Effect of breed and sire expected progeny difference for carcass weight on the expression of growth related genes in muscle of steers

S.M Keady[1], D.A Kenny[3], M.G Keane[4], S.M Waters[2]
[1]National University of Maynooth, Kildare, Ireland, [2]Teagasc, Animal Bioscience Centre, Grange, Co.Meath, Ireland, [3]School of Agriculture, Food Science & Veterinary Medicine, University College Dublin, Belfield, Dublin, Ireland, [4]Teagasc Beef Research Centre, Dunsany, Co.Meath, Ireland
Email: sarah.keady@teagasc.ie

Introduction Growth rate of bovine skeletal muscle is a trait of economic importance to beef production (Sudre *et al*. 2005). Selective breeding to increase muscle growth rate in cattle would enhance beef production in Ireland. Currently, the Irish Cattle Breeding Federation (ICBF) compiles breeding values for growth in cattle, expressed as expected progeny differences for carcass weight (EPD_{cwt}) but this is based on an amalgam of muscle, fat and bone growth. Elucidation of the molecular regulation of muscle growth rate may lead to the identification of molecular markers for growth traits which could subsequently be incorporated into breeding programs. The objective of this study was to examine the effect of breed and sire EPD_{cwt} on the expression of growth related genes in muscle of beef cattle.

Materials and methods This study utilised muscle samples harvested at slaughter from the study of Campion *et al*. (2009). The animals used were cross-bred Aberdeen Angus (AA; n=16) and Belgian Blue (BB; n=16) steers, born to Holstein Friesian dams and sired by AI bulls with either high (H) or low (L) expected progeny difference for carcass weight (EPD_{cwt}). The 32 animals represent the progeny of 16 different sires (AA; n = 7 and BB; n =9). At the end of their 2nd grazing season the animals were assigned to one of two mean slaughter weights (SW) *viz.*560kg (Light) or 620kg (Heavy), having been blocked within breed and sire EPD_{cwt} and balanced for live weight, sire and age. The finishing diet consisted of a total mixed ration with a grass-silage:concentrate ratio of 30:70 on a dry matter basis. Following slaughter, samples of *Longissimus dorsi* muscle were harvested from the animals; snap frozen in liquid nitrogen and stored at -80°C. RNA quantity and quality was determined prior to first strand cDNA synthesis. GAPDH was selected as the most suitable reference gene using GeNORM software. Quantitative real time reverse transcription RT-PCR reactions were carried out to measure the relative expression of a number of muscle growth related genes. The software package GenEx 4.2.2 (MultiD Analyses AB) was used for normalisation to the reference gene (GAPDH). Non-normally distributed data were transformed as appropriate by raising to the power of λ (TransReg procedure, SAS, 2001). Data were analysed using mixed models ANOVA (PROC MIXED, SAS 2001). Breed, genetic merit (GM) and slaughter weight were included as fixed effects in the statistical model, together with all appropriate two- and three-way interactions. Sire was included as a random effect.

Results No three-way interaction was detected. There were GM x SW interaction for IGFBP5 (P <0.05), IGF1 receptor (P <0.01) and IGF2 receptor (P <0.05), B x SW interactions (P <0.05) for IGFBP3, growth hormone receptor (GHR) and myostatin and a B x GM interaction for IGF2. There was no clear effect of the main factors of B or GM on the expression of any gene examined though IGFBP2 was higher at heavier SW.

Table 1 Effect of breed (B), sire EPD_{cwt} (GM) and slaughter weight (SW) on the relative expression of 10 genes examined (P <0.05, ** P <0.01, *** P <0.001)

	B		GM		SW		SEM	Statistical Significance					
Gene	AA	BB	H	L	Heavy	Light		B	GM	SW	BxGM	BxSW	GMxSW
IGFBP2	11.3	13.2	15.4	9.09	16.25	8.30	3.70	NS	NS	*	NS	NS	NS
IGFBP3	41.9	5.09	30.3	16.7	25.59	21.4	3.55	***	*	NS	NS	*	NS
IGFBP4	6.06	8.06	7.50	6.62	6.93	7.19	1.90	NS	NS	NS	NS	NS	NS
IGFBP5	14.8	19.0	19.4	14.5	9.53	24.4	8.23	NS	NS	NS	NS	NS	*
IGFBP6	3.8	3.54	4.50	2.79	3.97	3.33	0.56	NS	NS	NS	NS	NS	NS
IGF1-R	15.5	3.94	8.27	11.1	8.00	11.4	1.18	***	NS	NS	NS	NS	**
IGF2	16.1	21.1	15.6	21.6	14.32	22.9	2.32	NS	NS	*	*	NS	NS
IGF2-R	6.38	11.2	8.97	8.59	9.30	8.26	1.09	**	NS	NS	NS	NS	**
GHR	10.7	4.74	6.00	9.44	4.64	10.8	2.61	*	NS	*	NS	*	NS
Myostatin	10.6	5.50	7.09	9.04	4.99	11.1	4.12	*	NS	NS	NS	*	NS

Conclusion The data indicate that the local expression of some genes involved in muscle growth and proliferation can be influenced by the interaction of both genetic and management factors. These interactions are also consistent with the animal performance data of Campion *et al.* (2009) and merit further investigation. Overall, this information is important to the understanding of the biological control of muscle growth and to the interpretation and planning of gene expression based studied.

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