

Characterization of the F94L Double Muscling Mutation in Pure- and Crossbred Limousin Animals

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Summary and Implications

The objective of this study was to investigate the nature of the effect of the F94L variant in the myostatin (MSTN) gene on economic traits in Limousin and Limousin-Angus crossbred animals in the context of genomic analyses using Illumina BovineSNP50 Bead chip genotypes.

Introduction

Mutations in the MSTN gene have been identified at high frequencies in some heavily muscled beef cattle breeds. The mutations comprise deletions, insertions, or nucleotide substitutions that interrupt production or activity of the MSTN gene. There are at least nine identified mutations that cause muscular hypertrophy. The F94L mutation in MSTN is common in purebred Limousin and descendant crosses such as Lim-Flex. Lim-Flex is a cross between Limousin and (Red or Black) Angus, and is a popular Limousin hybrid in the United States. In this research, we characterize the effect of the F94L mutation on commonly recorded traits in Limousin cattle.

Materials and Methods

A total of 2,945 beef cattle including 1,912 purebred Limousin, 135 Lim-Flex, 800 Black Angus and 98 Red Angus were available in this study. The SNP marker data were from Illumina BovineSNP50 chips with 53,314 autosomal SNPs. The F94L mutation, which is not present in Angus or Red Angus cattle was genotyped by GeneSeek in most of the Limousin and Lim-Flex animals for whom DNA was still available, and the frequencies in each breed are in Table 1. The small number of missing SNP and F94L genotypes were imputed with BEAGLE software.

Published EPDs from national evaluation were expressed as EBVs and deregressed (Garrick et al., 2009 GSE). The parent average EBV (PA) was added back to the

deregressed estimated breeding values (DEBV) in order to account for breed and family differences in subsequent analyses. Bayes C method with $\pi = 0.99$ was used to estimate SNP marker effects and for the genome-wide association studies (GWAS) to calculate variances attributed to every 1 Mb genome window using GenSel software (Garrick and Fernando, 2013, CABI).

Results and Discussion

Results for the most significant windows from GWAS analyses are in Table 2. The F94L mutation, located on BTA2 at 6.21Mb, had the highest model frequency among SNPs within this genome region across many different traits (Birth Weight, Calving Ease Direct, Ribeye Area, Milk or Weaning Weight Maternal, Marbling and Yield Grade) in the purebred Limousin dataset, Lim-Flex dataset or the dataset pooling all these breeds. The GWAS results in this study confirm that the amino acid substitution at this position (F94L) is associated with dramatic phenotypic effects on growth and muscling traits and negative effects on Marbling.

Acknowledgments

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Table 1. Number of animals genotyped in each breed for F94L mutation (+ is the normally muscled wild type allele).

Breed	F94L genotype			Total
	Mh /mh	Mh /++	++ / ++	
purebred	1,271	586	55	1,912
crossbred	77	52	6	135
Angus	0	0	800	800
Red Angus	0	0	98	98
Total	1,348	638	959	2,945

Iowa State University Animal Industry Report 2015

Table 2. The most significant 1 Mb genome windows and lead SNPs associated with routinely recorded traits in Limousin and Limousin crossbred animals.

Trait	Breed	Most sig. window(s)			Lead SNP		
		BTA_Mb	No. SNP	% var	Name of most sig. SNP	Model Freq.	Additive effect
Birth Weight	purebred	2_6	12	2.33	F94L	0.9972	1.009
	crossbred	2_6	12	2.14	F94L	0.9950	0.990
	Pooled	2_6	12	2.97	F94L	1.0000	1.052
Calving Ease Direct	purebred	2_6	12	1.42	F94L	0.7185	-1.082
	crossbred	2_6	12	1.23	F94L	0.7387	-1.088
	Pooled	2_6	12	4.01	F94L	0.9893	-1.061
Ribeye Area	purebred	2_6	12	3.23	F94L	0.8672	0.071
	crossbred	2_6	12	2.87	F94L	0.6680	0.049
	Pooled	2_6	12	1.01	F94L	0.8478	0.087
Milk	purebred	24_22	22	0.65	Hapmap59298-rs29022301	0.3900	-0.750
		2_6	12	0.56	F94L	0.3664	-0.790
	crossbred	2_6	12	0.78	F94L	0.4795	-1.081
	Pooled	2_6	12	1.80	F94L	0.7850	-1.883
Marbling	purebred	25_180	13	1.04	ARS-BFGL-NGS-44798	0.9617	-0.024
		2_6	12	1.03	F94L	0.6424	-0.179
	crossbred	2_6	12	1.02	F94L	0.9403	-0.022
	Pooled	4_83	25	0.52	BTB-02092948	1.0000	-0.117
2_6		12	0.41	F94L	0.6843	-0.036	
Yield Grade	purebred	2_6	12	3.79	F94L	0.8278	-0.026
	crossbred	2_6	12	3.85	F94L	0.8752	-0.028
	Pooled	2_6	12	0.30	F94L	0.8295	-0.044