

QTL ANALYSIS OF MEAT QUALITY-RELATED TRAITS IN KOREAN NATIVE CHICKEN

Dongwon Seo¹, Hee Bok Park¹, Nuri Choi¹, Shil Jin¹, Muhammad Cahyadi¹

Kang Nyeong Heo², Samooel Jung¹, Cheorun Jo³, Jun Heon Lee¹

¹ Division of Animal & Dairy Science, Chungnam National University, Daejeon, Republic of Korea, ²National Institute of Animal Science, RDA, Seonghwan, Republic of Korea ³Department of Agricultural Biotechnology and Research Institute of Agriculture and Life Science, Seoul National University, Seoul 151-921, Korea

Abstract – The aim of this study is to identify genomic regions that affect meat quality traits by QTL (quantitative trait locus) mapping approach in Korean native chicken (KNC) resource population. For this study, 68 nuclear families were constructed by 15 sires mated with 4~5 dams. A total of 83 parents (G0) produced 597 progenies (G1). The genetic linkage map was established using 167 genetic markers. A multi-marker half-sib QTL mapping was performed using the least squares method implemented in GridQTL program. QTL with 5% chromosome-wide significance were detected in eleven (cAsh, cProtein, Cooking loss, Collagen, H₂O, L*, a*, WHC, pH1, pH2 and delta_pH) meat quality related traits. Especially, QTL for crude protein contents in breast muscle and thigh muscle were detected with 1% chromosome-wide significance QTL on GGA5 and GGA26, respectively. These results can provide useful information for the exploring positional candidate genes that affect meat quality traits related in Korean native chicken.

Key Words – QTL, Meat quality, Korean native chicken

I. INTRODUCTION

The chicken is one of the most important protein source for human and a valuable animal model for biological studies. Therefore, chicken was firstly chosen for genome sequencing among the livestock species [1]. Recently, when consumers choose meats, there are strong interests in the meat qualities including meat sensory and nutritional values compared to the price [2]. Therefore, it is justifiable to achieve genetic improvement of meat quality traits for consumer's preference. However, most of meat quality traits are quantitative traits that show continuous variations due to multiple genetic and environmental factors. Thus, it is very difficult to identify causal gene and variants [3, 4]. Quantitative

trait locus (QTL) mapping method can provide a solution for the finding candidate gene and causal variants that affect quantitative traits using various genetic marker information. Although Korean native chicken (KNC) have limitation in retarded growth rate, this breed is a well-known for unique meat quality related traits including taste. The aim of this study was to identify QTL that affect meat quality traits in breast and thigh meats in a nuclear pedigree of KNC comprising 683 birds.

II. MATERIALS AND METHODS

Animals

A total of 83 parents (founder; G0) birds which were consist of 3 sires mated with 4~5 dams in each lines were produced totally 597 progeny (G1) birds. All the animals were controlled in a standard feeding system and environment. Of this, blood samples in wing vein were collected for DNA extraction and slaughtered G1 birds for the measurement of meat quality traits.

Phenotypes and genotypes

Meat quality traits were analyzed following standard protocols in the Laboratory of Meat Science at Chungnam National University, Korea.

General linear model (GLM) was performed using the Minitab software to identify factors affecting phenotypic variation. Then, phenotypic values were pre-adjusted for fixed effects of sex, batch, line and carcass weight.

The linkage map was constructed using 128 microsatellite and 39 SNP for QTL mapping. The total autosomal map length was 2,921.4 cM. The average distance between makers was 17.5 cM.

QTL analysis

A multi-point QTL mapping was performed by the GridQTL program using paternal half-sib families

(Seaton et al., 2006). The conditional probability of alternative QTL genotypes given marker genotypes was computed at 1-cM intervals within and across the half-sib families. Then, the pre-adjusted phenotypic data of progeny were regressed onto the probability of QTL genotype to evaluate a significant effect of allele substitution using the following formula:

$$y_{ij} = m_i + a_i x_{ij} + e_{ij} \quad (\text{Model 1})$$

where, y_{ij} is the adjusted phenotypic observation of the j th animal, originating from the i th sire; m_i is

average effect for the i th half-sib family; a_i is the allelic substitution effect for a putative QTL within the i th sire; x_{ij} is the conditional probability for j th individual that transmits a given allele from the i th sire; e_{ij} is the residual effect. Of these, six QTL for general compounds (crude ash: cAsh, collagen, crude protein: cProtein, H₂O To address multiple testing issues in genome scans, chromosome-wide significance thresholds (1%, 5%) were computed by 1,000 permutations.

Table 1. Half-sib QTL mapping result for meat quality traits in Korean native chicken population.

Category	Phenotype	Half-sib QTLs					
		GGA	F	Position (cM)	Confidence Interval	Flanking Markers	
GC	Br_cAsh	9	2.15*	93cM	78-104	ADL0021	ADL0259
GC	Leg_Collagen	2	2.26*	173cM	151-191	MCW0288	MCW0282
GC	Br_cProtein	26	2.46**	30cM	10-37	MCW0069	LEI0074
GC	Leg_cProtein	5	3.03**	109cM	97-112	GEMIN2	PSMC1
GC	Br_H2O	3	2.51*	182cM	168-206	MCW0103	MCW0016
MC	Br_a*	17	2.22*	9cM	0-24	MCW0151	ADL0293
MC	Br_L*	3	2.23*	254cM	234-283	GCT0053	MCW0037
MC	Br_L*	5	2.2*	53cM	37-66	EFCAB4B	GPHN
MC	Leg_L*	8	2.14*	87cM	65-109	MCW0160	ADL0278
pH	Leg_Cooking Loss	10	2.12*	0cM	0-16	MCW0228	MCW0194
pH	Br_Delta_pH	27	2.15*	4cM	0-54	MCW0300	GCT0022
pH	Leg_Delta_pH	5	2.57*	148cM	131-167	MCW0081	ADL0298
pH	Br_pH1	27	2.07*	54cM	0-54	MCW0300	GCT0022
pH	Leg_pH1	5	2.23*	141cM	130-156	MCW0081	ADL0298
pH	Leg_pH1	7	2.1*	39cM	19-93	LEI0064	MCW0316
pH	Br_pH2	5	2.33*	106cM	81-115	MCW0078	PSMC1
pH	Br_pH2	15	2.1*	42cM	0-42	ADL0206	MCW0080
pH	Leg_pH2	7	2.08*	103cM	97-113	MCW0316	ADL0169
pH	Leg_pH2	17	2.06*	9cM	1-37	MCW0151	ADL0293
pH	Br_WHC	3	2.32*	27cM	5-45	MCW0261	UGP2
pH	Leg_WHC	8	2.03*	99cM	76-109	MCW0160	ADL0278
pH	Leg_WHC	24	2.12*	58cM	44-75	NTM	mir6612

Br: breast muscle; Leg: thigh muscle; L*: lightness; a*: redness; b*: yellowness; WHC: water holding capacity; § By using 1-LOD drop method

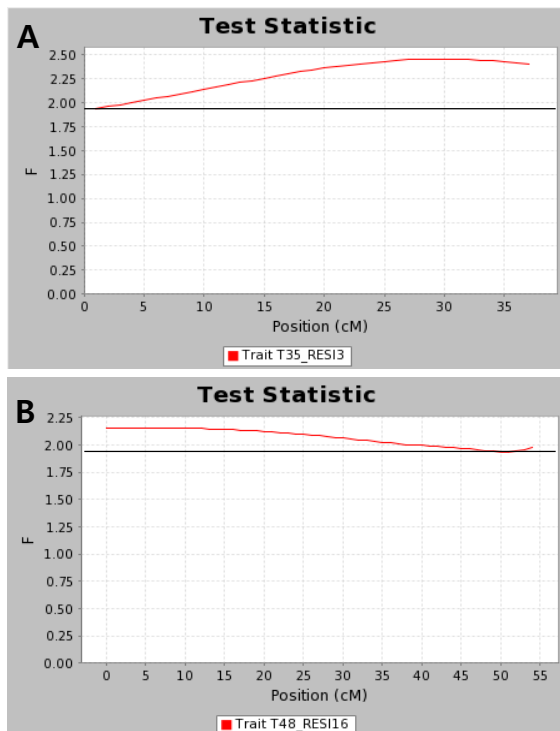


Fig. 1. Profile of test statistics (F -values) when a quantitative trait locus (QTL) is fitted across GGA5 for crude protein contents in thigh meat (**A**) and GGA26 for crude protein contents in breast meat (**B**) in 15 KNC paternal half-sib families. Map with distances in Kosambi cM is given on the x-axis. The y-axis represents the F -ratio testing the hypothesis of a single. QTL in a given position on the chromosome 5 and 26. Horizontal lines represent 1% chromosome-wide significance threshold.

III. RESULTS AND DISCUSSION

The half-sib QTL analysis mapped a total of 22 QTLs. Two of them on GGA5 and GGA26 were identified with 1% chromosome-wide significance (Table 1). Four QTLs on GGA 3, 5, 8, and 17 for meat color traits (a^* and L^* values) were detected with 5% chromosome-wide significance. In addition, Nine QTL that affect pH traits (initial pH: pH1, ultimate pH: pH2 and delta pH) were detected with five 5% chromosome-wide significance. Additionally, QTLs on GGA3, 8 and 24 for water holding capacity (WHC) were identified with 5% chromosome-wide significance. The most of QTL results revealed as novel QTL in the KNC population except breast pH and cProtein

traits which were reported similar positions in the previous results [6, 7].

IV. CONCLUSION

In conclusion, we identified 22 QTL that influence meat quality related traits in KNC. These results can provide important information to improve meat quality related traits.

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