

GENOTYPE FREQUENCIES OF A NON-SYNONYMOUS POLYMORPHISM IN THE CALPAIN I GENE VARY AMONG BREEDS



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Background:

A single nucleotide polymorphism (SNP) in exon 9 of the bovine calpain I gene results in an amino acid substitution of alanine (A) to glycine (G) in the proteolytic enzyme μ -calpain. Several studies have determined that genotypes at this locus are associated with Warner Bratzler Shear Force (WBSF) in bovine *longissimus thoracis et lumborum* aged for 14 days. AA and GA genotypes of the SNP are associated with lower shear force (increased tenderness) compared to the GG genotype. In order to assess the potential of this SNP in marker assisted selection programmes, it is first necessary to establish the baseline frequency of the desirable genetic variants in different breeds.

Objective:

The objectives of this study were to determine genotype and allele frequencies for the exon 9 locus of the calpain I gene in bulls of six of the main breeds in the Irish herd and determine if frequencies differ among breeds.

Materials & Methods:

DNA was extracted from muscle tissue of 262 bulls of six of the main beef breeds in the Irish herd (29 Aberdeen Angus, 10 Blonde d'Aquitaine, 38 Charolais, 48 Simmental, 24 Hereford and 61 Limousin) using the QIAamp® DNA mini kit (QIAGEN). Genotyping was carried out by Genetic Solutions Ltd, QLD, Australia. Genotype and allele frequencies for this locus were estimated for each breed. Tests for Hardy Weinberg equilibrium and pairwise genetic differentiation among breeds were carried in Genepop. Hierarchical F_{ST} which partitions genetic differentiation within and among samples (analogous to ANOVA) and pair wise F_{ST} were also estimated using Genepop.

Results:

The overall sample and individual breeds were found to be in Hardy-Weinberg equilibrium (Table 1), but overall allele frequencies differed significantly among breeds ($P < 0.001$). Genetic differentiation among breeds was moderate with global F_{ST} of 0.06 but no substructure was detected within breeds ($F_{IS} = -0.02$). Genotype and allele frequencies are presented in Figures 1 and 2. Pair wise comparisons indicated that there are significant differences in allele frequency between some pairs of breeds (Table 2). In the samples tested, the allele associated with reduced shear force (A) was at higher frequencies in Angus, Charolais and Limousin bulls (0.17-0.18) than Hereford (0.04) and was absent in Blonde d'Aquitaine and Simmental bulls (Figure 2).

Conclusion:

This evidence suggests that significant variation exists in allele frequencies among breeds at this calpain I SNP. The potential to increase beef tenderness in the Irish herd via marker assisted selection using this SNP thus varies depending on breed. Of the breeds tested, highest frequencies of the desirable genotypes were found in Angus, Charolais and Limousin bulls.

Table 1: Tests for Hardy-Weinberg equilibrium

Breed	P-val	S.E
Angus	0.558	0.0015
Blonde d'Aquitaine	-	
Charolais	1	0
Hereford	1	0
Limousin	1	0
Simmental	-	
Overall	0.999	

Figure 1: Genotype frequencies for the calpain I SNP

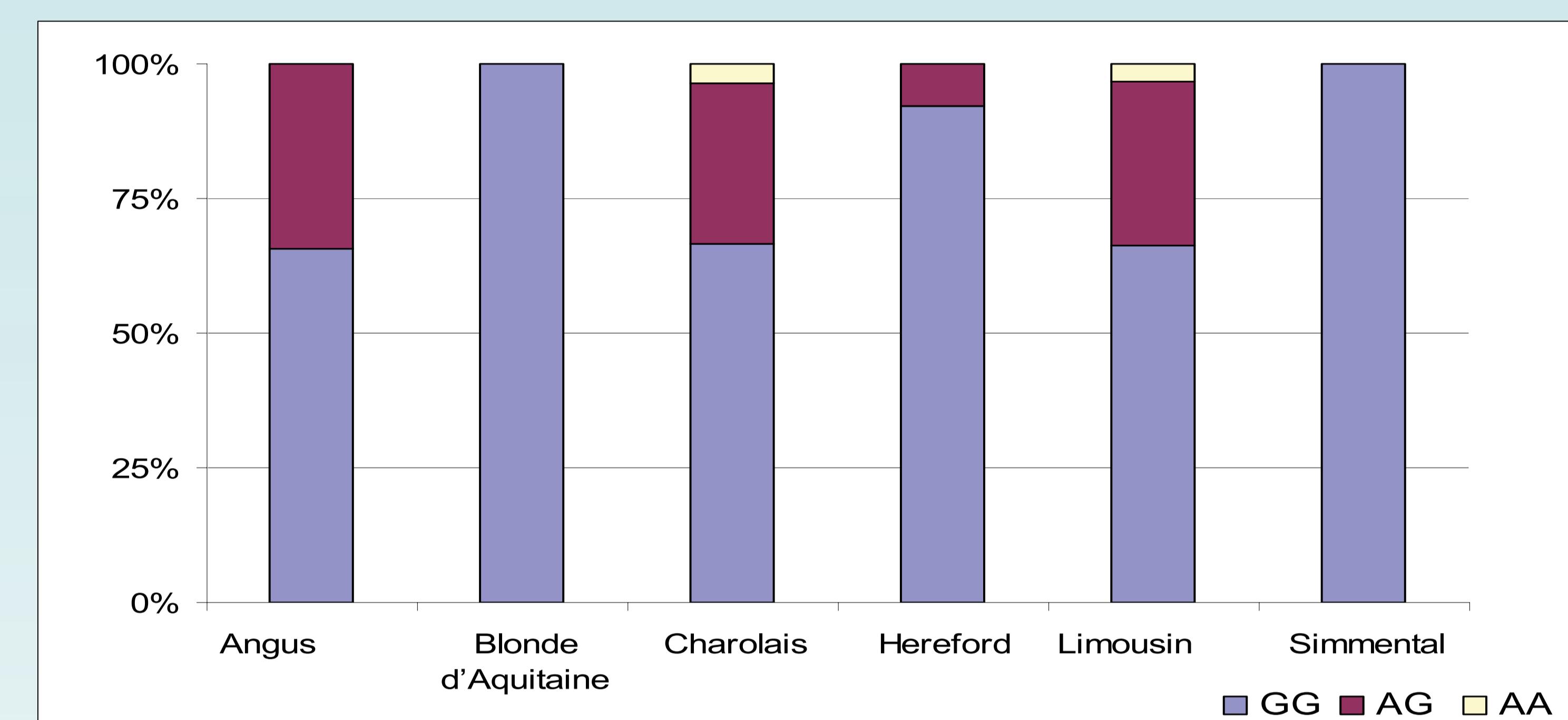


Figure 2: Allele frequencies for the calpain I SNP

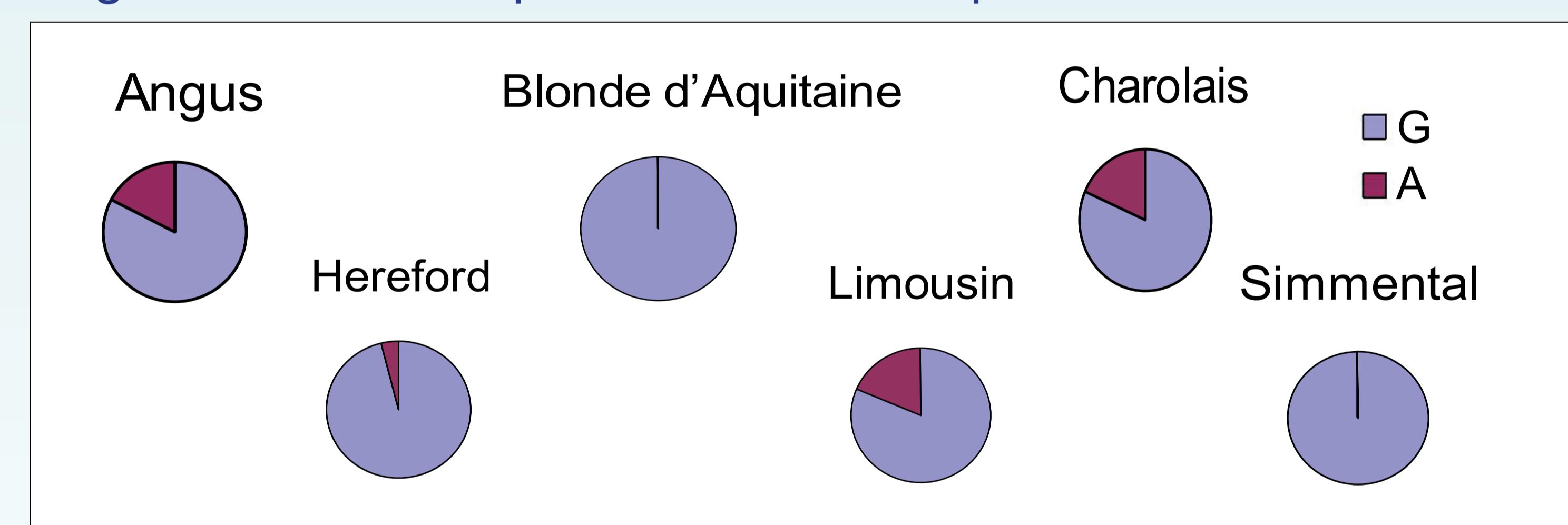


Table 2: Pairwise F_{ST} among breeds (lower diagonal) and P values for pair wise genic differentiation (upper diagonal)

	Angus	BldAquitaine	Charolais	Hereford	Limousin	Simmental
Angus		0.056	1.00	0.032*	1.00	<0.001**
BldAquitaine	0.099		0.044*	1.00	0.029*	-
Charolais	-0.012	0.091		0.013	1.00	<0.001**
Hereford	0.074	-0.007	0.072		0.008**	0.122
Limousin	-0.01	0.088	-0.007	0.067		<0.001**
Simmental	0.208	-	0.164	0.040	0.140	

* $P < 0.05$, ** $P < 0.01$, BldAquitaine = Blonde d'Aquitaine

Acknowledgements

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