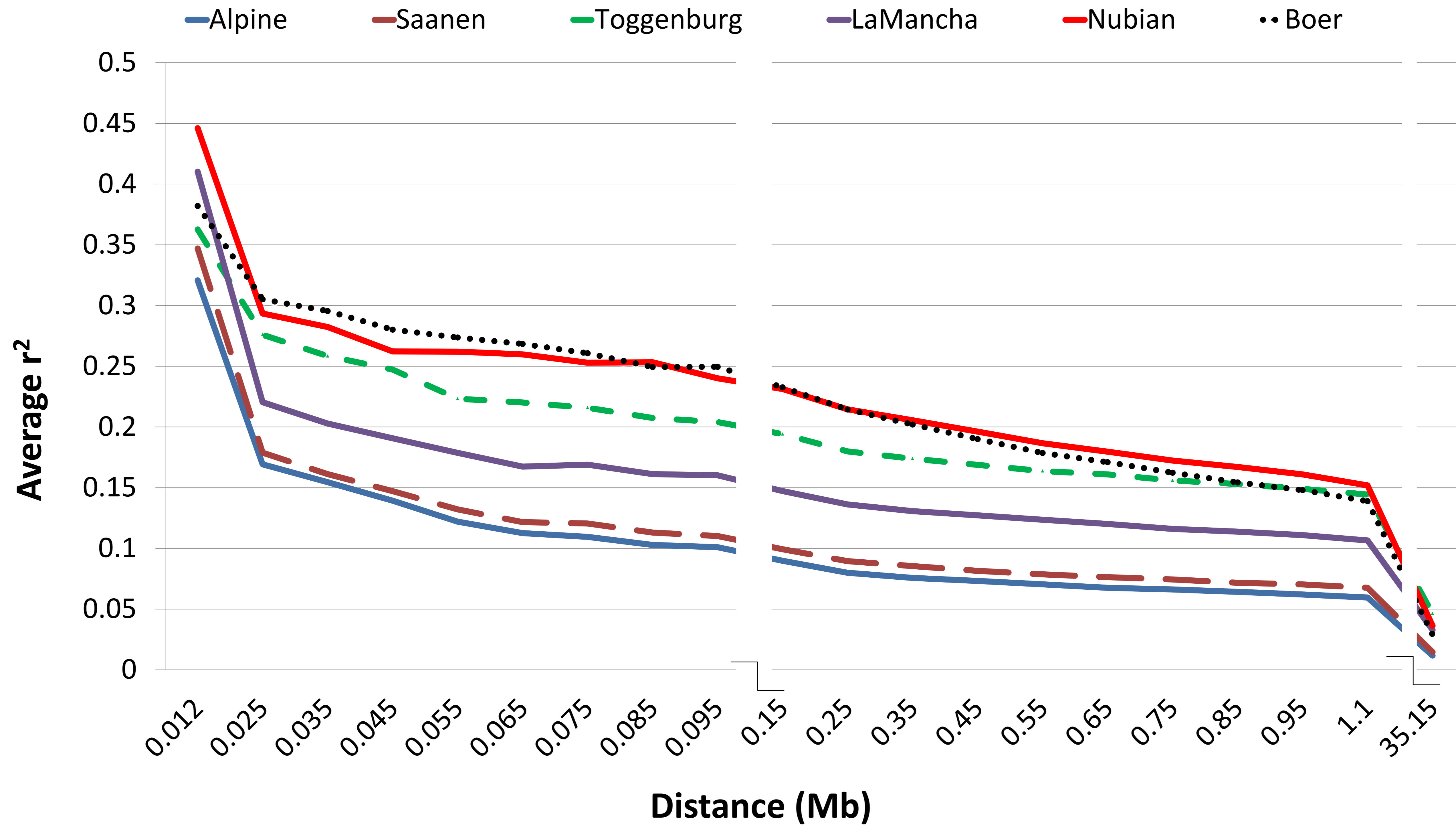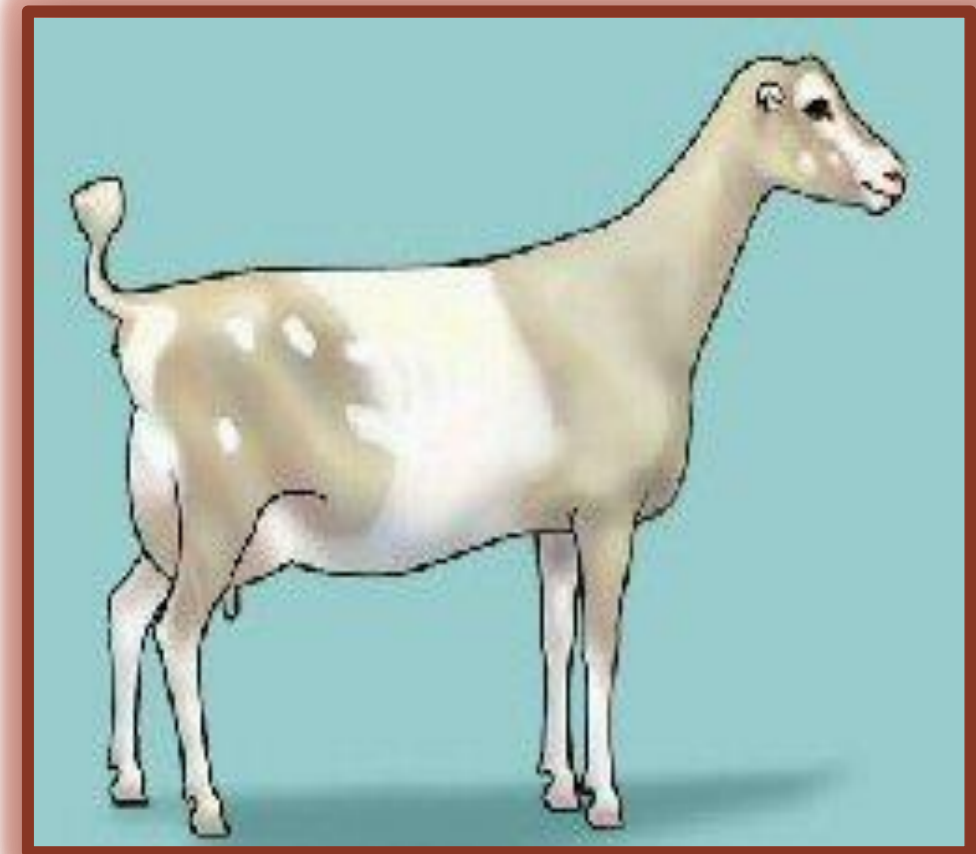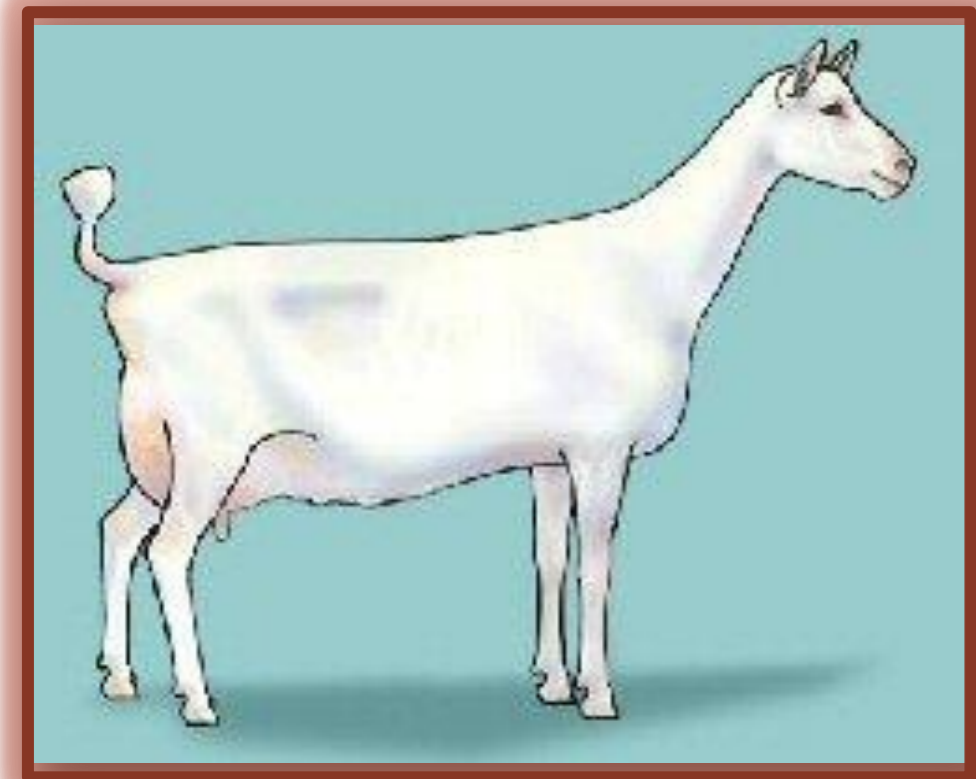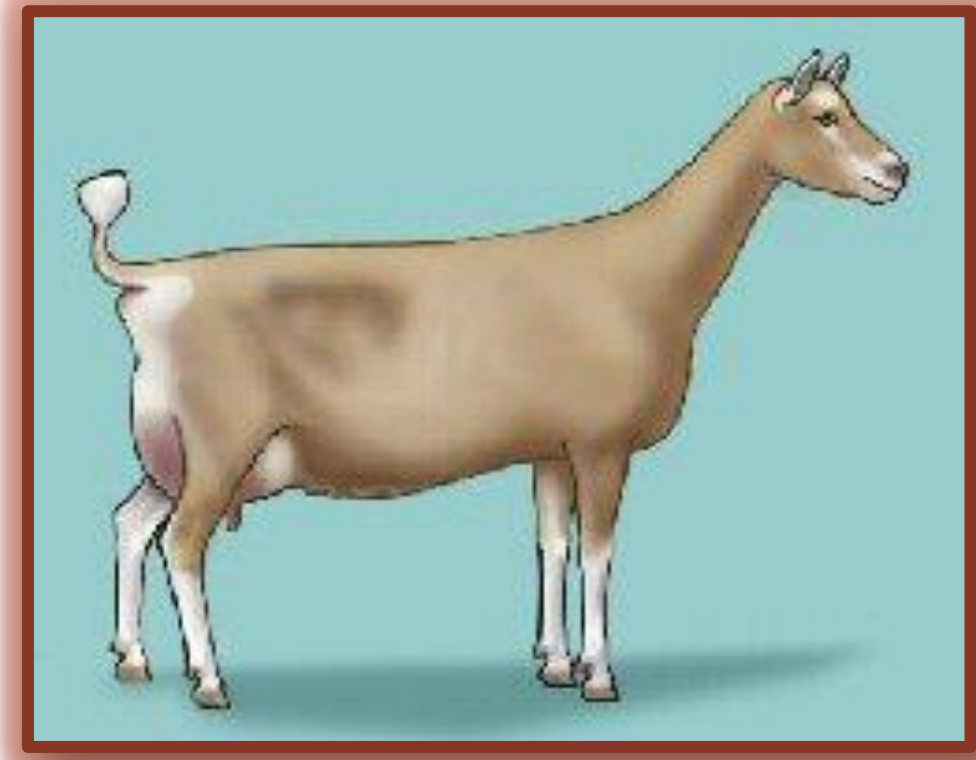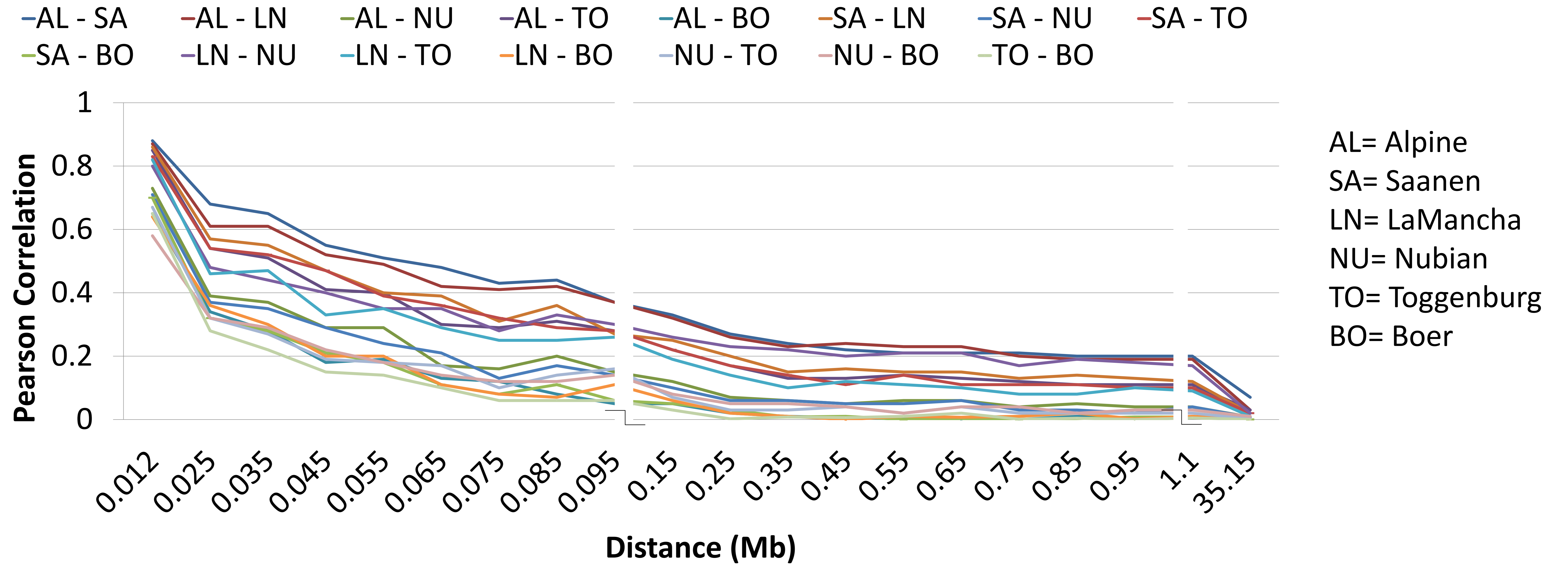
## Acknowledgements***

## Reference

Calus, M. (2008). *Genetics, 178*, 553.

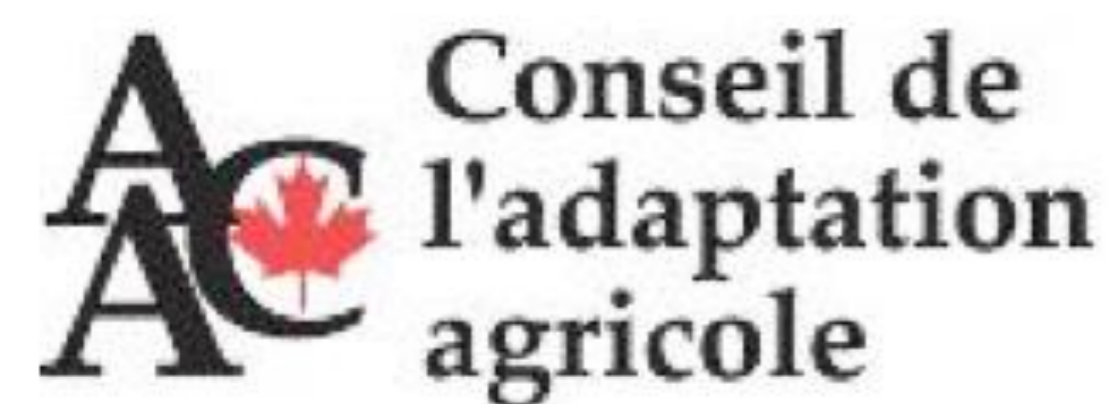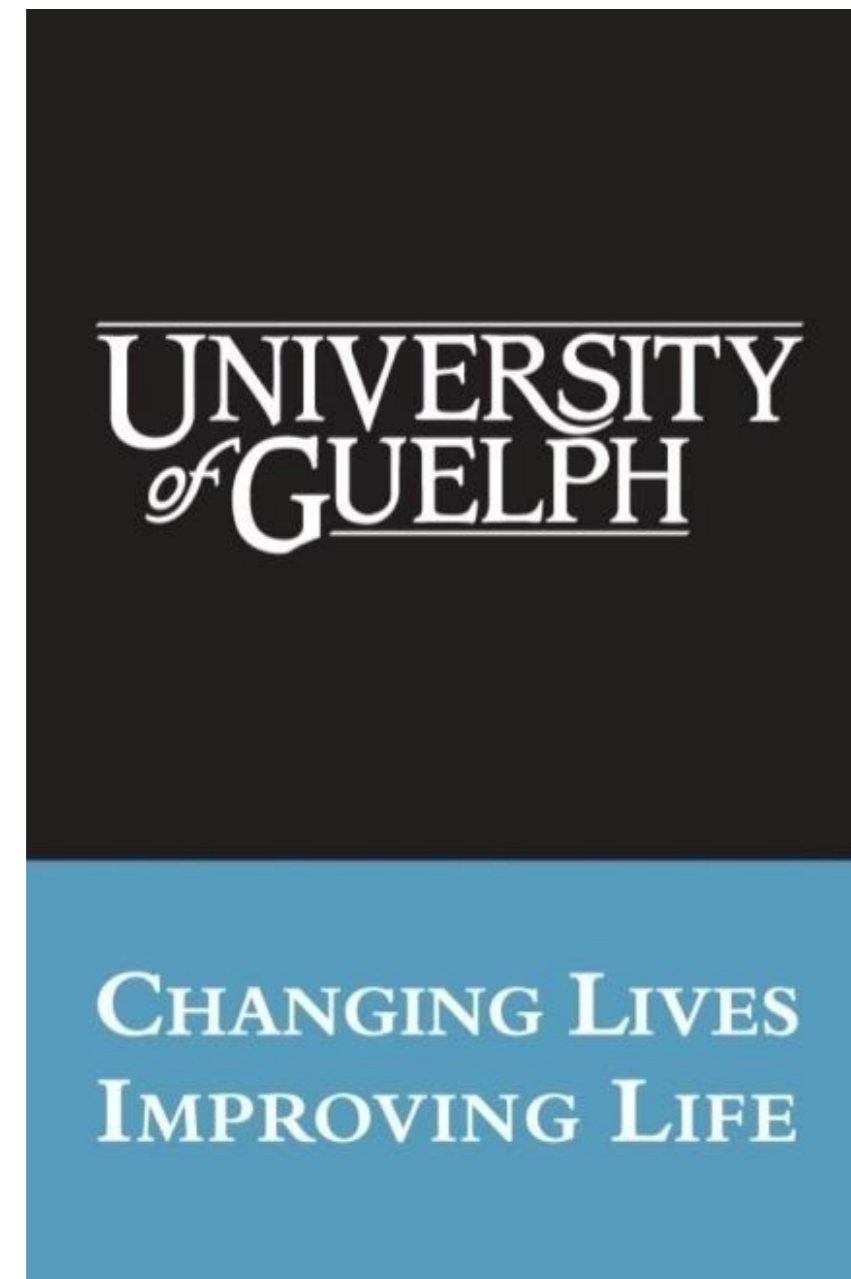Khatkar M. S., F. W. Nicholas, A. R. Collins et al. (2008). BMC Genomics. 9:187.

Figure 1: Average r² values at given distances for six goat breeds.

Figure 2: Consistency of gametic phase (Pearson correlations of signed r values) at given distances for 15 goat breed pairs.

# Acknowledgements



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