

Confirmation of the presence of a major gene for fecundity in Thoka Cheviot sheep by segregation analyses

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The putative Thoka gene, increasing fecundity, originated in Icelandic sheep and was introduced and subsequently established in a Cheviot sheep flock in the UK. This study applied segregation analysis to flock litter records to demonstrate the segregation of the Thoka gene within the flock

Data were collected over 13 years on 333 ewes with up to 5 parities per ewe. The total data set comprised 982 litter size records in a pedigree of 806 animals. Segregation analyses were performed using a MCMC method implemented using Gibbs Sampling. The gene was assumed to be purely additive and priors used for variance components were uniform. The polygenic heritability was set at a previous estimate of 0.1.

The results present very strong evidence for a major gene increasing litter size with an additive effect of 0.63 lambs per litter (s.e. 0.073). The gene frequency in the flock was 0.21 (s.e. 0.089) which was consistent with what would be expected given the mating structure. The true heritability of litter size (when taking account of the major gene effect) was 0.31 (s.e. 0.050).

The study detected the segregation of the Thoka gene. The challenge is now to combine this study with genetic marker data to find the chromosomal location of the gene.