

PROCEEDINGS OF II. INTERNATIONAL AGRICULTURAL, BIOLOGICAL & LIFE SCIENCE CONFERENCE

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MOLECULAR APPROACHES IN DETERMINING MEAT QUALITY

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ABSTRACT

Consumer requests are come at the beginning of the most important features in the quality of a meat. Meat color, pH, marbling score (MS) and tenderness of meat (texture) are the most important features that determine meat quality and are among the consumer requests. Characters such as tenderness and color of the meat come hereditary. Therefore, the tenderness of the meat stands out as quite an important feature. As well as meat tenderness, food analysis such as cooking loss, water holding capacity, MS, color, pH-temperature measurements are also taken as the basis for determining the quality of the meat offered for consumption. It is an important problem that beef is not as high quality as the consumers want. This is related to the animal's genotype and environmental conditions (age, species, race, care and feeding conditions, etc.). The fact that fattening is economical and qualified is a must for quality and economical meat production. This means too, that cattle of genotype known to produce better quality meat, By determining the genetic variations in the quantitative character locus (QTL) with technological and molecular genetic methods, today it is used in animal breeding studies for the production of quality beef. Gene markers are used to determine the genetic value of cattle and to increase genetic progression in populations by indirect selection. Marker Supported Selection (MAS) is performed by using QTL, which enable for the selection of cattle at a young age, regardless of gender and is not affected by environmental conditions. QTL analyzes are based on the link between some gene markers and QTL. The main purpose of the formed QTL maps is to identify the genes that cause variation in quantitative properties and mutations in these genes. Genetic studies have been performed on this topic in beef cattle, linear correlation relationship between single nucleotide polymorphisms (SNP) on meat quality has been revealed. Nowadays, Sequencing and PCR-RFLP method is most commonly used to detect mutations in marker genes.

Keywords: Meat quality, marker genes, QTL, MAS, SNP

INTRODUCTION

The importance of meat

Red meat protein is one of the main elements of a balanced diet in humans and an indispensable staple food that constitutes our best nutrient source in terms of biological value (Lawrie and Ledward, 2006). Animal-derived food products are important for nutrition and human health (Tosun and Hatırlı, 2006). High nutritional value is considerably important for consumers and red meat is known to be rich in proteins of high-quality essential amino group acids as well as fat, vitamins, minerals, iron, and zinc (Biesalski, 2005). Important essential amino acids such as histidine, isoleucine, leucine, lysine, methionine, phenylalanine, threonine, tryptophan, and valine are not found in plant proteins, but only in animal proteins (Kutlu et al., 2005). Consumer demands constitute the most important characteristics that define the quality of meat, and the fact that beef may often fail to meet the quality consumers demand creates a

major problem. This issue is related to both the genotype of the animal and the environmental conditions. Features such as meat colour, friability, marbling score (MS) and pH are among the consumer demands that determine meat quality.

Meat colour is the first important quality factor that determines whether the consumer is likely to purchase the product, and also an important feature that affects consumer preferences (Font-i-Furnols and Guerrero, 2014; Suman et al., 2014). The colour of meat is an inherited attribute and represents a key factor that defines meat quality (Girolami et al., 2013). Fresh and ripe meat of high quality is expected to be velvety red. In production and processing of food products, pH-metry is a commonly utilised measuring method. Technological features such as product yield and durability of the product, water-holding capacity, colourisation, and stability of the product as well as ripening and softness of the meat are all closely related to the final value pH reaches in 24 hours. The changes in pH in the post-mortem phase significantly affect the quality and appearance of the meat. The pH value of meat should be ideally between 5.2 with 5.5. Any pH above 6.2 indicates the onset of bacterial spoilage in meat. Cooking loss and water-holding capacity of meat are also taken into account in food analyses when determining the quality of meat offered for consumption (Mullen, 2002; Kök and Atalay, 2018).

Meat Texture and Marbling (Mosaic Fat Content)

The flavour and juiciness of are attributes of meat that can be improved by various methods of processing and cooking. However, tenderness is an inherited attribute that is directly associated with the animal breed (Thu, 2006). For this reason, the tenderness of meat stands out as a substantially important feature. The texture of meat determines juiciness and softness, thereby determining acceptability by customers and increasing the value of the meat (Weber et al., 2020). Texture is defined as the degree of hardness or softness that remains in the mouth as a result of chewing meat. In other words, tenderness of meat is the texture of cooked meat. The Warner-Bratzler Shear Force (WBSF) device is a mechanical texture fragmentation knife that simulations the process of chewing and shredding meat in the mouth. The WBSF texture device can measure that cooked and uncooked beef *Musculus Longissimus dorsi* (MLD) as mechanical and predict value sensory panel tenderness. This also refers to the time it takes to swallow the meat after chewing and break-down in the mouth. Force (kg) × Time (sec) graph showing the WBSF peak and mean values of the three samples obtained from each MLD beef (Figure 1). Tenderness is therefore a factor to be evaluated for cooked meat as well. The hardness and softness (tenderness) of meat is also related to the mosaic fat content, i.e. the marbling score. As showed in figure 2, Marbling is defined as the fat deposition between MLD fibres with a mosaic-like pattern, and the distribution of fat between these muscle fibres affects the meat texture (Barendse, 1999; George-Evins et al., 2004).

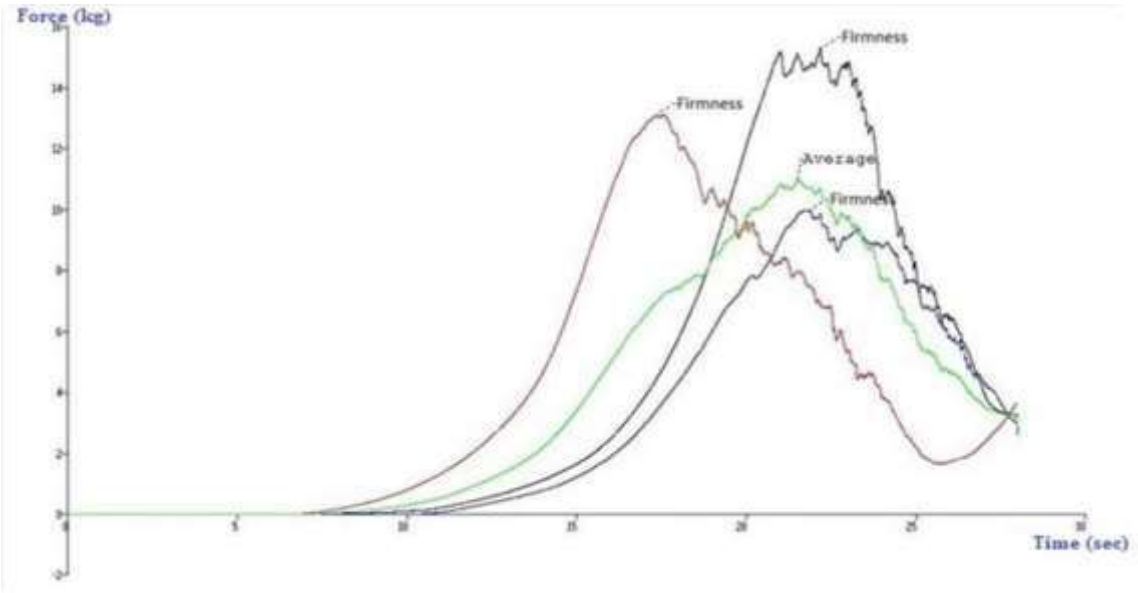


Figure 1. Force (kg) × Time (sec) graph showing the WBSF peak and mean values of the three samples obtained from each MLD beef, kg: Kilogram, sec: second (Vapur, 2019)

Measurement	Area	Unit
Total Area	142505,6819	px
Area	3012,620027	px
Area	5480,239694	px
Area	1955,281207	px
Area	2890,260631	px
Area	3896,021948	px
Area	969,2729767	px
Area	320,1646091	px
Area	488,340192	px
Area	341,2894376	px
Area	677,6406036	px
Area	307,2702332	px
Area	208,5048011	px
Area	436,7626886	px
Area	165,7064472	px
Area	225,5144033	px
Area	513,5734072	px
Total Fat	21888,46331	



Figure 2. Rib steak (MLD) cross-sectional area and rate of fat distribution, (Px): Pixel (Vapur, 2019)

Cattle are the main animal species that produce red meat worldwide. These consist of beef cattle and combined cattle breeds that have been specifically improved for meat production and quality, with ongoing efforts for further improvement. By using molecular genetic methods to detect genetic variations in quantitative trait loci (QTL) of cattle, the quality of meat may be determined at the calf stage, allowing cost-effective and high-quality meat yield in livestock production. In this respect, gene markers are used to determine the genetic value of cattle and to increase genetic progress in populations by indirect selection (Corva et al., 2007). The effect of marker-assisted selection (MAS), i.e. indirect selection using gene markers in cattle is a gender-independent process. Gene markers allow selection of young cattle and are not affected by environmental conditions (Andersson, 2001; Yamada et al., 2003; Andersson and Georges 2004). QTL analysis relies on the correlation between these markers and QTL (Knott and Haley 1992). The main aim of QTL mapping in reference cattle breeds is to identify the genes and

mutations that result in variation in quantitative traits (Gao et al., 2007; Hocquette et al., 2007; Allan and Smith, 2008). The yield characteristics of the same breed are determined by using QTL in different herds, leading to the appropriate use of these animals in terms of economics. Genetic studies have been conducted mostly in beef cattle and a linear correlation has been demonstrated between single nucleotide polymorphisms (SNPs) and the quality of meat (Zwierzchowski et al., 2001). A number of genes associated with meat quality have been identified and several candidate genes have been determined to be QTL with specific SNPs (Li et al., 2013). The functional candidate gene approach has been used to detect the polymorphisms associated with the quality and yield of meat (Georges, 2007; Pannier et al., 2010). DNA sequencing and polymerase chain reaction-restriction fragment length polymorphism (PCR-RFLP) have been suggested to be the most reliable and convenient tools in detecting genetic polymorphisms (Ahani Azari et al., 2012; López-Rojas et al., 2017). To date, candidate gene studies have focused on a number of genes in order to reveal the molecular basis of carcass and meat quality, and various genes have been investigated across different studies. Some of these genes are described below.

The 200 candidate genes have used for carcass and meat quality in beef cattle

Some of the marker genes most studied in cattle; Leptin (LEP) (Lagonigro et al., 2003; De Oliveira et al., 2013; Vapur, 2019), Thyroglobulin (TG) (Casas et al., 2005; Fortes et al., 2009; Vapur, 2019), Calpastatin (CAST), Calpains (Calcium Active Neutral Protease, CAPN1, Regulation of Calpain Activation) (Curi et al., 2010; Giusti et al., 2013; Kök et al. 2019), Diacylglycerol O-Acyltransferase 1 (DGAT1) (Giusti et al., 2013), Stearyl CoA deraturase (SCD), Peroxisome Proliferator Active Receptor –γ (PPARγ), Nebulin (NEB), Phosphatidylinositol 4-kinase alfa (Pik-4), Calcium / Calmodulin Dependent Protein Kinase II (CaM-K II), fatty acid binding protein (FABP4), Titin (TTN) (Lee et al., 2008), Ribosomal protein L27a (RPL27A), Akirin 2 (AKIRIN2) (Watanabe et al., 2011), endothelial differentiation sphingolipid G-protein-coupled receptor 1 (EDG1) (Sukegawa et al., 2010), Myostatin (Double Muscle Gene -GDF8), (Kambadur et al., 1997), Growth Hormone Receptor Gene (GHR) (Waters et al., 2011).

The Leptin gene (LEP)

The LEP gene in cattle consists of 3 exons and 2 introns. Containing 16,824 nucleotides, this gene is located on chromosome 4 (4q32) (Perucatti et al., 2006) and encodes the LEP protein, which consists of 167 amino acids (a.a). LEP has been considered a potential candidate gene associated with body size, muscle fattening, carcass characteristics and meat quality based on QTL studies in cattle (Lagonigro et al., 2003; De Oliveira et al., 2013; Vapur, 2019). The first study on the LEP gene was conducted by Zhang et al. in 1994 and Stone et al. mapped the LEP gene in 1996. Pomp et al. (1997) detected the polymorphisms in the intronic region of this gene by PCR-RFLP using the *Sau3AI* restriction enzyme. Konfortov et al. (1999) sequenced both the intronic and exonic regions of the LEP gene. The discovery of the association between the LEP gene and meat quality has led to an increase in relevant research studies (Shin and Chung, 2007a; Corva et al., 2009).

Table 1. The relationship of the LEP gene with meat quality (intramuscular fat, back fat thickness, meat texture, marbling, meat color, pH, water holding capacity, etc.)

Location / Position	**SNP Name**	**SNP**	**Phenotypic trait**	**Literature**
2. exon 305 (877-1342)	E2FB (C1180 T)	C/T	Carcass fat, Feed intake, Drip Loss (DL), Water holding Capacity (WHC), Meat color (L*,a*, b*), pH, Marbling score, Back fat thickness, WBSF, Meat quality	Buchanan et al., 2002; Nkrumah et al., 2004; Pinto et al., 2011; Papaleo Mazzucco et al., 2016; Schenkel et al., 2005; Da Silva et al., 2012; De Oliveira et al., 2013; Souza et al., 2009; Konfortov et al., 1999 ;Vapur G., 2019; Shin and Chung, 2007a; Gill et al., 2009
2. exon 252 (1008-1201)	E2JW (A1127 T)	A/T	Marbling score, Back fat thickness, meat color (L*,a*, b*), pH, WBSF, Intramuscular fat, Carcass weight	Yazdani et al., 2010; Kulig and Kmie´c, 2009; Geary et al., 2003; Silva et al., 2014; Ardıçlı et al., 2017; Shin and Chung, 2007a
2.exon (118026)	SNP2	C/T	Carcass yield, Backfat thickness	Corva et al., 2009
3. exon (2961-3456)	C3100T	C/T	-	Shin and Chung, 2007
3. exon 140	-	C/T	Carcass fat Intramuscular fat	Lagonigro et al., 2003
3. exon	A59V	C/T	Meat color (L*,a*, b*), Intramuscular fat, Carcass weight, meat quality	Friedman and Halaas, 1998; Yazdani et al., 2010; Da Silva et al., 2012; Kulig and Kmie´c, 2009; Geary et al., 2003; Silva et al., 2014; Ardıçlı et al., 2017
3. exon	A80V	C/T		
Promoter Region 207	UASMS 1	C/T	Marbling, Carcass fat, meat quality, Backfat, Body Weight, Serum lep concentration	Gill et al., 2009; Nkrumah et al., 2005; Da Silva et al., 2012
Promoter Region 528	UASMS 2	C/T		
Promoter Region	C963T	C/T	Marbling, Back fat thickness	Da Silva et al., 2012
Microsatellite	BM150 0	-	Back fat thickness	Silva et al., 2014

As shown in Table 1, SNPs in exons 2 and 3, and the promoter region in the LEP gene have been associated with marbling and muscle fattening in different cattle breeds (Lagonigro et al., 2003; Gill et al., 2009; Da Silva et al., 2012; De Oliveira et al., 2013; Aslaminejad et al., 2010; Silva et al., 2014). Several investigators have investigated SNPs in the LEP gene in relation to their effect on meat quality, associated the SNPs in exon 2 (E2JW, E2FB) with marbling, and identified these SNPs as markers (Lagonigro et al., 2003; Schenkel et al., 2005; Da Silva et al., 2012; De Oliveira et al., 2013; Vapur, 2019). Furthermore, these SNPs have been linked to attributes such as back fat thickness, muscle fattening, milk yield, live weight (LW) and feed consumption in addition to marbling. (Buchanan et al., 2002; Nkrumah et al.,

2004; Shin and Chung, 2007a; Souza et al., 2009; De Oliveira et al., 2013). The A80V polymorphism in exon 3 of the LEP gene has been reported as a candidate marker for milk yield and composition, while its association with attributes of meat quality currently remain unclear (Liefers et al., 2003; Kulig, 2005; Kulig et al., 2010). The A80V polymorphism of the LEP gene has also been reported to be an effective marker for weight and average daily body weight gain, marbling, and carcass characteristics (Kulig and Kmie´c, 2009, Geary et al., 2003; Silva et al., 2014). Friedman and Halaas (1998) and Yazdani et al. (2010) have reported that this polymorphism, also known as A59V, is a candidate marker for carcass characteristics and meat attributes. Briefly, QTL studies have revealed that the LEP gene is a potential candidate gene for performance, meat quality, marbling, carcass characteristics and muscle fattening in cattle. It has therefore been recommended to be included in MAS programmes (Buchanan et al., 2002; Gill et al., 2009).

The Thyroglobulin gene (TG)

The TG gene is located on chromosome 14q with a length of 235,941 nucleotides and consists of 48 exons and 47 introns in cattle (Smith et al., 1997; Vapur, 2019). The TG gene encodes 2769 amino acids, which constitute the thyroglobulin protein. Thyroid hormones have long been known to contribute to fat deposition between myocytes. Upon evaluation as a potential candidate gene in QTL studies, TG gene polymorphisms have been considered a candidate gene marker owing to their effects on yield grade, weaning, meat colour, meat pH, marbling, average daily live weight (LW) gain, birth weight and weaning characteristics, carcass fat thickness and fat deposits. TG is one of the important genes that affect the lipid metabolism. (Thaller et al., 2003; Barendse et al., 2001; Kneeland et al., 2004; Maltecca et al., 2009; McClure et al., 2010). Table 2 shows the association between marbling and the SNPs in the TG gene of various cattle breeds and buffalo (Pannier, et al., 2010; Yardibi et al., 2013; Dubey et al., 2014; Dubey et al., 2015). The marker SNPs in TG have been confirmed to affect intramuscular fattening in different cattle breeds (Barendse, 2004; Bonilla et al., 2010; Savaşçı and Atasoy, 2016). Genetic variations in the 5′ promoter region of the TG gene are widely used in MAS programmes to increase the marbling score of beef. Hou et al. (2011a) identified 6 new SNPs in the 3′ flanking region of the TG gene. They associated MLD marbling with the SNPs T354C, G392A, A430G and T433G. Thaller et al. (2003) demonstrated the association between the TG5 (C422T) marker and MLD muscle fat content in German Holstein cattle. Gan et al. (2008) showed the effect on marbling caused by a SNP in the 3′ flanking region of the TG gene. However, Fortes et al. (2009) reported a lack of correlation between TG gene polymorphism and fat accumulation or tenderness of meat. Three positions of the TG gene, namely position 257 (C257T), position 335 (A335G) and position 422 (C422T) have been investigated in Korean cattle and a positive correlation with marbling has been reported for these polymorphisms (Shin and Chung, 2007b). Unlike Shin and Chung, some studies report that cattle with the TT genotype at position 422 of the 5′ promoter region have higher MS than cattle with (C422T) CT and CC genotype (Barendse, 1999; Barendse et al., 2001; Thaller et al., 2003; Burrell et al., 2004). Casas et al. (2007) reported that the TT genotype has the highest MS across three different hybrid populations. Barendse et al. (2004), Wood et al. (2006) and Bonilla et al. (2010) revealed an important correlation between the T allele and marbling. On the other hand, Johnston and Graser (2010), McClure et al. (2010), Pannier et al. (2010) found no evidence of a linear correlation between marbling and the T allele.

Table 2. The relationship of TG gene with meat quality (Body Weight, intramuscular fattening, back fat thickness, meat texture, marbling, meat color, pH, water holding capacity)

Location	**SNP Name**	**SNPs**	**Phenotypic traits**	**Literature**
5′ Promoter Region	C422T (C422T)	C/T	Feed intake, marbling, intramuscular fat, fat thickness,*LMA, meat yield, meat color (l*, a*), meat quality	Barendse, 1999-2001; Thaller et al., 2003; Barendse et al., 2004; Burrell et al., 2004; Shin and Chung, 2007b; Casas et al., 2005-2007; Ağaoğlu et al., 2015; Savaşçı and Atasoy, 2016; Ardıçlı et al., 2018
	C257T	C/T	Marbling	Shin and Chung, 2007b
	A335G	C/T	Meat color (a*, b*), LMA, Marbling	Ribeca et al., 2014; Shin and Chung, 2007b
3′ Flanking Region	G133C G156A C220T A506C	G/C G/A C/T A/C	Marbling	Gan et al., 2008
	T354C G392A, A430G T433G	C/T G/C A/G T/G		Hou et al., 2011a;
5' Flanking Region	T1355C G1356A	T/C G/A	Meat percentage, body weight, LMA*	Zhang et al., 2015a
	G275A G277C G280A C281G	G/A G/C G/A C/G	Average daily earnings, carcass composition, meat quality traits, growth, intramuscular fat	Zhang et al., 2015b

*LMA; longissimus muscle area

The attempts to associate TG5 (C422T) markers with marbling or other traits of fat accumulation have led to the inclusion of TG5 in commercial SNP panels (Barendse, 1999; Thaller et al., 2003; Barendse et al., 2004). GeneSTAR is a DNA test to assess the quality and production characteristics in all cattle breeds. In order to improve the estimability of the quality and marbling level of beef, the SNP at position 422 of the 5′ promoter region (C422T) has been approved and launched by the company, GeneSTAR, as a TG5 marker in 2000. GeneSTAR marbling is a DNA-based diagnostic test for the TG gene and an available commercial marker for carcass quality attributes that is recommended for use in MAS programmes (Van Eenennaam et al., 2007; Pfizer, 2013). These DNA tests are used in USA, Japan, Canada, Argentina, and Australia (Shin and Chung, 2007b).

The Calpain gene (CAPN)

The decrease in the pH of meat upon slaughter activates the Calpains family. Calpains, which exert a calcium-dependent activity as natural proteinases, denature myofibrillar proteins, thereby increasing the texture of the meat. The CAPN gene is located on chromosome 29 in cattle (Smith et al., 2000). Among the Calpains, Calpain 1 and 2 have been shown to affect the tenderness of meat (Barendse, 2002; Kök et al., 2019; Page et al., 2002; White et al., 2005) while the exact effects of other Calpains (CAPN 5,7,10,12,14,15) currently remain unelucidated (Morris et al., 2006). The effect of relevant Calpains on palatability, juiciness, texture and meat

quality parameters of beef have been confirmed as direct effects on the phenotype by WBSF tests applied to MLD and with the genotype results obtained in polymorphism and SNP studies in CAPN1 loci (Curi et al., 2009; Van Eenennaam et al., 2007; Kök and Atalay, 2018). Studies have so far focused on three of the CAPN1 markers shown in Table 3 (CAPN 316, CAPN 530 and CAPN1 4751), which are known to be associated with the texture of meat (Barendse, 2002; Kök et al., 2017; Page et al., 2002; White et al., 2005). Page et al. (2002) have associated the μ-calpain (CAPN1) gene polymorphisms, CAPN1 316 and CAPN1 530, with the texture of meat. CAPN1 (316) is located in exon 9. The CAPN 316 C allele frequency has been shown to have a positive correlation with meat texture in *B. taurus* and *B. indicus* cattle (Curi et al., 2010; Gill et al., 2009; Kök et al., 2019; Page et al., 2002; Van Eenennaam et al., 2007; White et al., 2005). Page et al. (2004), Allais et al. (2011), Gill et al. (2009), Kök and Atalay (2018), and Costello et al.(2007) have shown increased tenderness in beef from cattle bearing the CC and CG genotype with the C allele compared to those of the GG genotype. CAPN1 (4751) is a polymorphism located on intron 17. Curi et al., (2009) have reported that the C allele of the CAPN1 4751 polymorphism is a favourable factor for the texture of meat (Kök and Atalay, 2018; Kök et al., 2017, White et al., 2005; Smith et al., 2009; Van Eenennaam et al., 2007; Curi et al., 2009). Overall, study results have shown that the cattle with the CAPN1 4751-CC genotype produce meat with increased tenderness, i.e. improved texture compared to those of the other genotypes (CC and CT) (Curi et al., 2009; Kök and Atalay, 2018; Smith et al., 2009; White et al., 2005). CAPN 530 is an amino acid polymorphism that occurs in exon 14 (Page et al., 2002,2004; White et al., 2005). For the CAPN 530 marker, the G allele is the allele that shows a positive correlation with tenderness (Allais et al., 2011; Corva et al., 2007; Costello et al., 2007; Page et al., 2004). Results of the studies in this field (Corva et al., 2007; Page et al., 2002, 2004), support the notion that beef with the CAPN 530 GG genotype is more friable than beef of other genotypes (AG and AA) based on the WBSF value. Investigators have also investigated the SNP, CAPN II/*HhaI* in Irish cattle breed (Costello et al., 2007) and the SNPs, CAPN1 5331 and 4753 in the Brahman breed (Casas et al., 2006; White et al., 2005); however, without concluding any positive correlation between the texture of meat and these SNPs. During the analysis of the CAPN1 polymorphism in Chinese Yanbian Yellow cattle, Xin et al. (2011) identified an important correlation between variants of this gene (E7-1, E7-2, E14-4, E14-5, E14-6) and pH, colour scores and other quality attributes such as fatty acids and amino acid content of meat. Hou et al. (2011b) evaluated the 3553A>G polymorphism and demonstrated higher marbling scores in those with the AA genotype compared to the other genotypes (AG and GG). Li et al. (2013) reported greater MS in animals of the CC genotype with the c.947G>C polymorphism than the scores in those bearing the CG or GG genotype among Angus, Charolais, Hereford and Limousin breeds. Cheong et al. (2008) determined that the T allele with the c.2151*479C>T polymorphism in the 3′ UTR region of cattle is responsible for low marbling scores in Korean Hanwoo cattle. Intramuscular fat content has been shown to be the lowest in cattle of the TT genotype and the highest in those of the CC genotype.

The Calpastatin gene (CAST)

The calpastatin gene is located on chromosome 7 in cattle (Bishop et al., 1993). Studies involving the CAST gene has revealed QTL, requiring this gene to be evaluated as a candidate gene in MAS since the SNPs, CAST-T1, and U*oG*-CAST are associated with the quality of meat (Van Eenennaam et al.,2007; Curi et al.,2010; Kök and Atalay 2018). CAST shows its effect on meat texture in an indirect manner, i.e. through CAPN (Barendse et al., 2007). The CAST gene also affects the inter-muscular fattening of the carcass (Juszczuk-Kubiak et al., 2008; Xiaomei et al., 2018). Juszczuk- Kubiak et al. (2008) identified 4 SNPs (using *AluI*, *BseYI* and *NdeI* enzymes) within intron 12 of the CAST locus in cattle. Investigating the CAST gene in *Bos taurus* breed, Allais et al., (2011) identified a novel SNP in intron 8, and two novel SNPs

in exon 30 and in the 3′ UTR region. In *Bos indicus* cattle, an A/T SNP in the 3′ UTR region, referred to as CAST-Brahman, has been identified and associated with the texture of meat (Frylinck et al., 2009) as well as a C/T SNP identified in hybrids (*Bos taurus* × *Bos indicus)* (Casas et al., 2006; Frylinck et al., 2009). SNPs have been determined by means of PCR-RFLP (*EcoRI* and *BamHI*) in the 3′ UTR region of the CAST gene in cattle and these polymorphisms have been recommended for use as gene markers to predict the texture of meat (Lonergan et al., 1995). In the CAST gene of *Bos taurus* and *Bos indicus* breeds, a positive correlation with the texture of meat has been mostly shown for two marker SNPs, namely UoG-CAST (Curi et al., 2010; Gill et al., 2009; Kök and Atalay 2018; Quaas et al., 2006; Reardon et al., 2010; Schenkel et al., 2006) and CAST-T1 (Allais et al., 2011; Corva et al., 2007; Curi et al., 2010; Smith et al., 2009; Van Eenennaam et al., 2007) (Table 3). The G/C base substitution in intron 5 of the CAST gene in cattle has been identified as the UoG-CAST polymorphism (Schenkel et al., 2006). The same polymorphism is also known as CAST/*RsaI* (Kök et al., 2013; Reardon et al., 2010). In the SNP, UoG-CAST, the C allele is responsible for the favourable effect on meat texture (Curi et al., 2010; Kök and Atalay, 2018; Schenkel et al., 2006). The UoG-CAST (CAST/*RsaI)* polymorphism has been reported in cattle of the CC genotype that produce meat with increased friability compared to those with the CG or GG genotype (Curi et al., 2010; Gill et al., 2009; Kök and Atalay, 2018; Schenkel et al., 2006; Van Eenennaam et al., 2007). The CAST-T1 polymorphism of the CAST gene in cattle has been found to have two different genetic variants (Allais et al., 2011; Corva et al., 2007; Curi et al., 2010; Morris et al., 2006; Smith et al., 2009; Van Eenennaam et al., 2007). One of these variants is located in exon 30 (2959A>G) while the other is the polymorphism (C/T) in the 3′ UTR region of the gene. The nucleotide polymorphism in the 3′ UTR region of the CAST gene in *Bos indicus* cattle, referred to as "CAST-Brahman SNP", has been associated with increased friability in beef from animals of the AA genotype compared to beef from animals bearing other genotypes (AT, TT) (Frylinck et al., 2009). In studies on other SNPs in the CAST gene, no positive correlation was observed between the texture of meat and the M/N polymorphisms in exon L region and intron 1 of the CAST gene (L14450-622) in Holstein cattle and buffalo (with frequency of the M allele 73% in Holstein and 22.5% in buffalo) (Yousefi and Azari 2012), the A/B polymorphism in intron 6 of the CAST gene in Nellore cattle breed (frequency of the B allele, 58%) (Alireza et al., 2009), the SNP2870 (AF159246) A/G polymorphism in the CAST gene in *B. taurus* cattle (frequency of the A allele, 33-53%) (Corva et al., 2007) and the Calpain II polymorphisms in Irish beef cattle (Costello et al., 2007) ($p>0.05$).

Table 3. The relationship of CAPN1 and CAST gene with meat quality (intramuscular fattening, meat texture, marbling, meat color, pH, water holding capacity, etc.)

Gene Name	SNP Name	Location	SNP	Phenotypic traits	Literature
Calpain-CAPN1	CAPN1 316	9. exon	G/C	Texture	Kök et al., 2017; Allais et al., 2011; Curi et al., 2010; Gill et al., 2009; Corva et al., 2007 Costello et al., 2007; Page et al., 2004
	CAPN1 4751	17. intron	C/T		Kök et al., 2017; Curi et al., 2009; Gill et al., 2009; Smith et al., 2009; Casas et al., 2006; White et al., 2005
	947G>C	1. intron	G/C	Marbling	Li et al., 2013
	SNP15	4.exon	C/T	Lean meat color score	Liu et al., 2015
	3553A>G	4. intron	A/G	Marbling	Hou et al.,2011b
	E7-1 E7-2 E14-4 E14-5 E14-6	7. exon 7. İntron 8. İntron 16. intron 17. Exon 18.exon	27 pcs SNPs	pH, meat color	Xin et al., 2011
	c.2151*479	3′ UTR	C/T	Marbling, carcass quality	Cheong et al., 2008
Calpastatin-CAST	*Uo*G-CAST	5. intron	G/C	Texture Tenderness	Kök et al., 2013; Costello et al., 2007; Gill et al., 2009; Reardon et al., 2010; Schenkel et al., 2006; Van Eenennaam et al., 2007
	CAST-T1	30. exon 3′ UTR	A/G C/T		Corva et al., 2007 Van Eenennaam et al., 2007
	c.155C>T	1. exon	C/T		Barendse et al.,2007; Kaplanová et al. 2013; Ekerljung, 2012
	61G>C		G/C	Tenderness, cooking lose	Juszczuk-Kubiak et al. 2004

CONCLUSION

In conclusion, genetic marker technology appears to be promising for the breeding of livestock. The SNPs in LEP, TG, CAST and CAPN1 gene loci are known to be associated with the quality of meat (texture, pH, MS, meat colour) and are therefore considered potential candidate genes. The gene markers, LEP (E2JW, E2FB), TG5 (C422T), CAST (UoG-CAST, CAST-T1) and CAPN1 (CAPN1 316, CAPN1 530 and CAPN1 4751), have been established to be among the markers with identified genetic potential for the production of meat with

improved quality. In the event that the LEP, TG, CAST and CAPN1 genes of a given cattle bear the favourable markers associated with improved meat quality, the genotype of these animals should be determined based on QTL by means of the MAS method without the impact of environmental factors at young age so that they may be separated from the cattle of other genotypes in livestock and allocated as breeding cattle or beef cattle for the production of high-quality meat.

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