INRAO

> Evolution of genetic variance in Manech Tête Rousse

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Why is genetic variance important?

Basically, because it is the basis for selection

$$\Delta G = \frac{i r_{A,\hat{A}} \sigma_{g}}{L}$$

(Bulmer, 1971 Am. Nat.; Dekkers, 1992 Anim. Prod.; Bijma, 2012 J. Anim. Breed. Genet.; Gorjanc et al., 2015 Geneti. Sel. Evol.)

Loss of genetic variance

Drift

- Due to the finite population
- Measure by the build-up of coancestry
- Well known and demonstrated

Selection

- Changes in allele frequencies
- Negative linkage disequilibrium or Bulmer effect:
 - Not constant
 - Becomes stable in a few generations
 - Well known in theory but not over real data

Objectives of this work

Estimate the yearly genetic variance of milk yield in Manech Tête Rousse dairy sheep

Estimate the loss of genetic variance due to drift

Estimate the loss of genetic variance due to selection (Bulmer effect)

Manech Tête Rousse

- Steady genetic progress $\sim 0.2\sigma_g/year$
- ~35 years of records
- ~60,000 records / year
- ~15,000 females / year
- ~200 elite (AI) males / year

Breeding Objectives

- Milk yield since 1990
- Milk composition since 2003
- Scrapie resistance from 2000 until 2010

Mating System

Limitation for Optimal Contribution:

Al with fresh semen: difficult to plan matings

Nevertheless:

- Matings among "cousins" are avoided: avoidance of recent inbreeding and hence no inbreeding depression.
- Males selection within grand-sire families.
- All females reproduce so there is no optimization to be made.









Data and model

- 540,999 individuals in pedigree
- 1,842,295 records of milk yield pre-corrected for heterogeneity of variances
- Model
 MY = contemporary groups + other fixed effects + animal + permanent
- Only pedigree information

Estimation of genetic variance

Genetic variance at base population σ_a^2

Genetic variance at time t is $\sigma_a^{2(t)} = \frac{1}{n_t} \sum_{i=1,n_t} (a_{i(t)} - \bar{a}_{(t)})^2$. **Estimated** using Gibbs sampling (Sorensen et al., 2001 Gen. Res.).

At each iteration, compute $\tilde{\sigma}_a^{2(t)} = \frac{1}{n_t} \sum_{i=1,n_t} (\tilde{a}_{i(t)} - \bar{\tilde{a}}_{(t)})^2$ where \tilde{a} are samples from the posterior distribution of breeding values

Separately for AI males (which are elite animals) and females (representative of the population).

Expected genetic variance due to build-up of coancestry

The theoretical **expected** genetic variance due to increased inbreeding and coancestry is

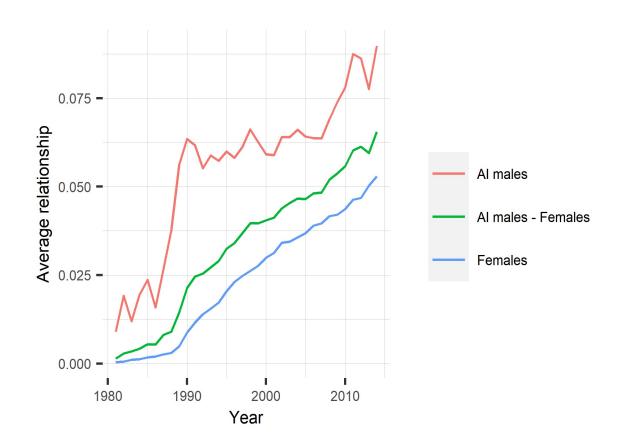
$$\sigma_a^{2(t)} = \sigma_a^2 \left(\overline{diag(\boldsymbol{A_t})} - \overline{\boldsymbol{A_t}} \right) \approx \sigma_a^2 (1 - \overline{\boldsymbol{F}_t})$$

where $\overline{diag(A_t)} = 1 + \overline{F_t}$ is average self relationship and $\overline{A_t}$ is average relationship of animals born in year t. Inbreeding and relationships estimated with INBUPGF90.

Quantification of Bulmer effect

The difference between <u>estimated</u> $\hat{\sigma}_a^{2(t)}$ and <u>expected</u> $\sigma_a^2(\overline{diag(A_t)} - \overline{A_t})$ is due to Bulmer.

Average Relationship

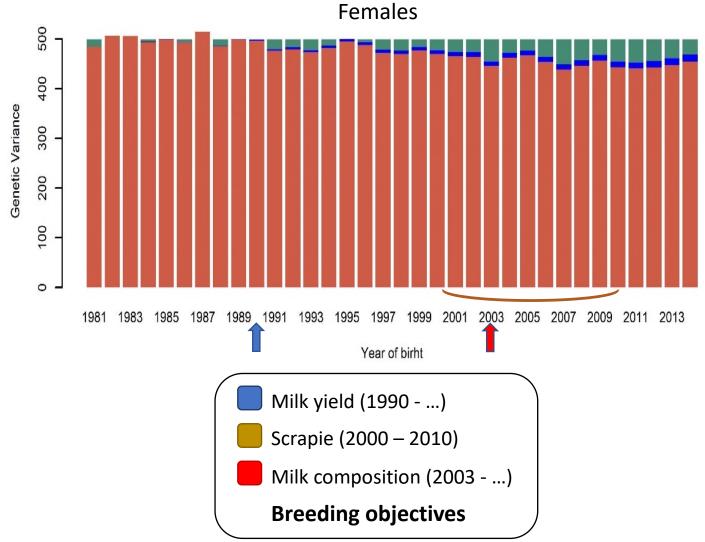


Continued increase of average relationship and inbreeding (not shown).

Low values of relationship.

We do not expect an important loss of genetic variance due to drift.

Genetic variance evolution



Loss due to Bulmer effect (~10%)
Loss due to Coancestry (~3%)
Estimated genetic variance

Stabilization of genetic variance after 2003 (loss of ~13%)

Conclusions

- Neither the loss due to buildup of coancestry (~3%) nor the Bulmer effect (~10%) appear to be important in Manech Tête Rousse
- Use of simple methods to handle diversity controlled well the loss of genetic variance due to drift.
- It is difficult to say if the genetic variance stabilization is due to the Bulmer effect or the changes in breeding objectives.
- Regular monitoring of genetic variance can be easily done and provide information for decision-making in a selection scheme.

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Computing and storage resources

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Thank you very much for your attention!





Questions or ideas?