S24-Ingrid.David@toulouse.inra.fr

Genetic parameters for growth traits in Romane sheep

I. David[1], D. François[1], F. Bouvier[2], L. Bodin[1], B. Bibé[1], J. Bouix[1]
INRA, UR631 Station d'Amélioration Génétique des Animaux, F-31320 Castanet-Tolosan, France
INRA, UE332 Domaine de la Sapinière, F-18390 Osmoy, France

Material and methods

The objective of this study was to estimate, in an experimental farm, the genetic parameters for growth traits. Data from multiparous Romane ewes were analyzed using an animal model including direct and maternal genetic effects, female and litter permanent random effects, significant environmental fixed effects and one way interactions (female age, sex, litter size at birth and weaning, year, season).

Experimental controlled indoor system
- >75% known sires
- Minimal sire misidentification
- Standardized weight measurements

293 sires — 3869 ewes

16350 Romane Lambs (2000-2009)

Results and discussion

		Direct heritability	Maternal heritability	Genetic correlation
Weight	D0 (Birth)	0.22 (0.02)	0.26 (0.02)	-0.19 (0.07)
	D45	0.17 (0.03)	0.10 (0.02)	-0.00 (0.11)
	D64 (Weaning)	0.19 (0.03)	0.07 (0.02)	0.07 (0.17)
	D90 (Slaughtering)	0.23 (0.03)	0.06 (0.02)	-0.08 (0.16)
Average daily gain	0-45	0.15 (0.02)	0.07 (0.02)	0.08 (0.14)
	45-64	0.24 (0.03)	0.04 (0.02)	-0.41 (0.15)

Table 1: Genetic parameters (se) for growth traits

➲ Direct heritabilities in accordance with literature

➲ Low heritabilities for maternal effect in comparison with other breeds

⇨ Small genetic variability for maternal effect in this specific flock (founder of a synthetic line)

⇨ Genetic variability is smaller in adult than in young females

⇨ This « good » controlled indoor system hides the importance of variability of maternal effects for growth traits

➲ No strong antagonistic correlations between direct and maternal effects

Due to …?

Omitting year*flock*sire random factor has been reported as a potential cause of the classical negative correlation estimate. This bias may not occur in this particular data set (results do not change when including sire*year effect).

Conclusion

On this well designed data set (sire identification, standardized measurements…), we do not found a negative genetic correlation between direct and maternal effects which seems more in accordance with the biology. Results will be confirmed with an experimental protocol.