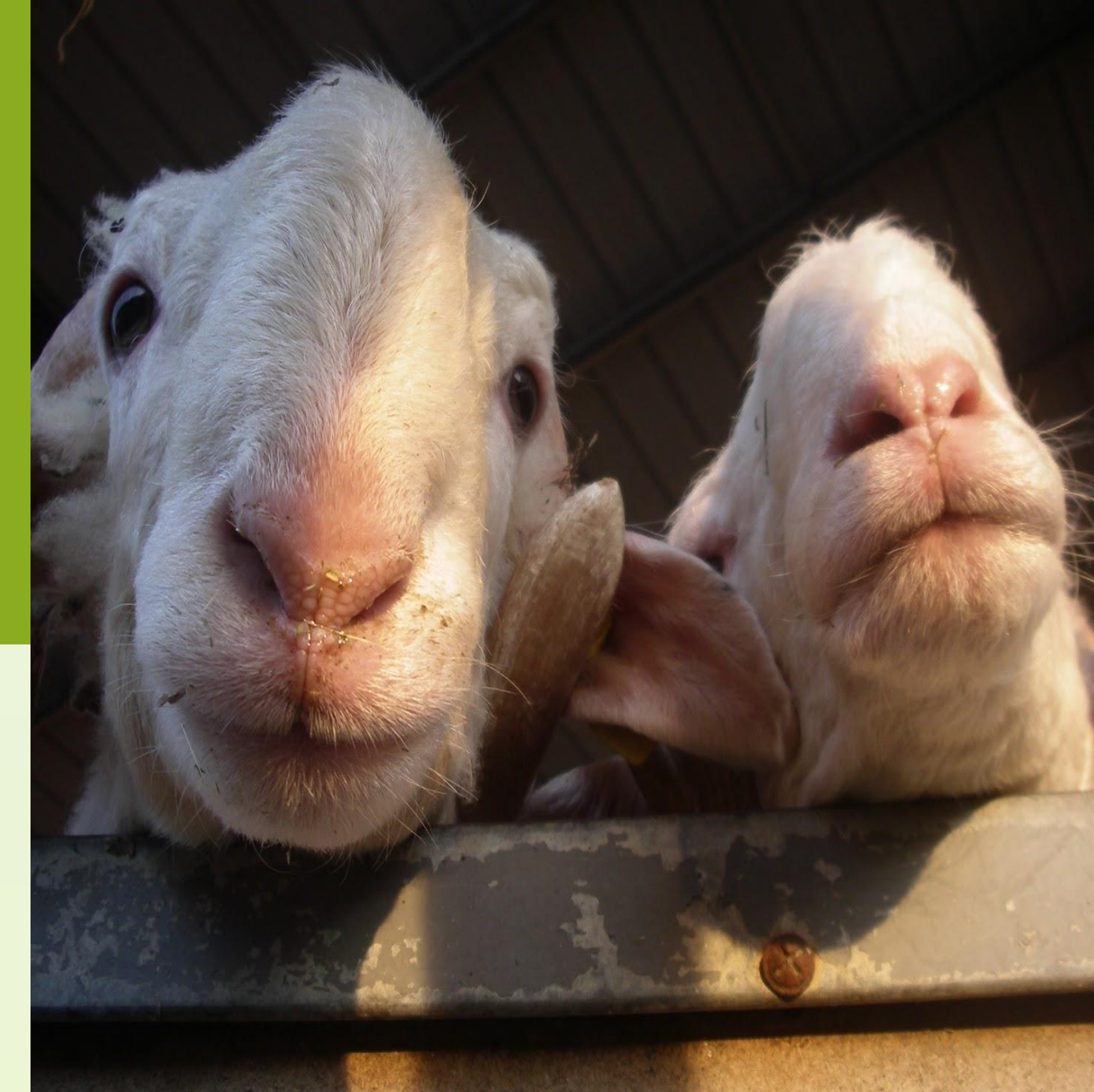


Toward a genomic monitoring of intra-breed sheep variability



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Introduction

Within domestic species genetic variability is in general estimated with pedigree method. Our **objective** was to look into the possibility to use genomic information from genetic evaluations to assess the genetic variability in sheep breeds, considering effective population size as an indicator.

Conclusion

It is possible to use linkage disequilibrium between unlinked loci to estimate the effective population size. However data used should be representative of the population, sufficient in size and contain the same type of animals over different generations.

Material and Methods

Three different methods used:

1. Linkage disequilibrium between physically unlinked loci – Ne_{LD} using the formula from Weir and Hill (1980) adapted by Waples (2006) (SNP data)
2. Inbreeding – Ne_F (Pedigree data, Gutiérrez (2009))
3. Kinship - Ne_K (Pedigree data, Cervantes (2011))

Populations

Four French dairy sheep breeds (Lacaune, Manech Tête Rousse, Basco-Béarnaise, Manech Tête Noire)

Reference populations:

Individuals born or genotyped over 4 years periods (1 generation interval)

Results

Using LD to estimate Ne requires a sufficiently large sample size. For smaller sample size there is a bias on the estimation (Fig. 1)

Problem: substructure is present in 2 breeds. It is possible to account for this substructure by using partial correlations for the estimation of Ne (Fig. 2)

When looking over 1 generation, there is a lot of variation present in certain breeds using LD to estimate Ne (full line). When using conventional pedigree methods (dotted line) we do not detect the same amount of variation (Fig. 3)

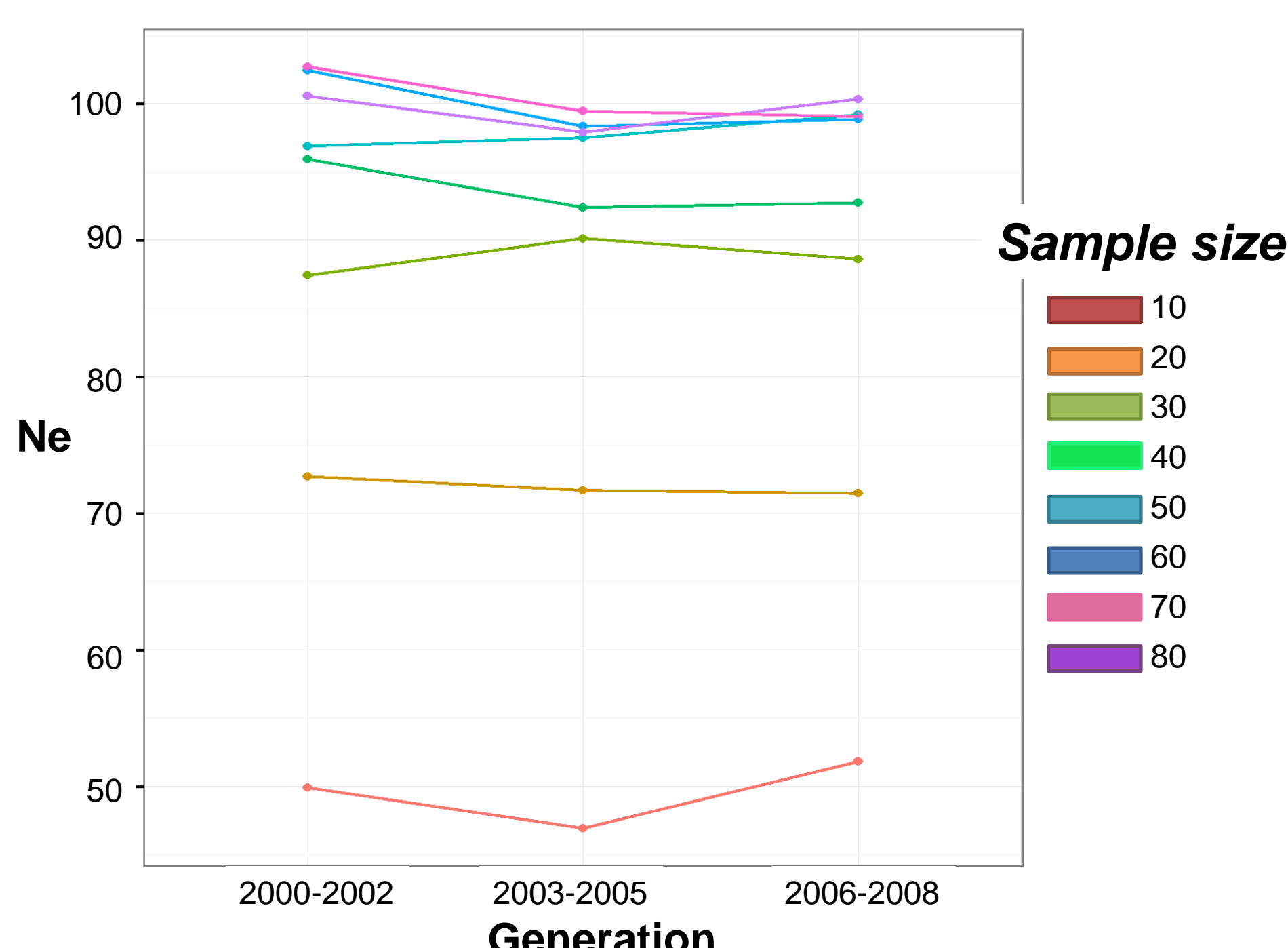


Fig. 1: Effect of sample size on the estimation of Ne

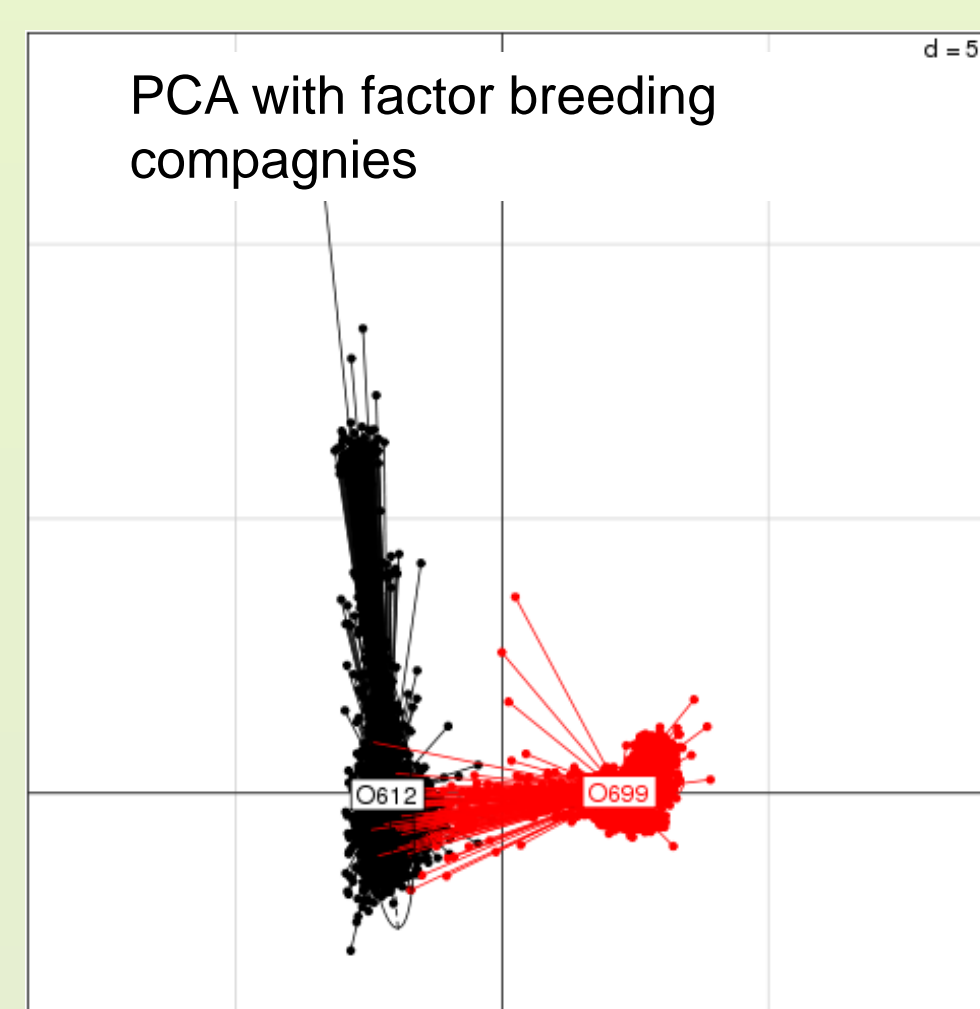


Fig. 2: PCA analysis showing substructure in Lacaune

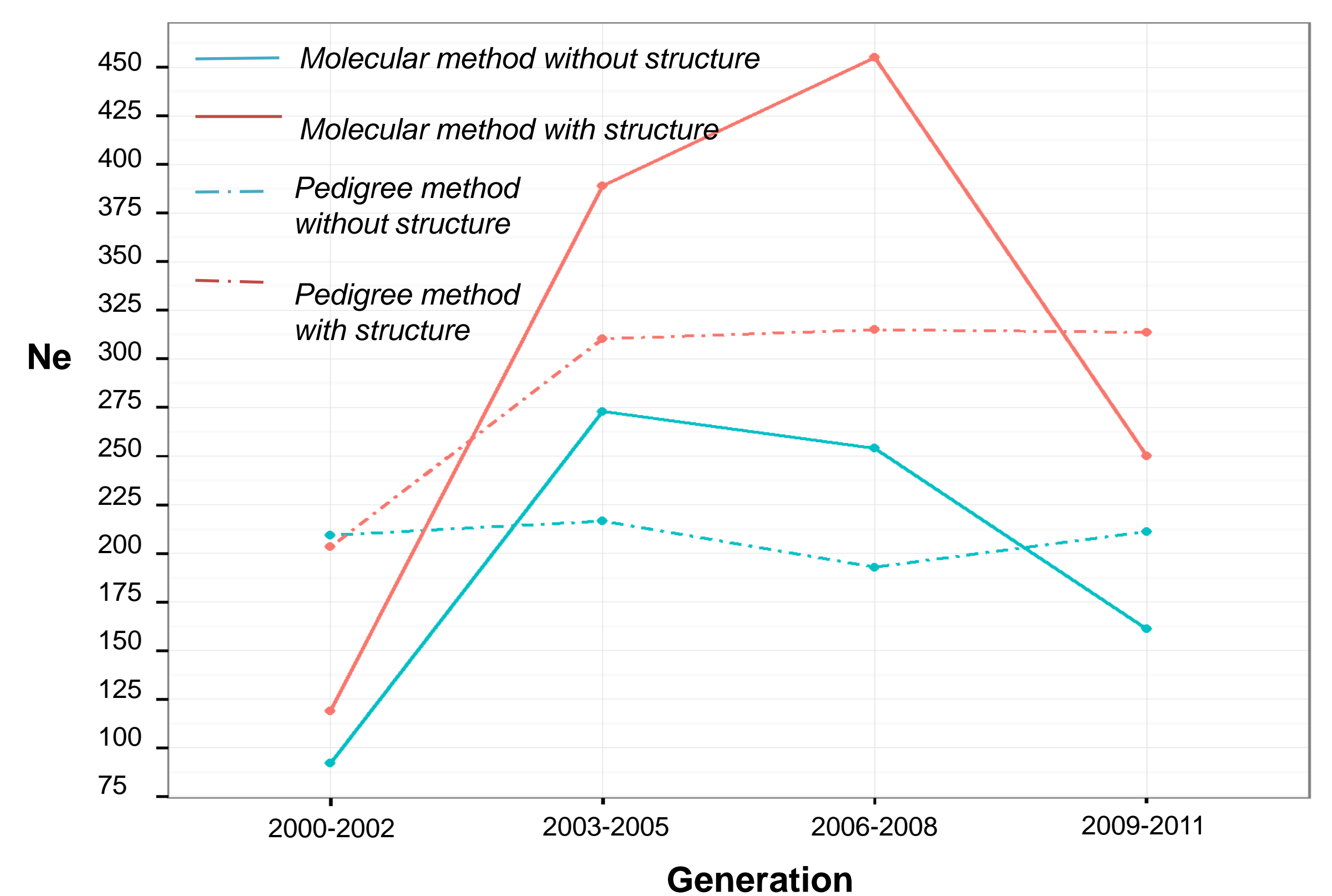


Fig. 3: Ne over small periods of time (1 generation)

Table 1: Ne over 4 generations

Breed	Ne_{LD}	Ne_{LD} (structure)	Ne_F	Ne_K
Lacaune	195	303	223	312
Manech Tête Rousse	118	145	153	148
Basco-Béarnaise	98	/	108	91
Manech Tête Noire	92	/	82	82

When we consider Ne averaged over the 4 generations, there are only minor differences between 3 methods (Table 1)

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