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Meat quality – genetic background and methods of its analysis

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Electronic supplementary material

Supplementary Table S1

Table S1. Effect of the selected SNP polymorphisms on the meat quality traits

Trait	Polymorphism localisation and its effect				References
Carcass traits	**Lipoprotein lipase – *LPL* effect on carcass traits** c. 322G > A*, P-value < 0.05				(Oh et al. 2013)
	Alleles	GG	AG	AA	
	Carcass weight (kg)	428.09^{b}	411.52^{a}	443.88^{c}	
	***MYOD* gene family - *MYOD1* effect on carcass traits** g. 1274A > G**, P-value < 0.05				(Bhuiyan et al. 2009)
	Alleles	AA	AG	GG	
	Live weight at 24 months-old (kg)	539.01^{b}	551.80^{a}	538.95^{b}	
	Carcass weight (kg)	312.29^{b}	321.19^{a}	311.30^{b}	
	***MYOD* gene family – *MYF5* effect on carcass traits** g. 1911A > G, P-value < 0.05				
	Alleles	GG	GA	AA	
	Live weight at 24 months-old (kg)	542.02^{b}	541.00^{b}	561.77^{a}	
	Leptin – *E2FB* effect on the carcass traits c. 305C > T, P-value < 0.05				(de Carvalho et al. 2012)
	Alleles	TT	TC	CC	
	Carcass fat thickness (mm)	6.08^{b}	5.28^{a}	4.72^{a}	
	Diacylglycerol O-acyltransferase – *DGAT1* effect on the longissimus muscle area c. 1416T > G, P-value < 0.05				(Yuan et al. 2013)
	Alleles***	EE	EF	FF	
	Longissimus muscle area (cm^2)	75.47^{a}	74.32^{a}	69.88^{b}	
	Diacylglycerol O-acyltransferase – *DGAT1* effect on the backfat thickness c. 1416T > G, P-value < 0.01				
	Alleles***	EE	EF	FF	
	Backfat thickness (cm)	0.91^{a}	1.02^{a}	1.27^{b}	
	Diacylglycerol O-acyltransferase – *DGAT1* effect on the longissimus muscle area c. 572A > G, P-value < 0.01				
	Alleles***	AA	AB	BB	
	Backfat thickness (cm)	0.97^{a}	1.01^{a}	1.29^{b}	
Meat colour	**Stearoyl-CoA desaturase 1 gene – *SCD1* effect on the meat colour – day 6 in air** SCD 1.878 – A293V, P-value < 0.05				(Li et al. 2013)
	Alleles	GG (AA amino acid sequence)	AG (AV amino acid sequence)	AA (VV amino acid sequence)	
	*a**	13.2^{b}	14.1^{a}	14.4^{a}	
	*b**	14.3^{b}	14.8^{a}	15.1^{a}	
	Chroma	19.6^{b}	20.6^{a}	20.9^{a}	
	OxyMb	0.66^{b}	0.68^{a}	0.69^{a}	
	Leptin gene – *LEP* effect on the meat colour – day 6 in air P-value < 0.05				
	Alleles	CC	CT	TT	
	Chroma	20.9^{a}	20.6^{a}	19.6^{b}	
	DeoxyMb	0.59^{b}	0.59^{b}	0.60^{a}	

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Table S1. To be continued

Trait	Polymorphism localisation and its effect				References
Meat colour	**Calpain – *CAPN* effect on the meat colour** CAPN4751, P-value < 0.05				(Pinto et al. 2011)
	Alleles	TT	TC	CC	
	a^* after 7 days	15.98^{b}	15.62^{a}	15.47^{a}	
	a^* after 14 days	16.53^{b}	16.00^{a}	15.77^{a}	
	a^* after 21 days	17.19^{b}	16.62^{a}	16.70^{a}	
	b^* after 7 days	13.53^{b}	13.11^{a}	13.12^{a}	
	b^* after 14 days	13.82^{b}	13.20^{a}	13.09^{a}	
	b^* after 21 days	14.74^{b}	14.18^{a}	14.17^{a}	
	Diacylglycerol O-acyltransferase – *DGAT1* effect on the fat colour c. 1416T > G, P-value < 0.05				(Yuan et al. 2013)
	Alleles***	EE	EF	FF	
	Fat colur (1–5)	1.41^{a}	1.16^{b}	1.12^{b}	
	Diacylglycerol O-acyltransferase – *DGAT1* effect on the fat colour c. 572A>G, P-value < 0.05				
	Alleles***	AA	AB	BB	
	Fat colur (1–5)	1.39^{a}	1.35^{b}	1.09^{b}	
Meat marbling score and the texture traits	**Leptin – *E2FB* effect on the drip loss,** c. 305C > T, P-value < 0.05				(Pinto et al. 2011)
	Alleles	TT	TC	CC	
	Drip loss after 7 days	4.30^{b}	4.52^{b}	2.95^{a}	
	Lipoprotein lipase – *LPL* effect on marbling score c. 322G > A, P-value < 0.05				(Oh et al. 2013)
	Alleles	GG	AG	AA	
	Marbling score (scale 1–9)	5.31^{a}	5.49^{a}	6.30^{b}	
	c. 329A > T, P-value < 0.05				
	Alleles	AA	AT	TT	
	Marbling score (scale 1–9)	5.62^{b}	5.36^{ab}	4.97^{a}	
	μ-calpain gene – *CAPN1* effect on marbling score c. 947G > C, P-value < 0.05				(Li et al. 2013)
	Alleles	CC	CG	GG	
	Marbling score (scale 1–5)	2.90^{a}	2.31^{b}	2.38^{b}	
	IMF (%)	3.32^{a}	2.54^{b}	2.63^{b}	
	Diacylglycerol O-acyltransferase 1 – *DGAT1* effect on marbling score K232A, P-value < 0.05				
	Alleles (Amino acid sequence)	AAAA (KK)	AAGC (KA)	GCGC (AA)	
	Marbling score (scale 1–5)	–	2.64^{a}	2.42^{b}	
	IMF (%)	–	2.99^{a}	2.67^{b}	
	Diacylglycerol O-acyltransferase – *DGAT1* effect on the marbling score (P-value < 0.05) and WBSF (P-value < 0.01), c. 1416T > G				(Yuan et al. 2013)
	Alleles	EE	EF	FF	
	Marbling score (1–5)	2.06^{a}	1.89^{a}	1.79^{b}	
	WBSF (kg)	5.19^{a}	4.21^{b}	4.06^{b}	

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Table S1. To be continued

Trait	Polymorphism localisation and its effect				References
Meat marbling score and the texture traits	**Diacylglycerol O-acyltransferase – *DGAT1* effect on the Marbling score** (P-value < 0.05) and WBSF (P-value < 0.01), c. 572A > G				(Yuan et al. 2013)
	Alleles***	AA	AB	BB	
	Marbling score (1–5)	1.89^{a}	1.79^{a}	1.12^{b}	
	WBSF (kg)	5.22^{a}	4.11^{b}	3.95^{b}	
	Leptin – *E2FB* effect on the shear force, C305T, P-value < 0.05				(de Carvalho et al. 2012)
	Alleles	TT	TC	CC	
	WBSF (kg)	5.75^{ab}	6.02^{b}	5.22^{a}	
Lipid profile	**Lipoprotein lipase – *LPL* effect on fatty acids composition** c. 322G > A, P-value < 0.05				(Oh et al. 2013)
	Alleles	GG	AG	AA	
	C18 : 2n6 (%)	3.06^{b}	2.82^{ab}	2.59^{a}	
	C18 : 3n3 (%)	0.33^{a}	0.36^{a}	0.45^{b}	
	SFA (%)	40.65^{b}	39.93^{ab}	39.02^{a}	
	MUFA (%)	52.72^{a}	53.80^{b}	54.83^{b}	
	MUFA/SFA (ratio)	1.31^{a}	1.36^{a}	1.42^{b}	
	c. 329A > T, P-value < 0.05				
	Alleles	AA	AT	TT	
	C18 : 2n6 (%)	2.97^{a}	2.96^{a}	3.23^{b}	
	C18 : 3n3 (%)	0.36^{b}	0.35^{ab}	0.30^{a}	
	SFA (%)	40.16^{a}	40.53^{ab}	40.95^{b}	
	MUFA (%)	53.38^{b}	52.91^{ab}	52.22^{a}	
	MUFA/SFA (ratio)	1.34^{b}	1.31^{ab}	1.28^{a}	
	c. 1591G > A, P-value < 0.05				
	Alleles	GG	AG	AA	
	C18 : 2n6 (%)	3.04^{a}	2.93^{a}	3.29^{b}	
	C18 : 3n3 (%)	0.34^{ab}	0.37^{b}	0.28^{a}	
	SFA (%)	40.34^{a}	40.38^{a}	41.81^{b}	
	MUFA (%)	53.03^{b}	53.11^{b}	51.66^{a}	
	MUFA/SFA (ratio)	1.33^{b}	1.33^{b}	1.25^{a}	
	Stearoyl-CoA desaturase – *SCD* effect on the lipid profile c. 878C > T – A293V, P-value < 0.001 (Taniguchi et al. 2004), P-value < 0.05 (Barton et al. 2010)				
	Alleles	CC (AA amino acid sequence)	CT (AV amino acid sequence)	TT (VV amino acid sequence)	(Taniguchi et al. 2004)
	MUFA (%)	58.8^{a}	58.2^{b}	57.1^{c}	
	C14:1 cis-9 [g $(100g)^{-1}$ total fatty acids]	0.45^{a}	0.36^{b}	0.28^{c}	(Barton et al. 2010)
	C18:1 cis-9 [g $(100g)^{-1}$ total fatty acids]	37.1^{a}	37.1^{a}	36.1^{a}	
	SFA [g $(100g)^{-1}$ total fatty acids]	47.3^{a}	47.5^{a}	48.7^{b}	
	MUFA [g $(100g)^{-1}$ total fatty acids]	42.9^{a}	42.9^{a}	41.8^{b}	
	MUFA/SFA (ratio)	0.91^{a}	0.91^{a}	0.86^{b}	

*Notation c. – addresses to the SNPs location in cDNA (complementary DNA) sequence; **notation g. – addresses to the SNPs location in genomic DNA sequence; ***alleles obtained after digestion of the PCR product using the restriction enzymes (c. 572*A* > *G* – enzyme *Mae*III, c. 1241*C* > *T* – enzyme *Hinf*I, c. 1416*T* > *G* – enzyme *Age*I)

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