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IDENTIFICATION OF SNPs AND CANDIDATE GENES ASSOCIATED WITH ABDOMINAL FAT DEPOSITION IN QUAILS (*Coturnix japonica*)

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Abstract

The rate of fat deposition, including abdominal fat, is one of the important indicators characterizing both meat performance and product quality, as well as the poultry welfare in general. This trait positively correlates with the bird's rapid growth and largely depends not only on feeding and housing conditions, but also on genetic factors. Mostly, data on the genetic mechanisms that determine fat metabolism and fat deposition rate have been obtained in chickens; SNPs and candidate genes that determine the deposition of both intramuscular and abdominal fat have been identified. The number of similar studies on quail is relatively small. To date, there is not enough information in the specialized literature about quantitative trait loci (QTLs) that are reliably associated with fat metabolism indices in quails. The present work reports for the first time the identified SNPs that are highly significantly ($p < 0.00001$) associated with the intensity of abdominal fat deposition in 8-week-old quails from the F_2 model resource population. In the region of identified SNPs, candidate genes reliably associated with this trait were established. The objective of the study was to search for SNPs and identify candidate genes associated with abdominal fat deposition in quails. The studies were carried out on F_2 males of the model resource population ($n = 146$) obtained by crossing two quail breeds contrasting in growth rate and meat quality, Japanese (slow growth) and Texas (fast growth). F_2 individuals were genotyped using the GBS (genotyping-by-sequencing) method. To identify associations between genome-wide genotyping data and the amount of abdominal fat, PLINK 1.9 software was used with accepted filter settings (geno 0.1, mind 0.1, maf 0.05). The threshold significance criterion was set to $p < 0.00001$. The resultant F_2 resource population of quail was characterized by high variability in the content of abdominal fat in the carcass. At the age of 56 days, this indicator varied from 0.01 to 10.46 g and averaged 2.41±0.16 g. Based on the GWAS (genome-wide association study) analysis, we identified 29 SNPs and 11 candidate genes located in the regions of these SNPs that were associated with abdominal fat deposition in quail. The determined SNPs are localized on chromosomes 1, 2, 7, 8, 17, 19, 21, 24 and 28. The candidate genes identified (*CNTN5*, *GNAL*, *PDE1A*, *RBMS1*, *PTPRF*, *SH3GLB2*, *SLC27A4*, *TRIM62*, *IGSF9B*, *USHBP1*, and *NR2F6*) were established on chromosomes CJA1 (1 gene), CJA2 (1 gene), CJA7 (2 genes), CJA8 (1 gene), CJA17 (2 genes), CJA21 (1 gene), CJA24 (1 gene) and CJA28 (2 genes). The detected SNPs and candidate genes can serve as genetic markers in breeding programs to improve the meat quality of quails and reduce the fat content in carcasses.

Keywords: *Coturnix japonica*, quail, QTL, SNP, genotyping-by-sequencing, GBS, genome-wide association study, GWAS, candidate genes, abdominal fat

Poultry products occupy a strong position in the overall structure of food products of animal origin [1, 2]. Both eggs and poultry meat are in great demand [3, 4]. Unlike other types of farm animals, poultry meat is a dietary product with high nutritional value and good taste [5, 6]. Poultry meat typically contains a small

amount of fat and a significant proportion of protein [3, 6].

The basis of a sustainable and competitive poultry meat industry is highly productive breeds and crosses. Therefore, constant breeding is required to search and identify valuable genotypes. For this purpose, modern methods are used to identify the molecular genetic mechanisms underlying economically valuable traits. One of the tasks of genomic selection to improve the quality of poultry products and increase the profitability of the industry is the search for SNPs and identification of candidate genes that determine selection-significant traits. In recent years, significant databases of SNPs and candidate genes associated with indicators of meat productivity of poultry have been formed [7, 8].

An important indicator of the meat quality of poultry is the intensity of fat deposition [9, 10]. There are intramuscular and internal (abdominal, abdominal) fat. Intramuscular fat determines the nutritional value of meat, its taste and texture [9]. Abdominal fat is deposited in poultry in the abdominal cavity and serves as a source of energy. Its content in the carcass can reach 3-4% of its weight [11]. Excessive abdominal fat deposition negatively affects poultry health [12, 13] and carcass quality [10, 11]. A number of studies have examined the use of abdominal fat to improve texture and palatability and to improve the nutritional value and nutritional value of poultry products [14, 15]. A number of factors influence fat metabolism and accumulation of fat deposits, e.g., living conditions [10], feeding [11, 16, 17], age [18, 19], sex [19), genetic predisposition [20-22]. Females have larger body fat than males [19]. The intensity of fat accumulation positively correlates with the rapid growth of birds, which makes it difficult to select birds simultaneously for growth rate and fat reduction in in carcasses [20].

Genome-wide association studies (GWAS) of single nucleotide polymorphisms (SNPs) with economically significant traits allow effective identification of candidate genes associated with their expression [23]. In chickens, compared to other types of poultry, the genetic mechanisms associated with fat metabolism and the intensity of fat deposition have been studied in more detail [24, 25], SNPs and candidate genes have been identified that determine the deposition of both intramuscular and abdominal fat [26-28]. For quail, such data are limited [29]. To date, there is insufficient information on quantitative trait loci (QTLs) reliably associated with fat metabolism in quail.

In this report, novel SNPs and candidate genes were identified in the F_2 model resource population of quails, with high confidence ($p < 0.00001$) associated with the intensity of fat deposition. The detected SNPs can be genetic markers in breeding to improve the meat qualities of quails and reduce the fat content in carcasses.

The purpose of this work is to search for SNPs and identify candidate genes associated with abdominal fat deposition in quails.

Materials and methods. The experiments were carried out on F_2 male quails of a model resource population ($n = 146$; vivarium of the Ernst Federal Research Center — VIZh, 2022-2023) derived from crossing two breeds contrasting in growth rate and meat qualities, the Japanese slow growing and Texas fast growing quails. At the first stage, four families were formed, each consisting of one male and five females of the original breeds. Among 20-30 F_1 individuals from each family, 12 families (F_1_1-F_1_12) were composed, each of one F_1 male and three F_1 females who were not close relatives, to create offspring. Of their F_2 progeny F_2 male groups F_2_1-F_2_12 were assembled for study.

After experimental slaughter at the age of 8 weeks, the carcass was cut up, and the carcass and abdominal fat were separately weighed. GWAS analysis was performed for both absolute and relative abdominal fat content. The relative abdominal fat content was calculated as the percentage of abdominal fat weight to

total carcass weight.

DNA was extracted from feather pulp using a Syntol kit for extracting DNA from animal tissue (NPF Syntol LLC, Moscow). The DNA concentration was measured (a Qubit® 3.0 fluorometer, Thermo Fisher Scientific, USA) and $OD_{260/280}$ was assessed (NanoDrop-2000, Thermo Fisher Scientific, USA) to control its purity. Quail genotyping was performed using the GBS (genotyping-by-sequencing) method according to the protocol described previously [30]. A reference genome was the Japanese quail (Coturnix_japonica_2.0) (https://www.ensembl.org/Coturnix_ja-ponica/Info/Annotation). Removal of adapters and the fastq file demultiplexing were carried out (https://cutadapt.readthedocs.io/en/stable/). Quality control of fastq files was carried out in the FastQC program [31]. For alignment to the reference genome, the bowtie2 package was used [32]. The R software system was used to convert to a file format suitable for further analysis [33]. Quality of SNPs detection was controlled in the PLINK 1.9 program (https://zzz.bwh.harvard.edu/plink/plink2.shtml). The genotyping efficiency filters (mind 0.1; maf 0.05) was applied, SNPs genotyped in less than 90% of samples (geno 0.1) were excluded.

To identify associations of SNPs with the abdominal fat content, regression analysis was performed PLINK 1.9 software. The significance of the SNP influence and the identification of significant regions in the quail genome were assessed by null hypothesis testing with a threshold value of $p < 0.00001$. Data were visualized in the qqman package in R [33]. The search for candidate genes located in the region of identified SNPs was carried out using the Ensembl Coturnix japonica 2.0 genomic resource (https://www.ens-embl.org/Coturnix_japonica/Info/Annotation).

Statistical indicators were calculated in Microsoft Excel 2013. Mean values (*M*), standard errors of means (±SEM), minimum (min) and maximum (max) values, and coefficient of variation (*Cv*, %) are submitted.

Results. The content of abdominal fat in the carcasses of 56-day-old F_2 male quails varied from 0.01 to 10.46 g and averaged 2.41±0.16 g. Note the high variability of the trait among the studied birds ($Cv = 78.7\%$), whereas the proportion of abdominal fat from the total carcass weight varied from 0.01% to 4.82% with $Cv = 73.2\%$ on average.

We also revealed a high variation in the absolute and relative content of abdominal fat in carcasses in the quail groups F_2_1-F_2_12 (Table 1).

1. Content of abdominal fat in carcasses of male quails (*Coturnix japonica*) of F_2 model resource population ($n = 146$; vivarium of the Ernst Federal Research Center for Animal Husbandry — VIZh, 2022-2023)

Group	*n*	Fat weight, г					Fat weigh to carcass weight, %				
		M	±SEM	max	min	*Cv*, %	*M*	±SEM	max	min	*Cv*, %
F_2_1	8	1.93	0.51	4.24	0.01	74.6	1.09	0.29	2.48	0.01	75.2
F_2_2	15	2.95	0.48	6.10	0.10	63.5	1.53	0.25	3.19	0.06	63.2
F_2_3	7	1.35	0.15	2.02	0.82	29.5	0.71	0.06	1.00	0.48	23.8
F_2_4	18	2.49	0.40	7.64	0.35	68.6	1.31	0.21	4.03	0.22	67.3
F_2_5	7	2.54	0.87	6.95	0.71	90.9	1.53	0.51	4.13	0.46	87.4
F_2_6	14	2.84	0.68	10.46	0.55	89.7	1.47	0.31	4.82	0.30	80.1
F_2_7	18	1.96	0.46	8.72	0.10	99.5	1.05	0.23	4.29	0.06	92.9
F_2_8	11	2.30	0.52	5.39	0.10	75.1	1.32	0.29	2.92	0.08	71.7
F_2_9	10	2.13	0.43	5.41	0.73	63.5	1.18	0.19	2.44	0.45	50.2
F_2_10	6	2.13	0.66	3.63	0.01	76.3	1.22	0.35	1.99	0.01	71.0
F_2_11	18	2.97	0.56	8.83	0.49	80.3	1.52	0.26	4.13	0.32	71.2
F_2_12	14	2.32	0.51	5.36	0.01	78.6	1.31	0.28	3.04	0.01	76.2
On average	146	2.41	0.16	10.46	0.01	78.7	1.30	0.08	4.82	0.01	73.2

A diagram (Fig. 1) shows the distribution of quails from the study sample according to the content of abdominal fat in the carcass depending on the genotype.

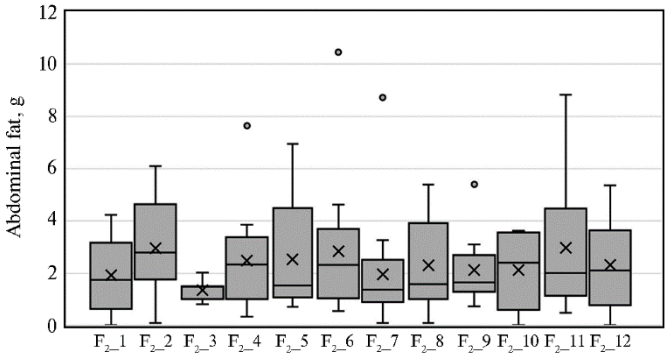

FIg. 1. Distribution of male quails (*Coturnix japonica*) of F2 model resource population according to the abdominal fat content in the carcass depending on the genotype (groups F2_1-F2_12, for the group size, see Table 1; vivarium of the Ernst Federal Research Center for Animal Husbandry — VIZh, 2022-2023). *Me*, *M*, min, max, and outliers of single data are given.

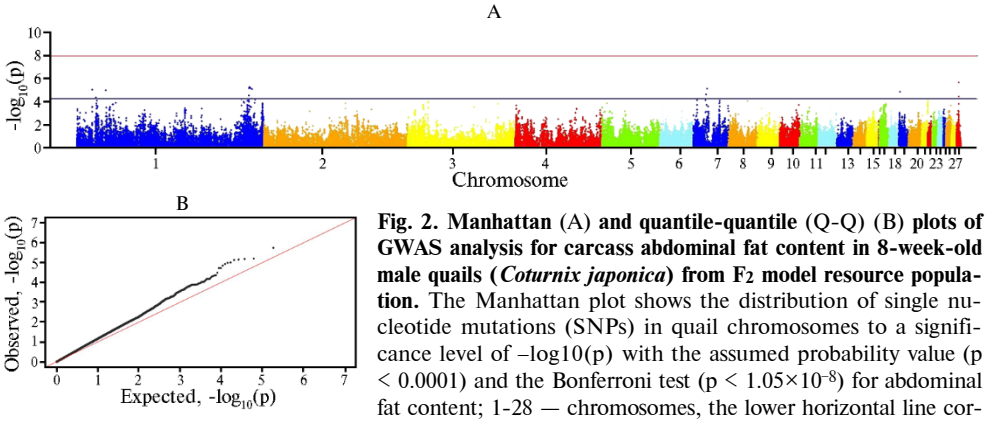

Fig. 2. Manhattan (A) **and quantile-quantile** (Q-Q) (B) **plots of GWAS analysis for carcass abdominal fat content in 8-week-old male quails (*Coturnix japonica*) from F2 model resource population.** The Manhattan plot shows the distribution of single nucleotide mutations (SNPs) in quail chromosomes to a significance level of –log10(p) with the assumed probability value ($p < 0.0001$) and the Bonferroni test ($p < 1.05\times10^{-8}$) for abdominal fat content; 1-28 — chromosomes, the lower horizontal line corresponds to $p < 0.0001$, the upper line is $p < 1.05\times10^{-8}$ (vivarium of the Ernst Federal Research Center for Animal Husbandry — VIZh, 2022-2023).

GWAS analysis for the abdominal fat rate in a carcass showed that in the F2 quails aged 8 weeks, this trait is associated with 29 SNPs ($p < 0.00001$) on chromosomes 1, 2, 7, 8, 17, 19, 21, 24 and 28 (Fig. 2). Chromosomes 1 and 7 contain the largest number of SNPs, 11 and 7 SNPs, respectively, and chromosomes 2, 17, 19, 21 and 24 the smallest number, 1-2 SNPs.

The identified SNPs ($p < 0.00001$) were used to annotate candidate genes associated with abdominal fat deposition in quail. Structural annotation identified 124 genes, including 11 genes, the *CNTN5*, *GNAL*, *PDE1A*, *RBMS1*, *PTPRF*, *SH3GLB2*, *SLC27A4*, *TRIM62*, *IGSF9B*, *USHBP1* and *NR2F6* located in the region of identified SNPs (Table 2). These genes were identified on 8 chromosomes, the CJA1 (1 gene), CJA2 (1 gene), CJA7 (2 genes), CJA8 (1 gene), CJA17 (2 genes), CJA21 (1 gene), CJA24 (1 gene) and CJA28 (2 genes).

The detected candidate genes and significant SNPs ($p < 0.00001$) associated with abdominal fat deposition in quail are submitted in Table 2.

Analysis of published research showed that for none of the 11 candidate genes (*CNTN5*, *GNAL*, *PDE1A*, *RBMS1*, *PTPRF*, *SH3GLB2*, *SLC27A4*, *TRIM62*, *IGSF9B*, *USHBP1*, and *NR2F6*) we identified in the region of the novel SNPs an association was previously reported with the deposition of abdominal fat in quails. However, seven candidate genes identified have been previously shown to influence lipid metabolism and body fat accumulation in other animal and poultry species. For example, it was reported that the *PTPRF* and *GNAL* genes are associated with the development, formation and accumulation of adipose

tissue [34] and abdominal fat deposition [35] in chickens, and the *TRIM62* and *SLC27A4* genes with the thickness [36] and lipid composition [37] of pig backfat. The influence of the *NR2F6*, *PDE1A* and *RBMS1* genes on adipogenesis and lipid metabolism, in particular on the accumulation of fat deposits in cold conditions [38] and obesity [39-41], has been shown in laboratory mice.

2. SNPs and potential candidate genes ($p < 0.00001$) **associated with abdominal fat deposition in the carcass of 8-week-old male quails (*Coturnix japonica*) of F_2 model resource population** (the Ernst Federal Research Center for Animal Husbandry — VIZh, 2022-2023)

Chromosome	Number of SNPs	SNP	p	Gene	
				in the SNP region	±0,2 Mb
1	11	1:14239735	1.03E-05	–	*GTSE1*, *TRMU*, *RAMD4*, *CERK*
		1:17986717	4.74E-05	–	*IL17REL*, *MLC1*, *MOV10L1*, *PANX2*, *TRABD*, *SELENOO*, *TUBGCP6*, *HDAC10*
		1:161416406	8.12E-05	–	*ATM*, *NPAT*, *ACAT1*, *ELMOD1*
		1:161611015	7.37E-06	–	*ALKBH8*, *CWF19L2*
		1:161611163	3.26E-05	–	*ELMOD1*, *ALKBH8*, *CWF19L2*, *GUCY1A2*
		1:161950040	6.55E-06	–	*GUCY1A2*, *ASDHPPT*, *KBTBD3*, *MSANTD4*
		1:162669404	6.99E-06	–	*PDGFD*
		1:164041425	6.53E-05	–	*PGR*, *ARHGAP42*, *CNTN5*
		1:164300065	9.84E-06	*CNTN5*	-
		1:18579785	9.30E-05	–	*PLXNB2*, *ZNF800*, *GRM8*
2	2	2:85104703	5.62E-05	–	*TMX3*
		2:87734460	1.35E-05	*GNAL*	*SPIRE1*, *AFG3L2*, *PRELID3A*, *MPPE1*
7	7	7:11751354	6.63E-05	–	*PARD3B*, *NRP2*, *INO80D*
		7:11751372	6.63E-05	–	
		7:12205885	1.88E-05	–	*DNAJC10*, *PIKFYVE*, *CYP20A1*, *NBEAL1*,
		7:12292293	1.88E-05	*PDE1A*	*IDH1*
		7:13285939	6.29E-06	–	*CWC22*, *ZNF385B*, *SESTD1*, *CCDC141*
		7:25004119	9.48E-05	*RBMS1*	*LY75*, *PLA2R1*, *ITGB6*
		7:3916979	9.88E-05	–	*AGAP1*, *GBX2*, *ASB18*, *IQCA1*, *ACKR3*
8	2	8:17793153	9.35E-05	*PTPRF*	*IPO13*, *KDM4A*, *ST3GAL3*
		8:17793157	9.35E-05	–	
17	2	17:4080998	4.98E-05	*SH3GLB2*	*SPTAN1*, *TBC1D13*, *ENDOG*, *LRRC8A*, *PHYHD1*, *NUP188*, *TBC1D13*, *PTPA*, *NTMT1*
		17:3724688	1.71E-05	*SLC27A4*	*NAIF1*, *EEIG1*, *SH2D3C*, *DPM2*, *AK1*
19	1	19:601237	1.42E-05	–	*CLDN4*, *LIMK1*, *CALN1*, *MTMR4*, *ABHD11*, *METTL27*, *SBDS*, *GALNT17*
21	1	21:5674628	8.43E-05	*TRIM62*	*WNT4*, *P3H1*, *ZMYND12*, *PHC2*, *USP48*, *ECE1*, *EIF4G3*, *CDC42*, *C1orf50*, *PPIH*, *SLC2A1*, *ALPL*
24	1	24:2070512	4.36E-05	*IGSF9B*	*OPCML*, *NCAPD3*, *THYN1*, *B3GAT1*, *JAM3*, *VPS26B*, *ACAD8*
28	2	28:2442148	4.46E-05	*USHBP1*	*REEP6*, *THOP1*, *GADD45B*, *ABHD8*,
		28:2436106	1.79E-06	*NR2F6*	*ANO8*, *YJEFN3*, *MAU2*, *NCAN*

N o t e. Dashes in the table mean that no genes are located in the position of identified SNPs.

For other candidate genes we discovered, a connection was established with meat productivity and meat quality prameters in other farm animals and poultry. In particular, the *CNTN5* gene has been reported to make association with feed efficiency in Peking ducks up to 42 days of age [42], which may indicate the effect of this gene on the feeding behavior of the bird and, therefore, on the accumulation of intramuscular and abdominal fat. The effect of the *CNTN5* gene on the pH of the *longissimus dorsi* muscle in F_2 sheep of the resource population Texel × Altai breed has also been shown [43]. A relationship was found between the *PTPRF* gene and bodyweight of Holstein cows [44].

Thus, GWAS analysis for abdominal fat deposition in quails identifies with high confidence ($p < 0.00001$) 29 SNPs on chromosomes 1, 2, 7, 8, 17, 19, 21, 24 and 28. In the regions of the novel SNPs, 11 candidate genes are identified that are significantly associated with abdominal fat deposition in quails at the age of 8 weeks. The functional annotation showed the involvement

of seven identified genes in lipid metabolism in other species of farm animals. The data obtained allow for searching associations of identified mutations with other indicators of breeding value.

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