

A bivariate model was used to estimate covariances and correlations per chromosome between growth traits in sheep. We found that 6 chromosomes have large covariance effects (Figure 2) and 5 have a negative covariance, e.g. chromosome 8, revealing that a small number of chromosomes appeared to ‘break’ the positive genetic correlation (overall genetic correlation ~ 0.5).

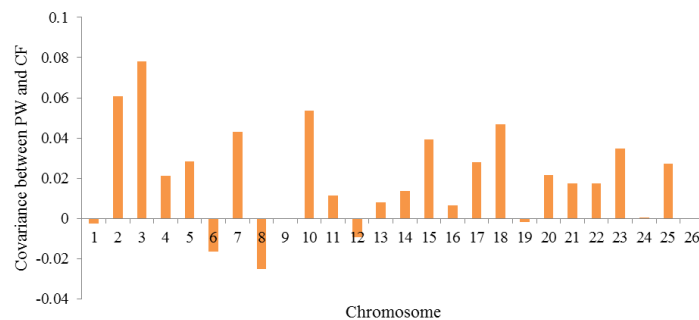


Figure 2. Covariance between post weaning weight (PW) and scanned C site back fat (CF) in merino lambs from bivariate analysis per chromosome.

The main conclusions from the present study are that the inclusion of PC in the model corrects for population structure avoiding co-linearity between the variance components. While the additive genetic variance explained per chromosome is partially related to chromosome length, considerable differences between chromosomes in the amount of additive genetic variance explained were found and a small number of chromosomes appeared to ‘break’ the positive genetic correlation.

The approach presented in our study provides relevant information to the understanding of the genetic underlying complex trait variation and represents a powerful source of information for genomic selection.

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