GENOME-WIDE ASSOCIATION STUDIES OF CHICKEN (*Gallus gallus* L.) BREAST MEAT COLOR CHARACTERISTICS

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The authors declare no conflict of interests

A b s t r a c t

One of the most important parameters of meat quality is its color characteristics, which largely determines consumer demand for these products. Special color scales are used to assess the quality of meat based on its color spectrum. The L*a*b* scale is common the effectiveness of which has been shown in meat livestock farming. A number of studies have established the genetic determination of meat color characteristics for farm animals and poultry. SNPs and candidate genes that determine the expression of this trait have been identified (J. Sun et al., 2022; X. Guo et al., 2023). Here, we submit data on genome-wide association studies of the spectrum of color parameters of breast meat of F_2 chickens of the resource population based on genome-wide genotyping data. The aim of research was to search for SNPs and identify genes associated with meat color in chickens. For the research, an F_2 model resource chickens population ($n = 260$, vivarium of the Ernst Federal Research Center for Animal Husbandry, 2021-2023) was obtained by crossing two chicken breeds contrasting in meat quality, the Russian White (slow growth) and Cornish (fast growth). The poultry of F_2 resource population was genotyped using high-density Illumina Chicken iSelect BeadChip 60k (Illumina, Inc., USA). At the age of 9 weeks, birds were slaughtered. The spectra of breast meat were measured according to the L*a*b* color scale using a portable spectrophotometer CM-700d (Konica Minolta, Japan). Based on the genotype and phenotype data, genome-wide association studies were carried out using PLINK 1.9 software with accepted restrictions (geno 0.1, mind 0.1, maf 0.03). The threshold significance criterion was set to $p < 0.000001$. The chickens of F_2 resource population was characterized by a high coefficient of variability in the green (a*) and blue (b*) spectrum of meat color, from 19.99 % to 97.23 %. According to the L parameter, chickens showed relatively low variability not exceeding 9.75 %. Based on the GWAS analysis, 60 significant SNPs were identified, including those associated with the color spectrum L* (28 SNPs), a* (48 SNPs), and b* (4 SNPs). These SNPs were located on chromosomes GGA1 (10 SNPs), GGA2 (3 SNPs), GGA3 (18 SNPs), GGA7 (2 SNPs), GGA8 (4 SNPs), GGA10 (2 SNPs), GGA12 (7 SNPs), GGA13 (9 SNPs), GGA17 (4 SNPs), and GGA18 (1 SNP). We identified 270 candidate genes associated with the studied traits, including 30 genes that contain the identified SNPs. The results of the study can be helpful in further genomic selection of chickens for improving meat quality.

Keywords: *Gallus gallus*, chicken, SNP, GWAS, candidate genes, meat quality, meat color, L*a*b* color scale

Progress in poultry farming is associated with high demand for the poultry products. Every year the requirements for the quality of poultry meat and its marketable yield are increasing [1, 2]. According to FAO, total production and consumption of this product is expected to increase annually by 1.8% until 2050, which is significantly higher than the expected growth in pork production and

consumption of 0.8% annually [3]. Chicken meat is a source of protein with high biological value, especially compared to plant proteins, in particular, in terms of the content of iron, phosphorus, vitamin A, thiamine, nicotinic acid [4]. In addition, the low energy value makes chicken meat a healthy food with a reduced fat content and a higher content of polyunsaturated fatty acids (PUFAs) compared to other types of meat [5].

Currently, poultry production emphasizes on improving quality for various characteristics of the final product, including appearance, texture and firmness, water holding capacity, color, pH, shelf life, collagen content, protein solubility, fat binding capacity [6]. Many of these parameters are significantly by poultry feeding, housing conditions [7], sex, age and breed [7, 8].

Color is an important indicator of meat quality and largely determines consumer demand [9]. Products with the desired color and without defects in appearance ensure better sales and final price [9, 10]. Pale, soft and exudative (PSE) meat is a color defect. PSE is becoming a growing problem in the meat industry. In the PSE condition, the water holding capacity (WHC) of the meat decreases and its texture becomes softer [11]. In broilers, meat PSE is influenced by various pre-slaughter factors, stunning methods, and cooling regimes [3, 12].

Poultry is the only animal species that has dark and light meat depending on the type of muscle. The breast meat is pale pink, the thighs and legs are dark red [13]. Direct correlations have been established between the meat color and pH. Dark meat, as a rule, has a higher pH, and very light meat has a lower pH value [14]. In the meat industry, pH also influences the PSE (pale, soft, exudative) and DFD (dark, firm, dry) appearance [15]. Fresh poultry meat is often classified as PSE based solely on high L* (lightness) color parameter and low pH, which also reduces WHC [16]. A number of studies have reported the genetic basis of meat color of farm animals and poultry, including loci of quantitative traits [17, 18], SNPs [19, 20] and candidate genes [19-22] for color parameters.

This paper results from a genome-wide association study of the color spectrum indicators of breast meat in F_2 chicken resource population. We identified novel SNPs and candidate genes that are highly significantly ($p < 0.00001$) associated with meat color parameters in chickens. In the future we plan to assess the discovered SNPs as genetic markers in breeding for chicken meat quality.

The goal of the work is to search for SNPs and identify genes associated with meat color in chickens.

Materials and methods. Experiments were carried out in 2021-2023 at vivarium of the Ernst Federal Center for Livestock Husbandry — VIZh (Moscow Province) on an F_2 chicken (*Gallus gallus* L.) model resource population ($n = 260$) derived from crossing Cornish meat breed and Russian White egg breed. Chicks up to 3 weeks of age were raised in brooders with a gradual decrease in temperature from 34 °C (in the first hours after hatching) to 23 °C, and then was floor-housed. The keeping conditions met the birds' age requirements and provided free access to complete feed, fresh water and normal lighting, good ventilation ensured the absence of dampness, drafts and gas pollution. The birds aged 9 weeks were slaughtered after starvation period of 8-10 h in accordance with the Russian Federation national standard the GOST R 52837-2007 "Agricultural poultry for slaughter. Technical conditions". After slaughter, the carcasses were scalded, the plumage was removed and the carcasses were deboned.

The color parameters of breast meat were measured using a portable spectrophotometer CM-700d (Konica Minolta, Japan) based on the L*a*b* system which is a three-dimensional space where negative values of a and b correspond to cold colors, positive values correspond to warm colors. The color index L characterizes the light reflection from meat surface [23]. Color spectra were recorded

24 h after slaughter at five points of the breast fillet sample and the average value was determined for each scale of the spectrum.

DNA was isolated from feather pulp using the commercial kit DNA Ekstran-2 (NPF Syntol LLC, Russia) according to the manufacturer's recommendations. The quality and integrity of the isolated DNA was assessed by a 1% agarose gel horizontal electrophoresis, the DNA purity spectrophotometrially (a NanoPhotometer® N60 spectrophotometer, Thermo Fisher Scientific, USA), samples with an $OD_{260/280} > 1.8$ were used. DNA concentration was assessed fluorometrically (a Qubit® 2.0 fluorometer, Invitrogen/Life technologies, USA) with the Qubit™ dsDNA BR Assay kit for 2-1000 ng DNA quantification (Invitrogen/Life technologies, USA).

Whole-genome genotyping was performed with the Illumina Chicken iSelect BeadChip DNA chip (Illumina, Inc., USA) for 60 thousand SNPs. Quality control and data filtering for each sample and each SNP were performed using PLINK 1.9 software in R (http://zzz.bwh.harvard.edu/plink/). The filters were --mind 0.10, --geno 0.10, --maf 0.05, --hwe 1e-3. Regression analysis commands −assoc, --adjust, --qt-means were used to perform genome-wide association studies (GWAS) and identify SNPs associated with muscle color indices. To confirm the influence of SNPs and identify significant regions in the chicken genome, a Bonferroni test for null hypotheses was used. Data were visualized in the qqman package (https://github.com/qqman). The candidate genes in the regions of identified SNPs were searched with the Genome Data Viewer in the NCBI Gallus gallus (chicken) database (https://www.ncbi.nlm.nih.gov/datasets/genome/). For functional annotations, the GeneCards database (http://www.genecards.org/) and the DAVID program (https://david.ncifcrf.gov/) were used.

Mean values (M), standard errors (±SEM), minimum (min), maximum (max), coefficient of variation (Cv, %) were calculated using the Microsoft Office 365 package.

Results. Table 1 shows the color parameters of breast meat in F2 chickens of the resource population studied.

1. Breast meat color parameters of chickens (*Gallus gallus* L.) from the F2 resource population ($n = 260$, vivarium of the Ernst Federal Research Center for Animal Husbandry — VIZh, 2021-2023)

Parameter	M	±SEM	min	max	Cv, %
L	38.88	1.98	42.08	62.28	7.62
a	2.12	0.19	-0.31	14.07	97.23
b	10.07	0.18	5.73	16.81	19.99

N o t e. a — spectrum from green (–128) to purple (127); b - spectrum from blue (–128) to yellow (127).

According to Table 1, the values of the a* and b* spectra of breast fillet highly fluctuated coefficient of variation, Cv of 97.23 and 19.99%, respectively. This indicates the influence of crossbreeding on the variability of these traits, when birds' feeding, housing and clinical health are controlled and stress during slaughter is minimized.

After data filtering, 16,630 SNPs were involved in genome-wide association studies. Figure 1 shows the distribution of identified SNPs across chromosomes.

Based on all the studied color indicators of meat in chickens from the F2 resource population, we eventually identified 60 significant SNPs (p < 0.00001) on chromosomes GGA1, GGA2, GGA3, GGA7, GGA8, GGA10, GGA12, GGA13, GGA17, GGA18 (Fig. 2).

Table 2 shows significantly significant SNPs (p < 0.00001) associated with the color characteristics of breast meat in chickens from the F2 resource population. It was found that 28 SNPs are associated with the color parameter L*.
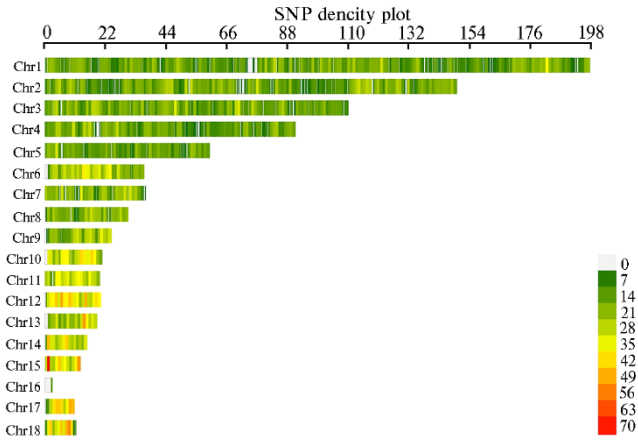
Fig. 1. Distribution density of SNPs for meat color parameters across chromosomes of chickens (*Gallus gallus* L.) from the F₂ resource population (n = 260, vivarium of the Ernst Federal Research Center for Animal Husbandry — VIZh, 2021-2023).

These SNPs are located at GGA1 (4 SNPs), GGA2 (5 SNPs), GGA3 (8 SNPs), GGA8 (1 SNP), GGA12 (4 SNPs), GGA13 (3 SNPs), GGA17 (2 SNPs) and GGA18 (1 SNP). In total, we identified 48 significant SNPs for the a* parameter on chromosomes GGA1, GGA2, GGA3, GGA7, GGA8, GGA10, GGA12, GGA13, GGA17 and GGA18. The largest number of SNPs was found on GGA3 (12 SNPs), the smallest on GGA18 (1 SNP). For breast meat color criterion b*, only 4 SNPs were identified on GGA3.
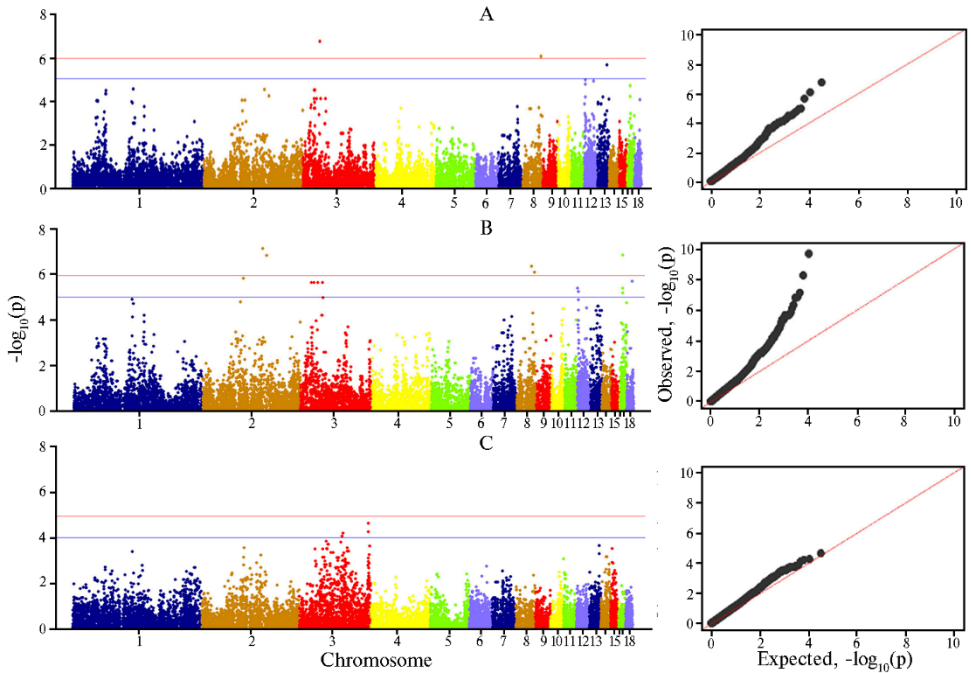

Fig. 2. Genetic structure of breast meat color parameters in chickens (*Gallus gallus* L.) from the F₂ resource population: on the left — genome-wide plots, on the right — Q-Q (probability) graphs; A — spectrum of color L*, B — spectrum of color a*, — spectrum of color b* (n = 260, vivarium of the Ernst Federal Research Center for Animal Husbandry — VIZh, 2021-2023).

2. Significant (p < 0.00001) **SNP associations with breast meat color parameters in chickens (*Gallus gallus* L.) from the F₂ resource population** (n = 260, vivarium of the Ernst Federal Research Center for Animal Husbandry — VIZh, 2021-2023)

Chromosome GGA	SNP	Position	p	Trait
1	GGaluGA017028	49518104...50473515	4.87E-05	L
	Gga_rs13865002		4.87E-05	
	GGaluGA017292		3.33E-05	
	Gga_rs13899455	88864063...90363842	1.27E-05	a
	Gga_rs14856616		7.36E-05	

	GGaluGA031490	91050938...91450938	2.87E-05	L, a
			1.95E-05	
	Gga_rs13917314	107440599...107940361	6.13E-05	a
	Gga_rs13917480		6.13E-05	
2	Gga_rs14187600	57548810...58000666	9.71E-05	L, a
			1.62E-05	
	Gga_rs14187774		9.71E-05	
			1.62E-05	
	GGaluGA150095	62037051...62437051	9.72E-05	L, a
			1.47E-06	
	Gga_rs14219701	91397215...91797215	2.99E-05	L, a
			7.47E-08	
	Gga_rs15133231	97797354...98197354	5.91E-05	L, a
			1.49E-07	
3	Gga_rs16228851	16704934...17317837	7.91E-05	L, a
			2.24E-06	
	GGaluGA210154		3.22E-05	
	Gga_rs14321392	18109888...18509888	3.22E-05	L
	Gga_rs14323710	20423383...20823383	7.91E-05	L, a
			2.24E-06	
	Gga_rs16239991	25213895...25613895	1.85E-07	L, a
			2.39E-11	
	Gga_rs15303835	26562059...26962059	7.91E-05	L, a
			2.24E-06	
	GGaluGA215531	32726056...34925170	6.15E-05	L, a
	Gga_rs16250047		6.15E-05	
	Gga_rs14337156		6.15E-05	
	Gga_rs16250652		6.15E-05	
	Gga_rs14337823		6.15E-05	
	GGaluGA215952		7.91E-05	
			2.24E-06	
	Gga_rs16251735		7.91E-05	
			2.24E-06	
	GGaluGA216144		1.04E-05	
	Gga_rs15375140	65279421...65679421	8.35E-05	b
	GGaluGA226948	66888191...67288191	6.24E-05	
	GGaluGA238450	105376493...105875531	5.50E-05	
	Gga_rs16338886		2.25E-05	
7	GGaluGA313956	16384962...16784962	9.96E-05	a
	Gga_rs13598324	28338012...28738012	6.98E-05	
8	GGaluGA330168	22596941...22996941	4.46E-07	a
	Gga_rs14653321	24397555...24797555	4.96E-05	a
	GGaluGA332278	27324733...27840907	8.92E-07	L, a
			2.06E-10	
	Gga_rs15937915		7.96E-07	
10	Gga_rs14953406	18446784...19677731	3.25E-05	a
	GGaluGA072861		3.25E-05	
12	GGaluGA080532	366564...1003693	4.08E-06	a
	GGaluGA080537			
	Gga_rs15628463			
	Gga_rs15630811	1703306...2418508	6.82E-05	L, a
			1.33E-05	
	GGaluGA081274		1.09E-05	
			5.67E-06	
	Gga_rs14031390		1.71E-05	
			3.72E-05	
	GGaluGA087110	14173406...14573406	1.21E-05	L, a
			3.01E-05	
13	GGaluGA093806	9428125...9828125	6.88E-05	L, a
			3.86E-05	
	Gga_rs15698305	11860386...13195035	5.92E-05	a
	Gga_rs14060024		2.46E-05	
	GGaluGA095191		2.46E-05	
	GGaluGA001139		2.46E-05	
	Gga_rs14063043	15435179...16143937	6.59E-05	L, a
	Gga_rs14063186		2.26E-06	
			5.55E-09	
	GGaluGA097116		3.85E-05	
	Gga_rs14065976	18469260...18869260	8.32E-05	L, a
			3.78E-05	
17	GGaluGA114289	4212179...5004176	6.34E-05	L, a
			4.00E-06	

	GGaluGA114391		2.04E-05	
			1.44E-07	
	GGaluGA114420		6.48E-06	
	Gga_rs15788572	10517209...10917209	1.78E-05	a
18	Gga_rs14114367	8362502...8762502	9.17E-05	L, a
			2.02E-06	

We identified candidate genes containing or linked to the identified SNPs (±0.2 Mb). Structural annotation revealed 270 genes that, according to a preliminary assessment, are responsible for the color spectra of breast sirloin, including 30 genes in the positions of identified SNPs (Table 3).

3. Structural annotation of candidate genes in the region of identified SNPs associated with breast meat color parameters in chickens (*Gallus gallus* L.) from the F₂ resource population (*n* = 260, vivarium of the Ernst Federal Research Center for Animal Husbandry — VIZh, 2021-2023)

Chromoosme GGA	Candidate gene			Trait
	SNP location		linked with SNP (±0,2 Mb)	
	gene ID	positions		
1	TEF	49701507..49717640	CD200, CD200L, CRYBG3, KCNJ15, MEI1, EP300, BTLA, CGGBP1, ARL6, KCNJ6, ETS2	L, a
	MKL1	50003390..50101264		
	TNRC6B	50146094..50287628		
	EPHA6	90900356..91399201		
	ERG	107658703..107811187		
2	VAPA	97965836..97997739	ACO2, RANGAP1, C1H3ORF52, EPHA3, CCDC134, L3MBTL2, ARL13B, PROS1, CSDC2, RBX1, NSUN3, STX19, XRCC6, XPNPEP3, POLR3H, ST13P5, TOB2, SGSM3, SREBF2, ADSL, SHISA8, GRAP2, PHF5A, FAM83F, DESI1, SNU13, DCDC2, NRSN1, MRS2, GPLD1, PHACTR1, EDN1, CNDP1, CNDP2, MOG, ALDH5A1, HIVEP1, CYB5A, FAM69C, APCDD1, PPP4R1, FBXO15, TIMM21, RAB31, RALBP1, TWSG1	L, a
3	TMEM63A	16879683..16908662	PARP1. CNIH3, HLX, SHKBP1, CAMKMT, SIX3, MCFD2, SCCPDH, PRKD3, SPAST, SRD5A2, QPCT, CEBPZ, ELP3, LIN9, MIXL1, DNAH14, MTARC1, CENPF, PTPN14, SIX2, CALM2, PPP1CB, NDUFAF7, SULT6B1, DPY30, MEMO1, SMYD3, CNST, TFB2M, ADSS2, COX20, DESI2, TUBE1, ARMC2, FBXO16, EXTL3	L, a, b
	KCNK2	20526712..20653121		
	TTC7A	26628446..26790506		
	KIF28P	33508507..33530730		
	AHCTF1	33454877..33507931		
	KIF26B	34003714..34297816		
	AKT3	34651696..34796287		
	LAMA4	65400812..65497195		
	AFG1L	67086571..67151321		
	FZD3	105634168..105686155		
7	−	−	ACBD3, SDE2, WDR26, PFN3, EFCAB2, HNRNPU, SDCCAG8, WISP3, FOXO3, INTS9, LEFTY1, ENAH, DEGS1, MARK1, FYN, SNX3, NR2E1, OSTM1, SEC63, CHN1, INSIG2, WIPF1, CCDC93, CHRNA1, DDX18	L, a
8	BEND5	22380811..23220947	GPR155, CIR1, SCRN3, SP9, OLA1, SP3, FOXD3, ALG6, LRP8, ITGB3BP, PGM1, ROR1, DMRTB1, YIPF1, NDC1	L, a
	GLIS1	24591950..24764561		
	EFCAB7	27494881..27547348		
10	−	−	DIO1, MEGF11, ANP32A, DIS3L, NOX5, MAP2K1, GLCE, TIPIN, KIF23, ZWILCH, PAQR5, LCTL, TLE3, RPL4, UACA, SNAPC5, SMAD6, SMAD3	L, a
12	PBRM1	771096..833446	TNNC1, RPL29, MAPKAPK3, CISH, NISCH, STAB1, NT5DC2, SMIM4, GNL3, SPCS1, GLT8D1, NEK4, ITIH3, MUSTN1, SFMBT1	L, a
	HEMK1	1847096..1930905		
	DOCK3	2034647..2317912		
	MAGI1	14181633..14474643		
13	GLRA1	12434258..12486014	SFXN1, DRD1, MFAP3, GRIA1, UBE2B, SKP1, BRD8, KIF20A, NMUR2, G3BP1, SPARC, ATOX1, PPP2CA, TCF7, RAPGEF6, GRK6, LMAN2, FAT2, CCDC69, GM2A, ANXA6, RGS14, ARL2, LACAAT2L, TNIP1, GPX3, DCTN4, PRR7, PDLIM7, NDST1, RPS14, CD74, TCOF1, B4GALT7, ADRA2BL2, SMIM3, RBM22, MYOZ3,	L, a
	FLT4	12951742..12998047		
	VDAC1	15589702..15650724		
	FSTL4	15845754..16032315		

			SYNPO, DOK3, DBN1, ARSI, CAMK2A, PDGFRB, CDX1, DDX41, RAB24, HMGXB3, CSF1R, TRIM105, NPY7R, PRELID1, NSD1, TBC1D9B, MGAT4B, SQSTM1, MAML1, CANX, HNRNPH1, DCK2	
17	*BRINP1*	4664527..4744154	*TLR4*	L, a
18	*LMX1B*	10665426..10802338	*GNA13, MVB12B, RGS9, ARSG, ALC,*	L, a
	ABCA9	8559320..8581766	*WIPI1, PRKAR1A, ANGPTL2, ABCA8, MAP2K6, RALGPS1, ABCA5*	

N o t e. Dashes in the table mean that the found SNP position was not localized within the gene

Of the 270 identified genes associated with the color characteristics of breast meat, 39 significant candidate genes for biological functions were selected, including 3 genes in which the identified SNPs were located (Table 4).

4. Functional annotation of genes associated with breast meat color parameters in chickens (*Gallus gallus* L.) from the F₂ resource population (*n* = 260, vivarium of the Ernst Federal Research Center for Animal Husbandry — VIZh, 2021-2023)

Gene	Position	Biological functions
In the SNP position:		
BRINP1	4664527..4744154	Cell cycle, cell death, behavior
FSTL4	15845754..16032315	Development of multicellular organisms, development of the nervous system
TTC7A	26628446..26790506	Cellular homeostasis of iron ions
Linked to the SNP position (±0,2 Mb):		
ARL13B	89891671..89940839	Looping the heart, forming a neural tube pattern
ABCA5	8582298..8608484	Lipid transport
ABCA8	8536924..8557588	Lipid transport
CD200L	88913076..88921182	Regulation of the immune response
DMRTB1	24557324..24563156	Development of germ cells, sex differentiation
FBXO15	91609665..91633896	Protein binding
FBXO16	105598226..105634014	Protein binding
FYN	65580445..65711082	Cardiac process, forebrain development, innate immune response
GNA13	8386712..8414335	Aging of a multicellular organism
G3BP1	12485905..12506960	Innate immune response, a protective response to the virus
GM2A	12614487..12617622	Lipid transport
LRP8	24349072..24499027	Regulation of the innate immune response
NDST1	12716758..12736200	Polysaccharide chain biosynthesis process
PDLIM7	9768860..9788764	Heart development
PRELID1	9812879..9814674	Lipid transport
SIX3	25520822..25523953	Eye development, maturation of epithelial cells
SMAD3	18814590..18878841	Response to hypoxia, development of the immune system
SP3	16704259..16735630	Liver development
B4GALT7	9710664..9712643	Carbohydrate metabolism, glycosaminoglycan biosynthesis
CCDC134	49550539..49554893	Angiogenesis, embryonic hematopoiesis, embryonic liver development
DIO1	24792883..24797740	Biosynthesis of hormones
DEGS1	17295979..17300997	Biosynthesis of fatty acids
EDN1	62406640..62411539	Cellular homeostasis of calcium ions, contraction of smooth muscle veins
GPX3	12661488..12663434	Response to oxidative stress
INSIG2	28449946..28462775	Cholesterol biosynthesis
LCTL	18547541..18551236	Carbohydrate metabolism
LEFTY1	16864275..16879586	Spleen development
LACAAT2L	12628444..12633004	Amino acid transport
MAP2K1	18496305..18527713	Heart development, thyroid development
NRSN1	57666592..57673732	Nervous system development
PGM1	27548636..27567569	Carbohydrate metabolism, glucose metabolism process
PPP1CB	26901055..26932174	Glycogen metabolism
SCCPDH	33530313..33540359	Biosynthesis of glycolipids
SFXN1	9634295..9669465	Ion transport, amino acid transport
STX19	89905548..89921452	Intracellular protein transport
TNNC1	643058..648527	Contraction of skeletal muscles, regulation of muscle contraction

Color is an important quality indicator closely related to glycolysis and intramuscular fat metabolism. The functions of a number of identified candidate genes (transport of lipids, amino acids, proteins, cholesterol, biosynthesis of fatty acids, development of the spleen, liver, heart, protein binding) directly or indirectly affect chicken meat color. The identified genes are responsible for the development of a multicellular organism and its organs, fatty acid homeostasis, and

biochemical processes. As is known, stress greatly affects the organoleptic characteristics of meat, therefore the function of nervous system is important meat color spectra. For the 7 candidate genes we identified, there are many reports about their connection with valuable traits in chickens. In particular, highly reliable associations of the *AKT3* gene with feather pigmentation in chickens [24] and the development of muscle fibers [25] have been established. The influence of the *FSTL4* and *VDAC1* genes on the moisture content in the egg yolk has been shown [26], and the *TTC7A* gene has been shown to influence the accumulation of glycogen in the muscles of chickens [27]. Association of the *FSTL4* gene with rapid muscle growth in broilers has also been reported [28]. The *MAGI1* and *VDAC1* genes influence immunity [29-31], and the *FZD3* and *EPHA6* genes influence the function and development of the nervous system [32]. For other candidate genes we identified, a number of studies have found a connection with indicators of meat productivity and quality in other species of farm animals. E.g., the *TTC7A* and *AFG1L* genes are associated with back fat thickness in pigs [33, 34], and the *BRINP1* gene is associated with growth indices in pigs [35] and linear measurements in goats [36].

Thus, we identified 60 significant SNPs associated with meat color in chickens, 28 SNPs for the L* color spectrum, 48 SNPs for the a* spectrum, and 4 SNPs for the b* spectrum. The SNPs we discovered are located in the chromosomes GGA1 (10 SNPs), GGA2 (3 SNPs), GGA3 (18 SNPs), GGA7 (2 SNPs), GGA8 (4 SNPs), GGA10 (2 SNPs), GGA12 (7 SNPs), GGA13 (9 SNPs), GGA17 (4 SNPs), and GGA18 (1 SNP). We also identified 270 candidate genes associated with the studied traits, of which 30 genes harbored SNPs. These results can promote genomic selection of chickens for meat quality.

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