



## QTL analyses of general compound, color, and pH traits in breast and thigh muscles in Korean native chicken



D.W. Seo<sup>a,1</sup>, H.B. Park<sup>a,1</sup>, S. Jung<sup>a</sup>, M. Cahyadi<sup>a,b</sup>, N.R. Choi<sup>a</sup>, S. Jin<sup>a</sup>, K.N. Heo<sup>c</sup>, C. Jo<sup>d</sup>, J.H. Lee<sup>a,\*</sup>

<sup>a</sup> Division of Animal and Dairy Science, Chungnam National University, Daejeon 305-764, Republic of Korea

<sup>b</sup> Department of Animal Science, Faculty of Agriculture, Sebelas Maret University, Surakarta 57126, Indonesia

<sup>c</sup> Poultry Science Division, National Institute of Animal Science, Rural Development Administration, Cheonan 331-801, Republic of Korea

<sup>d</sup> Department of Agricultural Biotechnology, Center for Food and Bioconvergence, and Research Institute for Agriculture and Life Science, Seoul National University, Seoul 151-921, Republic of Korea

### ARTICLE INFO

#### Article history:

Received 30 June 2015

Received in revised form

20 September 2015

Accepted 22 September 2015

#### Keywords:

Korean native chicken

QTL

General compound

Meat color

Meat pH

### ABSTRACT

Meat quality is one important selection criterion to consumers. In Asian countries, demands for native chicken breeds with better meat quality-related traits are increasing. In this study, 13 meat quality related traits in Korean native chicken were collected to identify QTLs that could affect the traits. A total of 20 novel QTLs, including 6 for general meat compounds (GC), 7 for the meat color (MC), and 7 for pH were identified. Significant QTLs (i.e., 1% chromosome wide significance) for crude protein contents in thigh and breast muscles were identified. Other QTLs were also identified with suggestive significance levels (i.e., 5% level of chromosome wide significance). Results presented here could provide useful information to find causal variants to improve meat quality traits in chicken.

© 2015 Elsevier B.V. All rights reserved.

### 1. Introduction

Chickens provide excellent protein sources for human. They are also useful animal models for biological researches. Chicken genome has been sequenced and used for various genetic and genomic studies (Wong et al., 2004). Most economically important traits (e.g. meat quality and growth related traits) are quantitative traits. They normally have continuous variations. These quantitative variations are mainly affected by multiple genetic and environmental factors. Thus, it is very difficult to identify causal genes and variants that affect quantitative traits (Lander and Schork, 1994; Abasht et al., 2006).

Recently, genome-wide mapping technologies such as genome sequencing and high-density array-based genotyping methods have been used to identify quantitative trait locus (QTL). In animal QTLdb (<http://www.animalgenome.org/cgi-bin/QTLdb/index>), 4,379 QTLs for 206 different traits have been reported from 210 papers in chicken. Of these, 10 traits (i.e., b color, breast pH, drip

loss, meat color, muscle dry matter content, muscle fiber cross-sectional area, muscle fiber density, muscle fiber diameter, muscle fiber number and muscle protein content) are meat quality-related traits in chicken. Based on consumers' perspective, these meat quality-related traits are very important. Hence, meat quality-related traits have excellent economic value. These traits can be investigated by analyzing general meat components (Berri et al., 2001). When consumers select meats in the market, their first selection standard is the meat color (Mancini and Hunt, 2005). Water holding capacity (WHC) is another important selection standard because meat WHC can show good texture to consumers. Crude fat, crude protein, and crude ash have sensory and functional importance. In previous research studies, hydrogen ion concentration (pH) has been used as an important criterion to evaluate the meat quality (Allen et al., 1997; Huff-Lonergan and Lonergan, 2005; Barbut et al., 2008). Lower meat pH can generally result in pale meat color and lower WHC. Therefore, pH is another important criterion for meat quality.

Korean native chicken (KNC) is an indigenous purebred in Korea (DAD-IS; <http://dad.fao.org/>). Based on their plumage colors, there are five lines of KNC: White, Black, Yellow, Gray, and Red. As the most indigenous chicken breed, KNC shows low growth rate and low feed efficiency. However, this breed has excellent and unique meat quality such as particular texture, which is because of

\* Correspondence to: Division of Animal and Dairy Science, College of Agriculture and Life Sciences, Chungnam National University, Daejeon 305-764, Republic of Korea. Fax: +82 42 825 9754.

E-mail address: [junheon@cnu.ac.kr](mailto:junheon@cnu.ac.kr) (J.H. Lee).

<sup>1</sup> These authors equally contributed to this work. Hence, they should be regarded as co-first authors.

the higher chewiness and cohesiveness, and different content of fatty acids compared with commercial broilers (Choe et al., 2010; Jeon et al., 2010). However, very limited research has been focused on the identification of genetic factors that affect the meat quality traits in KNC. Therefore, the objective of this study was to identify QTLs of meat quality related traits in KNC thigh and breast muscles in order to identify their causative variations that might be for future breeding purposes.

## 2. Materials and methods

### 2.1. Experimental animals

Two-generation nuclear pedigree KNC consisting of 83 G0 founders (i.e., 15 sires and 68 dams) and 597 G1 progeny were established to investigate genetic factors within Korean native chicken breed. No specific production related trait has been used for selection criterion during the establishment of KNC founder generation (G0). Three sires were mated with 4–5 dams within each line to produce G1 birds. Based on their plumage colors, the 597 G1 progeny were classified into the following five lines: Gray (G) ( $n=110$ ), Black (L) ( $n=90$ ), Red (R) ( $n=135$ ), White (W) ( $n=126$ ), and 136 Yellow (Y) ( $n=136$ ). This resource population consisted of 68 full-sib families ranging from 3 to 20 birds (average 10.6). In terms of half-sib family, the population comprised of 15 half-sib families ranging from 28 to 59 birds (average 44.5). All animals were reared with the standard breeding and maintenance procedures established by the National Institute of Animal Science (NIAS) of Korea. This study was conducted strictly in accordance with “The Guide for the Care and Use of Laboratory Animals” published by the institutional Animal Care and Use Committee of NIAS, Korea.

### 2.2. Genotype analysis

Previously, a total of 128 microsatellite (MS) and 8 SNP markers spanning 26 autosomes were used for constructing the 1st version of KNC genetic linkage map with a size of 2729.4 cM (Seo et al., 2015). For the current QTL analysis, we reconstructed the KNC genetic linkage map with additional 30 SNP markers. The newly incorporated SNP markers were genotyped by Fluidigm Genotyping Technology (Fluidigm, USA). The genetic marker order and genetic distance of the new map were determined using CRIMAP program version 2.4 (Green, 1992). The total autosomal map length was 2921.4 cM with average genetic distance between markers of 17.5 cM.

### 2.3. Phenotype analysis

After slaughtering, phenotypic data for meat quality traits were collected from breast and thigh muscles of 597 G1 birds. The pH value at 15 min post-slaughter was measured for the breast and thigh muscles using portable pH meter (SG2-SevenGo, Mettler-Toledo Into Inc., Schwerzenbach, Switzerland). The ultimate pH value was measured from pH of filtrated meat that was filtered with filter paper (No. 4, Whatman Ltd. Kent, UK) and centrifuge at 2090g for 15 min (Union 32R, Hanil Co., Ltd, Incheon, Korea) for 1 g of homogenized minced meat with 9 ml of distilled water. Water holding capacity (WHC; %) was measured using 1 g of minced meat sample on a round filter paper (No. 4, Whatman Ltd. Kent, UK). The filter paper with meat was centrifuged (CR 20B2, Hitachi Koki Co., Ltd. Fukuoka, Japan) at 6710g for 10 min. Water released from the filter paper was weighted and calculated as percentage of initial moisture in the meat. The moisture content of the meat was investigated by drying 3 g of the sample on an aluminum dish for

**Table 1**  
Descriptive statistics of meat quality-related traits.

Category	Type	Trait	N	Mean	SD	Range
<b>General compounds</b>	Br	cFat <sup>S</sup>	597	0.828	0.116	0–1.29
	Leg	cFat <sup>S</sup>	597	1.115	0.289	0–2.06
	Br	cAsh <sup>S</sup>	597	1.186	0.137	0.94–1.73
	Leg	cAsh <sup>S</sup>	597	0.208	0.180	–0.27 to 0.78
	Br	Collagen <sup>S</sup>	590	2.007	0.473	0.65–3.84
	Leg	Collagen <sup>L</sup>	590	2.075	0.314	1.26–3.01
	Br	H2O	597	73.032	0.742	28.64–94.45
	Leg	H2O	597	74.958	1.497	43.2–79.15
	Br	cProtein	597	24.394	0.517	71.26–75.76
	Leg	cProtein	597	21.962	1.701	71.26–78.05
<b>Meat color</b>	Br	L*	597	59.975	2.586	22.64–25.91
	Leg	L*	596	48.729	4.120	18.51–25.91
	Br	a* <sup>L</sup>	597	1.971	0.248	3.75–28.98
	Leg	a*	596	13.725	1.918	16.19–39.73
	Br	b*	597	21.246	1.587	1.75–1.94
	Leg	b*	596	20.357	1.665	4.7–1.92
<b>pH</b>	Br	WHC	596	64.092	7.655	1.65–1.9
	Leg	WHC	597	62.049	6.163	5.75–6.88
	Br	Cooking loss	597	20.597	2.846	–0.52 to 1.33
	Leg	Cooking loss	589(7)	30.038	3.827	–1.82 to 1.58
	Br	pH1 <sup>L</sup>	594(3)	1.822	0.041	44.65–68.2
	Leg	pH1	597	6.483	0.241	37.62–57.86
	Br	pH2 <sup>L</sup>	595(2)	1.762	0.033	1.24–2.83
	Leg	pH2	592(5)	6.210	0.162	8.73–18.81
	Br	Delta_pH	595(2)	0.367	0.328	16.83–27.12
	Leg	Delta_pH	597	0.270	0.283	14.97–23.89

Br: breast muscle; Leg: thigh muscle; cFat: crude fat content (%); cAsh: crude ash content (%); H<sub>2</sub>O: crude moisture (%); cProtein: crude Protein; L\*: CIE lightness value; a\*: CIE redness value; b\*: CIE yellowness; WHC; water holding capacity (%); pH1: after slaughter 15 min pH; pH2: ultimate pH; <sup>L</sup>Data transformed using natural log; <sup>S</sup>Data transformed using square root; For no. of animals (n), values in parenthesis are the number of animals omitted based on ascertainment of normality.

15 hour at 104 °C. Meat color for lightness (L\*), redness (a\*), and yellowness (b\*) of minced meat was measured using a colorimeter (CR-300, Minolta Inc., Tokyo, Japan). Two different areas were measured perpendicularly to the sample in quartz cell (3 cm × 1.5 cm). Crude protein (cProtein; %), crude fat (cFat; %), crude ash (cAsh; %), H<sub>2</sub>O (%), collagen (mg/g), and cooking loss (%) were measured with standard general compound methods as described previously (AOAC, 1995).

### 2.4. Statistical and QTL analyses

Before performing QTL analysis, basic descriptive statistics were obtained and normal distribution of the phenotype data were verified. If putative outliers were found, they were omitted based on normality ascertainment using Ryan–Joiner method implemented in Minitab software (Minitab, USA). The RJ score  $\geq 0.99$  was employed for the ascertainment of normality. Several meat quality related traits showed significant departure from normality. Therefore, they were transformed with natural logarithm or square root to eliminate their skewness (Table 1). A general linear model (GLM) was performed using the Minitab software (version 14, Minitab Inc. USA) to identify factors affecting phenotypic variation.

QTL mapping was conducted using two different methods: half-sib QTL analysis based on linear regression and full-sib QTL analysis based on variance components. Phenotypic values used for half-sib QTL analysis were pre-adjusted for fixed effects of sex, batch, line, and carcass weight. A half-sib QTL analysis was performed with GridQTL program using paternal half-sib families (Seaton et al., 2006). The conditional probability of alternative QTL genotypes of given marker genotypes was computed at 1-cM intervals within and across the half-sib families. The pre-adjusted

Download English Version:

<https://daneshyari.com/en/article/5789975>

Download Persian Version:

<https://daneshyari.com/article/5789975>

[Daneshyari.com](https://daneshyari.com)