The Genetic Influence on Sheep Meat Quality, Growth and Body Weight: A Review

Rodica Ştefania Pelmuş, Horia Grosu, Mircea Cătălin Rotar, Mihail Alexandru Gras, Cristina Lazâr, Florin Popa

Abstract

Background: Presently, the demand for sheep meat is directed mainly towards high quality products. Meat production improvement and meat quality are very important in sheep industry. The aim of this paper is focusing to review the papers to studies regarding the influence of genes to production and quality of meat.

Methods: Single nucleotide polymorphism microarrays are a molecular genetic method in searching the markers associated with meat production and meat quality traits in animal breeding.

Conclusion: Previous study had shown that genes like myostatin, leptin, calpastatin had influenced the meat production and meat quality traits. The meat production traits and meat quality traits have a moderate heritability and can be included in meat sheep breeding objectives.

Key words: Genes, Meat quality, Production, Sheep.

Meuwissen et al. (2001) published a visionary paper demonstrating the need for a large number of markers to predict the genetic merit of animals. A new tool that has been increasingly used in animal breeding in recent years is single nucleotide polymorphism (SNP) microarrays which allow genotyping thousands of polymorphic sites simultaneously. The sheep genome is analyzed using the Ovine SNP 50 Bead Chip, which has been developed for domestic sheep in collaboration with the International Sheep Genomics Consortium (ISGC) (Kawecka et al. 2016). The identification of genomic regions, genes associated with phenotypic traits and description of gene function are some of the applied research activities to understand the genetics of livestock species. Genome-wide association study is an important approach to identify candidate genes and molecular variants associated with different phenotypic traits. This will be quite useful for genetic improvement (Gebreselassie et al. 2020).

The aim of this review was the presentation the polymorphism of genes associated with body weight, growth and meat quality in sheep. The animals carried of best genotypes had heavier body weight and superior meat quality and will be selected for obtain descendants with superior performances.

Genes associated with growth and body weight

Growth traits are represented by weight at various ages, average daily gain and bone traits. Safari et al. (2005) have shown that the heritability for growth traits were generally moderate ranged from 0.15 to 0.41. Many studies were realized to identify functional genes associated with growth traits.

Jawasreh et al. (2019) identified three genotypes for the calpastatin Hha1 gene in Awassi sheep where polymorphic calpastatin gene affected final body weight and longissimus muscle width. Similarly, Myocyte Enhancer Binding Factor 2B (MEF2B) and Thyrotropin Releasing Hormone Degrading Enzyme (TRHDE) genes affected body weight and growth in sheep (Wang et al. 2015, Zhang et al. 2016).

A genome wide specific selection study has identified fat mass and obesity-associated protein (FTO) and Apolipoprotein B Receptor (APOBR) genes affecting body mass index in German mutton Merino and African white Dorper sheep breeds (Wang et al. 2015).

Genetic variants in myostatin (MSTN) gene were associated with muscling and growth in Madras Red, Mecheri and Texel sheep breeds. MSTN gene serves as a negative regulator for muscle growth. Thus, muscle growth increases by double when the function of MSTN is deteriorated in sheep (Broad et al. 2000, Sahu et al. 2017).

Shojaei et al. (2010) have analyzed the variance in exon 3 of the leptin gene in sheep breed in Iran. The genotypes found by those authors affected the body weight at three.
six and nine month of age. Hajhosseinio et al. (2012) investigated the effect of allele variance in exon 3 of the leptin gene on the growth traits of sheep in Iran and found different alleles and genotypes, some of which significantly improved some growth traits, such as weaning weight, six-month and nine-month weight and yearling weight. Abousoliman et al. (2020) identified 4s420693815 of the leptin (LEP) gene to be significantly associated with weaning weight and average daily gain. McMahon et al. (2001) and Moradian et al. (2013) have shown that growth hormone gene induces body growth and also reduces fat stores in sheep. The effect of the growth hormone gene was significant with six months weight (Moradian et al. 2013). Depison et al. (2017) reported that the growth hormone genes Mspl and Alul are associated with body weight, body weight gain, chest grid, chest depth, body length and chest width.

Yang (2014) reported that ADRB3 is highly variable in sheep. The variation of this gene was found to be associated with variation in weaning weight and post-weaning growth rate. Yang (2014) reported an association between variation in ovine UCP1 and variation in lamb carcass traits. USMG 5 is a gene with a function in muscle growth.

Xu et al. (2019) reported two novel indel loci within the ovine silent information regulator 7 SIRT7 gene, significantly associated with sheep growth traits.

Gene NCAPG was associated with body weight, post-weaning gain, bone-related traits (Al-Mamun et al. 2015, Bolormaa et al. 2016).

GWAS study had identified candidate genes associated with post-weaning gain in different sheep breeds. These genes include glutamate metabotropic receptor 1 (GRM1), methyl-CpG-binding domain protein 5 (MBD5), ubiquitin protein ligase E3 component n-recogin 2 (UBR2), ribosomal protein L7 (RPL7) and structural maintenance of chromosome 2 (SMC2) (Zhang et al. 2013). Regarding with the post-weaning gain trait, a GWAS study has reported three genes (POL, Complex Subunit 1 (MSL1) and Shisa Family Member 9 (SHISA9) in sheep breeds (Wang et al. 2015, Zhang et al. 2016).

Xu S. et al. (2017) realized a review regarding the genes associated with economically important traits. The genes NPR2, HMGA2 and BMP2 are associated with skeletal morphology and body size, GRM1, POL, MBD5, UBR2, RPL7 and SMC2 affecting post-weaning gain and accounting for body growth (GHR and ANKS1B) (Kijas et al. 2012, Riggio et al. 2013, Zhang et al. 2013). STRBP and TRAML1 affected body weight at 53 and 83 week stages, DAAM1 and APIP had a central role in controlling weaning weight. The genes PHF15, PRSS12 and MAN1A1 were involved in the six-month-weight. SYNE1, WAPAL and DAAM genes were associated with the yearling weight. Yang et al. (2016) identified genes associated with body size in sheep (GPX3, FSTL1, PVR, EXT2, ALT 4, SOX6, HAND2, PDGF and BMPR2). Zobin et al. (2019) studied the QTLs focusing on single nucleotide polymorphisms associated with growth and meat traits in sheep. The database contains about 163 SNP trait associations – 130 unique SNPs and a list of 172 associated genes. Al-Mamun et al. (2015) using GWAS analysis detected 39 SNPs associated with body weight in sheep and a major region was identified on OAR6.

Tahmoorespur et al. (2009) and Bahrami et al. (2013) studied the genetic polymorphism of Insulin-like growth factor 1 (IGF1) and its association with growth traits. Trukhachev et al. (2016a) studied the polymorphisms of the IGF1 gene in Russian sheep breeds and their influence on some meat production parameters. 18 single nucleotide polymorphisms (SNP) were found in Russian Merino sheep breed. Two allele of the gene were correlated with a high live weight in a heterozygous state.

Genes associated with meat quality

Meat quality traits are important in sheep meat industry. Mortimer et al. (2014) reported that the meat quality traits had a moderate heritability.

The animals with Callipyge phenotype display a 30-40% increase of the postnatal development of the back and rump muscles and 6-7% decrease of the fat percentage (Koohmarai et al. 1995; Freking et al. 1998, 1999, Duckett et al. 2000; Jackson et al. 1997). Callipyge phenotype in sheep results from A/G mutation at locus CLPG. One of 4 markers for the callipyge gene, TGLA 122 on chromosome 18 was found to be present in Australian animals exhibiting increased muscling (Barendse, 1995; Nicoll et al. 1998). The CPPG mutation had a negative impact on meat quality, the tenderness decreased (Koohmarai et al. 1995, Schackelford et al. 1997). Cockett et al. (1996, 2005) had shown that the callipyge phenotype is linked with postnatal hypertrophy of muscle tissue with simultaneous reduction of carcass fatness. Freking et al. (2002) reported that a small genetic region near the telomere of ovine chromosome 18 was previously shown to carry the mutation causing the callipyge muscle hypertrophy phenotype in sheep. White et al. (2008) realized analysis of the callipyge phenotype through skeletal muscle development.

The studies of calpastatin (CAST) gene polymorphism and their correlation with meat quality were done on sheep by Szkudlarek-Kowalczyk et al. (2011). Palmer et al. (1998, 1999) identified polymorphism in the CAST gene in sheep and presented their association with daily body weight gain, age-corrected carcass weight and shear force of longissimus dorsi muscle. Polymorphism in CAPN gene had been identified in different breeds of sheep (Mahrous et al. 2016). The CAPN gene was investigated as a potential candidate gene for growth and meat tenderness as reported in earlier studies of Koohmarai (1995), Arora et al. (2014) and Naveen et al. (2015). Arora et al. (2014) identified nine novel SNPs in four candidate genes, including CAPN4, for mutton quality traits across 11 Indian sheep breeds. Nassiry et al. (2006) reported that calpastatin polymorphism is associated with average daily gain from birth to weaning and nine month to yearling in Kurdi sheep. Aali et al. (2017) identified polymorphism in calpastatin gene, affecting meat quality and fatty acid composition in Chall and Zel sheep breeds.
Fatty acid binding protein 4 (FABP4) gene polymorphism influences IMF level, shear force and marbling of the longissimus dorsi muscle. Allele A of this gene has a positive effect on lamb tenderness (Xu et al. 2011).

Boucher et al. (2006) identified three single nucleotide polymorphisms in the ovine LEP gene (A103G, C154 T and C617 G). In the Suffolk breed, the A103G SNP is associated with reduced muscle thickness (-1.36 mm) and loin eye area (-137.58 mm²) and with increased shear forces (+1.091 kg), pH (+0.168) and cross-sectional area of the slow-twitch oxidative fibers (+818 μm²) of the longissimus muscle. In the Dorset breed, the A103G variant is also associated with an increased citrate synthase activity in the longissimus muscle (+3.19 IU g⁻¹) and in subcutaneous fat (+0.36 IU g⁻¹). The genetic variants increase the weight of the carcass and body fat in Shal sheep and decrease cold carcass and lean meat weight in Zel sheep (Barzehkar et al. 2009). Hajhosseinlo et al. (2012) and Sadeghi et al. (2014) had shown that SNPs in the LEP gene in sheep influence the fat content in carcasses, muscle growth, meat quality traits.

A variant of the myostatin gene (MSTN) has been reported to be segregating in Texel sheep in New Zealand (Broad et al. 2000). The mutation affects muscle and fat traits in some Texel sired lambs (Johnson et al. 2005a) with no effect on shear force, color and pH of the muscle longissimus and muscle semimembranosus (Johnson et al. 2005b). Laville et al. (2004) reported a shift towards more glycolytic muscle fibers in lambs carrying the A variant. Kijas et al. (2007) reported a reduction in intramuscular fat and sensory scores, but no effect on shear force. MSTN has an effect on carcass fatness (Boman et al. 2010; Hadjipavlou et al. 2008). Clop et al. (2006) identified a mutation in the 3’UTR region (G6723A) thus causing muscular hypertrophy in Texel sheep. Gan et al. (2008) identified several mutations of the myostatin gene. Two haplotypes were suggested to be associated with double-muscled trait. Hadjipavlou et al. (2008) had shown that two single nucleotide polymorphisms in the myostatin gene have significant association with muscle depth of commercial Charollais sheep. Johnson et al. (2009) have shown that testing for g+6723G-A SNP and selection of animals carrying the A allele therefore offers breeders the chance to improve rates of genetic gain for lean-meat yield. Hickford et al. (2010) and Praneth et al. (2020) studied the polymorphisms in the ovine myostatin gene (MSTN) and their association with growth and carcass traits. Five variants of the myostatin gene were identified in Romney sheep. The presence of allele A in a lamb’s genotype was associated with decreased lean, loin and total yield of lean meat, whereas the presence of allele B was associated with increased loin yield and proportion loin yield. Han (2012) studied the association between the MSTN haplotypes and variation in lamb growth and various carcass traits in New Zealand Romney sheep. Bagatolli et al. (2013) confirmed association between expression level of MSTN and calpastatin genes and lamb meat quality, lower values of lamb meat tenderness. Grochowska et al. (2020) studied the effects of intronic SNPs in the myostatin gene on growth and carcass traits in colored Polish Merino sheep. The MSTN genotype was found to have significant effect on body weight at second day of life and loin shank weights. Twenty-three genes were identified to be related to biological process associated with fatty acid content in skeletal muscle such DGAT2, TRIHDE, TPH2, ME1 (Rovadosci et al. 2018). Fatty acids have important roles in meat quality in regulating fat firmness, shelf life and color (Wood et al. 2005). Supplementation of Selenium can improve the stability of meat products (Liebien-Jimenez et al. 2015). The incorporation of the omega-3 fatty acid synthesis gene and knockdown of myostatin gene in sheep has improved the quality of sheep mutton (Kumar et al. 2016). Quirino et al. (2016) had identified the polymorphisms in the myostatin and leptin genes of Santa Ines breed and crossbreed sheep and association with carcass trait. The mutant allele of the myostatin gene showed association with increased measures of cold carcass weight, fat thickness and with reduced hot carcass yield. The three alleles of the leptin gene increased cold carcass weight.

Trukhachev et al. (2016b) have shown that a candidate gene defining productive qualities of sheep is MEF2B. Protein from the MEF2B group encoded by it affects the production of myostatin and the expression of the gene responsible for the growth of skeletal muscle fibers.

The regulatory factor X associated Ankyrin containing protein (RFXANK) gene and receptor-interacting serine/threonine-protein kinase 2 (RIPK2) gene affected post-weaning gain in sheep (Zhang et al. 2013).

Xu et al. (2009) observed the influence of mutation Ala 487Ala T>C of diacylglycerol acyltransferase1 (DGAT1) gene on important quality traits of lambs. The genotype was associated with increase of marbling score and intramuscular fat (IMF) content, lower shear force and drip loss rate. (DGAT1) gene controls carcass traits (Mohammadi et al. 2013). UCP1 (uncoupling protein1) is a gene associated with subcutaneous carcass fat depth (Cannon et al. 2004, Yang et al. 2014).

Fast skeletal muscle troponim C (TNNC2) gene is associated with meat productive traits. Xu et al. (2008) reported that a single nucleotide polymorphism in intron 1 influenced carcass weight and meat quality traits: muscle longissimus thoracis and muscle lumbarum shear force, water-holding capacity, marbling and pH value. Sheep with TT genotype were characterized by improved meat tenderness and marbling, but lower carcass weight.

Bahrami et al. (2015) presents an association between carcass traits and genetic polymorphism and changes in the protein structure of the growth hormone 1 (GH1) gene in Mehraban sheep. Gene ACACA was associated with muscle depth, fatty acid formation and several multivariate phenotypes related to carcass (Bolormaa et al. 2016, Garza Hernandez et al. 2018).

Gene LCORL was associated carcass multivariate phenotypes (Al-Mamun et al. 2015, Bolormaa et al. 2016).
Kashani et al. (2017) studied the SNP of ovine ADRB3 gene (adrenergic-receptor beta 3) in crossbred Australian sheep. Eleven SNPs in both the coding and non-coding regions of this gene were detected.

Hopkins et al. (2011) have shown that meat quality includes many factors including palatability, water-holding capacity, color, nutritional value and safety.

Hu et al. (2016) reported that in Sheep QTL database have been annotated 175 QTLs related with carcass traits, 33 with meat composition, 6 with meat color and 5 with meat texture.

The QTL for final and carcass weight on chromosome 2 was the only one that corresponded to Aqtl for live weight in Scottish Blackface and Suffolk, Texel sheep (Karamichou et al. 2006, Walling et al. 2001). The association between the ovine leptin gene and its association with growth and carcass traits in three Iranian sheep breeds. Iranian Journal of Biotechnology. 7(4): 241-246.

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