# SCRAPIE GENOTYPE : A CORRELATION WITH LEAN GROWTH RATE ?

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## INTRODUCTION

Scrapie in sheep has been recognised for over two centuries in several countries (e.g. Stamp, 1962 ; Parry, 1983). It is an important transmissible spongiform encephalopathy (TSE) that is fatal and incurable. The incidence of natural scrapie in the Suffolk breed is associated with codon 171 of the prion protein (PrP) gene. Three polymorphisms for codon 171 are known : $Q_{171}$ - recessive allele associated with manifestation of scrapie ; $R_{171}$ – dominant allele associated with resistance ; and, $H_{171}$ – allele considered as neutral with respect to scrapie susceptibility (Hunter *et al*., 1997a).

Since the only known effect of these polymorphisms in the PrP gene in sheep is to confer susceptibility to this fatal disease, both the frequency of the susceptible allele and the incidence of scrapie are expected to be rare. However, the disease remains widespread (Hunter *et al.*, 1997b). This in part may be due to the extended incubation period of the disease, which renders natural selection against scrapie less effective. Another possible explanation could be selective advantage (Woolhouse *et al*., 1999 ; 2001). The susceptible allele may confer a selective advantage in the absence of scrapie or may be linked to traits favoured by breeders.

This study deals with an experimental flock of Suffolk sheep, which became affected by scrapie. The flock was split into two breeding lines, a selection line selected for lean meat production and an unselected control line. Between November 1991 and January 1996 there were 93 cases of scrapie in the flock primarily in the selection line, with no cases earlier. It has been postulated that the selection line might not only have been selected for lean meat but also inadvertently for susceptibility to scrapie (Hunter *et al*., 1997a). The aim of this study was to assess whether there is an association between selection for lean meat production and susceptibility to scrapie.

## MATERIALS AND METHODS

The Suffolk flock considered was established in the early 1980s at the East of Scotland College of Agriculture, now part of the Scottish Agricultural College (SAC). The flock numbered about 140 ewes when closed to outside imports in 1985. It was split into two breeding lines : a selection line (two-thirds of the flock) and an unselected control line. The selection line was selected on a Lean Growth Index in which the breeding goal comprised carcass lean weight and carcass fat weight at a constant age, with relative economic values of

+3 and –1 per kg respectively, as proposed by Simm and Dingwall (1989). The selection criteria were live weight, ultrasonic fat depth, and ultrasonic muscle depth adjusted to 150 days of age. The husbandry of the flock and the details of the selection process are described elsewhere (Simm *et al.*, 2002).

**Scrapie genotypes.** PrP genotypes were established by sequencing polymerase chain reaction (PCR) products and using oligonucleotide probes, as described by Hunter *et al*. (1996, 1997a). Only a proportion of the flock was genotype tested. For the remainder, a predicted genotype was obtained using the procedure of van Arendonk *et al*. (1988). In this procedure the PrP genotypes of individuals were predicted using pedigree information and principals of Mendelian inheritance (Grundy and Lewis, 2001). The level of confidence (or probability) with which a predicted genotype reflected the true genotype was also obtained. Where the probability exceeded 0.90, the predicted genotype was accepted as known.

**Field data.** All animals of $QQ_{171}$, $QR_{171}$ or $RR_{171}$ genotype that had a complete set of information for both performance and scrapie genotype were included. Animals with $QH_{171}$ and $RH_{171}$ genotypes were excluded because they were few in number (as a proportion, 0.05 of total). This limited the data to that on 502 animals born between 1988 and 1994, when the selection component of the experiment ended. Among the animals considered, as a proportion 0.81 had been genotype tested. Estimated breeding values (EBVs) for live weight at scanning, ultrasonic fat depth, and ultrasonic muscle depth were obtained by best linear unbiased prediction (BLUP) using full information from relatives. Simm *et al.* (2002) describe the genetic model used in the analyses. Lean Growth Index score was used as a measure of an animal's overall merit for lean growth rate.

**Statistical analysis.** The performance data (EBV) were analysed using the Residual Maximum Likelihood procedure (REML ; Patterson and Thompson, 1971) in Genstat 5.4 (1998). The fixed effects considered were line, birth year, scrapie genotype and their two-way interactions. Sire nested within line was considered as a random effect for EBVs and Lean Index score. The goodness-of-fit was based on a deviance test.

## RESULTS AND DISCUSSION

The distribution of $PrP_{171}$ genotypes among animals included in the study, and the mean EBVs and Lean Growth Index score of animals of different $PrP_{171}$ genotypes, are shown in table 1 and table 2, respectively. For EBVs and Lean Growth Index score there were no significant line by genotype or year by genotype interactions ($P>0.05$). As expected, there was an interaction between year and line ($P<0.05$), reflecting genetic gain in the selection line. The differences between the means of the three genotypes were small and not significant ($P>0.05$) for any of the four measures studied.

**Table 1. The distribution of $PrP_{171}$ genotypes among animals included in the study**

| Year | Line | Total no. of animals | Genotype | | |
|---|---|---|---|---|---|
| | | | $QQ_{171}$ | $QR_{171}$ | $RR_{171}$ |
| 1988 | Selection | 10 | 3 | 4 | 3 |
| | Control | 7 | 0 | 3 | 4 |
| 1989 | Selection | 55 | 14 | 27 | 14 |
| | Control | 34 | 3 | 11 | 20 |
| 1990 | Selection | 26 | 6 | 18 | 2 |
| | Control | 15 | 1 | 8 | 6 |
| 1991 | Selection | 34 | 15 | 14 | 5 |
| | Control | 18 | 1 | 10 | 7 |
| 1992 | Selection | 59 | 16 | 34 | 9 |
| | Control | 39 | 3 | 17 | 19 |
| 1993 | Selection | 4 | 40 | 34 | 10 |
| | Control | 43 | 7 | 14 | 22 |
| 1994 | Selection | 47 | 47 | 0 | 0 |
| | Control | 31 | 4 | 17 | 10 |
| Total | | 502 | 98 | 210 | 140 |

**Table 2. Last squares means for EBVs and Lean Growth Index score of animals for animals of different $PrP_{171}$ genotype (± standard error)**

| Trait | Sig.[A] | Line | Overall | Genotype | | |
|---|---|---|---|---|---|---|
| | | | | $QQ_{171}$ | $QR_{171}$ | $RR_{171}$ |
| Lean Growth Index score (units) | n/s | **Overall** | **3.23 (±0.21)** | **3.29 (±0.31)** | **3.56 (±0.25)** | **2.85 (±0.31)** |
| | | Selection | 6.48 (±0.29) | 6.51 (±0.35) | 6.75 (±0.34) | 6.34 (±0.49) |
| | | Control | -0.02 (±0.32) | 0.11 (±0.65) | 0.43 (±0.38) | -0.55 (±0.40) |
| Scanning weight (kg) | n/s | **Overall** | **1.35 (±0.20)** | **1.14 (±0.28)** | **1.55 (±0.23)** | **1.37 (±0.28)** |
| | | Selection | 2.77 (±0.28) | 2.64 (±0.33) | 2.91 (±0.31) | 2.73 (±0.43) |
| | | Control | -0.07 (±0.30) | -0.73 (±0.57) | -0.20 (±0.34) | -0.03 (±0.36) |
| Fat depth[B] (mm) | n/s | **Overall** | **-0.67 (±0.07)** | **-0.71 (±0.11)** | **-0.71 (±0.09)** | **-0.59 (±0.11)** |
| | | Selection | -1.11 (±0.10) | -1.08 (±0.12) | -1.17 (±0.12) | -1.76 (±0.17) |
| | | Control | -0.22 (±0.11) | -0.64 (±0.23) | -0.25 (±0.13) | -0.07 (±0.14) |
| Muscle depth[B] (mm) | n/s | **Overall** | **0.79 (±0.08)** | **0.92 (±0.13)** | **0.87 (±0.10)** | **0.59 (±0.13)** |
| | | Selection | 1.77 (±0.11) | 1.92 (±0.14) | 1.82 (±0.14) | 1.58 (±0.20) |
| | | Control | -0.19 (±0.13) | -0.18 (±0.27) | -0.08 (±0.15) | -0.40 (±0.16) |

[A] statistical significance of genotype effect : n/s = not significant
[B] ultrasonic measurement

These results are consistent with those of Roden *et al*. (2001). They found no evidence of a relationship between PrP genotype at codon 171 and performance for these same four measures in the three Suffolk flocks they studied. They found a slight tendency for $QQ_{171}$

genotype animals to have lower EBVs and Lean Growth Index score then the $QR_{171}$ and $RR_{171}$ genotype animals. In both the Roden *et al.* (2001) and this study the performance of $QR_{171}$ animals was numerically the best for scan live weight and Lean Growth Index score.

## CONCLUSION

Our results suggest that breeding for scrapie resistance in sheep is a feasible option in that it is unlikely to have a negative impact on lean growth rate because of any genetic association. From related investigations, the increase in the susceptible allele frequency in the selection line was likely due to chance sampling of animals in the early stages of selection (Grundy and Lewis, 2001). The resistant $PrP_{171}$ allele was not associated with performance in this study. However, if the frequency of this desirable allele is low within a breed and if $RR_{171}$ genotype individuals are heavily favoured as parents, genetic gain in other traits may be slowed.

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