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The T3811>G3811 mutation in the Blonde d'Aquitaine myostatin gene: effects on beef traits

G. Renand¹, A. Vinet¹, G. Caste², B. Picard³, I. Cassar-Malek³, M. Bonnet³, C. Bouyer⁴, V. Blanquet⁴ and A. Oulmouden⁴

¹INRA-AgroParisTech, UMR 1313, 78350 Jouy en Josas, France, ²INRA, UE 0333, 81400 Blaye les Mines, France, ³INRA-VetAgroSup, UMR 1213, 63122 Saint-Genès-Champanelle, France, ⁴INRA-Université de Limoges, UMR 1061, 87060 Limoges, France; gilles.renand@jouy.inra.fr

The mutation (T3811>G3811) recently discovered in the myostatin gene of Blond d'Aquitaine cattle is suspected to result in a reduction in functional Myostatin and consequently to explain the high muscularity in this breed. In order to evaluate the actual effect of this mutation on beef traits, experimental crossbred calves were procreated and tested. Three Blond d'Aquitaine sires were mated to Holstein cows to obtain 3 F1 sires and 9 F1 dams. F2 embryos were implanted into beef heifers. Backcross calves were also obtained mating of F1 sires to Holstein cows. Fifty six calves (43 F2, 13 backcross) were intensively fattened and slaughtered at 169±10 days of age. Birth weight, daily gain and muscularity score were recorded on live animals. Slaughter yield, carcass length, carcass muscularity and fatness scores were recorded at slaughter. The following muscle characteristics were recorded on both Longissimus thoracis (LT) and Triceps brachii (TB) muscles: Isocitrate dehydrogenase (ICDH: oxidative) and Lactate dehydrogenase (LDH: glycolytic) activity, proportions of myosin heavy chain isoforms (MyHC) I, IIa, IIx. ICDH and LDH activities were also recorded in kidney fat. The genotype at the mutation was determined: 18 T/T, 30 G/T, 8 G/G. Highly significant substitution effects (above +1.3 phenotypic s.d.) were shown on carcass yield and muscularity scores. Birth weight was positively affected by the mutation (+0.8 s.d.) but not growth rate, while carcass length and fatness scores were negatively affected (-0.6 to -0.8 s.d.). The TB muscle of calves with a mutated copy had lower oxidative activity and higher proportion of MyHC IIx (around 0.9 s.d.). The mutation had no effect on the LT muscle characteristics neither on the enzymatic activities of kidney fat.

Genetic growth profiles for carcass traits in steers

T.M. Englishby^{1,2}, R.D. Evans³, G. Banos², M.P. Coffey², K.L. Moore² and D.P. Berry¹

¹Teagasc, Animal & Grassland Research and Innovation Centre, Moorepark, Fermoy, Cork, Ireland,

²Scotland Rural College, Roslin Institute Building, Easter Bush, Midlothian EH25 9RG, United Kingdom,

³Irish Cattle Breeding Federation, Bandon, Cork, Ireland; tanya.englishby@sruc.ac.uk

Livestock mature at different rates depending on their genetic merit; therefore, the optimal age at slaughter for progeny of certain sires may differ. The objective of this study was to generate sire genetic profiles for carcass weight, carcass conformation and carcass fat, in steers of multiple beef and dairy breeds, including crossbreeds. Slaughter records from 124,641 steers, aged between 360 and 1,200 days, from 7,949 sires were available from the Irish national database. Variance components for each trait were generated using sire random regression models that included quadratic polynomials for fixed and random effects; heterogeneous residual variances were assumed across ages. Heritability for carcass weight, conformation and fat score across age at slaughter varied from 0.44 (801 days) to 0.53 (650 days), from 0.40 (650 days) to 0.45 (759 days), and from 0.24 (1,183 days) to 0.31 (673 days), respectively. Genetic correlations within each trait weakened as the interval between ages compared lengthened, suggesting a different genetic background for different ages. Eigenvalues and eigenfunctions of the additive genetic covariance matrix substantiated this but also revealed genetic variation among animals in the shape of the growth profiles for carcass traits. Genetic correlations between carcass weight and conformation were positive, reaching a peak correlation of 0.56 at 824 days. Genetic correlations between carcass conformation and fat score were weak (-0.07 at 650 days to 0.06 at 1,010 days), as were the correlations between carcass weight and fat score, ranging from -0.25 (770 days) to 0.17 (1,010 days). Genetic parameters presented indicate genetic variability in growth rate at different ages exists, which can be exploited through breeding programs and used in decision support tools.