GENETIC TRENDS AND ECONOMIC TRAIT LOCI IN ASTURIANA BEEF CATTLE

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INTRODUCTION

The breeders of Asturiana de los Valles cattle keep detailed performance records for many traits including birth and weaning weight and dates (Silva *et al.*, 2002). The breed displays a QTL for muscular hypertrophy, *mh*, which has recently been mapped to chromosome 2, and a marker is available within the locus sequence (Grovet *et al.,* 1997). Previous estimates of additive and dominant effects of its alleles were based on phenotypes (Baro *et al.,* 1998) and now, an increasing number of genotypes along with more adequate statistic tools (Hofer and Kennedy, 1993 ; Baro *et al.,* 2002) are available allowing for better estimates.

MATERIAL AND METHODS

Data. The data set consisted of 10 038 records of average daily gain (adg) from birth to weaning of animals born between 1/7/1997 and 1/2/2002. A summary of genotypes and data is collected in table 1. Several individuals have data available on their performance and that of their progeny (284 sires and 81 dams), and some of these have been typed for the *mh* gene (21 sires and 28 dams).

Table 1. Data and genotypes

	no.	adg	mh/mh	mh/+	+/+
sires of calves	1388	284	20	1	0
dams of calves	7743	81	16	12	0
individuals	23158	-	720	542	57

Model. The data were analysed under the following mixed linear model :

$$adg = id + dam + hmy + cn + sex + mh$$

where adg is average daily gain from birth to weaning, id is the additive genetic effect of the calf, dam is a maternal effect, hmy represents the combined effect of dam's grazing regime, bi-month, and year of calving, cn is the calving number for the dam, sex the calf's gender, and mh is the calf's genotype for the *mh* gene. The same data was analysed under a model not accounting for the the *mh* gene effect.

We used the *Loki* set of programs (Heath, 1997) for Markov chain Monte Carlo segregation

and linkage analysis of quantitative traits under mixed inheritance. Their original aim was multipoint linkage analyses on large pedigrees. Released under an Open Source license, the code is free for anybody to modify and distribute under certain conditions. Inspection of the code revealed that it keeps internally samples from the distribution of the infinitesimal breeding value of each animal in the pedigree file, and minor modifications turned it into a genetic evaluation program capable to account simultaneously for oligo- and poligenic genetics.

RESULTS AND DISCUSSION

Figure 1 shows the course of the Markov chains. The chains stabilised after 500 iterations, and the dispersion of the realizations did not improve after 5000 rounds.

Variance partition. The estimated heritability for the trait adg was 37.58 %, with a standard error of 2.50. The heritability estimated ignoring the *mh* gene was 36.64 % (s.e. 2.41). Segregation of the *mh* gene accounts for 1.12 % (s.e. 0.36) of the total variance, much less than the combined effect of grazing regime and calving season, 26.09 % (s.e. 11.76), or 24.94 % under the simpler model. Fostering is very unlikely, making estimates of maternal effect unreliable at 12.02 % (s.e. 25.68), probably due to error correlations with other parameters, i.e. the individual's additive genetic effect. Changes in frequencies of the *mh* allele, a tendency that has been explored by (Cañón *et al.,* 1998), do not seem to affect the genetic trend for the breed. There was a significant (at the 0.05 level), negative genetic trend of –7.61 gr/d (s.e. 2.98).

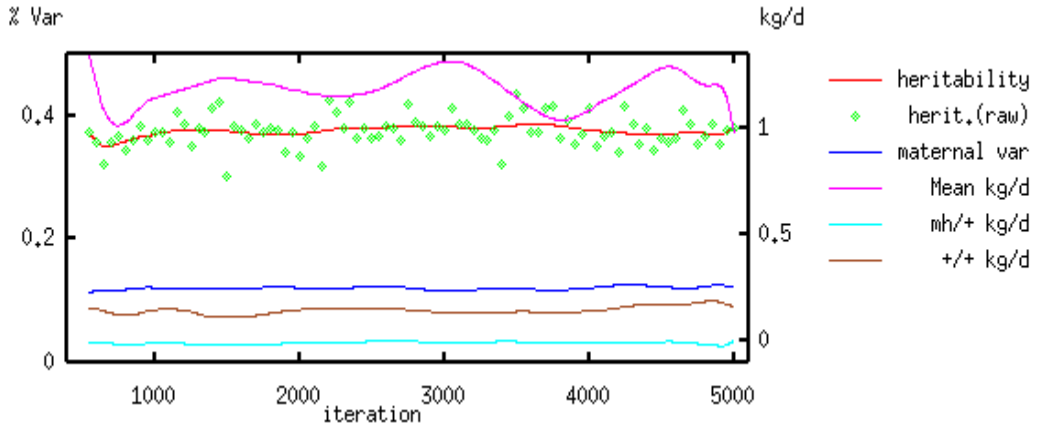

Figure 1. Realizations of the main parameters. Raw data was spline-smoothed into lines

Allele effects. The mh allele of the *mh* gene has an estimated frequency of 78.66 % (s.e. 1.009). It presents full dominance, as the mh/+ genotype is not significantly different from 0, value that corresponds to the homozygous mh/mh : 10.677 g/d (s.e. 16.340). The wild genotype, +/+, increasingly rare, made a particularly better growing individual than the double muscling, homozygous mh/mh : 143.989 g/d (s.e. 57.371)

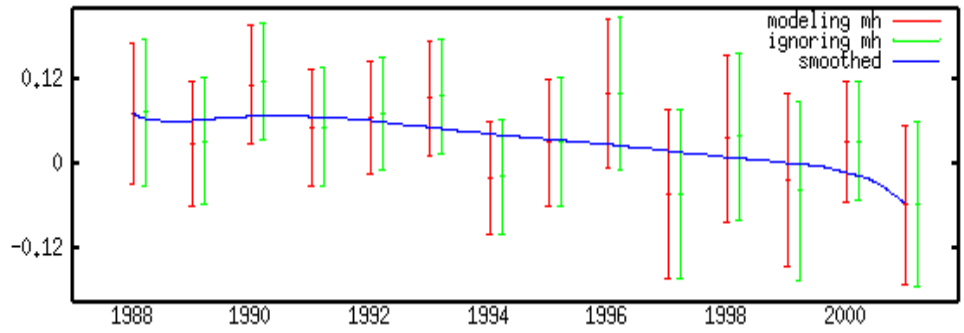

Figure 2. Confidence intervals (95 %) for the year's genetic group

CONCLUSION

Loki constitutes a very powerful tool for the exploration of traits affected by an unknown number of genes of diverse effect sizes. Here we explored its possibilities as an all-purpose, open source genetic evaluation tool capable to handle a more general scenario than the classical "phenotype plus pedigree". Some of the animals are typed for markers with a small number of alleles, which constitutes a very realistic setup. Markers may not necessarily lay within the sequence of a gene of economic importance as in this case. The fact that some individuals may not be typed can be partially overcome by use of segregation information within the genotype update step of the MCMC sampler.

It may be concluded that the mh allele shows full dominance with regard to average daily gain. It had been hinted by previous studies (Baro, 1998 ; Baro *et al.,* 2000) that dominance plays a major role in the expression of muscular hypertrophy, and its impact on poligenic heritability estimates (negligible for the trait under study) deserves further investigation on other traits. It makes it possible to take advantage of breeding double muscling individuals without the risk of loosing the wild, +/+ allele for the sake of diversity.

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