



Study on the Fat-related Genes of Chicken

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Abstract

For chicken, the study about fat-related traits is one important aspect of the breeding and economic benefit. The intramuscular fat can enhance the taste and flavor of muscle, and study of chicken on the level of DNA has become into a research spot for modern biologics. In this article, we summarized deeper research developments of fatty acid-binding protein gene (FABP), leptin receptor gene (OBR), peroxisome proliferators-activated receptor gene (PPAR), thyroid hormone response albumen Spot14 gene (THRSP), melanocortin receptor gene (MCR), apolipoprotein B and lipoprotein lipase gene (LPL) about chicken fat-related traits in recent years.

Keywords: O, O-diethyl acrylamide phosphate, Intumescent flame retardant, LOI, SEM

With the enhancement of human living, people require more and more chicken quality. The intramuscular fat is the fat in the muscle. On the one hand, it can dissolve the muscular fasciculi and enhance the taste and flavor of the muscle when the muscular fat is oxidated. On the other hand, because the muscular fat largely contains phosphatide which can produce aroma though Mailard reaction (Oleagineux et al, 1997), so the content of muscular fat is the important factor to influence the quality and taste of animal meat. With the accomplishment of the chicken genome plan, as the important biological representative biology, the chicken will certainly exert larger function in the age of post genome. Numerous genes, which compose the chicken production traits and special idioplasm inheritance base will be developed and the function of genes will be analyzed. Therefore, the study of relative genes of fowl fat traits has become into one of spots studied by many fowl inheritance and breeding scholars.

1. Fatty acid-binding protein gene (FABP)

In the species of bird, as one part of dissoluble non-enzyme albumen in the cytoplasm, FABP is broad distributed in multiple histocytes, and it occupies 3%~8% of the total protein in cytoplasm, and its molecular weight is 14~16k. Albumens combining with fatty acid are some small proteins existing in the cell (Wang, 2002). FABPs participate to incept the fatty acid in the cell, and help to carry fatty acid to the locales of β -oxygenation (such as plastosome or peroxide enzyme) and the combination part of triglycerides and phophatide (Veerkamp and Maatman, 1995). When studying the adjustment of rat fatty acid absorption, Ockneir et al found FABP in the intestinal mucosa. At present, there are nine sorts of FABP including small intestine type (I), heart type (H), lipocyte type (A), liver type (L), brain type (B), ileum type (II), epidermal cell type (E), phospholipids (MY) and spermary type (S). The main function of FABP is to combine with the long chain fatty acids (LCFAs), and different types of FABP have different abilities to combine with LCFAs (Wang, 2002), and the type H and the type A are regarded as the candidate gene of intramuscular fat (IMF).

The gene of H-FABP is positioned in the sixth chromosome of pig, the fourth chromosome of small rat and the first chromosome of human being. As the candidate gene of intramuscular fat, the researches about the gene of A-FABP and H-FABP in birds have achieved some results. Wang, Qigui (2004) cloned the genes of A-FABP and H-FABP of chicken, and found different gene types produced by part SNPs had important influences to the avoirdupois and ventral fat traits, and speculated that the reason is in the major gene influencing these traits or the close linkage with the major gene. Ye, Manhong et al (2003) used the method of PCR-RFLP found that the polymorphism existed in the third intron of chicken A-FABP and the second intron of chicken H-FABP. The sequence length of EX-FABP gene is 5148bp, and it includes 6 exontras and 178 amino acids codes, and the polymorphism of chicken EX-FABP has significant correlation with ventral fat (Wang, 2001). Ao, Jinxia (2003) cloned and tested the goosey A-FABP gene code area, and its length was 399bp, and the homology of nucleotide acid sequence with chicken A-FABP gene code area achieved 94%, and the

homology after deducting amino acid achieved 97%. And she also measured the intron 2 of the gene, and the length was 221bp, and she found that the expression quantity of goosey A-FABP gene is higher in fat, heart and liver, and it had no expression in spleen and small intestine (Gerbens F, 1998).

2. Leptin receptor gene (OBR)

The gene of OBR was found and cloned by Tartaglia (1995) through the strategy of clone. It is a sort of trans-membrane albumen, and it belongs to the I type cell factor super family acceptor which has five isomers including OBRa, OBRb, OBRc, OBRd and OBRe, and they possess same exterior area of cell, but their interior structures of cell are different in length and sequence. The main physiological function of OBR is to combine with leptins and make leptins to adjust body energy balance and fat storage. There are few researches about birds OBR gene, and Guy et al (2000) first cloned the sequency of chicken OBR cDNA, and its homology with mammals could averagely achieve 60%. Dunn et al (2000) oriented the chicken OBR gene in the eighth chromosome (Carre W, 2001, p.289-297). Gu, Zhiliang et al (2002) found one base mutation on the exontra 9 of OBR gene, and speculated that the allele A might be related with much ventral fat. Wangying et al (2004) found two gene mutations of T →C and G→A in the intron 8 of chicken OBR gene, and the different gene types were obviously different in the ventral fat weight and ventral fat rate, and the individual ventral fat weight and ventral fat rate of BB type were significantly higher than the individual of AB type, and the significance was higher than the individual of AA type (Hardiman, 1996, P.461-467 & Jeffrey, 1998, P.763-770). So we can primarily judge that the gene OBR might be the major gene influencing the chicken fat traits or closely linked with the major gene.

3. Peroxisome proliferators-activated receptor gene (PPAR)

The existing researches indicated that three PPARs including PPAR α , PPAR β (orPPAR δ or NUC1) and PPAR γ (Robert, 1998). According to the report of Diot, the cDNA sequences of PPAR gene among different species are highly homologized. As same as other steroid hormones acceptor super-family members, PPAR has six regions (A-F) or four functional structure regions. The region C in the center of the acceptor molecule is the DNA-binding domain (DBD), the E/F region of carboxyl port is the ligand-binding domain (LBD) which exerts important function in the process that the hormone signals are converted into the transcriptional activation signals, and the A/B region of amido port is the adjustment domain.

PPAR can promote fat metabolism, adjust glucide metabolism and differentiate lipocytes. Menghe adopted the PCR-SSCP technology and found three types of gene in the chicken samples with eight weeks old, and he found a mutation from C to T at the point of 297bp, but the statistical analysis showed the gene type of the point had no significant difference in ventral fat rate, ventral fat weight and other six traits (Lemberger, 1996, P.335-363). Grindflek implemented PCR-RFLP analysis to the PPAR γ gene of Norway pig and found a polymorphism point, and statistical analysis indicated that the waist muscle fatty acid composing is different of the individuals with different gene types, but the indexes of back-fat and intramuscular fat had no obvious differences (Meng, 2002 & Meng, 2002, p. 119-123).

4. Thyroid hormone response albumen Spot14 gene (THRSP)

The gene of THRSP is a sort of acidic protein with less molecular weight in mammals, and it was found in the research about the reaction of thyroxin in the fat (Seeling et al, 1981). The gene mainly exists in fat-produced organizations such as liver, ventral fat and galactophore (Compe E, 2001, P.175-183). Because this albumen can produce response reaction to the stimulation of thyroxin and the high dextrose level, so the chromosome domain where the genes exist is related with the adiposity, and the gene is thought to possess important function for the production of fat. The researches about the gene mainly concentrated in human, big rat and small rat, and the THRSP gene of chicken was first confirmed by Cogbum et al (2000) who used the micro-array method to separate the chicken liver. The gene was oriented in the chromosome of lq41244 (Beccavin, 2001, 297-306). The chromosome domain contains sebum traits points and the ventral fat quantity traits points (Ikeobi et al, 2002). The gene can be divided into THRSP α and THRSP β 2 according to its polymorphism (Kinlaw, 1995, 16615-16618 & Liu H C, 1994, 1021-1037). The gene of THRSP α was related with the ventral fat traits in the crossbreed resource colony of table poultry and leghorn. Yan, Wenlong et al (2004) pointed out the chicken gene of THRSP α was significantly correlated with the fat bandwidth and fat weight, and various gene types of this gene were significantly correlated with the influences of traits (Cunningham, 1997, 5184-5188). Li, Huifeng et al (2005) applied the gene chip technology to analyze the expressions of 20 genes in the fat metabolism approaches in different growth periods of Beijing oil chicken, established the Bayesian interactive network of these genes, and found the spot14 β and H-FABP genes which largely influenced the fat traits, and deeply analyzed the influences of these two genes to the fat traits (Liu H C, 1994, 1021-1037). The gene of H-FABP presented significantly negative correlation with the intramuscular fat content of Beijing oil chicken. Li, Zhihui et al (2005) pointed out the combination gene type of OBR and UCP significantly influenced ventral fat weight and ventral fat rate of table poultry, and the individual of BBBB was lower 17.81g than the individual of AAAA, its inheritance contribution rates to ventral fat weight and ventral fat rate aberrance respectively could achieve 16.61% and 11.04% (Cao, 2008, 258-288).

5. Melanocortin receptor gene (MCRs)

The family is the smallest G albumen coupling acceptor sub-family at present, and they all belong to the 7 trans-membrane α helix G albumen acceptor of A class, and they are the production of a series of small gene (SchiothHB, 2003, 504-509). Up to now, there are five melanocortin receptor genes (MC1R-MC5R) to be cloned, identified and oriented. The melanocortin receptor board participates in the controls of multiple physiological channels including pigmentation, food intake behaviors, weight and energy metabolism and balance, anti-infection, sex function and ache. High homology exists in all MCRs which possess common molecule structure character (Vaisse C, 1998, p.113-114 & Jeffrey M, 1997, P.119-120). The human chromosome database sequence in Gene bank has not the similar sequence with rat MC2R α and its flank sequence, which indicates that the human fat organization has no the expression of MC2R because of the deficiency of exon1f. Blondet et al also found an E-box (oriented in -1020bp) participated in restraining the expression of MC2R in the adrenal gland cell. The electrophoresis analysis shows the restriction function is implemented by the mutual function of various factors such as catalytic albumen enzyme-4. Jiang, Siwen et al took the Plymouth rock 3 as the experiment materials and found 5 new MC3R genes SNPs including T452G, A549G, C564T, A882G and C894T, and the first mutation produced Len151Arg amino acid substitution, and the second mutation produced a new Dde I limited endonuclease enzyme cutting site which could be utilized to establish the MC3R gene type PCR-RFLP molecule test method. The variance analysis result showed that the MC3R gene could significantly influence the weight of cock and hen, and the ventral fat content of cock, and the result advised that the MC3R gene could be as the reason to explain the significant difference of crossbreed chicken weights (Jiang, 2002, 322-325).

6. Apolipoprotein B gene

Apolipoprotein B (ApoB) gene possesses important function in the processes of energy absorption, transportation and metabolism (Glickman et al, 1986). In mammals, ApoB is expressed in small intestine and liver, and it is the VLDL synthesis of triglyceride and excretory framework albumen which has important function of the transportation and metabolism of fat (Schumaker et al, 1994). The ApoB albumen in mammals mainly includes two forms, i.e. ApoB-100 and ApoB-48, and they are coded by same gene, and formed by special compiling mechanism (Glickman et al, 1986 & Schumaker et al, 1994). The mRNA of ApoB in the chicken small intestine is not be compiled, so the expression of ApoB-48 doesn't exist in the chick small intestine. ApoB is the component of VLDL, IDL, LDL, and it is the frame albumen of fat albumen synthesis exudation and transportation, and it has important function for the energy transportation and metabolism, and it can directly or indirectly influence the fat accumulation and growth (Innerarity et al, 1996). Zhangsen et al (2005) found a T→G synonymy mutation on exon 26 of chicken ApoB gene, and it had large influence to the weight and ventral fat traits, and 1 week weight and 3 week weight of GG gene type were significantly lower than other gene type, but the ventral fat weight and ventral fat rate of TT gene type were significantly higher than GT gene type and GG gene type (Zhang, 2006).

7. Lipoprotein lipase gene (LPL)

The research about the LPL gene of chicken is clear. In 1989, Cooper et al separated the chicken fat LPLcDNA clone from a λ -gt11 expression library and tested its sequence. According to the analysis of cDNA sequence and purification enzymatic N-port sequence, the chicken fat LPL is a mutual protein containing 465 amino acids, and possesses the signal peptide with 19 or 25 amino acids. All chicken LPL genes have been separated and determined by the primer extension and sequence analysis (Cooper, 1992), and the length of the gene is 17kb. All cutting sites of all introns and exons must abide the rule of gt-ag. As same as human LPL gene, the chicken LPL gene also contains 10 exons and 9 introns. Raisonier (1995) implemented linear arrangement to the LPL nucleotide acid and amino acid sequence of 8 species (human, pig, cattle, sheep, small rat, big rat, guinea pig and chicken), and found the main structure domain including catalytic action, N-candy base and liver element combination point are highly conservative, and the sequence of amino acid chain with same code is in the end of the second exon to the start of the third exon. In 7 sorts of mammal, exon 10 has not been completely translated and it contains special deficiency, insert or A and A+T components of species, but in chicken, the start of exon 10 is translated, and the linear arrangement of these 8 species will offer useful tool for further studying the function of LPL. The experiment result of Whitehead et al (1982) showed that under the condition of raising HFD, the sum of VLDL and LDL is closely related with the fat weight of 7 weeks old, and the type correlation was 0.45. In addition, the research by Griffin et al (1982) also indicated that strong correlation existed in VLDL and the accumulation of fat. But the physiological function of LPL is the triglyceride in VLDL which charges in the storage of fat. Therefore, it has extensive research foreground to study the relationship between different gene types of LPL and the intramuscular fat content, confirm the molecule inheritance sign of the intramuscular fat content, and enhance the veracity of chicken high quality traits breeding (Wang, 2007).

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