

Research Article

Genomic statistical profiles and genetic parameter of taste-active compounds in breast meat of the Korean native chicken red brown line

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ABSTRACT

Improving the flavor of chicken meat while maintaining productivity has become an important goal in poultry breeding. This study investigated the genetic characteristics of 20 taste-active compounds (TACs) and carcass weight (CW) in the Korean native chicken red-brown line. The TACs encompassed a wide range of metabolites, including free amino acids, peptides, organic acids, and nucleotide-related compounds. Genetic parameters were estimated using data from 829 birds, applying a multi-trait genomic model. Most TACs showed moderate heritability. Among them, inosine and carnosine stood out with relatively high heritability estimates of 0.45 and 0.34, respectively, indicating strong potential for genetic improvement. Trait correlations reflected known metabolic relationships. For example, leucine and methionine were positively correlated with a coefficient of 0.68, while inosine and its metabolic precursor inosine-5-monophosphate (IMP) showed a strong negative correlation of 0.71, suggesting regulatory competition. In addition, several TACs demonstrated undesirable associations with CW. Acetate, in particular, had a phenotypic correlation of -0.44 with CW, implying that selection for flavor-related traits may affect growth performance if not properly balanced. These findings reveal that many flavor compounds are under moderate genetic control and have biologically meaningful interactions. Integrating these compounds into breeding objectives can help develop chickens with improved sensory qualities while maintaining acceptable production levels. This strategy supports a more consumer-oriented approach to native chicken breeding.

Keywords: Korean native chicken, taste-active compound, genetic parameter estimation, heritability, genomic selection

INTRODUCTION

Over the past century, global meat consumption has steadily risen due to factors such as economic advancement, increased urbanization, and innovations in meat production techniques (Thornton, 2010; Graça et al., 2014). Recently, however, consumer preferences have shifted toward meat that is both nutritious and of high quality (FAO, 2013; Bryant et al., 2019; Bryant and Barnett, 2020; Henchion et al., 2021). Compared to

other meats, chicken is particularly favored for its affordability, high protein content, and low-fat composition (Shu et al., 2010; Chumngoen and Tan, 2015; Marangoni et al., 2015). Meat quality encompasses various characteristics, including pH, color, tenderness, water-holding capacity, intramuscular fat, and flavor, all of which contribute to consumer preference and market value (Jayasena et al., 2013; Jung et al., 2013; Sun et al., 2013; Ono et al., 2019). Multiple studies have shown that various traits positively correlate with meat quality, influencing consumer acceptance and meat price.

Taste and flavor, regarded as the most important traits of meat quality, are influenced by taste-active compounds such as IMP, which is the predominant nucleotide-related compound (NT) in meat. Additionally, free amino acids (FAAs) such as glutamic acid, glycine, and alanine also play key roles in enhancing meat flavor. These compounds contribute to the umami, sweet, and overall savory qualities of meat that are essential for consumer satisfaction. Together, these taste-active compounds interact to determine the characteristic flavor profile of meat, making them important targets for genetic improvement in meat production (Dashdorj et al., 2015).

Korean native chicken (KNC) represents an indigenous chicken population in Korea, classified into five lines based on feather color: white (KNC-W), black (KNC-B), yellow-brown (KNC-Y), gray-brown (KNC-G), and red-brown (KNC-R) (Jayasena et al., 2015; Seo et al., 2016; Jin et al., 2017; Kim et al., 2022). The KNC breed is valued for its high meat quality, with consumers often favoring KNC meat over that of commercial broilers for its unique flavor and taste profile (Choe et al., 2010; Jayasena et al., 2014; Seo et al., 2017). In particular, the KNC-R is recognized for its significant contribution to Woorimatdag, a popular commercial breed in Korea, as it was selected by the National Institute of Animal Science (NIAS) for its enhanced meat quality and production characteristics (Jung et al., 2013; Choi et al., 2015; Jung et al., 2015). This study aims to explore the potential of TAC traits as valuable selection criteria in breeding programs. Specifically, this research estimates the heritability and genetic correlations of TAC traits in breast meat of the KNC-R line, providing foundational insights for the genetic improvement of these flavor-related attributes.

MATERIALS AND METHODS

Animals

In this study, chickens from the KNC-R line, maintained as a purebred line at the Poultry Research Institute of NIAS in Korea, were used. A total of 829 (320 male and 509 female) chickens were selected across four generations (one generation spanning 52 weeks) for this experiment. For population continuity, 30 male and 210 female birds were chosen annually as breeding parents to establish each new generation. Importantly, the selection criteria excluded nucleotide-related traits, ensuring that selection practices did not impact the results obtained from this population. All chickens in each generation were hatched simultaneously and reared in battery cages within a controlled, windowless facility at the Poultry Research Institute. From hatching until 10 weeks of age, birds were provided with ad libitum access to feed and water. A starter diet was given from hatch to 6 weeks, followed by a grower diet from 7 to 10 weeks. Environmental factors, including temperature, humidity, housing conditions, and stocking density, were carefully regulated throughout the study. At 10 weeks, blood samples were collected from the experimental chickens before they were rendered unconscious through CO₂ exposure. The birds were then exsanguinated via neck cut, after which carcass weight and breast meat samples were collected. Breast meat samples were stored at -80 °C until analysis, while blood samples were kept at -20 °C for subsequent DNA extraction. All animal procedures adhered to the guidelines set by the Institutional Animal Care and Use Committee of NIAS (Approval number: NIAS 20212219) and the Animal Ethics Committee of Chungnam National University (Approval number: 202209A-CNU-141).

Phenotyping

For phenotype data collection, we used nuclear magnetic resonance spectroscopy to measure 12 FAA (alanine, asparagine, aspartic acid, glutamate, glutamine, glycine, isoleucine, leucine, methionine, phenylalanine, tyrosine, valine), 2 peptide (anserine, carnosine), 3 organic acid (acetate, creatine, lactate), and 3 NT (hypoxanthine, IMP, inosine) contents in the breast meat samples (Kim et al., 2021). The measured TAC values were calculated in units of mM. Additionally, CW was measured from each bird after slaughter. For the outlier trimming, values that were larger or smaller than three standard deviations from the mean value of the data were removed. Finally, from 817 to 828 samples across 21 traits including TAC contents and CW were filtered and used in variance component analysis. R software v 3.6.3 was used for preprocessing (Table 1).

Table 1. Descriptive statistics of phenotype measured from KNC-R population.

Trait	Category	Mean	SD	Min	Max	N
CW	CW	677.977	136.936	358	1135	824
Alanine	FAA	1.195	0.262	0.520	1.984	820
Asparagine	FAA	0.401	0.297	0.011	1.543	819
Aspartic acid	FAA	0.63	0.249	0.164	1.458	817
Glutamate	FAA	0.874	0.267	0.308	1.743	817
Glutamine	FAA	1.137	0.451	0.341	2.49	828
Glycine	FAA	1.266	0.660	0.316	3.305	826
Isoleucine	FAA	0.235	0.097	0.045	0.535	822
Leucine	FAA	0.678	0.210	0.24	1.345	822
Methionine	FAA	0.306	0.222	0.07	1.032	819
Phenylalanine	FAA	0.222	0.071	0.067	0.447	822
Tyrosine	FAA	0.523	0.201	0.117	1.153	824
Valine	FAA	0.331	0.127	0.088	0.729	823
Anserine	Peptide	29.457	3.819	17.956	40.547	818
Carnosine	Peptide	11.065	3.040	1.85	20.437	825
Acetate	Organic acid	0.315	0.109	0.057	0.664	819
Creatine	Organic acid	25.142	2.972	15.41	35.157	817
Lactate	Organic acid	83.809	11.293	47.342	120.123	818
Hypoxanthine	NT	0.433	0.210	0.096	1.532	827
IMP	NT	5.046	0.930	2.318	7.854	823
Inosine	NT	1.197	0.418	0.178	2.422	822

KNC-R, Korean native chicken red brown line; Min, Minimum; Max, Maximum; N, Number of samples used for analysis; CW; Carcass weight; FAA, Free amino acid; NT, Nucleotide-related compound; IMP, Inosine 5'-monophosphate

Genotyping and preprocessing

Genomic DNA was extracted from blood samples using a commercial extraction kit (GeNet Bio, Daejeon, Korea). Genotyping was conducted using the Illumina chicken 60K SNP chip (Illumina Inc., San Diego, CA, USA), generating a dataset of 57,636 SNPs from the extracted DNA. Quality control was performed with PLINK 1.9 software (v1.90b5.2) (Purcell et al., 2007), removing SNPs with a call rate below 0.9, minor allele frequency under 0.01, or a Hardy-Weinberg equilibrium p-value of less than 10^{-6} . After filtering, 44,638 variants remained and were included in the subsequent association analysis.

Statistical analysis

Genetic parameter estimation was conducted using the BLUPF90+ software with the EM REML algorithm. To accurately estimate variance components, sex and experimental batch were included as covariates in the model. A multi-trait genomic model was applied to capture genetic correlations among traits, thereby enhancing the precision of parameter estimates.

For this multi-trait model, genomic data were used to create the genomic relationship matrix (G), following VanRaden's method:

$$G = \frac{MM'}{\sum 2p_i(1 - p_i)}$$

, where M represents the matrix of centered genotypes, and p_i is the allele frequency at locus i. The estimation of additive genetic variance and residual variance was recorded in the log file (VanRaden, 2008). Heritability (h^2) for each trait was calculated as the proportion of genetic variance (σ_g^2) to the total variance (sum of genetic and residual variances), based on the formula:

$$h^2 = \frac{\sigma_g^2}{\sigma_g^2 + \sigma_r^2}$$

, where h^2 denotes heritability of a trait, σ_g^2 is the genetic variance, and σ_r^2 is the residual variance. This process enabled the estimation of heritability values for various TAC and CW traits in the KNC-R population.

To assess the relationships among traits, genetic correlations were calculated. These correlations provide insights into shared genetic influences among traits. Genetic correlations (r_g) were derived from the covariance between traits as follows:

$$r_g = \frac{cov_g}{\sqrt{V_{g1}V_{g2}}}$$

, where r_g represents the genetic correlation, cov_g is the genetic covariance between two traits, and V_{g1} and V_{g2} denote the genetic variances of traits 1 and 2, respectively.

RESULTS

Basic statistics

The descriptive statistics for the phenotypic values of TAC traits, including FAAs, peptides, organic acids, and NTs, in the KNC-R chicken population are presented in Table 1. Histograms and quantile-quantile (Q-Q) plots illustrating the distributions of these traits are displayed in Fig. 1. In this population, the mean values of FAA phenotypes such as alanine and leucine were 1.195 and 0.678 mM, respectively. Among the FAAs, valine exhibited a relatively narrow range (0.102-0.729 mM), whereas glycine had a wider range (0.316-3.305 mM), reflecting the variability of these amino acids in the population. Regarding NTs, inosine showed a mean of 1.197 mM with a range from 0.178 to 2.422 mM, while IMP exhibited a higher mean of 5.046 mM, with values ranging from 2.318 to 7.854 mM. For organic acids, lactate displayed the highest mean value at 83.809 mM, ranging from 43.342 to 120.123 mM, indicating its prominent presence among organic acid compounds in KNC-R breast meat. Peptides like anserine and carnosine also exhibited considerable mean values, with anserine reaching 29.457 mM and carnosine averaging 11.065 mM. The histograms and Q-Q plots in Fig. 1 illustrate the normality of trait distributions. Traits such as carnosine and inosine show distributions close to normal, while others like acetate exhibit slight deviations.

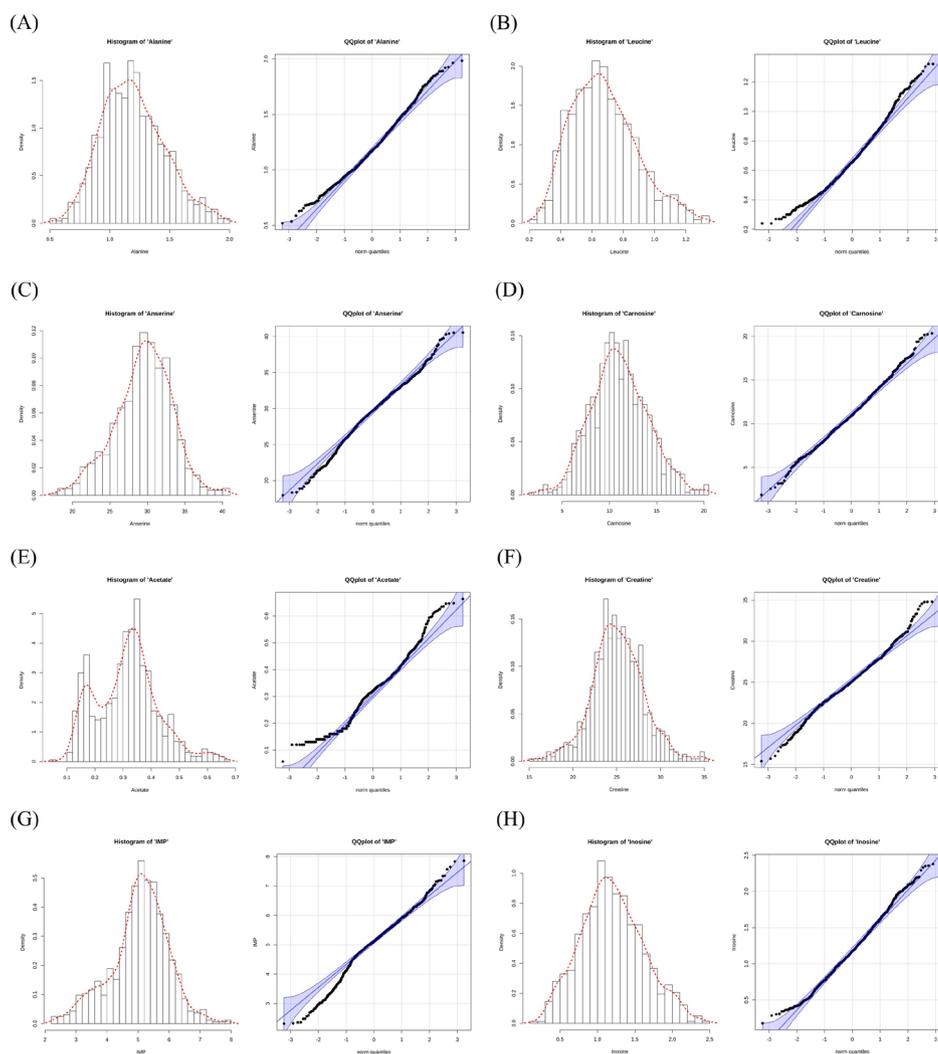


Figure 1. Histogram and quantile-quantile plot of taste-active compound data. (A) Alanine, (B) Leucine, (C) Anserine, (D) Carnosine, (E) Acetate, (F) Creatine, (G) Inosine 5'-monophosphate (IMP) (H) Inosine.

Heritability and variance components

Table 2 presents the heritability estimates and variance components for various TAC traits in the KNC-R chicken population. Overall, the heritability estimates for most FAA, peptide, organic acid, and NT traits were moderate, indicating that both genetic and environmental factors contribute to the observed phenotypic variance. For FAAs, alanine and asparagine exhibited the highest heritability at 0.27, suggesting a relatively stronger genetic influence on these traits. Other FAAs such as glutamate, glutamine, isoleucine, leucine, phenylalanine, and valine showed heritability estimates ranging from 0.18 to 0.21, highlighting their moderate genetic variance within this population. Among the peptide traits, carnosine displayed a heritability of 0.34. Anserine, another peptide, showed a lower heritability of 0.17. For organic acids, acetate, creatine, and lactate had heritability values of 0.12, 0.13, and 0.16, respectively. NTs, including hypoxanthine, IMP, and inosine, demonstrated heritability estimates between 0.24 and 0.45. Notably, inosine had the highest heritability at 0.45 among all analyzed TAC traits, suggesting a strong genetic component in its phenotypic variance. The NT traits tended to have higher heritability values compared to other categories in TAC, while organic acids displayed the lowest heritability estimates.

Table 2. Estimated heritabilities and variance components of taste-active compound and carcass weight (CW) traits.

Trait	Category	σ^2_a	σ^2_r	h^2
CW	CW	2973.5	3977.6	0.43
Alanine	FAA	0.016	0.043	0.27
Asparagine	FAA	0.008	0.022	0.27
Aspartic acid	FAA	0.003	0.024	0.11
Glutamate	FAA	0.006	0.025	0.20
Glutamine	FAA	0.009	0.038	0.20
Glycine	FAA	0.014	0.096	0.13
Isoleucine	FAA	0.001	0.004	0.21
Leucine	FAA	0.005	0.025	0.18
Methionine	FAA	0.001	0.004	0.15
Phenylalanine	FAA	0.001	0.003	0.18
Tyrosine	FAA	0.003	0.016	0.14
Valine	FAA	0.001	0.006	0.18
Anserine	Peptide	1.715	8.459	0.17
Carnosine	Peptide	2.181	4.282	0.34
Acetate	Organic acid	0.001	0.005	0.12
Creatine	Organic acid	0.895	5.995	0.13
Lactate	Organic acid	13.395	68.724	0.16
Hypoxanthine	NT	0.005	0.017	0.24
IMP	NT	0.105	0.327	0.24
Inosine	NT	0.066	0.080	0.45

σ^2_a , Estimated genetic variance of the trait; σ^2_r , Estimated residual variance of the trait; h^2 , Estimated heritability; CW, Carcass weight; FAA, Free amino acid; NT, Nucleotide-related compound; IMP, Inosine 5'-monophosphate

Genetic and phenotypic correlations

The genetic and phenotypic correlations among the TAC traits reveal distinct patterns within and across these trait categories (Fig. 2). Within the FAA category, alanine showed a strong positive genetic correlation with phenylalanine (0.65) and methionine (0.53), while methionine and leucine also demonstrated a high correlation (0.68). Additionally, glutamate displayed moderate to high positive genetic correlations with isoleucine (0.55), leucine (0.74), and methionine (0.67). Carnosine, a peptide, exhibited a negative genetic correlation with anserine (-0.59). For organic acids, creatine and lactate showed positive genetic correlation (0.59). For NTs, inosine and hypoxanthine displayed a strong positive genetic correlation (0.63). Whereas, inosine showed strong negative genetic correlation with IMP (-0.71). Notably, across different TAC categories, acetate, an organic acid, exhibited moderate genetic correlations with alanine (0.52) and phenylalanine (0.56), isoleucine (0.60) and glutamate (0.53) from the FAA category. Lactate showed moderate positive correlations with tyrosine (0.571). Creatine exhibited negative correlation with asparagine (-0.58) from FAA trait. Hypoxanthine, an NT trait, displayed a positive genetic correlation with glutamate (0.57) from the FAA category. In terms of phenotypic correlations, alanine and phenylalanine showed a moderate positive correlation (0.52), as did glutamate and glutamine (0.54). Among the NTs, inosine and hypoxanthine also exhibited a high positive correlation (0.50), indicating a consistent relationship in both genetic and phenotypic dimensions. Inosine and IMP showed moderate negative phenotypic correlation (-0.31). CW showed a mild negative correlation with acetate (-0.44), phenylalanine (-0.34), and IMP (-0.33). Whereas, CW generally showed weak phenotypic correlations with TAC traits.

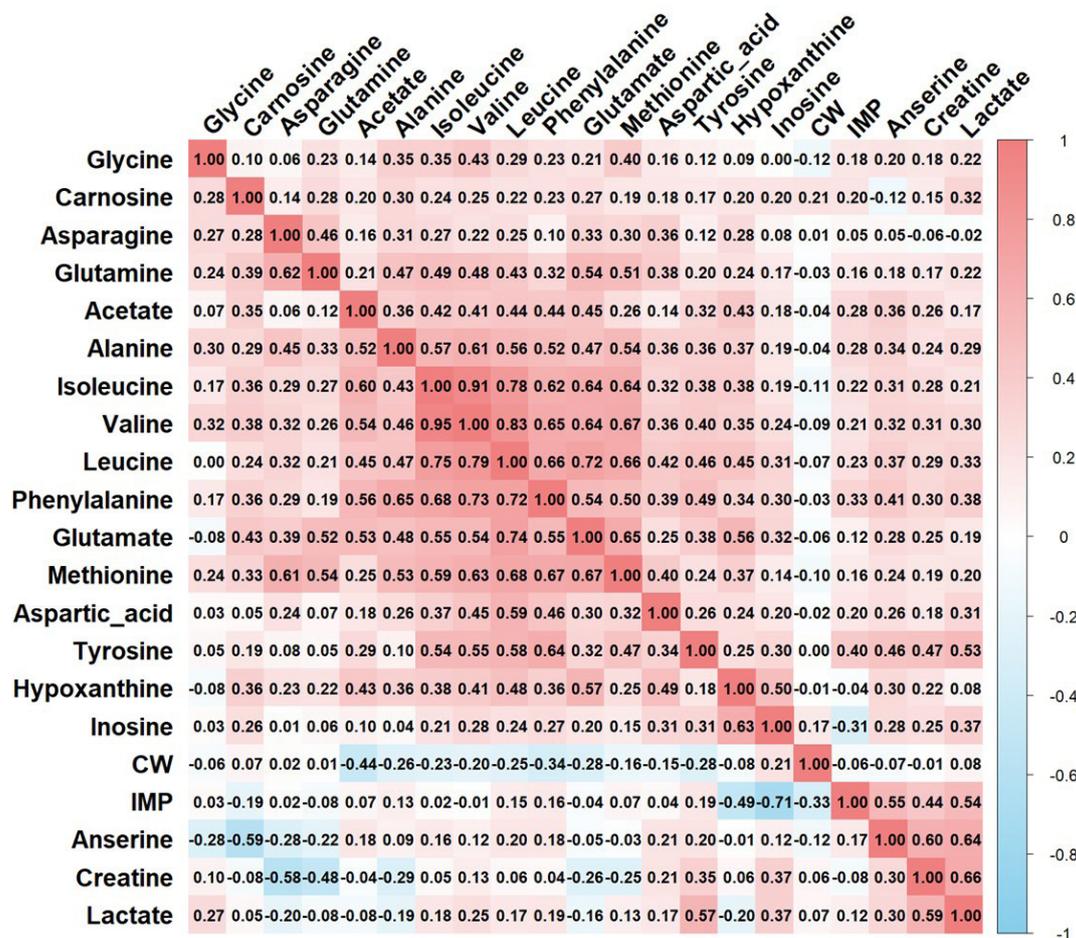


Figure 2. Genetic and phenotypic correlation of taste-active compound and carcass weight (CW) traits. Genetic correlations are shown in the lower diagonal, while phenotypic correlations are shown in the upper diagonal.

DISCUSSION

In this study, we analyzed the heritability and genetic correlations of CW and TAC in the breast meat of the KNC-R line, focusing on FAAs, peptides, organic acids, and NTs. The results revealed a complex genetic architecture underlying these compounds, with notable variability in heritability estimates across different TAC categories. The heritability values for FAAs were generally moderate in this research, with alanine and asparagine showing the highest values (0.27). This aligns with previous study indicating that free amino acids in skeletal muscle involved in protein metabolism tend to be easily affected by nutritional condition for broiler (Watanabe et al., 2020). In that study, low dietary lysine levels were reported to increase protease expression, leading to the release of FAAs in muscle tissue. Additionally, muscle FAA content in poultry has been shown to vary in response to environmental effects, such as protein metabolism induced by heat stress (Qaid and Al-Garadi, 2021).

In the results, the peptides anserine and carnosine displayed heritability estimates of 0.17 and 0.34, respectively, with carnosine exhibiting one of the highest heritability among TAC traits. Histidine-containing dipeptides like anserine and carnosine are known for their antioxidant properties in muscle tissue, and studies suggest that their concentrations in muscle may be genetically influenced due to their roles in pH buffering and antioxidation in animals, including chickens. These dipeptides help delay muscle acidification during anaerobic metabolism, where lactate and hydrogen ions accumulate, thereby stabilizing muscle pH under conditions of metabolic stress (Dolan et al., 2018; Baldi et

al., 2021). This buffering role may explain the moderate heritability observed for peptide traits.

Lactate, an organic acid, is produced in skeletal muscle during high-intensity exercise through anaerobic metabolism. Its levels can fluctuate as it is further utilized as an energy source (Gladden, 2004). Creatine, on the other hand, tends to decrease with intense muscle activity, as it is consumed for ATP production (Casey and Greenhaff, 2000). Acetate levels can also vary based on muscle energy demands; during active metabolism, fatty acids and amino acids break down to form acetyl-CoA, which may then convert to acetate (Wolfe, 1998; Foster, 2004). Given these dynamics, individual differences in activity levels likely influenced the phenotypic value of organic acid traits, contributing to the lower genetic variance observed in these traits.

The NT traits IMP, inosine, and hypoxanthine are products of the purine metabolism pathway, where ATP is broken down to supply energy for muscle tissue. In chicken muscle, both the synthesis and degradation of IMP, inosine, and hypoxanthine are regulated by several metabolic enzymes. Genes encoding these enzymes, such as Glutamine-PRPP amidotransferase (*GPAT*), Adenylosuccinate lyase (*ADSL*), and Aminoimidazole ribonucleotide carboxylase (*AIRC*), have been previously identified as markers associated with individual variation (Huang et al., 2022). In the present study, inosine demonstrated notably high heritability, indicating a substantial genetic influence on its concentration. This finding may suggest a significant genetic effect on 5'-nucleotidase, the enzyme responsible for degrading IMP to inosine.

We observed distinct genetic and phenotypic correlations within and across the TAC traits in the KNC-R chicken population, reflecting their underlying metabolic relationships. Within the FAA category, several strong positive genetic correlations were identified, such as between alanine and phenylalanine (0.65) and between methionine and leucine (0.68). These correlations suggest that these amino acids share a common genetic basis, likely due to their interconnected roles in amino acid metabolism. For instance, the metabolic link between branched-chain amino acids, like leucine, isoleucine, and valine, is well-documented and supported by shared enzymes in their synthesis and degradation pathways (Harris et al., 2005; Wu, 2009). Additionally, glutamate's moderate to high positive genetic correlations with amino acids like leucine (0.74) and methionine (0.67) align with its role as a central amino acid in nitrogen transport and amino acid biosynthesis (Temple et al., 1998; Watford, 2015). In the peptide category, anserine and carnosine showed a negative genetic correlation (-0.59). Based on the chicken Kyoto Encyclopedia of Genes and Genomes (KEGG) database, in the histidine metabolism pathway (gga00340) describe how carnosine convert to anserine (Kim et al., 2024). The observed negative correlation suggests that these dipeptides synthesis may be regulated in opposing ways, perhaps due to physiological trade-offs in muscle tissue. For organic acids, creatine and lactate exhibited a moderate positive genetic correlation (0.59), indicating co-regulation within energy metabolism in muscle tissue. Lactate is produced during anaerobic metabolism, while creatine serves as an immediate energy reserve. The positive correlation may reflect their combined role in energy production and utilization under high metabolic demands (Gladden, 2004). Additionally, acetate's moderate genetic correlations with several FAAs, such as alanine (0.52) and phenylalanine (0.56), indicate potential metabolic links between amino acid and organic acid pathways. Acetate, as a derivative of acetyl-CoA in active metabolism, may interact with amino acid catabolism, aligning with findings in prior studies (Foster, 2004). In the NT category, inosine and hypoxanthine displayed a strong positive genetic correlation (0.63), consistent with their sequential roles in purine degradation. The negative genetic correlation observed between inosine and IMP (-0.71) highlights the metabolic flux in purine pathways, where the accumulation of one compound can lead to the depletion of another, as each compound represents a step in ATP degradation (Huang et al., 2022).

The phenotypic correlations generally followed the genetic trends but with some differences in magnitude, likely due to environmental influences. Inosine and hypoxanthine displayed a moderate positive phenotypic correlation (0.50), consistent with their shared metabolic pathway. The moderate negative phenotypic correlation observed between CW and TAC traits like acetate (-0.44) and phenylalanine (-0.34) suggests that larger carcass size may be associated with reduced concentrations of specific TACs, potentially reflecting metabolic shifts in larger birds. Given the observed correlations, breeding strategies aimed at increasing CW in meat-type chickens should carefully consider the traits that display negative correlations with CW. Specifically, TACs, which showed moderate negative phenotypic correlations with CW, may be

influenced in ways that could impact the flavor profile if CW is significantly increased. Increasing CW without accounting for these negative correlations could lead to a reduction in certain flavor-related compounds, potentially affecting meat taste.

CONCLUSION

This study provides foundational insights into the genetic architecture of TAC traits in the KNC-R chicken line, offering direction for breeding strategies aimed at enhancing both growth and flavor. The moderate heritability values for FAAs, peptides, organic acids, and NTs suggest potential for genetic selection, though environmental influences remain significant. Inosine and carnosine, with higher heritability, emerge as promising targets for flavor enhancement. However, the negative correlations observed between CW and specific TACs, such as acetate and phenylalanine, imply that increasing carcass weight could impact flavor. Thus, a balanced breeding approach is recommended to maintain both carcass yield and the distinct flavor profile of KNC-R chicken meat.

CONFLICT OF INTERESTS

No potential conflict of interest relevant to this article is reported.

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