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Development of Muscle-related Genes and Their Effects on Meat Quality

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Abstract

Myofibre is the basic unit of muscle tissue, muscle fibre types and the proportion of fibre types affected meat quality directly. Four adult MyHC isoforms have been identified in skeletal muscles, types I, IIa, IIx and IIb isoforms are corresponding to four MyHC isoforms. Muscle fibre types are influenced by forkhead transcription factor family, myogenic determination gene family and calpain gene family.

Keywords: Meat quality; Muscle fibre; Gene

1. Introduction

Over the last few decades, in all species raised for meat production, genetic selection and improvement of nutrition and breeding conditions has led to a tremendous increase in the efficiency of animal production and carcass composition by decreasing carcass fatness, and increasing muscle yield. Several studies suggest that such practice would have adversely affected some aspects of lean meat quality[1-2].

Currently, consumers focus on meat quality more than meat quantity. It is a new Challenge for enterprises and scientist to improve production performance as well as meat quality to meet the increasing demand of the consumers for high quality meat. With the rapid development of molecular biology, structure and function of genes have been researched deeply; the study on genetic mechanism of meat quality and quantity is a hot spot now. Modern molecular biology and genomics opened a new era of the study of meat quality.

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2. Meat quality and its genetic characteristics

Meat quality is a complex trait, it is difficult be measured by a single index[3]. Depending on the different demand, meat quality has different definitions. Meat quality is known to be influenced by numerous factors such as genetic, pre-slaughter and slaughter conditions, p.m.processing, as well as nutritional and environmental conditions during the rearing phase. Generally, meat quality includes many aspects such as pH value, intramuscular fat, color, water holding capacity, tenderness, juiciness and flavor.

Many meat quality traits are quantitative traits, controlled by multiple genes. Several genes play a major role; these genes are called major genes. Major gene is a gene with pronounced phenotypic effects, in contrast to a modifier gene, which modifies the phenotypic expression of another gene[4]. A candidate gene is a gene, located in a chromosome region suspected of being involved in the expression of a trait such as a disease, whose protein product suggests that it could be the gene in question. A candidate gene can also be identified by association with the phenotype and by linkage analysis to a region of the genome[5]. Through the investigation of major gene and candidate gene, meat quality will be improved. Now gene affecting muscle fibre is hot.

3. Muscle fibre types impact on meat quality

Through deferent method, muscle fibre can be classified as different type. Histochemical staining with Sudan black-B has been used to classify fibres into red and white fibres[6]. Based on differences in the sensitivity of the acto-myosin ATPase activity to pH preincubation, three main fibre types have been conventionally determined by histochemistry in adult skeletal muscle, i.e. types I, IIA and IIB fibres[1]. Muscle fibres could also be classified as slow-twitch red (βR), fast-twitch red (αR) or fast-twitch white (αW) or also slow-twitch oxidative (SO), fast-twitch oxidative glycolytic (FOG) or fast-twitch glycolytic (FG) based on the activities of ATPase and oxidative enzymes[7]. However, four adult MyHC isoforms have been identified in mouse, rat, guinea pig and rabbit skeletal muscles, i.e. types I, IIa, IIx and IIb isoforms[1].

Muscle fibre type composition, fibre areas and the capillary density of specific muscles are important factors influencing many of the peri- and post-mortal biochemical processes and thereby meat quality[8]. Ryu and Kim (2006) found that accelerated metabolic rates and poor meat quality in fast-glycolyzing PSE and RSE pork were explained by an increase in percentage of type IIb fibres. A high proportion of type IIb fibres may be more prone to undesirable pork because of its anaerobic nature[9]. Seideman's study (1986) show that the low-energy diet resulted in higher red fibres, and larger white fibre area than the higher-energy diet, Breed × sex interactions were observed for muscle fibre characteristics. Correlations between muscle fibre characteristics and carcass and meat quality characteristics are presented. Red fibre area was significantly correlated with hot carcass wt. and fat thickness; few other correlations between fibre characteristics and carcass quality characteristics were significant. Higher area of red fibres is correlated with low off-flavour incidence. Large fibre area, either red or white, was positively correlated with objective tenderness[10]. Choi's study (2008) shows that muscles with low glycogen and lactate content at early postmortem are composed of significantly higher fibre type I and lower fibre type IIB as compared to muscles with high glycogen and lactate content[11].

4. Genes affecting muscle fibre

4.1. Forkhead transcription factor family

The forkhead (Fox) gene family comprises a large and diverse group of transcription factors that share a 'winged helix' DNA binding domain, first defined in 1990, consisting of three alpha helices flanked by two 'wings' of beta strands and loops[12]. In November 1998, at the first International Meeting on Forkhead/Winged Helix Proteins, held in La Jolla, California, a proposal was developed to standardize the nomenclature for these proteins. A winged helix/forkhead nomenclature committee was elected to implement this proposal. In 2000, unified nomenclature for the winged helix/forkhead transcription factors had been given[13]. Over 100 proteins with forkhead domains have been found, comprising at least 17 subclasses, from FoxA to FoxQ[12].

FoxO is the most diverse subclasses of Fox family. In mammals, there are four FOXO genes, FOXO1, 3, 4, and 6. FOXO factors are evolutionarily conserved mediators of insulin and growth factor signaling[14]. In 2004，Kamei Y, et al created transgenic mice specifically over expressing FOXO1 in skeletal muscle. These mice weighed less than the wildtype control mice, had a reduced skeletal muscle mass, and the muscle was paler in color. Microarray analysis revealed that the expression of many genes related to the structural proteins of type I muscles (slow twitch, red muscle) was decreased. Histological analyses showed a marked decrease in size of both type I and type II fibres and a significant decrease in the number of type I fibres in the skeletal muscle of FOXO1 mice. These results suggest that FOXO1 negatively regulates skeletal muscle mass and type I fibre gene expression and leads to impaired skeletal muscle function[15]. YANG Yan-Jun got same result in his study on expression of FoxO1 mRNA in muscle tissue of Bamei, Landrace and Landrace × Bamei. It suggests that FoxO1 expression level has the negative correlation with the content of type Ⅰ muscle fibre[16].

4.2. MYOD gene family

The MYOD gene family consists of four structurally and functionally related genes: MYOD1 (MYF3), MYOG (myogenin), MYF5 and MYF6 (herculin). All four genes are composed of three exons and (Fujisawa-Sehara et al., 1990). Myogenic differentiation (MYOD) genes encode for skeletal muscle-specific transcription factors with highly conserved basic helix–loop–helix domain. These genes play key roles in growth and muscle development, and are therefore considered as candidate genes for meat production traits in farm animals[17].

In 2002, Muroya's study suggested that MyoD and Myf5 influence the MyHC isoform expression, and skeletal muscles are characterized as fast and slow muscles, according to the expression pattern of myosin heavy chain (MyHC) isoforms in the muscle fibres, so it suggested that MyoD and Myf5 influence the muscle fibertypes[18].

The MYOD1 and MYF5 genes are involved in myoblasts proliferation and they were found to directly affect the proportion of fast-twitch oxidative fibres and the fast-twitch low-oxidative fibres of pigs being crosses of Pietrain x (Polish LW x Polish Landrace) and thereby also influence the metabolic properties of muscle[19]. Several investigations have been focused on the detection of polymorphisms in MYF5 gene in pig and revealed significant association with production and meat quality traits[20-21]. The myogenin (MYF4) genotype showed a significant effect on most of the studied meat characteristic[22].

4.3. The calpain gene family and its inhibitors

Calpains (EC 3.4.22.17) are intracellular non-lysosomal calcium-dependent cysteine proteinases, consisting of two subunits with molecular masses of 80 and 30 kDa. The calpain large subunit constitutes a family classified into two major species: ubiquitous and tissue-specific. Ubiquitous calpains are predominantly composed of two molecular species, m- and m-calpain, which are activated, respectively, by micromolar and millimolar calcium ion concentrations. Many reports have already suggested that m-

calpain could be involved in myoblast fusion. It has been shown that during myogenesis, the appearance of m- and m-calpain and the appearance of their specific mRNAs are not simultaneous events, suggesting that these two isoenzymes could have different biological functions: the increase in m-calpain specific activity is very large during the burst of myoblast fusion, whereas m-calpain expression reaches a maximum during the later stages of muscle cell differentiation[23-25].The μ - and m-calpain seem to have different biological functions during myogenesis, revealed by their differential distribution, expression and activity during the early stages of myogenesis. While m-calpain seems to be directly involved in early myoblast differentiation, because its mRNA appears before fusion and its activity increases all along myotube formation, μ-calpain expression is delayed and increases in later stages of myogenesis[24].

5. Conclusion

Meat quality is a complex trait; improvement of meat quality has great economic value. So investigation into the relevance of these genes and meat quality will meet the increasing demand of the consumers for high quality meat.

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