O-04-02

Polymorphisms in the genes of glycolysis are associated with beef production and quality traits in South African purebred bulls (#537)

Annie Basson[1, 2], Lorinda Frylinck[1], Phillip Strydom[1]

[1] Agricultural Research Council, Animal Production, Pretoria, South Africa; [2] University of Pretoaria, Animal and Wildlife Sciences, Pretoria, South Africa

Introduction

Intermediary metabolic processes of the sarcoplasm play a critical role in determining the cellular conditions, which in turn influence both structural and biochemical processes of the conversion of muscle to meat. In these processes, glycolysis plays a key role in determining the rate of pH decline, which in turn can influence a range of beef quality traits. Analysis of single nucleotide polymorphisms (SNPs) of causal genes is a useful tool to verify genes for beef production and quality traits, in order to design custom SNP panels for specific subpopulations, or even individual herds.

Methods

To determine the role of polymorphisms in the genes for the enzymes of glycolysis, 144 SNPs of the Bovine-HD SNP BeadChip (Illumina) were used in a correlation analysis for beef traits, including growth, colour, tenderness, calpain protease activity, water-holding capacity (WHC), drip and cooking loss, and metabolite concentrations. All bulls were feedlot-finished, purebred South African beef breeds (n=166) and loins were used to determine meat quality. Data were analysed using PLINK, with Bonferroni correction of *P*-values (a=0.05).

Results

There were 35 associations with average daily gain over the last 35 days of the finishing period (ADG35), where individual SNPs explained between 6.9-19.8% of the variation in ADG35. The most notable associations were observed for the hexokinase 1 gene (*hk1*), which could favour energy supply to cellular metabolic processes, by maintaining the glucose concentration gradient into muscle fibres. Of the 19 SNPs in the *hk1* gene that correlated with ADG35, 11 exhibited R^2>10% (up to 19.8%, P<0.0001).The *hk3* gene (R^2<13.9%) and the gene for the M isomer of lactate dehydrogenase (*ldha*) also exhibited strong correlations with growth.

There were 9 correlations with lightness (L*), particularly for SNPs in the muscle-type phosphofructokinase (*pfkm*), *hk1* and *ldhb* genes (R^2=6.6-8.9%). Yellowness (b*) and chroma (C*) both exhibited seven correlations with glycolysis enzyme SNPs, where both traits were particularly influenced by the muscle-type phosphofructokinase gene (*pfkm*), *ldhb* and *hk1* (R^2=6.7-14.4%), although *ldhd* made an important contribution to the C* phenotype.

Individual SNPs in glycolytic genes affected tenderness, measured as myofibril fragment length (MFL, R^2=6.9-11.0%) and Warner-Bratzler shear force (WBSF, R^2=6.7-9.8%). Notable genes that affected tenderness were *ldha* and *ldhd*, enolase 1 (*eno1*), *hk1* and phosphoglycerate kinase (*pgk1*). These associations can be linked to correlations between the glycolytic SNPs and protease activities, where 35 correlations between genotypes and calpain, calpastatin and/or relative calpastatin were observed in the *eno1*, *hk1* and *ldhd* gene, as well as the G6P isomerase gene (*gpi*).

Although the SNPs of the enzymes of glycolysis did not correlate with WHC or drip loss, several associations with cooking loss were identified. The SNPs in the gene for enolase a (*eno1*) explained between 12.6-15.5% of the variation in cooking loss, while *gpi* and *hk1* SNPs also contained several SNPs related to cooking loss. Both *ldha* and *ldhb* contributed to cooking loss, but only a few associations were significant. The regulatory kinase mitogen-activated protein kinase (*mapk14*) explained between 8.8% to 12.1% of the variation in cooking loss.

The *hk*1 and *hk3* genotypes correlated with glycogen, glucose and glucose 6-phosphate (G6P) concentrations in the first day post-mortem (individual SNPs explained 7.2-11.4% of the variation in metabolites). Other genes (*hk3*, *ldhd* and *pfkm*) explained 6.8-7.5% of the variation in lactate concentration.

Conclusion

Several genes were shown to correlate with colour changes post-mortem, which could be linked to lactate build-up from anaerobic glycolysis (i.e. the rate of pH decline). The genes of glycolysis that determine the variation in tenderness and those that determine protease activity were found to be similar. Because glycolytic activity is linked to the rate of pH decline, it can have profound effects on calpain system activities, which in turn determine the tenderness of beef. The rate of the post-mortem pH decline can also affect the WHC of meat, which can result in differences in drip loss, cooking loss and thawing drip. This could in turn influence the juiciness of steaks, having a potentially negative impact on consumer satisfaction. The SNPs of glycolytic enzymes were verified for beef quality traits in South African purebred beef bulls. The SNPs from the first and the last step of glycolysis (*hk* and *ldh* genes) were identified as important sites for identifying genotypes for selection purposes and should be considered for inclusion in customised SNP chips.

Notes

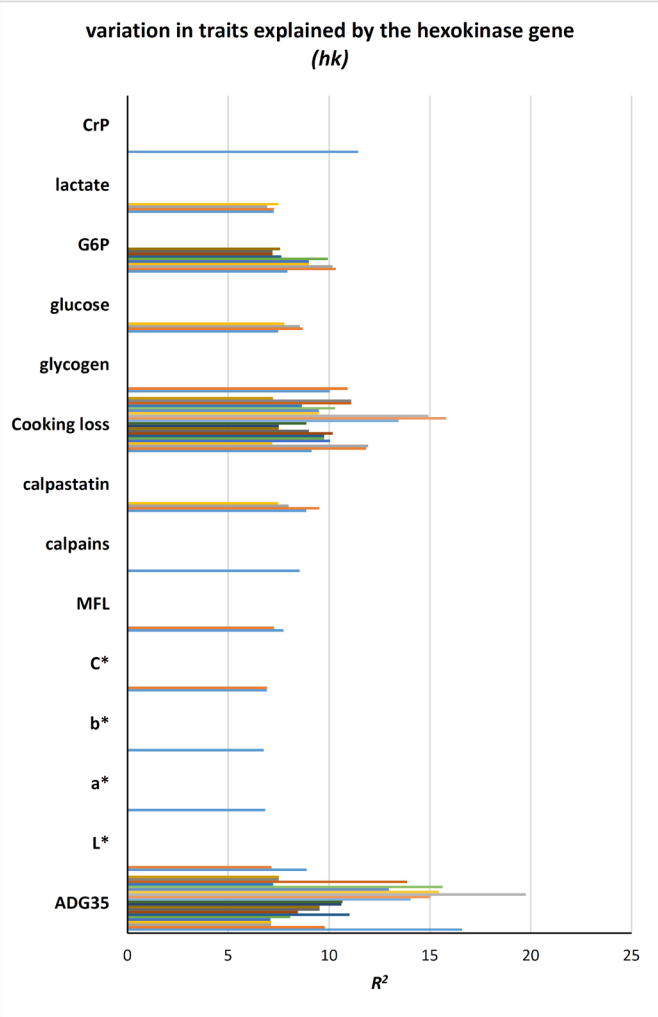

Figure 1: Correlations between SNPs in the hexokinase genes and beef production and quality traits i

Table 1: Illumina bovine-HD SNP BeadChip genes used in association analysis

No	Chrom	gene	"HD"SNPs	Enzyme	Start	End
1	BTA5	*pfkm*	14	muscle-type phosphofructokinase	32,308,621	32,360,654
2	BTA5	*ldhb*	10	lactate dehydrogenase H isomer	88,960,749	88,983,080
3	BTA5	*tigar*	2	TP53-inducible glycolysis and apoptosis regulator	106,221,574	106,239,537
4	BTA7	*hk3*	9	hexokinase 3	39,691,174	39,715,578
5	BTA10	*pkm*	8	pyruvate kinase M isomer	18,963,315	18,995,310
6	BTA11	*hk2*	32	hexokinase 2	9,715,757	9,798,674
7	BTA16	*eno1*	4	enolase alpha	45,400,205	45,417,949
8	BTA18	*gpi*	7	glucose 6-phosphate isomerase	44,976,771	45,010,450
9	BTA19	*eno3*	1	enolase beta	27,072,902	27,080,026
10	BTA22	*pgam2*	1	muscle-type phosphoglycerate mutase 2	370,735	373,562
11	BTA25	*aldoa*	2	glucose 1-phosphate aldolase A	26,469,195	26,484,685
12	BTA28	*hk1*	20	hexokinase 1	25,844,165	25,932,411
13	BTA29	*ldha*	2	lactate dehydrogenase M isomer	26,542,651	26,557,096
14	Chr X	*pgk1*	10	phosphoglycerate kinase 1	79,280,439	79,307,654

Table 1: Illumina bovine-HD SNP BeadChip genes used in association analysis

Notes

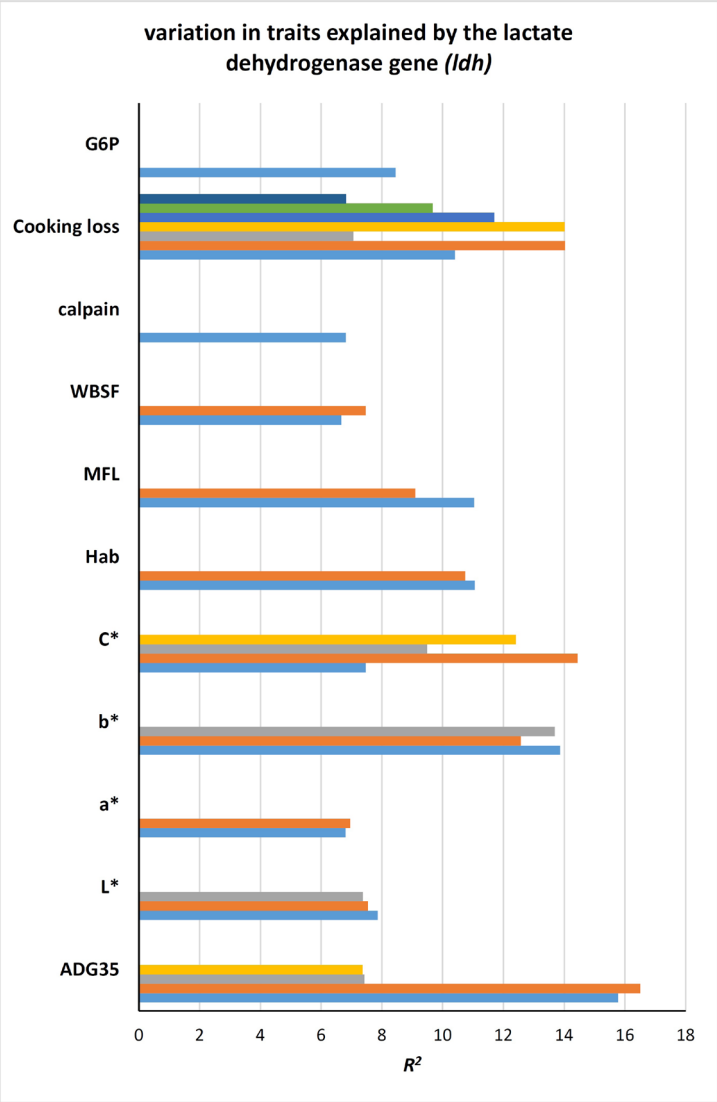

Figure 2: Correlations between SNPs in the lactate dehydrogenase genes and beef production and quali

Notes