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ESTIMATION OF HETEROSIS, COMBINING ABILITY AND RECIPROCAL EFFECTS FOR PRODUCTION, REPRODUCTION, CARCASS CHARACTERISTICS AND EGG QUALITY TRAITS IN FOUR GENETIC GROUPS OF CHICKEN FROM A FULL DIALLEL CROSS

PhD Dissertation

By

Philimon Teshome Feyisa

Department of Animal Production Studies

PhD Program in Animal Production

February 2026

Bishoftu, Ethiopia

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Dissertation submitted to the College of Veterinary Medicine and Agriculture of Addis Ababa University in partial fulfillment of the requirements for the degree of Doctor of Philosophy in Animal Production

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DEDICATION

I dedicate this PhD dissertation to my beloved family for their love, patience, understanding, and support throughout my studies.

STATEMENT OF THE AUTHOR

First, I declare that this thesis/dissertation is my bona fide work and that all sources of material used for this thesis have been duly acknowledged. This thesis has been submitted in partial fulfillment of the requirements for a PhD degree at Addis Ababa University, College of Veterinary Medicine and Agriculture and is deposited at the University/College library to be made available to borrowers under rules of the library. I solemnly declare that this dissertation has not been submitted to any other institution for the award of an academic degree, diploma, or certificate.

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BIOGRAPHICAL SKETCH

Philimon Teshome was born on October 20, 1988 in Adama, Ethiopia. He attended his elementary and high school education at Holy Angels School in Adama, and he followed his preparatory education at Atse Gelawdios Preparatory School in Adama. After completion of his high school education, he joined Jimma University, College of Agriculture and Veterinary Medicine in October 2007 and graduated with a BSc degree in Animal Science in 2010. Soon after graduation, he rejoined Jimma University for his second degree in Animal Production and graduated in July 2012. Upon completion of his MSc study, he joined the Ethiopian Institute of Agricultural Research in January 2013 and started working in the livestock research department for over seven years until he was granted leave of absence to pursue his PhD study in October 2019. During this time, Philimon collaborated with his fellow researchers and conducted relevant research studies that examined various livestock production issues in the pastoral areas of Ethiopia. Similarly, he authored and coauthored relevant research articles in his research engagements, which contributed to information generation for the improvement of livestock production in the above-mentioned areas of the country.

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LIST OF ABBREVIATIONS

ADFI	Average Daily Feed Intake
AFE	Age at First Egg
AH	Albumen Height
AW	Albumen Width
BW	Body Weight
BWSM	Body Weight at Sexual Maturity
DW	Dressed Weight
EL	Egg Length
EM	Egg Mass
EN	Total Egg Numbers
EW	Egg Width
EWAFE	Egg Weight at First Egg
EWT	Egg Weight
FCR	Feed Conversion Ratio
HDEP	Hen-day Egg Production
HFE	Hatchability of Fertile Eggs
HHEP	Hen-housed Egg Production
HTES	Hatchability of Total Eggs Set
HU	Hugh Unit
MO	Moisture Content
SR	Shell Ratio
ST	Shell Thickness
SW	Slaughter Weight
SWT	Shell Weight
WHC	Water Holding Capacity
YH	Yolk Height
YR	Yolk Ratio
YW	Yolk Width
YWT	Yolk Weight

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Estimation of Heterosis, Combining Ability and Reciprocal Effects for Production, Reproduction, Carcass Characteristics and Egg Quality Traits in Four Genetic Groups of Chicken from a Full Diallel Cross

ABSTRACT

Crossbreeding is an effective strategy for improving productivity and adaptability of chickens under diverse production environments. This study evaluated heterotic effects (H^e), general combining ability (GCA), specific combining ability (SCA), reciprocal effects (RE), and maternal effects (M^e) for production, reproduction, carcass characteristics, and egg quality traits in a 4×4 full diallel cross involving four chicken breeds: Improved Horro (H), Commercial Sasso (S), Potchefstroom Koekoek (K), and Dz-white feathered (D). The experiment was conducted at the poultry research farm of Werer Agricultural Research Center (WARC), located in Amibara Woreda of the Afar Regional State, Ethiopia. A total of 960 purebred and F1 hybrid chickens representing sixteen genetic groups were reared in a completely randomized design to evaluate growth performance, with body weight (BW) recorded from hatch to 14 weeks of age. At 24 weeks, 288 chickens (144 males and 144 females), comprising 18 birds per genotype (9 males and 9 females), were used for carcass component analysis. Fertility and hatchability traits were monitored throughout the incubation period. Egg production data were collected from 672 hens, with eggs recorded twice daily from the onset of lay until 40 weeks of age to determine egg production. Egg quality traits were evaluated using 480 eggs (30 eggs per genetic group) randomly sampled at peak production (32 weeks of age). Heterosis estimates revealed that crosses between S males and K or D females (including reciprocals) exhibited the strongest positive H^e for BW throughout the growth period, whereas K×D crosses showed negative H^e, and H×K crosses displayed low and showed decreasing trend after WK 10. The GCA effects were highly significant ($P < 0.0001$), underscoring the importance of additive gene effects on BW, while SCA significantly influenced early-age BW (hatch, WK 2, 4, and 10), highlighting non-additive genetic contributions. The RE was significant only at hatch, WK 2, and WK 10, suggesting transient maternal or paternal influences. These findings suggest prioritizing parental GCA for consistent BW gains and developing broiler lines from S sires crossed with K or D dams and H sires with S dams. Carcass traits showed moderate to high heterosis in several crosses, particularly H×S, S×K, S×D, and H×K, with stronger

responses in males. The S breed exhibited the highest positive GCA for slaughter, dressed, and eviscerated weights, while H showed negative GCA effects. Favorable SCA estimates were observed mainly in H×S, S×K, and K×D, and significant reciprocal effects indicated important maternal influences. Reproductive traits showed generally positive heterosis, with H×K and H×S crosses exhibiting superior fertility and hatchability. Genotype K showed the highest positive GCA for fertility and hatchability traits, whereas H showed negative GCA effects. The H×K cross demonstrated the best SCA for reproductive performance, and significant reciprocal effects confirmed the importance of cross direction. For egg production traits, 800 chickens were evaluated over 40 WK, with significant genotypic variations ($P < 0.0001$) in age at first egg (AFE), body weight at sexual maturity (BWSM), egg weight at first egg (EWAFE), egg number (EN), hen-housed egg production (HHEP), hen-day egg production (HDEP), and egg mass (EM). Heterosis varied widely: BWSM and EM showed positive H^e in most crosses, while AFE consistently exhibited negative H^e. Notably, the K×H cross demonstrated the highest H^e for HHEP (26.85%), HDEP (29.44%), EM (40.88%), and EN (28.27%), while D×H and K×S crosses also displayed strong heterosis for key traits. Reciprocal crosses generally showed positive H^e for all traits except AFE. Both GCA and SCA were highly significant ($P < 0.0001$), with GCA/SCA ratios indicating non-additive dominance for AFE, additive influence for EWAFE, and balanced additive/non-additive effects for HHEP, HDEP, EM, and EN. RE and M^e further modulated trait expression, supporting optimized crossbreeding strategies such as using K sires with H/S dams and D sires with H dams to enhance egg production. Egg quality traits were assessed using 480 eggs from purebreds and crossbreds, evaluating egg weight (EWT), egg length (EL), egg width (EW), shell weight (SWT), shell thickness (ST), shell ratio (SR), albumen height (AH), albumen width (AW), yolk height (YH), yolk width (YW), yolk weight (YWT), yolk ratio (YR), and Haugh unit (HU). Positive H^e was observed for most traits, with significant GCA effects ($P < 0.001$) for EWT, EL, EW, AW, YW, YWT, and YR, while SCA influenced all traits ($P < 0.001$). The K×S cross showed positive RE for EWT and AW, whereas D×S had the highest RE for ST. Additive effects primarily governed EWT and YWT, while non-additive effects dominated EL, EW, ST, and YR. Maternal effects significantly varied across genotypes, emphasizing their role in egg quality. In conclusion, these findings underscore the importance of tailored breeding

strategies based on trait-specific genetic architectures. For growth, leveraging high-GCA parents is critical, while crossbreeding programs should prioritize synergistic heterotic combinations like S×K/D for broilers and K×H/S for layers. Egg quality improvement requires balancing additive and non-additive selection, supported by molecular tools for precision. This integrated approach enhances genetic gains across production traits in poultry breeding.

Keywords: Combining ability, Diallel cross, Heterosis, Maternal effect, Reciprocal effect

1. INTRODUCTION

1.1. Background and Justification

Poultry production has emerged as one of the most transformative sectors in global agriculture, demonstrating unprecedented growth over the past three decades. According to the Food and Agriculture Organization (FAO, 2023), worldwide poultry meat production increased by 150% between 1990 and 2020, outpacing all other livestock sectors. This remarkable expansion can be attributed to several key factors that make poultry uniquely positioned to address contemporary food security challenges. The biological efficiency of chickens, characterized by their rapid growth rates, high feed conversion ratios, and short generation intervals, gives them distinct advantages over larger livestock species. A broiler chicken, for instance, can reach market weight in just 5-6 weeks, compared to 18-24 months for cattle, while producing 1 kg of meat from just 1.6 kg of feed (World Bank, 2022). This efficiency translates into greater affordability, making poultry products the most accessible animal protein source for low-income populations globally.

The nutritional importance of poultry cannot be overstated. Chicken eggs are considered nature's perfect food, containing all nine essential amino acids required by humans, along with critical micronutrients like vitamin B12, selenium, and choline (Passarelli *et al*., 2022). In developing countries where malnutrition remains prevalent, regular consumption of poultry products has been shown to reduce stunting prevalence by up to 32% in children under five (Global Nutrition Report, 2023). The sector's labor-intensive nature also makes it a powerful engine for rural employment, particularly benefiting women and youth. These multidimensional benefits explain why poultry development has become a cornerstone of food security strategies across the Global South.

Within the African context, Ethiopia presents a paradoxical case of immense potential constrained by systemic limitations. The country boasts the second-largest chicken population in Africa, estimated at 57 million birds, with 85% kept under traditional smallholder systems (CSA, 2021). This vast resource base theoretically positions Ethiopia to be a regional leader in the sector. However, productivity metrics reveal staggering inefficiencies: average annual egg production stands at just 40-60 eggs per hen compared

to 280-300 in commercial systems, while broilers require 4-5 months to reach 1.5 kg compared to 5-6 weeks in intensive systems (Solomon *et al*., 2013; Damte *et al*., 2024). These performance gaps become even more concerning when contextualized against demographic pressures, with Ethiopia's population projected to reach 160 million by 2040, the current poultry production system would need to expand by 400% just to maintain per capita consumption levels (UNDP, 2022).

The root causes of these productivity constraints are multifaceted and deeply entrenched. At the biological level, indigenous chicken breeds; while admirably adapted to local conditions, exhibit several limiting traits including extended broodiness periods (3-4 weeks), late sexual maturity (6-8 months), and small egg size (35-45 g) (Tewodros and Mebrate, 2019). Management challenges compound these biological limitations, with scavenging systems exposing birds to high predation rates (15-20%) and disease prevalence (Newcastle disease alone causes 50-60% mortality in unvaccinated flocks) (Kassa *et al*., 2021). The feed scarcity situation is particularly dire, with only 12% of poultry farmers accessing formulated feeds and most relying on nutritionally inadequate kitchen scraps and grain by-products (Mengesha *et al*., 2022). These technical challenges are exacerbated by structural weaknesses in the value chain, including fragmented market systems, inadequate processing infrastructure, and limited cold storage facilities that result in post-harvest losses exceeding 30% (MoA, 2022).

The persistent underperformance of Ethiopia's poultry sector demands urgent intervention, and genetic improvement emerges as the most sustainable solution. Previous efforts to improve poultry productivity through the direct introduction of exotic breeds have largely been unsuccessful due to poor adaptability, as demonstrated by the 2015–2020 Exotic Chicken Distribution Program, which recorded mortality rates of up to 70% within the first year (MoA, 2022). These experiences have shifted the paradigm toward crossbreeding strategies that combine the hardiness of indigenous breeds with the productivity of exotic lines. Modern breeding science offers sophisticated tools for this purpose, with combining ability analysis standing out as particularly valuable for the Ethiopian context.

The concept of combining ability, first formalized by Griffing (1956), provides a robust framework for evaluating parental stocks in breeding programs. General Combining

Ability (GCA) measures the average performance of a parent across multiple crosses, primarily reflecting additive genetic effects. In practical terms, a hen with high GCA for egg production will consistently transmit this trait to its offspring regardless of mating partner. Specific Combining Ability (SCA), by contrast, captures non-additive genetic effects that emerge in particular crosses, explaining why some breed combinations outperform expectations based on parental averages (Hayman, 1954). These metrics become particularly powerful when applied through diallel crossing designs, where multiple parental lines are systematically intercrossed to evaluate all possible combinations (Narinc *et al*., 2014).

Recent advances in quantitative genetics have refined these approaches, enabling more precise prediction of cross performance. Mixed model methodologies now allow breeders to account for genotype-by-environment interactions, crucial for Ethiopia's diverse agroecologies (Duenk *et al*., 2021). Molecular markers are increasingly being used to complement phenotypic selection, with genes associated with disease resistance (e.g., the NRAMP1 gene for Newcastle disease resilience) and heat tolerance (e.g., HSP70 polymorphisms) offering new opportunities for precision breeding (Abdullah, 2021). When integrated with Ethiopia's rich avian biodiversity; including unique ecotypes like the long-term adapted Horro and Tepi breeds, these tools can catalyze a genetic revolution in the country's poultry sector.

The Ethiopian government has demonstrated growing recognition of poultry's transformative potential through policy instruments like the 10-Year Poultry Sector Development Plan (2022-2031) and “Yelemat Tirufat” Program. This ambitious roadmap aims to double national egg and meat production by 2030 through a combination of genetic improvement, feed security interventions, and value chain development (MoA, 2022). However, critical knowledge gaps hinder effective implementation, particularly regarding optimal breed combinations for different production systems and agroecological zones.

Existing research on poultry genetics in Ethiopia remains fragmented, with most studies limited to single-location and small sample sizes (Assefa *et al*., 2023). A comprehensive review reveals that only two published studies (Wondmeneh, 2015; Damte *et al*., 2024) have employed full diallel designs to estimate combining abilities. This represents a

significant constraint to evidence-based breeding policy formulation. The international experience offers valuable lessons in this regard. Kenya's success with Kuroiler chickens demonstrates how hybrid vigor can be harnessed when breeding programs align with smallholder realities (Okeno *et al*., 2012). Ethiopia stands to benefit tremendously from adapting these proven approaches while innovating to address its unique challenges.

This study emerges at a critical juncture in Ethiopia's agricultural development trajectory, seeking to provide the scientific foundation for the country's poultry genetic improvement strategy. By employing a comprehensive diallel crossing design, the research generated robust estimates of general and specific combining abilities for key economic traits.

The timing of this research aligns with several strategic priorities. The African Union's Agenda 2063 identifies livestock genetic improvement as essential for continental food sovereignty (AU, 2023). At the national level, Ethiopia's Homegrown Economic Reform emphasizes agricultural modernization as the centerpiece of structural transformation (Berihu, 2022). Most immediately, the findings will directly inform implementation of the 10-Year Poultry Sector Development Plan, providing the evidence base for establishing regional breeding centers and multiplication hubs.

From a scientific perspective, this study contributes to advancing breeding methodology in two key ways: First, it establishes a framework for continuous genetic improvement that can be adapted to other livestock species. Second, it helps to catalyze a sustainable intensification of Ethiopia's poultry sector, one that boosts productivity while preserving genetic diversity and meeting smallholder needs.

1.2. Objectives of the Study

This research was conducted with the following specific objectives:

- To evaluate the comparative performance of the genotypes (H, S, K, D and H×S, H×K, H×D, S×K, S×D, K×D, S×H, K×H, D×K, K×S, D×S, D×K) for growth, feed efficiency, and carcass characteristics;
- To evaluate the comparative performance of the genotypes (H, S, K, D and H×S, H×K, H×D, S×K, S×D, K×D, S×H, K×H, D×K, K×S, D×S, D×K) for fertility, and hatchability;
- To evaluate the comparative performance of the genotypes (H, S, K, D and H×S, H×K, H×D, S×K, S×D, K×D, S×H, K×H, D×K, K×S, D×S, D×K) for egg production and egg quality; and
- To estimate the heterosis effects, combining abilities, and reciprocal effects for growth, feed efficiency, carcass quality, hatchability, fertility, egg production, and egg quality traits on the genotypes (H, S, K, D and H×S, H×K, H×D, S×K, S×D, K×D, S×H, K×H, D×K, K×S, D×S, D×K).

2. LITERATURE REVIEW

2.1. Historical Overview of Poultry Breeding

Poultry breeding has a rich and evolving history, extending over thousands of years, as humans have dedicated efforts to domesticate and enhance chickens to serve as a reliable source of protein, companionship, and cultural significance (FAO, 2007; Miao *et al*., 2013). The domestication of chickens, achieved through the breeding of indigenous chickens, spans a history of roughly 8,000 years (Hata *et al*., 2021). Early efforts in domestication centered on selecting birds for traits like docility, high egg yield, and superior meat quality, establishing the foundation for the diverse breeds present today (Diamond, 2002; FAO, 2007). Over the centuries, chickens spread worldwide through trade networks and human movement, evolving to thrive in diverse environments and align with different cultural practices (Peters *et al*., 2022).

The agricultural revolutions of the 18th and 19th centuries brought a more structured and deliberate approach to poultry breeding. Breeders started focusing on specific traits, such as size, plumage color, and egg production, which resulted in the creation of specialized breeds (Hoffmann, 2005; Nasser *et al*., 2007). These breeds were typically chosen for their practical purposes, with some tailored for meat yield and others for their ability to lay eggs (Hoffmann, 2005).

The 20th century marked a pivotal shift in poultry breeding, fueled by the rise of industrial agriculture and the expansion of large-scale commercial poultry farming (Tixier *et al*., 2012; Rothschild and Plastow, 2014; Saxena and Kolluri, 2018). The growing need for efficient meat and egg production led to the development of hybrid chickens through targeted crossbreeding initiatives (Nasser *et al*., 2007). Breeders began to focus on traits like rapid growth, improved feed conversion rates, and high egg yields, leading to the development of specialized breeds like broilers for meat and layers for eggs (Tixier *et al*., 2012). Advances in genetic selection methods and the adoption of artificial insemination further propelled progress, allowing breeders to achieve significant improvements in productivity (Mohan *et al*., 2018; Saxena and Kolluri, 2018).

In recent years, poultry breeding has been transformed by breakthroughs in biotechnology and genomics (Andersson and Georges, 2004). The mapping of the chicken genome in 2004 opened new opportunities to pinpoint and select genes linked to advantageous traits, such as disease resistance, heat tolerance, and better feed efficiency (International Chicken Genome Sequencing Consortium, 2004). Contemporary breeding initiatives now leverage advanced techniques like marker-assisted selection and genomic prediction to increase the accuracy and effectiveness of genetic enhancements (Andersson and Georges, 2004). Moreover, there is a rising focus on sustainability and animal welfare, with breeders aiming to develop chickens that are not only high-performing but also robust and capable of thriving in shifting environmental conditions (Hoffmann, 2005; Perini *et al*., 2020).

2.2. Genetic Principles of Poultry Crossbreeding

2.2.1. Heterosis in chicken production

Heterosis, commonly known as hybrid vigor, is a fundamental concept in crossbreeding that describes the phenomenon where crossbred offspring exhibit superior performance compared to their purebred parents (Abdullah, 2021; Wang *et al*., 2022; Li *et al*., 2024). This occurs due to the combination of genetic diversity from two distinct parental lines, leading to enhanced growth rate, egg production, disease resistance, and overall vitality (Khalil and Aboukhadiga, 2020; Wu *et al*., 2021).

Heterosis is a key driver of the success of crossbreeding programs in poultry, particularly in commercial farming, where maximizing productivity and efficiency are critical (Mancinelli *et al*., 2023). One of the most significant benefits of heterosis is its impact on growth and productivity (Shambel, 2022). In meat production, for example, crossbreds often demonstrate faster growth rates and better feed conversion efficiency than their purebred counterparts (Siwendu *et al*., 2013; Khalil *et al*., 2018; Tolasa *et al*., 2020; Shambel *et al*., 2022). This is because the genetic combination of two complementary breeds can mitigate the negative effects of inbreeding depression, which often plagues purebred lines. Similarly, in egg-laying breeds, crossbred hens frequently produce more eggs and exhibit greater longevity in their laying cycles (Waleed and Shaheen, 2011; Basant *et al*., 2013; Emad, 2014; Shambel, 2022). These improvements are attributed to

the synergistic effects of combining favorable alleles from both parent breeds, resulting in offspring that outperform either parent.

Heterosis also plays a crucial role in enhancing the resilience and adaptability of crossbred chickens (Sungkhapreecha *et al*., 2022). While often specialized for specific traits, exotic lines may lack the genetic diversity needed to cope with environmental stressors or disease challenges under tropical condition (Sebho, 2016; Assefa *et al*., 2023). Crossbreeding introduces genetic variation, which can improve traits like heat tolerance, cold resistance, and immune response (Fathi *et al*., 2022). For instance, crossbred chickens may inherit disease resistance from one parent and adaptability to harsh climates from the other, making them better suited to diverse farming conditions (Islam and Nishibori, 2010). This adaptability is particularly valuable in regions with variable climates or limited resources (Juiputta *et al*., 2023).

Another important aspect of heterosis is its contribution to reproductive performance (Williams *et al*., 2002; Offermann and Peterhansel, 2014). Crossbred chickens often exhibit higher fertility rates, better hatchability, and improved chick viability compared to purebred lines (Sola and Ayorinde, 2011; Dzungwe *et al*., 2024). This is especially beneficial in breeding programs aimed at producing large numbers of healthy offspring for commercial purposes.

Despite its advantages, the benefits of heterosis are not always consistent across all traits or generations (Williams *et al*., 2002). Heterosis typically has a greater impact on reproduction traits than on growth potential (Fairfull, 1990) and its expression is influenced by maternal genetics and nutrition (Liu *et al*., 1993). The magnitude of heterosis depends on the genetic distance between the parent breeds, with greater diversity typically leading to more pronounced hybrid vigor (Liu *et al*., 1993; Yalçin *et al*., 2000).

2.2.2. Combining ability in chicken crossbreeding

Combining ability is a critical concept in chicken crossbreeding that refers to the performance of specific parental combinations in producing hybrid offspring with desirable traits (Adebambo *et al*., 2010). It measures how well the genes of two parent breeds complement each other to create superior hybrids. Combining ability is divided into two

main types: general combining ability (GCA) and specific combining ability (SCA) (Fasahat, 2016; Khalil *et al*., 2018). General combining ability reflects the average performance of a breed when crossed with multiple other breeds, while SCA refers to the performance of a specific cross between two particular breeds (Griffing, 1956). Understanding and utilizing combining ability is essential for optimizing crossbreeding programs and achieving targeted improvements in traits such as growth rate, egg production, and disease resistance (Emad *et al*., 2017).

General combining ability (GCA) is particularly important for identifying breeds that consistently contribute favorable traits to their offspring, regardless of the other parent breed (Julius and Louis, 2019; Temesgen, 2021). For example, a breed with high GCA for egg production will likely produce high-performing hybrids when crossed with various other breeds (Shambel and Mahilet, 2024). This makes GCA a valuable tool for selecting parent breeds that can serve as reliable foundations for crossbreeding programs (Siwendu *et al*., 2013). Breeds with high GCA are often used in commercial poultry production, where consistency and predictability are crucial for meeting production goals.

Specific combining ability (SCA), on the other hand, focuses on the unique interaction between two specific parent breeds (Griffing, 1956). Some crosses may exhibit exceptional performance due to the synergistic combination of their genes, even if the individual breeds do not have high GCA (Nath *et al*., 2007; Rajkumar *et al*., 2011; Musa *et al*., 2015). For instance, a cross between Fayoum with White Leghorn and Koekoek exhibited the highest SCA for body weight and body weight gain than either parent breed (Fikrineh *et al*., 2023a). Identifying such high-performing combinations is a key objective of crossbreeding programs, as it allows breeders to capitalize on the benefits of heterosis and breed complementarity (Mancinelli *et al*., 2023).

Combining ability also plays a significant role in addressing challenges related to inbreeding and genetic diversity (Shambel, 2022). By selecting parent breeds with high GCA and identifying crosses with high SCA, breeders can maintain genetic variation while achieving consistent improvements in performance (Fasahat, 2016; Temesgen, 2021). This is particularly important in commercial poultry production, where the focus on a few highly specialized breeds has led to reduced genetic diversity. Crossbreeding strategies that

leverage combining ability can help reintroduce genetic variation and reduce the risks associated with inbreeding depression (Rothschild and Plastow, 2014).

2.2.3. Reciprocal effects in diallel crosses

Reciprocal effects in chicken diallel crosses refer to the differences in offspring performance based on which parent contributes specific genetic or maternal effects (Dubey *et al*., 2020). These effects are crucial in poultry breeding because they influence traits such as growth rate, egg production, and disease resistance. Diallel crossing designs help breeders assess both additive and non-additive genetic variances, including reciprocal cross differences (Franky, 2024). Understanding these effects allows for optimized mating strategies to enhance desirable traits in poultry (Dzungwe *et al*., 2024).

Maternal effects, a key component of reciprocal differences, arise from the hen's influence on egg quality, incubation conditions, and early chick development (Fairfull, 1982). Studies have shown that mitochondrial DNA inheritance, which is exclusively maternal, can also impact metabolic efficiency in chickens (Kong *et al*., 2020). Additionally, epigenetic modifications transferred through the maternal line may further contribute to phenotypic variation in offspring (Ramírez *et al*., 2019; Dunislawska *et al*., 2021).

Reciprocal effects can lead to asymmetrical results in crossbreeding programs, where the same genetic combination yields different outcomes depending on parental direction (Fairfull *et al*., 1983). For example, crossing indigenous Egyptian chickens as the sire line (rather than the dam line) with a commercial Lohmann breed resulted in late sexual maturity (Soliman *et al*., 2020). Accurate estimation of these effects is essential for predicting hybrid performance in commercial poultry (Ni *et al*., 2023).

Statistical models, such as Griffing's or Hayman's diallel analyses, are commonly used to partition reciprocal effects from general combining ability (GCA) and specific combining ability (SCA) (Griffing, 1956). These methods help distinguish between nuclear genetic effects and maternal or cytoplasmic influences. Advanced genomic tools, including SNP markers, have further refined the detection of reciprocal differences in poultry crosses (Cha *et al*., 2023; Sharma *et al*., 2023). Integrating these approaches ensures more precise breeding value estimations (Afrin *et al*., 2024).

2.3. Chicken Breeds and their Suitability for Crossbreeding

2.3.1. Genetic and phenotypic variation among breeds

Chicken breeds exhibit remarkable genetic and phenotypic diversity, reflecting centuries of domestication, selective breeding, and adaptation to various environments and human needs (Lawal and Hanotte, 2021; Wattanadilokcahtkun *et al*., 2023). This diversity is a valuable resource for poultry breeders, as it provides a wide range of traits that can be harnessed to improve productivity, resilience, and sustainability in poultry production systems (Yang *et al*., 2022; Atiyat *et al*., 2023). Understanding the genetic and phenotypic variation among chicken breeds is essential for developing effective breeding programs and conserving genetic resources for future generations (Musa *et al*., 2023; Shambel, 2024).

Genetic diversity refers to the variety of alleles and genetic material present within and among chicken breeds (Ben *et al*., 2018; Malomane *et al*., 2021). This diversity arises from mutations, genetic recombination, and the historical divergence of breeds as they adapted to different regions and purposes (Sheng *et al*., 2024). For example, some breeds, such as the Leghorn, have been selected for high egg production, while others, like the Cornish, are prized for their meat quality (Bell, 2002).

Genetic studies, including genome sequencing and marker analysis, have revealed significant differences in the genetic makeup of chicken breeds, even among those with similar phenotypes (Rubin *et al*., 2010; Lawal *et al*., 2020; Weng *et al*., 2020). This genetic variation is crucial for addressing challenges such as disease resistance, climate adaptation, and improving production traits (Habimana *et al*., 2021; Dou *et al*., 2022; Yang *et al*., 2025).

Phenotypic diversity, on the other hand, refers to the observable differences in physical and physiological traits among chicken breeds (Tixier *et al*., 2008; Wragg *et al*., 2012). These traits include body size, plumage color, comb type, egg size, growth rate, and behavior. For instance, the Silkie breed is known for its unique fluffy plumage and black skin, while the Ayam Cemani is famous for its entirely black appearance, including feathers, skin, and internal organs (Dorshorst *et al*., 2011, 2015). Phenotypic diversity is a direct result of

genetic variation and selective breeding, as humans have historically chosen birds with desirable traits for reproduction (Rubin *et al*., 2010; Zuidhof *et al*., 2014). This diversity not only serves practical purposes but also contributes to the cultural and aesthetic value of chickens (Desta *et al*., 2013).

The conservation of genetic and phenotypic diversity is critical for the long-term sustainability of poultry production (FAO, 2019). Many traditional and indigenous chicken breeds possess unique traits, such as disease resistance, heat tolerance, or adaptability to low-input farming systems, that are increasingly valuable in the face of climate change and emerging diseases (Psifidi *et al*., 2016; Gu *et al*., 2020; Kebede *et al*., 2021). However, the focus on a few highly specialized commercial breeds has led to the erosion of genetic diversity, putting many traditional breeds at risk of extinction (FAO, 2019). Efforts to conserve and utilize these breeds, such as through gene banks or IN SITU conservation programs, are essential for maintaining a broad genetic base for future breeding efforts (Paiva *et al*., 2016).

Advances in genomics have revolutionized the study of genetic and phenotypic diversity in chicken breeds. Tools like whole-genome sequencing, genome-wide association studies (GWAS), and genomic selection allow researchers to identify the genetic basis of specific traits and track the distribution of genetic variation across breeds (Rubin *et al*., 2010; Kranis *et al*., 2013; Lawal *et al*., 2018). This knowledge enables breeders to make more informed decisions about which breeds and traits to incorporate into their programs.

2.3.2. Indigenous versus exotic breeds: complementarity for crossbreeding

Chicken breeds can be broadly categorized into indigenous (local or native) and exotic (foreign or commercial) breeds, each with distinct characteristics, advantages, and challenges. Indigenous breeds have evolved over centuries in specific regions, adapting to local environmental conditions, cultural practices, and resource availability (Manyelo *et al*., 2020). Exotic breeds, on the other hand, are often developed through intensive selective breeding for high productivity and are typically used in commercial poultry farming (Tewodros and Mebrate, 2019). A comparative analysis of these two groups highlights their unique contributions to poultry production and the trade-offs associated with their use.

Indigenous chicken breeds are renowned for their adaptability to local environments and resilience to harsh conditions (Shambel, 2024). These breeds have evolved to thrive in specific climates, resist local diseases, and utilize available feed resources efficiently (Chencha *et al*., 2022). For example, indigenous breeds in tropical regions often exhibit heat tolerance and resistance to parasites, making them well-suited to free-range or backyard farming systems (Kennedy *et al*., 2022; Nawaz *et al*., 2023). In contrast, exotic breeds, while highly productive, may struggle to adapt to extreme climates or low-input systems (Ayalew *et al*., 2023). Their reliance on controlled environments and high-quality feed can limit their suitability for small-scale or resource-constrained farming.

Exotic chicken breeds, such as the Cornish Cross (broilers) and White Leghorn (layers), are bred for high productivity, making them the backbone of commercial poultry production (Tixier *et al*., 2012). Broilers exhibit rapid growth rates and efficient feed conversion, while layers produce a high number of eggs annually (Havenstein *et al*., 2003). Indigenous breeds, however, generally have lower productivity in terms of growth and egg production. For instance, an indigenous hen might lay 60-100 eggs per year, compared to 250-300 eggs from a commercial layer (Zaheer, 2015; Mengesha *et al*., 2022). Despite this, indigenous breeds often produce eggs and meat with desirable sensory qualities, such as taste and texture, which are highly valued in local markets (Senbeta and Zeleke, 2015; Jaturasitha *et al*., 2017).

Indigenous chicken breeds play a vital role in the livelihoods and cultural practices of rural communities (Kondombo *et al*., 2003; Padhi, 2016). They are often raised in free-range or backyard systems, providing a source of income, nutrition, and food security for smallholder farmers (Abdelqader *et al*., 2007). These breeds are also integral to local traditions and ceremonies, contributing to their cultural value. Exotic breeds, while economically significant in commercial farming, are less accessible to small-scale farmers due to their higher input requirements and reliance on specialized infrastructure (Tadelle, 2003). However, their high productivity makes them indispensable for meeting the growing global demand for poultry products (Havenstein *et al*., 2003; Alders and Pym, 2009).

Indigenous breeds are a critical component of global genetic diversity, possessing unique traits that can be leveraged for future breeding programs (Nigussie *et al*., 2010). Their

conservation is essential for maintaining genetic resources that may be needed to address challenges such as climate change, disease outbreaks, or changing consumer preferences (Tixier *et al*., 2011; Zhang *et al*., 2024). Exotic breeds, while valuable for their productivity, contribute less to genetic diversity due to their narrow genetic base (Rubin *et al*., 2010). Efforts to conserve indigenous breeds, such as through community-based programs or gene banks, are crucial for ensuring the sustainability of poultry production systems.

2.4. Crossbreeding Strategies and Diallel Mating Designs

2.4.1. Full diallel cross: applications and advantages

One effective approach for evaluating combining ability is through a diallel cross (Hayman, 1954). Griffing (1956) described four methods of diallel crosses, which vary based on the inclusion of parents and reciprocal crosses. Additionally, diallel crosses can be categorized as either full or half diallel. A full diallel set incorporates reciprocal crosses, whereas a half diallel set includes only one set of F_1s, omitting reciprocals (Griffing, 1956). A full diallel cross is an optimal approach for studying genetic effects because it systematically evaluates all possible parental combinations, enabling comprehensive analysis of combining ability (Franky, 2024).

A key advantage of the full diallel cross is its ability to capture reciprocal maternal effects and dominance interactions, which are often significant in species like poultry. Unlike a half diallel cross, which omits reciprocals, the full diallel provides complete genetic information, making it ideal for studying heterosis and genotype-by-environment interactions (Wearden *et al*., 1965). This method is widely applied in breeding programs to identify superior parental lines, optimize hybrid combinations, and improve traits such as yield, disease resistance, and growth efficiency (Griffing, 1956; Franky, 2024). Additionally, it helps researchers understand the genetic architecture of complex traits, guiding selection strategies in both crops and livestock.

Despite its advantages, the full diallel cross requires a large number of crosses, making it more resource-intensive than partial designs (Griffing, 1956). However, its thoroughness in estimating GCA (overall parental performance) and SCA (specific cross performance) justifies its use in precision breeding. By incorporating reciprocal effects, the full diallel

ensures a more accurate assessment of genetic contributions, particularly in traits influenced by cytoplasmic inheritance (Antony *et al*., 2024). Thus, despite its complexity, the full diallel cross remains a powerful tool for advancing genetic research and breeding efficiency (Dubey *et al*., 2020).

2.4.2. Selection of parental stocks for meat and egg traits

The poultry industry relies heavily on the careful selection of parental stocks to enhance meat and egg production (Havenstein *et al*., 2003; Sonesson *et al*., 2012). The success of a crossbreeding program in chickens hinges on the careful selection of parental breeds (Leroy *et al*., 2016). Choosing the right breeds to cross is critical for achieving the desired improvements in traits such as growth rate, egg production, disease resistance, and adaptability (Saxena and Kolluri, 2018).

Choosing the right parental stocks is crucial for maintaining and improving the genetic potential of poultry flocks (Bedere *et al*., 2022; Barani *et al*., 2024). Birds selected for meat traits should exhibit fast growth rates, efficient feed conversion, and high muscle yield, while those chosen for egg production must demonstrate high laying capacity, strong eggshell quality, and longevity (Jiang and Groen, 1999). By selecting superior parents, breeders can enhance profitability and meet the increasing demand for poultry products.

Advances in genetics have revolutionized poultry breeding by enabling precise selection of desirable traits (Saxena and Kolluri, 2018; Fikrineh *et al*., 2021). Techniques such as marker-assisted selection (MAS) and genomic selection allow breeders to identify superior genes early in the breeding process (Dekkers, 2012; Heidaritabar *et al*., 2014). Despite technological advancements, challenges remain in selecting ideal parental stocks. Balancing multiple traits (e.g., growth rate vs. reproductive health) can be difficult, as some characteristics may be negatively correlated but growth and reproduction have positive covariance at earlier age. Because puberty needs 2/3rd of mature body weight of the species. Negative covariance comes when the body begins depositing fat to undesirable level (Aggrey *et al*., 2010; Wolc *et al*., 2016). Additionally, maintaining genetic diversity is essential to prevent inbreeding depression, which can reduce fertility and overall fitness (Muir *et al*., 2008; FAO, 2019).

2.5. Impact of Crossbreeding on Production Traits

2.5.1. Body weight and growth performance

Crossbreeding in chickens has been widely adopted in the poultry industry as a strategy to improve growth performance and body weight, which are critical traits for both meat (broiler) and dual-purpose poultry production (Siwendu *et al*., 2013). By combining the genetic potential of different breeds, crossbreeding exploits heterosis, or hybrid vigor, resulting in offspring that often outperform their purebred parents in terms of growth rate, feed efficiency, and overall body weight (Mokoena *et al*., 2024). This phenomenon is particularly valuable in broiler production, where rapid growth and high meat yield are economically essential (Zuidhof *et al*., 2014).

One of the most significant effects of crossbreeding is the enhancement of growth rate and body weight in chickens (Tahawy and Habashy, 2021). For example, crossing a fast-growing broiler line with a robust, disease-resistant layer line can produce hybrids that not only grow quickly but also maintain better health and survivability. Studies have shown that crossbred chickens often achieve higher body weights at market age compared to their purebred counterparts, making them more profitable for producers (Iraqi *et al*., 2013; Wang *et al*., 2022). This improvement is largely attributed to heterosis, which maximizes the expression of favorable genes while minimizing the impact of deleterious ones (Khalil *et al*., 2018). Additionally, crossbreeding can lead to better feed conversion ratios (FCR), meaning that crossbred chickens require less feed to achieve the same weight gain, further enhancing their economic value (Dawud *et al*., 2019).

Despite the clear advantages, the effects of crossbreeding on growth performance and body weight can vary depending on environmental factors and management practices (Ssewannyana *et al*., 2008; Besbes, 2009; Nigussie *et al*., 2010; Wolc *et al*., 2012). For example, nutrition, housing conditions, and disease pressure can all influence the expression of genetic potential in crossbred chickens. Optimal management practices are essential to ensure that the benefits of crossbreeding are fully realized. Additionally, while crossbreeding can improve growth and body weight, it may not always address other important traits, such as egg production or meat quality, unless these are specifically

targeted in the breeding program (FAO, 2007, 2008; Dekkers, 2012). This highlights the importance of a balanced approach that considers multiple traits and their interactions.

Another consideration is the potential trade-offs associated with crossbreeding (Wolc *et al*., 2016). While crossbred chickens often exhibit superior growth performance, maintaining the purebred lines required for crossbreeding can be resource-intensive (Hillel *et al*., 2003). Furthermore, the genetic diversity of parental lines must be carefully managed to avoid inbreeding depression, which can negate the benefits of heterosis. Long-term sustainability of crossbreeding programs depends on continuous genetic improvement and the preservation of genetic variation within breeding populations (Tixier *et al*., 2011; FAO, 2015).

2.5.2. Meat yield and carcass characteristics

One of the most significant effects of crossbreeding is the improvement in meat yield (Neeteson *et al*., 2023). Crossbred broilers often exhibit faster growth rates and higher body weights at market age compared to their purebred counterparts (Mancinelli *et al*., 2023; Dzungwe *et al*., 2024). This is particularly important in commercial poultry production, where maximizing meat output per bird is essential for profitability (Sungkhapreecha *et al*., 2022). For example, crossing a fast-growing broiler line with a breed known for its muscular development can result in hybrids that achieve higher breast meat yields, a highly valued trait in the poultry industry (Barbut *et al*., 2024). Heterosis plays a key role in these improvements, as it enhances the expression of favorable genes while minimizing the impact of less desirable ones. Additionally, crossbred broilers may exhibit better feed conversion ratios (FCR), meaning they require less feed to achieve the same weight gain, further enhancing their economic value (Jie *et al*., 2024).

Carcass characteristics, such as meat-to-bone ratio, breast muscle development, and fat deposition, are also significantly influenced by crossbreeding (Chi *et al*., 2023; Huang *et al*., 2023). Breeders often select parental lines with complementary traits to optimize these characteristics. For instance, a broiler line with excellent breast muscle development might be crossed with a line that has low fat deposition, resulting in hybrids with leaner, more desirable carcasses (Abdullah *et al*., 2010). Advances in genetic technologies, such as genomic selection and marker-assisted breeding, have further refined this process by

enabling breeders to identify and select for specific genes associated with superior carcass traits (Fikrineh *et al*., 2021; Tan *et al*., 2022). These tools have accelerated genetic progress, allowing for the development of crossbred broilers that meet the stringent demands of consumers and processors.

In conclusion, crossbreeding has a profound impact on meat yield and carcass characteristics in chickens, making it a cornerstone of modern broiler production (Dzungwe *et al*., 2024). By leveraging heterosis and selecting complementary parental lines, breeders can develop hybrids that grow faster, achieve higher meat yields, and produce more desirable carcasses than purebred broilers (Sharifuzzaman *et al*., 2023). However, the success of crossbreeding programs depends on careful planning, optimal management practices, and ongoing genetic improvement. As the poultry industry continues to evolve, crossbreeding will remain a key strategy for meeting the growing global demand for high-quality poultry meat while addressing challenges related to sustainability, animal welfare, and food security (Shambel, 2022).

2.5.3. Egg production and egg quality

Crossbreeding in chickens has been widely utilized to enhance egg production and quality, making it a key strategy in the poultry industry, particularly for layer breeds and dual-purpose poultry systems (Dzungwe *et al*., 2024; Mokoena *et al*., 2024). One of the most significant effects of crossbreeding is the increase in egg production (Tahawy and Habashy, 2021; Atsbaha *et al*., 2023). Crossbred layers often exhibit higher egg-laying rates compared to their purebred counterparts, which is a critical factor for commercial egg production. For example, crossing a high-yielding layer breed with a breed known for its robustness and disease resistance can result in hybrids that not only lay more eggs but also maintain better health and longevity (Shambel, *et al*., 2022). This improvement in productivity is primarily attributed to heterosis, which enhances the expression of favorable genes while mitigating the impact of less desirable ones.

Egg quality is another important aspect influenced by crossbreeding (Dzungwe *et al*., 2024). Traits such as shell thickness, yolk color, albumen height, and overall egg size can be significantly improved through strategic crossbreeding (Jones *et al*., 2010; Sreenivas *et al*., 2013). For instance, crossing a breed known for strong eggshells with one that produces

eggs with vibrant yolk color can result in hybrids that lay eggs with both durable shells and appealing visual qualities (Yaman *et al*., 2020). These attributes are highly valued by consumers and can command premium prices in the market. Furthermore, crossbreeding can enhance the nutritional quality of eggs, such as increasing the levels of omega-3 fatty acids or other beneficial nutrients, by selecting parental lines with these specific traits (Sabrout *et al*., 2022).

2.5.4. Feed efficiency and nutrient utilization

Crossbreeding has become a vital tool in poultry production, particularly for improving feed efficiency and nutrient utilization, which are critical factors for the economic and environmental sustainability of the industry (Havenstein *et al*., 2003). Crossbred chickens often exhibit better feed conversion ratios (FCR), meaning they require less feed to achieve the same level of growth or egg production compared to purebred lines (Dawud *et al*., 2019). This is particularly important in broiler production, where feed costs account for a substantial portion of total production expenses. For example, crossing a fast-growing broiler line with a breed known for its efficient nutrient utilization can produce hybrids that grow rapidly while consuming less feed (Jie *et al*., 2024). Similarly, in layer systems, crossbreeding can result in hens that produce more eggs with the same or less feed input (Dawud *et al*., 2019).

Nutrient utilization is another critical area influenced by crossbreeding. Crossbred chickens often demonstrate enhanced ability to digest and absorb essential nutrients, such as proteins, fats, and carbohydrates, from their feed (Baldinger and Bussemas, 2021). This can lead to better growth rates, higher egg production, and improved overall health. For instance, crossbreeding programs that combine a breed with high digestive efficiency and another with strong immune function can produce hybrids that not only utilize nutrients more effectively but also maintain better health under challenging conditions (Mancinelli *et al*., 2023).

Advances in genetic technologies, such as genomic selection and marker-assisted breeding, have further refined this process by enabling breeders to identify and select for specific genes associated with improved nutrient utilization (Yuan *et al*., 2015; Neeteson

et al., 2023). These tools have accelerated genetic progress, allowing for the development of crossbred chickens with superior metabolic efficiency (Ye *et al*., 2025).

In conclusion, crossbreeding has a profound impact on feed efficiency and nutrient utilization in chickens, making it a cornerstone of modern poultry production. By leveraging heterosis and selecting complementary parental lines, breeders can develop hybrids that convert feed more efficiently and utilize nutrients more effectively than purebred chickens. However, the success of crossbreeding programs depends on careful planning, optimal management practices, and ongoing genetic improvement (Leroy *et al*., 2016; Vanvanhossou *et al*., 2025).

3. MATERIALS AND METHODS

3.1. Framework of the Study

The present study consists of four separate studies. The first study focused on estimating the heterosis effects, maternal effect, combining abilities, and reciprocal effects on growth and feed utilization performance, meat and carcass characteristics, fertility and hatchability, egg production performance and egg quality traits in four genetic groups using a full diallel mating design. The second study focused on the comparative growth performance, meat, and carcass characteristics of the four chicken breeds using a full diallel cross. The third study evaluated the comparative fertility, and hatchability performance of four genetic groups of chicken from a full diallel cross. The final and fourth study investigated the egg production performance and egg quality traits of the four genotypes crossed in full diallel mating.

3.2. Descriptions of the Study Area

This study was conducted at the poultry farm of Werer Agricultural Research Center (WARC), in Amibara *woreda* of the Afar Regional State of Ethiopia, from February 2023 to August 2024. The Center is located 280 km from the capital Addis Ababa, at an altitude of 750 meters above sea level and at 9º 55' N latitude and 40º, 40' E longitude (Jemal *et al*., 2019). The study area is found in the Middle Awash Valley, where sugarcane and cotton are major crops grown. From the total land area of the region, Amibara *woreda* covers 294, 106 ha (Figure 1). Typically, the mean annual rainfall is less than 590 mm, with May and June being the driest months. The highest rain season accounts for 60% of the yearly total rainfall from July to September whereas slight rainy season appears in March and April which accounts for 20% of the total rainfall. It is characterized by high temperatures ranging from 19.3 ºC to 45 ºC (Metrological data from WARC station). Woods and bush vegetation type are found along the major perennial rivers. The area is evergreen due to continuous water supply from Awash River and browsed by the livestock during the dry season.

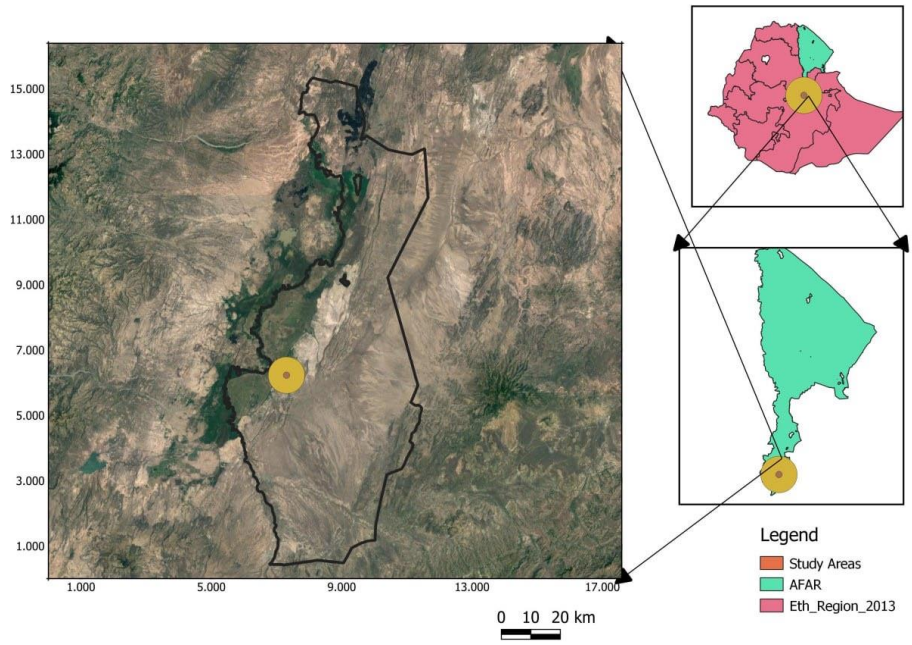

Figure 1. Map of the Study Area

3.3. Descriptions of Experimental Birds

The chicken breeds included in this study were, Improved Horro (H), Dz White feathered (D), Potchefstroom Koekoek (K), and Sasso (S). All chicken breeds used in the present study were previously introduced in the study area for adaptation and crossbreeding works by WARC and the Regional Research Institute starting from 2016 G.C.

Improved Horro chicken breed: Horro chicken ecotype is named after the particular area from Ethiopia called 'Horro'. There were 30,000 chickens restricted to this original environment (Nigussie *et al*., 2010). Now adays, the chicken breed has been distributed to a wider area in Ethiopia in particular through research institutions and Universities. These birds were reported for the potential of 171 eggs per year during their 7th generation on the selection program at Bishoftu Agricultural Research Center (BARC) (Wondmeneh, 2015). The Horro chicken breed used in the present study was their 16th generation from the National Poultry Research Program at BARC.

DZ White-feathered chicken breed: DZ White is a white colored composite chicken breed produced at the BARC through selective cross breeding. This breed of chicken was produced with a combination of Lohmann Silver, Potchefstroom Koekoek, and local white

colored chicken ecotype of Ethiopia (Samrawit *et al*., 2020). The synthetic Dz white-feathered chicken used in this particular study was their 13th generation at BARC. At the end of the production period, the breed attains relatively high body weights of 2.48 kg for males and 1.44 kg for females (Habtamu *et al.,* 2023).

Potchefstroom Koekoek chicken breed: The Koekoek chicken breed is a composite of the White Leghorn, Black Australorp and Bared Plymouth Rock bred at the Potchefstroom Agricultural College, in south Africa during the 1950s (Grobbelaar *et al*., 2010). The Koekoek's colour pattern is a sex-linked gene that is very useful for colour sexing in crossbreeding for egg producing types of hens used in medium input production systems. The breed is popular among rural farmers in South Africa and neighboring countries for egg and meat production as well as their ability to hatch their own offspring (Grobbelaar *et al*., 2010). Potchefstroom Koekoek breed was used in Ethiopia for more than 10 years. This breed was selected based on good performance as seen in BARC poultry farm, with 200 eggs per hen per year, relatively high body weight of male (2.65 kg) and female (1.87 kg) at the end of production (Wondmeneh *et al*., 2011).

Sasso chicken breed: Sasso is a dual-purpose, hardy chicken breed which thrives among rural smallholder farmers. Besides performing as a dual protein source, this bird is easy to manage and meant to thrive especially in free-range rearing conditions. The Sasso chicken breed was developed through intensive selection of traditional colored chicken lines from France (Guni *et al*., 2021). This bird was distributed in Ethiopia by Ethio-chicken private farm (Aman *et al*., 2017). According to the same author, the male Sasso weight (2.73 kg) at sexual maturity. In Ethiopia, under village production system the breed produces up to 229 eggs per year (Aman *et al*., 2017).

3.4. Breeding Plan and Birds Management

For this study, a 4×4 full diallel cross involving Improved Horro, Sasso, Potchefstroom Koekoek, and DZ white feathered chickens were used. The mating was random, and the pullet to cockerel ratio maintained at 5:1 for all breed groups. For Horro dams, due to their small size, artificial insemination was used by collecting semen from sires of S, K, and D chicken breeds. Fertile eggs were collected, cleaned, and recorded daily according to

breeds and crossbreds. After seven days collection the eggs were weighed and set for incubation separately according to their different breeds category. Accordingly, from the diallel cross, four purebreds (H, S, K, D), six crossbreds (H×S, H×K, H×D, S×K, S×D, K×D), and six reciprocal crossbreds (S×H, K×H, D×K, K×S, D×S, D×K) progenies were obtained. A total of 960 experimental chickens (160 male and 800 female) were obtained. The number of the different genotypes used for this study are detailed in Table 1. Chickens of four purebreds and twelve crossbred genotypes were randomly distributed in to 48 pens (16 genotypes with three replications) in a completely randomized design (CRD).

Table 1. The diallel crossing system used, the purebred and F_1 crossbreed produced

Sire Line	Chicken Breeds			
	Dam line			
	H♀	S♀	K♀	D♀
H♂	$p^{H\times H}$ (N=48)	$d^{H\times S}$ (N=61)	$d^{H\times K}$ (N=72)	$d^{H\times D}$ (N=54)
S♂	$r^{S\times H}$ (N=54)	$p^{S\times S}$ (N=72)	$d^{S\times K}$ (N=66)	$d^{S\times D}$ (N=54)
K♂	$r^{K\times H}$ (N=72)	$r^{K\times S}$ (N=54)	$p^{K\times K}$ (N=59)	$d^{K\times D}$ (N=54)
D♂	$r^{D\times H}$ (N=60)	$r^{D\times S}$ (N=54)	$r^{D\times K}$ (N=54)	$p^{D\times D}$ (N=72)

♂ Sire, ♀ Dam; H: Improved Horro, S: Sasso, K: Potchefstroom Koekoek, D: DZ White; p: Purebreds, d: Direct crosses, r: Reciprocal crosses.

For the experimental chicks, a wire mesh partitioned (size of 2*1.5 m^2) deep litter floor house was used. The pens were arranged in a ratio of 20 pullets and 4 cockerels. Before starting the experiment, the pens, watering and feeding troughs, and laying nests were disinfected (with 10% formalin) and sprayed against external parasites (with 12.5% amitraz). All experimental chickens were vaccinated against Newcastle disease (HB1 and Lasota), Gumboro (Infectious Bursal disease), fowl typhoid, and fowl pox based on producer's manual. Starting from hatch chickens were provided with a starter ration (20% CP and 3000 kcal/kg of ME) until the 8^{th} wk, followed by grower ration (18% CP and 2950 kcal/kg of ME) from 9 to 20 wk of age, and then the ration was changed into layer (16% CP and 2800 kcal/kg of ME) from 21 to 40 wk. Feed was purchased from Alema Feeds Co., Ltd., Bishoftu, Ethiopia, and clean water was always available in a drinker. During the growing stage (from hatch upto wk 8) fluorescent lamps were placed to provide lighting for the chickens. For the first five days, 16-18 hours of light was provided, afterwards 12 hours of light up to the 8^{th} wk.

3.5. Studied Traits and Data Measurements

3.5.1. Body weight gain and feed efficiency traits

Body weight (BW) of 960 experimental chicks from a full-diallel cross of four breeds was measured in a group per pen using a sensitive balance (Brand Name: Bioevopeak; Model: BEPXYDZ220824032; Capacity: 5000 grams). Body weight was recorded at the end of each two wk period from hatch up to the 20th wk of age. Average BW per pen was calculated for weights at hatch, 2nd, 4th, 6th, 8th, 10th, 12th, and 14th wk. Feed conversion ratio (FCR) was calculated as the ratio of feed consumed (average feed intake; FI) by each genetic group for every four weeks to body weight gain of the birds recorded over the same period.

3.5.2. Meat and carcass traits

The study evaluated key meat quality traits, including carcass component yield, pH (initial and ultimate), color coordinates (Lightness, L*; redness, a*; yellowness, b*), water holding capacity (WHC), and tenderness.

Carcass component yield analysis

At 24 weeks of age, a total of 288 chickens (144 males and 144 females) were used for the analysis, with 18 birds per genotype (nine males and nine females). Following ethical approval by the Institutional Animal Care and Use Committee (IACUC), the chickens were fasted for 12 hours with free access to water before slaughter.

The slaughter process was conducted at Bishoftu Agricultural Research Center. It began with stunning and exsanguination, followed by scalding at 53 °C to facilitate feather removal. The defeathered carcasses were then eviscerated and manually dissected into breast, back, drumstick, thigh, wings, and giblets (heart, liver, and gizzard). Each component was weighed using a precision scale, with measurements recorded in grams (g) and as a percentage of live weight. The processed carcasses were thoroughly rinsed, sealed in airtight plastic bags, and chilled at 4°C for 24 hours to standardize post-mortem conditions. Finally, carcass yield percentages were calculated relative to the live weight at slaughter, following established methodologies (Santos *et al*., 2005; Cömert *et al*., 2016).

pH measurement

The pH values were assessed at two critical time points: initial pH (measured 45 minutes post-slaughter) and ultimate pH (measured 24 hours post-slaughter). For each experimental group, breast muscle samples from six randomly selected chickens were analyzed in triplicate following a standardized protocol. The samples were homogenized before measurement to ensure consistency. A high-precision digital pH meter, equipped with a sensitive electrode, was used for all measurements. To guarantee accuracy, the instrument was carefully calibrated before each use with standard buffer solutions at pH 4.0 and 7.0 (Choo *et al*., 2014).

Water-holding capacity analysis

The water-holding capacity (WHC) of chicken breast meat was assessed following the method described by Jang *et al*. (2011), Approximately 0.5 g of meat was placed on a round plastic plate within a Millipore Ultrafree-MC tube (Millipore, Bedford, MA). The sample was then heated in a water bath at 80°C for 20 minutes, cooled to 23 ± 1°C, and centrifuged at 2,000 × g for 10 minutes at 4°C. Water loss was calculated, and WHC was expressed using the following formula:

WHC (%) = [(Moisture content – Water loss) / Moisture content] × 100

Water loss (%) = [(Weight before centrifugation – Weight after centrifugation) / (Sample weight × Fat factor)] × 100

Fat factor = 1 – (Crude fat / 100)

Color determination

The surface color of breast meat samples was quantified using a Konica Minolta Chroma Meter CR-400 (Konica Minolta Sensing, Inc., Japan) calibrated with a white standard tile. Samples were equilibrated to room temperature (20°C) and placed on a clean, uniform surface under standardized D65 illuminant (daylight) conditions. The chroma meter's 8-mm aperture was positioned perpendicular to the sample surface, ensuring no shadow interference. Three random readings per sample were taken for lightness (L*), redness (a*),

and yellowness (b*) values, and the average was recorded. Between measurements, the instrument was recalibrated to minimize drift.

Proximate composition analysis

Proximate analysis of raw breast meat samples was conducted on six independent samples per genotype to determine crude protein, fat, and ash content. Samples were stored at −20°C until analysis at the Food Science Laboratory, Addis Ababa Science and Technology University (AASTU). Crude protein was measured using the Kjeldahl method (AOAC 984.13) with a nitrogen-to-protein conversion factor of 6.25. Total fat content was determined by Soxhlet extraction (AOAC 960.39) using petroleum ether as the solvent. Ash content was quantified by incineration in a muffle furnace at 550°C for 6 hours (AOAC 942.05) until constant weight was achieved. All procedures adhered to the AOAC International guidelines (Lee, 1995).

Shear force measurement (Tenderness)

To evaluate meat tenderness, chicken breast samples were sealed in polyethylene bags and heated in a water bath at 75°C for 45 minutes. After heating, the samples were cut into uniform blocks (1 × 2 × 2 cm), and shear force was measured using a TA1 texture analyzer (Lloyd Instruments, Berwyn, IL) equipped with a V-shaped blade. The device was set to a 500 N load cell with a crosshead speed of 50 mm/min. The maximum shear force (N) required to cut through the sample was recorded as an indicator of tenderness, with lower values corresponding to more tender meat. Six samples from each genotype were analyzed. Data acquisition and analysis were performed using NEXYGENPlus software (Lloyd Instruments), ensuring standardized force-displacement curve interpretation.

3.5.3. Fertility and hatchability measurements

Fertility and hatchability parameters were systematically evaluated throughout the incubation process. Before incubation, eggs were stored under optimal conditions in a climate-controlled room maintained at 12°C with 75% relative humidity. The eggs were then transferred to Pass Reform incubators, where they underwent a two-phase incubation protocol. During the initial 18-day setter phase, eggs were maintained at 37.5°C with 55% relative humidity, while being automatically turned 45° every hour to ensure proper

embryonic development. The final three days (days 19-21) constituted the hatcher phase, where temperature was reduced to 36.9°C and humidity increased to 65% to facilitate hatching.

Egg viability was assessed on day 18 through candling using a specialized mass candler in a darkened room. This process allowed for clear differentiation between fertile eggs, which appeared opaque with visible vascular networks indicating viable embryos, and infertile eggs that remained translucent. Following candling, all infertile eggs were removed from the incubation process, while viable eggs were transferred to the hatcher compartment according to their respective genotypes. Three key metrics were calculated to quantify reproductive performance: fertility percentage (based on candling results), hatchability of total eggs set (measuring overall efficiency), and hatchability of fertile eggs (assessing incubation effectiveness). Data on Fertility and Hatchability was computed as:

$$\text{Fertility (\%)} = \frac{\text{Number of set eggs} - \text{Number of infertile eggs at candling}}{\text{Number of set eggs}} \times 100$$

$$\text{Hatchability of Total Eggs Set (\%)} = \frac{\text{Number of day old chicks}}{\text{Number of set eggs}} \times 100$$

$$\text{Hatchability of Fertile Eggs Set (\%)} = \frac{\text{Number of day old chicks}}{\text{Number of set eggs} - \text{Number of infertile eggs}} \times 100$$

3.5.4. Egg production traits

The four purebred and twelve F_1 crossbred chickens obtained from the diallel crosses were evaluated for age at first egg (AFE), body weight at sexual maturity (BWSM), egg weight at first egg (EWAFE), total egg numbers (EN), hen-housed egg production (HHEP), hen-day egg production (HDEP), and egg mass (EM).

Data for AFE, BWSM, EN, EWAFE, and EM were collected from 672 hens. AFE was calculated from the hatching date of the hen to the production of the first egg laid (at least 5% of birds) by the flocks. BWSM was measured as the weight of hens in the group at AFE. In order to determine EN, eggs laid were collected twice a day (morning and afternoon) from start of lay upto 40 WK of age and the number of eggs were recorded. The average weight of the first ten eggs laid consecutively in each pen was recorded to

determine EWAFE. HHEP was calculated as the total number of eggs produced by the hens, divided by the number of hens initially housed and the number of days the birds were in lay, while HDEP was calculated as the total number of eggs produced by the hens, divided by the number of hens alive at the time of egg collection (Hunton, 1995). EM was determined as the product of EN per hen and average egg weight.

3.5.5. Egg quality traits

A total of 480 eggs (30 from each genetic group) were randomly chosen at the pick production period (at 32 WK). Sampled eggs were evaluated for egg weight (EWT), egg length (EL), egg width (EW), shell weight (SWT), shell thickness (ST), shell ratio (SR), albumen height (AH), albumen width (AW), yolk height (YH), yolk width (YW), yolk weight (YWT), yolk ratio (YR), and hugh unit (HU).

Eggs were weighed using a sensitive balance then length and width of each egg were measured using a compass. Then, the eggs were broken within 24 hours on a table glass cover and YH and AH were measured using a spherometer. YW and AW were measured using a compass. Then yolk of each egg was separated from the albumen, then weighed in grams and expressed as a percentage relative to the EWT. The ST were measured at 3 different points of the eggshell and the calculated average of the three points were used. The shell and member were weighed together in grams for each egg and expressed as a percentage relative to the egg weight. Haugh unit was calculated according to the equation of (Haugh, 1937): $HU = 100 \log (AH - 1.7EW^{0.37} + 7.6)$, where; H = observed height of the albumen (mm) and W = weight of the eggs in grams.

3.6. Methods of Data Analysis

3.6.1. Relative performance of the genotypes

Date were analyzed for variation between the genotypes using the general linear model procedure of R (Version 4.4.2) (R Core Team, 2023). Differences considered to be significant ($P < 0.05$) were compared by Duncan's Multiple Range Test (Duncan, 1955). The statistical model used was:

$$Y_{ij} = \mu + g_i + e_{ij} \qquad \text{Model (1)}$$

Where, Y_{ij} is the performance of bird of the j^{th} observation on the i^{th} genetic group, μ is the overall mean, g_i is the effect of the i^{th} genetic group, and e_{ij} is the random error.

3.6.2. Estimation of crossbreeding effects

Diallel analysis was carried out only when the differences among the genotypes were significant, fixed model of (Griffing, 1956) Model 1, Method 1, a commonly used approach for assessing the genetic potential of breeding lines, especially in diallel crossing experiments was used. The mathematical model for the combining ability analysis used was:

$$Y_{ij} = \mu + G_i + G_j + S_{ij} + r_{ij} + e_{ij} \qquad \text{Model (2)}$$

Where, Y_{ij} is the observed performance of the i^{th} genotype crossed with the j^{th} genotype, μ is the overall mean of the population, G_i and G_j are the general combining abilities of the i^{th} and j^{th} genotypes (represents the additive genetic effect of genotype i and j), S_{ij} is the specific combining ability for the i^{th} and j^{th} cross (represents the non-additive genetic interaction between i and j genotypes), r_{ij} is the reciprocal effect involving the reciprocal crosses between the i^{th} and j^{th} parents, and e_{ij} is random error term, which accounts for any variation not explained by the fixed effects.

Heterosis was calculated on the percentage of mid-parents (Williams *et al*., 2002) by the application of the following formula: H% = {F1 – [(P1 + P2)/2)] / [(P1 + P2) /2] * 100}.

Where F1 represents the mean performance of crossbred progeny, and P1 and P2 are parents in diallel and reciprocal crosses.

Maternal effects were estimated using a set of linear contrasts of the genetic group means (Dickerson, 1969) as follows: ½ [(A×B) - (B× A)].

4. RESULTS

4.1. Growth Performance and Feed Efficiency

Breed effect on body weight

The growth performance of the genotypes was evaluated based on BW measurements taken from hatch, 2nd, 4th, 6th, 8th, 10th, 12th, and 14th WK of age (Table 2). According to the results of this study, the purebred S (1567.47 g) weighed the heaviest at WK 14, followed by K (1435.47 g) and D (1398.13 g). However, crossbred chickens, particularly S×K, significantly outperformed all purebreds, reaching 1646.47 g at WK 14. The S×D and K×S crosses also surpassed purebred S, demonstrating the clear advantage of crossbreeding for growth performance. Among purebreds, H was consistently the lightest at all ages (1160.40 g at WK 14), but even the poorest-performing crossbred (H×K: 1300.47 g) exceeded H in weight.

Among twelve crossbred groups, the S×K crossbred not only dominated from hatch to WK 14 but also maintained superiority over its reciprocal cross K×S, though K×S initially led at WK 2 (125.72 g), WK 4 (349.15 g) and WK 6 (569.78 g) before being overtaken by S×D from WK 8 onward. Notably, the cross H×S and its reciprocal S×H showed the 5th (1478.60 g) and 6th (1447.53 g) highest BW among the crossbreds at the 14th WK of age. However, H×S cross recorded similar BW with S×H from hatch up to WK 14. The crossbred H×K, except at WK 6, weighed the lowest for the entire period of the study.

Breed effect on feed intake and feed conversion ratio

Table 3 presents the average daily feed intake (ADFI) and feed conversion ratio (FCR) across different age intervals for the various genotype groups. Across the experimental period, both feed intake and feed conversion ratio exhibited considerable variation among the different genotypes. In terms of ADFI, genotype S consistently demonstrated higher consumption across all ages, with values rising from 20.92 g/bird/day in WK 0–4 to 73.33 g/bird/day by WK 13–16. Similarly high intakes were observed in genotype K, ranging from 19.98 to 72.61 g, and genotype D, which ranged from 20.18 to 71.49 g. In contrast, genotype H had the lowest feed intake throughout, increasing from only 17.79 g in WK 0–4 to 65.60 g by WK 13–16.

When looking at the crossbreds, the highest ADFI values in the final growth stage (WK 13–16) were observed in combinations such as H×S (74.74 g), H×D (74.02 g), S×K (74.70 g), S×D (74.67 g), K×D (74.54 g), S×H (74.52 g), K×H (74.47 g), and K×S (74.75 g), all showing a marked improvement over the pure H genotype. These crossbreds also started with relatively high ADFI in the early weeks, notably S×K and K×S with the highest initial intake at 21.23 g and 21.24 g, respectively.

Feed conversion ratio (FCR) further distinguished the genotypes in terms of efficiency. Genotype H had the highest and least efficient FCR values, especially in WK 0–4 (4.23) and WK 13–16 (5.70). In contrast, genotype S showed excellent efficiency with FCR values as low as 2.52 in WK 0–4 and 4.12 in WK 13–16. The crossbreds reflected this trend, with S×K and K×S exhibiting outstanding efficiency. K×S had the lowest FCRs among all genotypes, starting at just 2.10 in WK 0–4, dipping to 1.75 in WK 5–8, and maintaining strong performance with only 2.31 in WK 9–12 and 3.73 in the final phase. S×H also performed well, especially early on, with FCRs ranging from 2.25 to 4.45 across the periods. Other notable crossbreds included S×D and H×K, which maintained moderate to low FCRs throughout. However, crosses involving genotype H such as H×D and D×H displayed variable efficiency, with elevated FCR values in the final stage (4.96 and 4.54, respectively), though still better than pure H. Some crossbreds like D×K showed relatively high FCR values (e.g., 3.53 in WK 0–4 and 4.60 in WK 13–16), suggesting that not all crosses guaranteed improved efficiency.

Table 2. Least square means (SE) for body weight (grams) as affected by chicken genotype at different growth stages

Genotype	Age (weeks)							
	Hatch	WK 2	WK 4	WK 6	WK 8	WK 10	WK 12	WK 14
Pure								
H	27.37±0.52^{h}	91.51±0.74^{g}	225.88±8.38^{h}	404.60±29.50^{h}	606.80±14.10^{h}	722.00±40.40^{h}	932.93±47.50^{h}	1,160.40±52.00^{f}
S	32.49±0.44^{b}	132.68±0.87^{a}	345.84±12.40^{ab}	557.01±10.40^{ab}	790.38±4.65^{abc}	1,018.27±23.20^{ab}	1,261.87±2.07^{abc}	1,567.47±21.10^{ab}
K	30.23±0.52^{def}	109.45±1.72^{d}	293.45±12.30^{de}	498.63±9.14^{cde}	696.93±19.80^{ef}	895.87±18.90^{cdef}	1,207.07±2.10^{bcd}	1,435.47±15.30^{cd}
D	30.73±0.49^{de}	100.70±0.79^{ef}	250.54±20.40^{fgh}	430.39±3.72^{gh}	633.01±51.40^{gh}	845.58±38.00^{efg}	1,079.07±91.80^{efg}	1,398.13±80.90^{cde}
Cross								
H×S	31.26±0.17^{cd}	117.85±2.29^{c}	308.85±1.95^{cd}	511.90±6.92^{c}	740.80±2.77^{cde}	932.80±1.62^{c}	1,188.20±1.73^{bcd}	1,478.60±4.04^{bc}
H×K	29.06±0.29^{g}	100.83±1.27^{ef}	265.18±15.40^{fg}	468.57±4.31^{ef}	655.01±9.71^{fgh}	825.70±0.98^{g}	1,074.80±14.70^{efg}	1,300.47±13.10^{e}
H×D	29.69±0.18^{efg}	102.45±1.36^{ef}	256.51±6.29^{fg}	449.44±12.10^{fg}	675.17±9.69^{fg}	861.67±30.50^{defg}	1,091.27±44.80^{efg}	1,351.87±76.6^{de}
S×K	33.99±0.30^{a}	134.53±1.10^{a}	367.13±5.35^{a}	586.32±1.74^{a}	820.76±10.50^{a}	1,069.93±10.70^{a}	1,309.53±2.60^{a}	1,646.47±17.50^{a}
S×D	32.37±0.17^{b}	120.94±1.20^{bc}	345.70±3.80^{ab}	532.46±5.06^{bc}	795.98±2.13^{ab}	1,037.03±0.80^{ab}	1,284.80±2.19^{ab}	1,612.67±2.23^{a}
K×D	28.81±0.36^{g}	97.28±0.45^{f}	248.73±3.84^{gh}	425.37±5.68^{gh}	622.67±11.00^{gh}	828.00±9.70^{g}	1,067.20±20.80^{fg}	1,380.67±36.40^{cde}
RE								
S×H	31.07±0.42^{cd}	116.64±1.32^{c}	304.82±5.51^{cd}	509.92±14.50^{cd}	730.00±9.41^{de}	920.27±10.70^{cd}	1,167.67±11.10^{cde}	1,447.53±11.00^{cd}
K×H	28.99±0.46^{g}	102.80±2.40^{e}	268.27±1.15^{efg}	452.22±10.80^{fg}	665.73±11.00^{fg}	838.23±9.85^{fg}	1,090.73±3.45^{efg}	1,303.29±0.64^{e}
D×H	29.54±0.28^{fg}	100.71±1.17^{ef}	251.86±8.53^{fgh}	430.75±7.31^{gh}	642.50±6.44^{gh}	820.07±5.22^{g}	1,055.13±21.50^{g}	1,354.60±10.30^{de}
K×S	32.37±0.35^{b}	125.72±1.26^{b}	349.15±6.09^{ab}	569.78±4.67^{a}	783.13±6.45^{abc}	1,020.13±2.40^{ab}	1,278.13±10.30^{ab}	1,589.33±3.37^{a}
D×S	32.04±0.38^{bc}	119.84±3.42^{c}	325.96±4.91^{bc}	531.88±10.30^{bc}	766.53±3.24^{bcd}	997.87±9.78^{b}	1,239.07±4.74^{abcd}	1,558.07±21.20^{ab}
D×K	30.82±0.05^{d}	109.27±2.15^{d}	277.91±2.72^{ef}	475.85±9.56^{def}	669.33±9.70^{fg}	900.27±3.34^{cde}	1,155.73±7.56^{def}	1,422.80±26.90^{cd}
SEM	0.84	3.79	20.83	25.48	36.89	42.63	68.67	79.64
P-value	***	***	***	***	***	***	***	***
CV	1.99	2.60	5.21	4.02	3.98	3.61	4.52	4.21

$^{a-h}$Means with the same letter in a column are not significantly different (P > 0.05); ***P ≤ 0.001; H, Improved Horro; S, Sasso; K, Potchefstroom Koekoek; D, Dz-white; Males are listed first in the cross; SEM, standard error of the means; CV, coefficient of variation; RE, reciprocal crosses.

Table 3. Least square means (SE) for feed intake and feed conversion ratio

Genotype	ADFI, (g/bird/day)				FCR (g/ feed intake /g weight gain)			
	WK 0-4	WK 5-8	WK 9-12	WK 13-16	WK 0-4	WK 5-8	WK 9-12	WK 13-16
Pure								
H	17.79±0.19^{d}	39.45±0.72^{d}	58.86±0.49^{c}	65.60±0.46^{d}	4.23±0.22^{a}	3.95±0.12^{a}	4.26±0.29^{b}	5.70±0.15^{a}
S	20.92±0.25^{ab}	43.03±0.14^{abc}	62.49±0.01^{a}	73.33±0.25^{b}	2.52±0.08^{d}	2.71±0.23^{cde}	3.29±0.17^{ef}	4.12±0.11^{ef}
K	19.98±0.07^{abc}	41.50±0.26^{a-d}	62.24±0.25^{a}	72.61±0.08^{b}	3.06±0.22^{c}	2.76±0.13^{cd}	3.74±0.10^{cde}	4.19±0.06^{def}
D	20.18±0.24^{abc}	40.71±0.17^{cd}	60.63±0.14^{b}	71.49±0.04^{c}	3.31±0.17^{bc}	2.97±0.13^{cd}	3.79±0.13^{cd}	5.02±0.16^{b}
Cross								
H×S	20.69±0.29^{ab}	43.23±0.13^{ab}	62.49±0.00^{a}	74.74±0.01^{a}	3.06±0.09^{c}	2.94±0.08^{cd}	3.44±0.19^{def}	4.73±0.13^{bcd}
H×K	19.62±0.30^{bc}	42.65±0.05^{abc}	62.41±0.08^{a}	72.90±0.34^{b}	3.52±0.04^{bc}	2.35±0.28^{de}	3.58±0.23^{de}	4.50±0.20^{b-e}
H×D	20.17±0.14^{abc}	40.98±2.77^{bcd}	61.10±1.39^{ab}	74.02±0.39^{a}	2.40±0.12^{d}	3.95±0.13^{a}	4.14±0.22^{bc}	4.96±0.26^{b}
S×K	21.23±0.01^{a}	43.45±0.12^{ab}	62.49±0.00^{a}	74.70±0.03^{a}	2.10±0.25^{d}	2.61±0.10^{de}	2.99±0.05^{f}	3.57±0.17^{g}
S×D	20.31±0.26^{ab}	43.15±0.60^{abc}	62.24±0.26^{a}	74.67±0.04^{a}	2.32±0.06^{d}	2.47±0.27^{de}	3.55±0.19^{de}	4.70±0.21^{bcd}
K×D	20.22±0.49^{ab}c	43.29±0.23^{ab}	61.84±0.44^{ab}	74.54±0.17^{a}	3.63±0.04^{b}	2.55±0.10^{de}	4.82±0.12^{a}	4.84±0.12^{bc}
RE								
S×H	20.18±0.30^{abc}	43.58±0.17^{a}	61.10±0.49^{ab}	74.52±0.24^{a}	2.25±0.11^{d}	2.11±0.17^{ef}	3.32±0.11^{def}	4.45±0.27^{b-e}
K×H	19.71±0.76^{bc}	43.54±0.21^{a}	62.18±0.31^{a}	74.47±0.20^{a}	3.55±0.22^{bc}	2.42±0.25^{de}	3.72±0.13^{cde}	4.35±0.09^{cde}
D×H	20.52±0.23^{ab}	42.53±0.15^{abc}	62.14±0.18^{a}	71.21±0.40^{c}	3.08±0.29^{c}	3.33±0.09^{bc}	4.50±0.15^{ab}	4.54±0.17^{b-e}
K×S	21.24±0.01^{a}	43.75±0.00^{a}	62.50±0.00^{a}	74.75±0.00^{a}	2.10±0.05^{d}	1.75±0.21^{f}	2.31±0.07^{g}	3.73±0.15^{fg}
D×S	19.76±0.86^{bc}	43.44±0.18^{ab}	62.22±0.28^{a}	74.73±0.02^{a}	2.35±0.07^{d}	2.92±0.27^{cd}	3.77±0.09^{cde}	4.47±0.18^{b-e}
D×K	18.89±0.52^{cd}	41.38±0.19^{a-d}	61.51±0.53^{ab}	73.07±0.26^{b}	3.53±0.03^{bc}	3.59±0.30^{ab}	3.75±0.09^{cde}	4.60±0.10^{b-e}
P-value	***	**	***	***	***	***	***	***
CV	3.42	3.07	1.29	0.57	9.08	11.85	6.82	6.46

[a-f] Means with the same letter in a column are not significantly different (P > 0.05); ns= non-significant; **P ≤ 0.01; ***P ≤ 0.001; N, number of birds; H, Improved Horro; S, Sasso; K, Potchefstroom Koekoek; D, Dz-white; Males are listed first in the cross; CV, coefficient of variation; RE, reciprocal crosses; ADFI, average daily feed intake; FCR, Feed conversion ratio.

4.2. Meat and Carcass Characteristics

Table 4 presents the effects of genotype and sex on various carcass weights: slaughter weight (SW), dressed carcass weight (DW), and eviscerated weight (EW) across different genotypes. The study findings demonstrated a significant influence ($P < 0.05$) of genotype and sex on SW, DW, and EW.

Among purebreds, the S breed stood out, with males achieving the highest SW (2507.67 g), DW (2016.67 g), and EW (1720.00 g). Females of the S breed also led their purebred counterparts, though their weights were markedly lower than males, reflecting the pervasive sex-based disparity. The K and D purebreds showed intermediate performance, while H consistently ranked lowest, particularly in females, which had the poorest SW (1266.67 g) and EW (726.67 g) of all purebreds.

Crossbred results revealed even more striking patterns. The Sasso-Koekoek crosses (S×K and K×S) emerged as top performers, with K×S males yielding the highest EW (1900.00 g) and females nearly matching purebred S in SW (2020.00 g). On the other hand, crosses involving Horro, such as H×D and H×K consistently underperformed, reinforcing the breed's limitations for meat production. The D breed's crosses showed mixed results: while D×S females achieved respectable DW (1580.00 g), D×H and D×K were among the poorest performers.

Table 5 demonstrated significant ($P < 0.05$) effects of genotype and sex on thigh, drumstick, breast, and wing weights, except for wing weight in females, where the difference was not significant ($P = 0.330$). In all cases, male birds possessed higher individual cut weights than females across genotypes. Among the purebred genotypes, the S males had the highest thigh (346.67 g), drumstick (310.00 g), and breast weights (533.33 g), while H males had the lowest values for these cuts. Similarly, in females, S birds also maintained superiority in thigh (206.67 g), drumstick (223.33 g), and breast (473.33 g) weights, with Horro females exhibited the lowest values.

Among the crossbred genotypes, the S×K males achieved the highest values for thigh (366.67 g), drumstick (336.67 g), breast (574.67 g), and wing (94.33 g) weights. D×S and K×S crosses also showed strong performance, particularly in females, with D×S females

exhibiting the highest thigh (215.00 g), drumstick (198.33 g), and wing (55.00 g) weights. Overall, crossbred genotypes exhibited improved cut weights compared to pure lines, especially those involving S chickens, reflecting the positive impact of crossbreeding on meat yield traits.

Furthermore, while wing weights showed significant variation among males ($P < 0.0001$), the differences were not statistically significant among females ($P = 0.330$). The highest wing weights in males were observed in S×K (94.33 g) and S (81.33 g) genotypes, whereas among females, although D×S recorded the highest value (55.00 g), differences across groups were not statistically meaningful.

The analysis of back, gizzard, heart, and liver weights revealed varied effects of genotype and sex (Table 6). Differences in back weight were not statistically significant for either males ($P = 0.315$) or females ($P = 0.673$). S (170.00 g) and K×S (163.33 g) showed the highest back weights in females. For gizzard weight, significant differences were observed ($P > 0.05$) for both sexes. Among males, the highest gizzard weights were recorded in pure K (36.47 g) and crossbred S×K (35.17 g), while the lowest was seen in H (24.10 g). In females, the highest gizzard weight was noted in D (38.57 g) and K×S (32.77 g) crosses, with the lowest in D×H (18.73 g).

Heart weight also varied significantly ($P < 0.05$) among males, with S×K (14.00 g) and D×S (13.87 g) genotypes achieving the highest values, while H males (9.13 g) had the lowest. In females, although differences were not statistically significant ($P = 0.082$), D×S (10.07 g) and S (8.53 g) females displayed relatively higher heart weights. Liver weight showed highly significant differences ($P < 0.001$) in both sexes. Among males, K×S crossbred birds exhibited the heaviest livers (58.83 g), followed by H×S (45.33 g), whereas the lightest was found in H×D (15.37 g). Among females, K×S had the highest liver weight (70.33 g), with D×K (18.37 g) and D×H (19.17 g) females having the lowest.

Table 4. Effect of genotype and sex on slaughter, dressed, and eviscerated carcass weights

Genotype	Slaughter Weight (g)		Dressed Carcass Weight (g)		Eviscerated Weight (g)	
	Male	Female	Male	Female	Male	Female
Pure						
H	1847.67±13.30^{f}	1266.67±12.00^{i}	1503.33±14.50^{e}	1043.33±8.82^{i}	1186.67±14.50^{f}	726.67±21.90^{i}
S	2507.67±12.00^{ab}	2063.33±47.00^{a}	2016.67±17.60^{b}	1643.33±8.82^{ab}	1720.00±5.77^{b}	1240.00±15.30^{a}
K	2417.67±24.00^{bcd}	1590.00±5.77^{ef}	1910.00±20.80^{bc}	1263.33±8.82^{efg}	1553.33±18.60^{c}	903.33±14.50^{ef}
D	2117.67±64.90^{e}	1640.00±26.50^{de}	1686.67±52.40^{d}	1330.00±5.77^{de}	1206.67±43.30^{f}	863.00±8.50^{fg}
Cross						
H×S	2440.00±11.50^{bcd}	1753.33±12.00^{c}	2020.00±25.20^{b}	1456.67±54.90^{c}	1562.33±16.20^{c}	1043.33±26.00^{c}
H×K	2090.00±28.90^{e}	1636.67±31.80^{de}	1690.00±28.90^{d}	1310.00±5.77^{def}	1260.00±28.90^{ef}	970.00±17.30^{d}
H×D	1893.33±24.00^{f}	1510.00±11.50^{fgh}	1503.33±14.50^{e}	1223.33±38.40^{gh}	1213.33±43.30^{f}	833.33±8.82^{gh}
S×K	2583.33±8.82^{a}	1686.67±20.30^{cd}	2193.33±35.30^{a}	1356.67±12.00^{d}	1740.00±35.10^{b}	953.33±18.60^{de}
S×D	2517.67±52.40^{ab}	1476.67±28.50^{h}	2145.00±20.20^{a}	1220.00±11.50^{gh}	1646.67±24.00^{bc}	803.33±8.82^{h}
K×D	2040.00±30.60^{e}	1706.67±12.00^{cd}	1590.00±45.10d^{e}	1360.00±20.80^{d}	1193.33±32.80^{f}	926.67±17.60^{de}
RE						
S×H	2397.67±13.30^{cd}	1566.67±14.50^{efg}	1946.67±17.60^{bc}	1276.67±12.00^{defg}	1570.00±37.90^{c}	910.00±5.77^{ef}
K×H	2050.00±32.10^{e}	1493.33±46.70^{gh}	1616.67±66.90^{d}	1230.00±46.20^{fgh}	1216.67±52.10^{f}	806.67±39.30^{gh}
D×H	2113.00±18.60^{e}	1326.67±14.50^{i}	1663.33±12.00^{d}	1073.33±14.50^{i}	1320.00±30.60^{de}	776.67±12.00^{hi}
K×S	2567.67±20.30^{a}	2020.00±36.10^{ab}	2176.67±46.30^{a}	1670.00±49.30^{a}	1900.00±30.60^{a}	1253.33±21.90^{a}
D×S	2495.00±54.80a^{bc}	1945.00±29.30^{b}	1925.00±31.80^{bc}	1580.00±11.50^{b}	1590.00±17.30^{c}	1176.67±12.00^{b}
D×K	2337.67±43.30^{d}	1466.67±33.80^{h}	1840.00±55.70^{c}	1173.33±18.60^{h}	1393.33±53.60^{d}	793.33±18.60^{h}
P-value	***	***	***	***	***	***
CV	2.53	2.90	3.39	3.45	3.75	3.44

$^{a-i}$ Means with the same letter in a column are not significantly different (P > 0.05); ***P ≤ 0.001; H, Improved Horro; S, Sasso; K, Potchefstroom Koekoek; D, Dz-white; Males are listed first in the cross; CV, coefficient of variation; RE, reciprocal crosses.

Table 5. Effects of genotype and sex on thigh, drumstick, breast, and wing weights

Genotype	Thigh (g)		Drumstick (g)		Breast (g)		Wing (g)	
	Male	Female	Male	Female	Male	Female	Male	Female
Pure								
H	233.33±8.82^{g}	123.33±12.00^{e}	220.00±11.50^{e}	116.33±9.13^{d}	393.33±21.90^{fg}	266.67±39.3^{0f}	60.00±5.77^{def}	40.00±10.00
S	346.67±26.00^{ab}	206.67±6.67^{a}	310.00±32.10^{abc}	223.3324.00^{a}	533.33±8.82^{ab}	473.33±34.8^{0a}	81.33±2.96^{ab}	46.67±3.33
K	293.33±16.70^{cd}	156.67±12.00^{b-e}	310.00±15.30^{abc}	143.33±14.50^{bcd}	466.67±8.82^{cde}	316.67±12.00^{c-f}	60.00±5.77^{def}	36.67±3.33
D	246.67±8.82^{fg}	160.00±10.00^{bcd}	243.33±8.82^{e}	143.33±6.67^{bcd}	380.00±20.80^{g}	313.33±28.50^{def}	63.33±12.00^{e-f}	40.00±5.77
Cross								
H×S	296.67±12.00^{cd}	180.00±10.00^{abc}	266.67±12.00^{b-e}	143.33±24.00^{bcd}	525.00±2.52^{abc}	403.33±23.30^{a-d}	71.67±1.67^{bcd}	50.00±5.77
H×K	232.50±4.33^{g}	170.00±17.30^{bcd}	250.00±5.77^{de}	153.33±14.50^{bcd}	415.00±2.89^{efg}	386.67±44.10^{a-e}	54.33±2.33^{def}	40.00±0.00
H×D	253.33±3.33^{efg}	160.00±5.77^{bcd}	226.67±3.33^{e}	140.00±5.77^{bcd}	376.67±8.82^{g}	323.33±6.67^{c-f}	53.33±3.33^{ef}	40.00±5.77
S×K	366.67±8.82^{a}	170.00±20.00^{bcd}	336.67±14.50^{a}	150.00±25.20^{bcd}	574.67±17.40^{a}	356.67±58.40^{b-f}	94.33±2.33^{a}	43.33±6.67
S×D	326.67±6.67^{abc}	146.67±14.50^{cde}	310.00±15.30^{abc}	130.00±15.30^{cd}	534.67±2.91^{a}	310.00±25.20^{d-f}	83.67±1.86^{ab}	36.67±3.33
K×D	246.67±3.33^{fg}	166.67±3.33^{bcd}	230.00±15.30^{e}	150.00±11.50^{bcd}	450.00±55.70^{def}	336.67±24.00^{b-f}	46.67±3.33^{f}	40.00±0.00
RE								
S×H	313.33±12.00^{bcd}	156.67±12.00^{b-e}	296.67±20.30^{a-d}	140.00±10.00^{bcd}	516.67±8.82^{abc}	343.33±29.60^{b-f}	66.67±3.33^{b-e}	40.00±0.00
K×H	250.00±5.77^{fg}	143.33±6.67^{cde}	236.67±14.50^{e}	130.00±10.00^{cd}	400.00±10.00^{fg}	300.00±25.20^{ef}	66.67±6.67^{b-e}	40.00±0.00
D×H	280.00±23.10^{def}	136.67±8.82^{de}	260.00±28.90^{cde}	123.33±6.67^{d}	410.00±20.00^{efg}	286.67±18.60^{ef}	56.67±8.82^{def}	36.67±3.33
K×S	330.00±5.77^{abc}	210.00±0.00^{a}	296.67±8.82^{a-d}	190.00±10.00^{abc}	496.67±23.00^{bcd}	426.67±3.33^{ab}	80.00±5.77^{abc}	50.00±5.77
D×S	335.00±20.20^{abc}	215.00±8.66^{a}	320.00±11.50^{ab}	198.33±28.30^{ab}	500.00±17.30^{bcd}	415.00±21.80^{abc}	70.00±5.77^{b-e}	55.00±5.00
D×K	326.67±13.30^{abc}	186.67±8.82^{ab}	300.00±10.00^{a-d}	166.67±37.10^{a-d}	425.00±2.89^{efg}	330.00±36.10^{b-f}	56.67±3.33^{def}	46.67±6.67
P-value	***	***	***	*	***	**	***	ns
CV	7.83	11.37	10.22	20.68	7.04	14.77	13.92	20.42

$^{a-g}$ Means with the same letter in a column are not significantly different (P > 0.05); ns= non-significant; *P ≤ 0.05; **P ≤ 0.01; ***P ≤ 0.001; H, Improved Horro; S, Sasso; K, Potchefstroom Koekoek; D, Dz-white; Males are listed first in the cross; CV, coefficient of variation; RE, reciprocal crosses.

Table 6. Effects of genotype and sex on back, gizzard, heart, and liver weights

Genotype	Back (g)		Gizzard wt. (g)		Heart wt. (g)		Liver wt. (g)	
	Male	Female	Male	Female	Male	Female	Male	Female
Pure								
H	193.33±6.67	113.33±8.82	24.10±1.14^{e}	20.40±0.62^{de}	9.13±1.29^{cd}	4.97±0.41	19.87±0.87^{ef}	28.33±3.15^{def}
S	234.33±5.67	170.00±20.80	32.33±0.66^{abc}	29.63±0.75^{bcd}	13.07±0.42^{ab}	8.53±1.67	32.50±0.99^{c}	32.07±4.32^{c-f}
K	216.67±18.60	146.67±12.00	36.47±2.56^{a}	29.00±1.61^{bcd}	11.40±0.31^{a-d}	5.80±0.30	24.50±2.35^{c-f}	22.97±0.95^{def}
D	190.00±25.20	146.67±8.82	31.23±0.97^{a-d}	38.57±2.98^{a}	10.63±0.69^{bcd}	7.67±1.68	41.50±5.05^{b}	52.53±9.10^{b}
Cross								
H×S	226.67±12.00	150.00±17.30	28.27±0.44^{b-e}	26.10±1.89^{b-e}	10.70±0.44^{bcd}	6.37±0.48	45.33±5.02^{b}	44.77±9.17^{bc}
H×K	200.00±5.77	143.33±12.00	26.53±0.33^{cde}	26.93±1.66^{b-e}	8.60±0.12^{d}	6.50±1.08	32.93±0.33^{c}	26.53±3.76^{def}
H×D	190.00±5.77	133.33±12.00	24.07±2.91^{e}	24.23±2.64^{cde}	8.57±0.78^{d}	6.17±0.32	15.37±2.19^{f}	22.53±2.87^{def}
S×K	246.67±8.82	143.33±31.80	35.17±0.71^{a}	21.53±7.75^{de}	14.00±0.90^{a}	6.67±0.94	30.23±1.17^{cd}	24.33±5.65^{def}
S×D	220.00±5.77	123.33±13.30	32.37±1.44^{abc}	27.13±3.44^{b-e}	12.60±0.30^{ab}	5.27±0.34	25.60±0.98^{cde}	35.23±2.59^{cde}
K×D	186.67±14.50	143.33±20.30	26.33±1.42^{de}	33.90±1.89^{ab}	9.47±0.23^{cd}	5.50±0.95	30.63±2.13^{cd}	37.37±5.27^{cd}
RE								
S×H	203.33±16.70	140.00±10.00	26.83±1.54^{cde}	24.97±1.58^{b-e}	11.97±1.84^{abc}	6.70±0.31	24.60±1.24^{c-f}	22.40±0.78^{def}
K×H	183.33±14.50	133.33±14.50	23.43±1.94^{e}	23.17±1.09^{de}	11.03±1.89^{a-d}	5.90±0.85	27.93±5.98^{cde}	33.77±5.61^{c-f}
D×H	203.33±39.30	110.00±10.00	25.43±2.29d^{e}	18.73±3.24^{e}	9.07±0.52^{cd}	6.03±1.53	24.07±0.79^{c-f}	19.17±0.44^{ef}
K×S	223.33±20.30	163.33±20.30	33.07±2.04^{ab}	32.77±1.34^{abc}	11.07±0.93^{a-d}	8.23±0.73	58.83±4.33^{a}	70.33±2.50^{a}
D×S	210.00±17.30	158.33±14.20	25.17±0.09^{e}	28.60±1.19^{bcd}	13.87±1.07^{a}	10.07±1.43	22.17±1.65^{def}	36.13±6.29^{cd}
D×K	200.00±5.77	140.00±35.10	32.27±3.72^{abc}	26.07±1.62^{b-e}	11.80±0.59^{abc}	6.20±0.85	28.23±2.73^{cde}	18.37±1.15^{f}
P-value	ns	ns	***	**	**	ns	***	***
CV	13.94	22.34	10.8	17.83	14.59	26.05	16.90	25.16

$^{a-f}$ Means with the same letter in a column are not significantly different (P > 0.05); ns= non-significant; **P ≤ 0.01; ***P ≤ 0.001; H, Improved Horro; S, Sasso; K, Potchefstroom Koekoek; D, Dz-white; Males are listed first in the cross; CV, coefficient of variation; RE, reciprocal crosses.

Proximate composition and physicochemical properties of breast meat

As presented in Table 7, the proximate composition analysis of breast meat revealed significant variations ($P < 0.05$) across most parameters among the different chicken genotypes and their crosses, except for energy content ($P = 0.341$).

Among the purebreds, D and K chickens exhibited the highest crude protein (CP) contents at 22.70% and 22.49%, respectively, while S chickens had the lowest at 19.34%. Moisture (MO) content ranged from 73.29% in D chickens to 75.39% in H chickens. Crude fat (CF) was highest in S chickens (3.56%) and lowest in K and D (2.82%), with ash (CA) values ranging from 1.08% in H to 1.73% in S. Energy content did not vary among genotypes, though D and K chicken breeds showed the highest values at 116.14 kcal and 115.36 kcal, respectively.

Among crossbreds, the highest CP was recorded in K×H (23.78%) and D×H (23.83%), surpassing even their purebred counterparts. On the other hand, the lowest CP value in crossbreds appeared in D×S at 19.00%, aligning with the lower values seen in its parent S line. MO varied slightly, with D×K exhibiting the highest at 75.79% and D×H the lowest at 72.46%. CF content among crossbreds ranged widely; D×S had the highest value at 4.07%, while combinations like S×K and K×H maintained lower values at 1.39% and 1.40%, respectively. Ash content ranged from 1.10% in D×K to 1.76% in K×H. Energy values remained generally steady across groups, with K×D (113.26 kcal), K×S (114.42 kcal), and D×H (115.07 kcal) among the higher end.

The physicochemical characteristics of breast meat from the purebreds and their crossbreds showed varying degrees of significance across the measured parameters (Table 8). Meat pH, both at 45 minutes postmortem (pH 45 min) and 24 hours postmortem (pH 24 h) did not differ significantly among the genotypes ($P = 0.215$ and $P = 0.627$, respectively). The pH 45 min values ranged from 6.11 in K×H to 6.58 in both S and H×D, while pH 24 h values varied slightly between 5.53 (S×H) and 5.83 (D).

Instrumental color values of the breast meat, however, showed significant differences ($P < 0.05$). Lightness (L*) values ($P < 0.05$) ranged from 35.07 in D×K to 48.07 in purebred D. Generally, pure D and crosses like H×K, K×H, and K×S exhibited higher lightness,

indicating paler meat, whereas S×K, D×S, and D×K had lower L* values, reflecting darker meat. Redness (a*) values showed highly significant variation ($P < 0.0001$). H×K recorded the highest redness (1.88), followed by H×S (1.62) and K×D (1.61). In contrast, D×H (0.42) and K×S (0.53) showed the lowest a* values. These differences indicate that crosses involving H and K tend to enhance redness intensity in breast meat. Yellowness (b*) also varied significantly ($P < 0.0001$), ranging from 2.00 in D×H to 4.21 in S×D. Generally, S×D, D×K, and S×K exhibited higher b* values, indicating more yellow pigmentation, while D×H, K×H, and H×S recorded lower values.

In comparing the different genotypes of chicken breast meat, distinct variations were observed in both water holding capacity (WHC) and shear force, with several notable values highlighting these differences. The pure genotype H recorded the highest WHC at 85.85%, standing out significantly from the others. In contrast, the pure genotype K had the lowest WHC at 78.61%.

Among the crossbreeds, H×S showed a high WHC of 84.21%**,** closely following the pure H line, suggesting some retention of favorable traits. Meanwhile, combinations like K×S and D×K were among the lowest, with WHC values of 78.70% and 79.42%, respectively, aligning more closely with the lower end of the spectrum seen in pure K.

Shear force, which reflects the meat's tenderness, and the highest values found in the S×D and K×D crosses, at 23.83 N and 23.70 N, respectively, indicating tougher meat. On the other hand, the D×S genotype had the lowest shear force at 19.53 N, suggesting a more tender meat texture. Most other genotypes, including pure lines and various crosses, showed intermediate shear force values ranging from approximately 20.3 N to 22.8 N.

Table 7. Proximate composition of breast meat from different genetic groups

Genotype	MO (%)	CP (%)	CF (%)	Ash (%)	Energy (kcal)
Purebred					
H	75.39±0.19^{ab}	20.31±0.25^{eh}	3.22±0.16^{abc}	1.08±0.02^{g}	110.22±0.99
S	75.37±0.80^{abc}	19.34±0.63^{gh}	3.56±0.33^{ab}	1.73±0.16^{a}	109.41±4.94
K	73.48±0.42^{cde}	22.49±0.33^{ad}	2.82±0.05^{bc}	1.20±0.06^{d-g}	115.36±1.63
D	73.29±0.64^{de}	22.70±0.22^{abc}	2.82±0.42^{bc}	1.20±0.05^{d-g}	116.14±4.56
Crossbred					
H×S	74.46±0.28^{ad}	21.40±0.60^{cf}	3.02±0.39^{abc}	1.11±0.04^{fg}	112.81±1.58
H×K	74.71±0.70^{ad}	20.18±0.32^{fgh}	3.84±0.73^{ab}	1.27±0.09^{d-g}	115.27±5.93
H×D	74.88±0.53^{ad}	21.11±0.17^{cf}	2.85±0.32^{bc}	1.16±0.04^{d-g}	110.07±3.56
S×K	73.90±0.57^{be}	23.50±0.69^{ab}	1.39±0.30^{e}	1.21±0.03^{d-g}	106.54±2.29
S×D	73.47±0.74^{cde}	23.64±0.48^{ab}	1.53±0.37^{e}	1.36±0.07^{b-e}	108.33±4.83
K×D	73.69±0.65^{b-e}	22.25±0.82^{a-d}	2.70±0.22^{bcd}	1.37±0.05^{bcd}	113.26±2.47
RE					
S×H	73.51±0.81^{be}	23.48±0.66^{ab}	1.68±0.17^{de}	1.33±0.05^{c-f}	109.06±4.17
K×H	73.00±0.45^{de}	23.78±0.36^{a}	1.40±0.10^{e}	1.76±0.10^{a}	108.24±2.36
D×H	72.46±0.72^{e}	23.83±0.70^{a}	2.19±0.24^{cde}	1.50±0.10^{bc}	115.07±3.21
K×S	73.95±0.42^{ae}	21.96±0.61^{be}	2.95±0.30^{abc}	1.13±0.03^{efg}	114.42±1.90
D×S	75.35±0.44^{abc}	19.00±0.38^{h}	4.07±0.47^{a}	1.57±0.03^{ab}	112.64±3.80
D×K	75.79±0.52^{a}	20.91±0.79^{dg}	2.21±0.28^{cde}	1.10±0.02^{fg}	103.49±1.03
P-value	**	***	***	***	ns
CV	1.31	4.11	22.65	9.14	5.25

$^{a-h}$ Means with the same letter in a column are not significantly different (P > 0.05); ns= non-significant; **P ≤ 0.01; ***P ≤ 0.001; H, Improved Horro; S, Sasso; K, Potchefstroom Koekoek; D, Dz-white; Males are listed first in the cross; CV, coefficient of variation; RE, reciprocal crosses; MO, moisture content; CP, crude protein; CF, crude fat.

Table 8. Breast meat pH, instrumental color, WHC, and shear force from different genetic groups

Genotype	Meat pH		Meat color			WHC (%)	Shear force (N)
	pH 45min	pH 24h	L*	a*	b*		
Pure							
H	6.49±0.12	5.71±0.09	41.11±2.83^{ab}	1.23±0.10^{bc}	3.37±0.25^{bcd}	85.85±0.79^{a}	20.53±1.07^{bcd}
S	6.58±0.10	5.62±0.07	40.38±1.20^{ab}	1.45±0.27^{ab}	3.58±0.15^{abc}	80.74±0.32^{cde}	20.30±1.13^{bcd}
K	6.54±0.15	5.61±0.06	42.93±0.88^{ab}	1.45±0.20^{ab}	2.59±0.11^{def}	78.61±0.70^{h}	21.47±0.72^{a-d}
D	6.17±0.04	5.83±0.15	48.07±5.46^{a}	1.44±0.18^{ab}	2.92±0.37^{cde}	79.36±0.22^{gh}	20.77±0.85^{a-d}
Cross							
H×S	6.39±0.22	5.82±0.31	42.00±1.24^{ab}	1.62±0.09^{ab}	2.41±0.16^{ef}	84.21±0.33^{b}	22.20±0.40^{a-d}
H×K	6.54±0.21	5.54±0.06	47.55±3.45^{a}	1.88±0.07^{a}	2.83±0.08^{cde}	80.99±0.50^{cde}	21.77±0.64^{a-d}
H×D	6.58±0.10	5.72±0.01	38.63±0.95^{ab}	1.15±0.08^{bc}	3.58±0.07^{abc}	81.54±0.20^{c}	21.40±0.80^{a-d}
S×K	6.53±0.18	5.82±0.01	37.58±2.34^{b}	1.49±0.17^{ab}	3.78±0.34^{ab}	81.25±0.09^{cd}	19.73±0.80^{cd}
S×D	6.40±0.13	5.79±0.03	39.84±2.46^{ab}	1.10±0.05^{bc}	4.21±0.23^{a}	80.24±0.09^{d-g}	23.83±0.66^{a}
K×D	6.35±0.09	5.77±0.25	43.11±2.30^{ab}	1.61±0.04^{ab}	2.76±0.28^{def}	79.89±0.09^{efg}	23.70±0.92^{a}
RE							
S×H	6.37±0.14	5.53±0.03	38.57±1.31^{ab}	0.57±0.24^{d}	3.35±0.12^{bcd}	80.86±0.20^{cde}	21.83±0.48^{a-d}
K×H	6.11±0.08	5.61±0.07	47.21±4.35^{a}	0.80±0.17^{cd}	2.46±0.26^{ef}	80.15±0.09^{d-g}	23.10±1.21^{ab}
D×H	6.42±0.18	5.66±0.01	39.26±1.60^{ab}	0.42±0.17^{d}	2.00±0.39^{f}	80.58±0.08^{c-f}	21.47±1.62^{a-d}
K×S	6.18±0.06	5.81±0.01	47.97±4.49^{a}	0.53±0.18^{d}	3.55±0.20^{abc}	78.70±0.47^{h}	22.80±0.35^{abc}
D×S	6.31±0.15	5.79±0.02	37.51±0.56^{b}	1.51±0.06^{ab}	2.73±0.09^{def}	79.48±0.05^{fgh}	19.53±1.07^{d}
D×K	6.15±0.10	5.80±0.05	35.07±1.72^{b}	1.12±0.21^{bc}	4.06±0.30^{ab}	79.42±0.09^{gh}	22.40±1.47^{a-d}
P-value	ns	ns	*	***	***	***	*
CV	3.69	3.46	11.60	22.96	13.20	0.76	7.29

$^{a-h}$ Means with the same letter in a column are not significantly different ($P > 0.05$); ns= non-significant; *$P \leq 0.05$; ***$P \leq 0.001$; H, Improved Horro; S, Sasso; K, Potchefstroom Koekoek; D, Dz-white; Males are listed first in the cross; CV, coefficient of variation; RE, reciprocal crosses; WHC, water-holding capacity; L*, lightness; a*, redness; b*, yellowness.

4.3. Egg Production Performance

The least square means for AFE, BWSM, and EWAFE across various genetic groups are shown in Table 9. Significant differences ($P < 0.0001$) were observed for all traits among genotypes. The K×H crossbred showed the earlier AFE (140.13 days), while among purebreds, breed D (150.93 days) matured earliest. K×S crossbred exhibited the highest BWSM (2032.22 g), and H purebred the lowest (1369.78 g). For EWAFE, K×S laid the heaviest eggs (41.14 g), while H×D laid lighter egg (33.67 g).

The performance of genotypes was also assessed for EN, HHEP, HDEP, and EM. (Table 10) highlights significant differences ($P < 0.0001$) for all traits among all genetic groups. K×H and K×S had the highest EN and egg production rates, while S×D and H×D performed the poorest. K×S, K×H, and D×K showed the highest EM, with the H breed showing the lowest performance.

Table 9. Least square means (±SE) for AFE, BWSM, and EWAFE

Genotype	HH (n)	HD (n)	AFE (days)	BWSM (g)	EWAFE (g)
Pure					
H	40	39	157.03 ± 1.75^{a}	1369.78 ± 17.90^{h}	32.23 ± 0.50^{i}
S	60	56	153.70 ± 1.48^{ab}	1779.50 ± 8.95^{d}	39.10 ± 0.41^{cd}
K	50	50	151.43 ± 0.69^{bc}	1683.56 ± 5.61^{fg}	37.52 ± 0.64^{e}
D	60	60	150.93 ± 2.11^{bc}	1669.56 ± 7.00^{fg}	35.04 ± 0.08^{fg}
Cross					
H×S	50	49	151.47 ± 0.68^{bc}	1758.00 ± 27.70^{d}	36.16 ± 0.21^{f}
H×K	60	60	$145.10\pm2.51^{d-g}$	1757.67 ± 2.17^{d}	34.14 ± 0.24^{gh}
H×D	45	44	148.10 ± 1.13^{cde}	1644.89 ± 20.60^{g}	33.67 ± 0.24^{h}
S×K	55	54	150.40 ± 1.36^{bc}	1953.78 ± 22.10^{b}	38.14 ± 0.04^{de}
S×D	45	43	150.03 ± 0.18^{bc}	1858.67 ± 10.70^{c}	36.18 ± 0.52^{f}
K×D	45	45	143.47 ± 0.48^{fgh}	1687.11 ± 17.00^{fg}	36.09 ± 0.12^{f}
RE					
S×H	45	44	148.93 ± 1.33^{bcd}	1740.89 ± 16.10^{de}	39.55 ± 0.09^{bc}
K×H	60	60	140.13 ± 1.14^{h}	1778.44 ± 10.40^{d}	38.18 ± 0.37^{de}
D×H	50	50	$144.13\pm1.60^{e-h}$	1678.22 ± 2.47^{fg}	37.33 ± 0.67^{e}
K×S	45	43	149.27 ± 1.02^{bcd}	2032.22 ± 12.10^{a}	41.14 ± 0.65^{a}
D×S	45	44	$147.27\pm2.29^{c-f}$	1884.00 ± 28.60^{c}	40.72 ± 0.38^{ab}
D×K	45	45	142.37 ± 1.23^{gh}	1701.11 ± 21.20^{ef}	39.92 ± 0.16^{bc}
P-value			***	***	***
CV			1.67	1.68	1.84

[a-i] Means with the same letter in a column are not significantly different ($P > 0.05$); ***$P \leq 0.001$; H, Improved Horro; S, Sasso; K, Potchefstroom Koekoek; D, Dz-white; AFE, age at first egg; BWSM, body weight at sexual maturity; EWAFE, egg weight at first egg.

Table 10. Least square means (±SE) for total EN, HHEP, HDEP, and EM

Genotype	Total EN per hen (n)		Egg production (%)		EM per hen (g)
	HH	HD	HHEP	HDEP	
Purebred					
H	47.64±1.85^{k}	48.71±1.15^{h}	35.90±1.16^{i}	36.70±0.54^{e}	2048.95±37.50^{j}
S	55.32±0.59^{j}	59.32±1.61^{fg}	41.53±1.15^{h}	44.54±1.67^{d}	2876.02±70.70^{ghi}
K	66.57±0.04^{e}	66.57±0.04^{de}	51.10±0.69^{d}	51.10±0.69^{c}	3335.67±32.10^{ef}
D	60.43±0.36^{g}	60.43±0.36^{fg}	46.26±0.65^{e}	46.26±0.65^{d}	2848.24±27.20^{ghi}
Crossbred					
H×S	59.30±0.43^{gh}	60.33±0.79^{fg}	44.14±0.23^{efg}	44.92±0.80^{d}	2963.18±7.84^{gh}
H×K	59.55±1.18^{gh}	59.55±1.18^{fg}	43.78±0.60^{fgh}	43.78±0.60^{d}	3000.53±43.60^{g}
H×D	56.44±0.31^{ij}	57.80±1.61^{g}	42.98±0.41^{gh}	44.03±1.45^{d}	2758.50±86.00^{i}
S×K	59.01±0.41^{gh}	60.03±0.66^{fg}	45.63±0.43^{ef}	46.44±1.01^{d}	3208.97±29.80^{f}
S×D	57.78±0.28^{hi}	60.52±1.09^{fg}	43.12±0.27^{gh}	45.16±0.84^{d}	2996.35±45.40^{g}
K×D	71.24±0.70^{bc}	71.24±0.70^{bc}	53.85±0.82^{bc}	53.85±0.82^{bc}	3404.05±55.80^{de}
RE					
S×H	60.29±0.75^{g}	61.70±1.01^{f}	44.88±0.45^{efg}	45.93±0.76^{d}	2796.89±92.10^{hi}
K×H	73.93±0.36^{a}	73.93±0.36^{ab}	55.18±0.42^{ab}	55.18±0.42^{b}	3792.82±39.60^{b}
D×H	68.03±0.50^{de}	68.03±0.50^{cde}	51.42±0.63^{d}	51.42±0.63^{c}	3246.25±37.10^{ef}
K×S	72.04±0.31^{ab}	75.48±1.77^{a}	56.78±1.16^{a}	59.45±0.94^{a}	4158.47±92.20^{a}
D×S	64.04±0.27^{f}	65.56±1.26^{e}	50.09±1.24^{d}	51.26±1.21^{c}	3556.08±78.30^{cd}
D×K	69.62±0.49^{cd}	69.62±0.49^{cd}	52.49±0.71^{cd}	52.49±0.71^{bc}	3708.55±50.80^{bc}
P-value	***	***	***	***	***
CV	1.94	2.91	2.81	3.39	3.21

$^{a-j}$ Means with the same letter in a column are not significantly different ($P > 0.05$); ***$P \leq 0.001$; H, Improved Horro; S, Sasso; K, Potchefstroom Koekoek; D, Dz-white; EN, total egg number; HHEP, hen housed egg production; HDEP, hen day egg production; EM, egg mass.

4.4. Fertility and Hatchability

The fertility and hatchability performances of purebred and crossbred chickens are presented in Table 11. All measured parameters, fertility, hatchability of total eggs set (HTES), and hatchability of fertile eggs (HFE) showed highly significant differences among the genotypes ($P < 0.01$).

Fertility percentages ranged from 78.78% in pure H to 92.80% in the D×S cross. Among the purebreds, S (90.45%), K (89.21%), and D (88.34%) exhibited higher fertility rates than H (78.78%). Crossbred combinations generally showed improved fertility, with the highest values observed in D×S (92.80%), followed by S×K (91.42%), H×K (91.40%), and K×D (91.19%).

Hatchability of total eggs set (HTES) varied from 60.93% in pure H to 81.56% in D×S, mirroring the fertility pattern. Crosses involving D, S, and K, particularly D×S (81.56%), K×H (78.24%), K×S (77.83%), and K×D (77.68%), achieved superior HTES percentages, while pure H and reciprocal crosses involving H (S×H and D×H) exhibited lower hatchability rates. HFE ranged from 77.36% in pure H to 89.85% in the H×S cross. Crosses such as H×S (89.85%), D×S (87.91%), and K×H (86.44%) recorded higher HFE percentages, reflecting better survival rates of fertile embryos to hatch. In general, the H chickens consistently demonstrated lower fertility and hatchability outcomes compared to other purebreds and most crosses.

Table 11. Fertility and hatchability of eggs from different genetic groups

Genotype	Fertility (%)	HTES (%)	HFE (%)
Pure			
H	78.78±1.10^{f}	60.93±0.61^{f}	77.36±0.90^{f}
S	90.45±0.54^{ad}	73.60±0.51^{bcd}	81.38±0.98^{bf}
K	89.21±0.45^{bcd}	76.72±0.89^{abc}	85.99±0.56^{abc}
D	88.34±1.63^{cd}	74.43±0.87^{bcd}	84.27±0.68^{af}
Cross			
H×S	83.60±2.07^{e}	75.13±2.10^{bcd}	89.85±0.30^{a}
H×K	91.40±0.91^{ab}	76.21±0.82^{bcd}	83.39±1.12^{af}
H×D	87.91±0.99^{d}	71.32±0.94^{d}	81.15±1.58^{bf}
S×K	91.42±0.76^{ab}	77.59±0.49^{ab}	84.88±0.45^{ae}
S×D	89.28±1.72^{bcd}	75.93±0.92^{bcd}	85.08±1.06^{ad}
K×D	91.19±1.03^{abc}	77.68±0.70^{ab}	85.20±0.57^{ad}
RE			
S×H	84.64±0.94^{e}	65.97±5.24^{e}	78.03±6.60^{ef}
K×H	90.51±0.57^{ad}	78.24±1.53^{ab}	86.44±1.63^{abc}
D×H	83.94±0.91^{e}	66.65±0.34^{e}	79.44±1.23^{cf}
K×S	90.63±0.68^{ad}	77.83±1.71^{ab}	85.92±2.47^{ad}
D×S	92.80±1.60^{a}	81.56±1.70^{a}	87.91±1.78^{ab}
D×K	90.97±0.49^{abc}	71.76±1.42^{cd}	78.87±1.31^{def}
P-value	***	***	**
CV	1.71	3.62	4.35

$^{a-f}$ Means with the same letter in a column are not significantly different ($P > 0.05$); **$P \leq 0.01$; ***$P \leq 0.001$; H, Improved Horro; S, Sasso; K, Potchefstroom Koekoek; D, Dz-white; Males are listed first in the cross; CV, coefficient of variation; RE, reciprocal crosses; HTES, hatchability from total eggs set; HFE, hatchability from fertile egg.

4.5. Egg Quality Traits

The least square means for external egg quality traits (EWT, EL, EW, SWT, ST, and SR) across different genotypes are detailed in Table 12. Differences ($P < 0.05$) were observed for all traits. From the results, K×S crossbred demonstrated the heaviest EWT of 55.10 g, followed by D×S (53.91 g). S×K, S×H, D×K, and S also displayed notable EWT, while the purebred H recorded the lightest EWT of 46.08 g. The purebred D stood out with the longest EL at 53.89 mm, trailed by S breed at 53.50 mm. On the other hand, the D×S crossbred exhibited the shortest EL at 42.79 mm.

Table 12. Least square means (±SE) for external egg quality traits

Genotype	EWT (g)	EL (mm)	EW (mm)	SWT (g)	ST (mm)	SR (%)
Pure						
H	46.08 ±0.28^{j}	51.14±0.17^{ab}	39.57±0.41^{abc}	5.23±0.05^{ad}	0.33±0.03^{e}	11.36±0.06^{a}
S	52.15±0.11^{de}	53.50±0.39^{a}	41.82±0.43^{a}	5.97±0.04^{a}	0.35±0.00^{de}	11.44±0.06^{a}
K	50.44±0.34^{g}	51.29±0.48^{ab}	38.93±0.14^{abc}	5.05±0.02^{bcd}	0.32±0.01^{e}	10.02±0.11^{abc}
D	49.13±0.36^{h}	53.89±0.47^{a}	41.46±0.40^{ab}	5.52±0.21^{abc}	0.32±0.01^{e}	11.24±0.50^{ab}
Cross						
H×S	48.80±0.42^{hi}	53.17±0.85^{a}	39.55±0.90^{abc}	5.06±0.23^{bcd}	0.43±0.02^{ab}	10.39±0.57^{abc}
H×K	51.07±0.22^{fg}	53.17±1.08^{a}	39.47±0.41^{abc}	5.38±0.26^{ad}	0.42±0.01^{abc}	10.53±0.50^{abc}
H×D	50.38±0.26^{g}	53.29±0.36^{a}	40.94±0.52^{abc}	4.85±0.32^{cd}	0.37±0.01^{cde}	9.61±0.59^{c}
S×K	53.46±0.57^{bc}	51.66±1.67^{ab}	40.04±0.54^{abc}	5.42±0.30^{ad}	0.33±0.02^{e}	10.16±0.66^{abc}
S×D	50.85±0.06^{fg}	45.63±2.13^{c}	34.05±2.28^{d}	5.72±0.14^{ab}	0.47±0.01^{a}	11.26±0.28^{ab}
K×D	50.11±0.19^{g}	49.30±1.98^{b}	37.74±2.04^{c}	5.25±0.18^{ad}	0.43±0.02^{ab}	10.48±0.34^{abc}
RE						
S×H	53.31±0.28^{bc}	51.07±0.87^{ab}	39.93±0.75^{abc}	5.18±0.30^{ad}	0.40±0.01^{bcd}	9.71±0.52^{bc}
K×H	51.63±0.22^{ef}	52.66±0.51^{ab}	38.92±0.44^{abc}	4.83±0.08^{cd}	0.45±0.02^{a}	9.36±0.19^{c}
D×H	48.05±0.14^{i}	50.63±0.62^{ab}	38.34±0.42^{bc}	4.66±0.05^{d}	0.40±0.01^{bcd}	9.69±0.08^{bc}
K×S	55.10±0.13^{a}	52.59±0.81^{ab}	41.42±0.28^{ab}	5.33±0.05^{ad}	0.33±0.01^{e}	9.68±0.07^{bc}
D×S	53.91±0.32^{b}	42.79±0.72^{c}	31.76±0.63^{d}	5.56±0.51^{abc}	0.37±0.03^{cde}	10.32±1.00^{abc}
D×K	52.61±0.50^{cd}	52.59±0.46^{ab}	41.50±1.08^{ab}	4.92±0.35^{bcd}	0.42±0.01^{ab}	9.35±0.65^{c}
P-value	***	***	***	*	***	*
CV	1.05	3.56	4.27	7.93	7.12	8.07

$^{a-j}$ Means with the same letter in a column are not significantly different ($P > 0.05$); *$P \leq 0.05$; ***$P \leq 0.001$; EWT, egg weight; EL, egg length; EW, egg width; SWT, shell weight; ST, shell thickness; SR, shell ratio.

For EW, S breed achieved the largest measurement at 41.82 mm, followed by D×K and D. On the lower end, the D×S crossbred recorded the narrowest EW at 31.76 mm. SWT was highest in the purebred S at 5.97 g, while the D×H crossbred displayed the lightest shells.

ST varied significantly, with the S×D crossbred showing the thickest shells (0.47 mm), whereas the purebred K and D exhibited the thinnest shells at 0.32 mm. The SR was highest in the purebred S at 11.44%, with the crossbreds K×H and D×K recording the lowest at 9.36% and 9.35%, respectively.

The least square means for internal egg quality traits (AH, AW, YH, YWT, YR, and HU) are indicated in Table 13. The analysis revealed differences ($P < 0.05$) across all traits. The crossbred K×H (7.28 mm) and its reciprocal H×K (7.00 mm) exhibited the highest AH, surpassing other genotypes. Followed by H×D (6.93 mm) and its reciprocal D×H (6.83 mm), while the lowest AH values were recorded in S×D (5.72 mm), D (5.55 mm), and K (5.17 mm).

In terms of AW, the H×D crossbred stood out with the highest measurement, trailed by D×K, D, and K×S. The H×K crossbred exhibited the narrowest AW. The purebred D (19.44 mm), crossbred K×S (19.33 mm), and purebred S (19.11 mm) demonstrated the highest YH. On the other hand, D×S (42.69 mm), S (42.33 mm), and S×D (41.22 mm) exhibited the highest YW. In contrast, the H×K crossbred displayed the smallest YH (15.94 mm) and YW (34.98 mm) values. The purebred S (16.36 g) emerged with the heaviest yolk, outperforming all other genotypes.

For YR, the purebred H (34.26%) and crossbred H×S (32.78%) achieved the highest value, with H×D (24.30%) and D×K (22.80%) showing the lowest values. The K×H crossbred exhibited the highest HU score (87.67). This was closely followed by D×H (86.21) and H×K (85.97). Other genetic groups displayed moderate HU values, while K×S (77.12) and K (73.87) recorded the lowest scores.

Table 13. Least square means (±SE) for internal egg quality traits

Genotype	AH (mm)	AW (mm)	YH (mm)	YW (mm)	YWT (g)	YR (%)	HU
Purebred							
H	6.33±0.51^{ad}	62.40±2.58^{efg}	18.67±0.33^{ab}	40.51±0.86^{abc}	15.79±0.47^{abc}	34.26±1.00^{a}	83.57±3.13^{ad}
S	6.33±0.67^{ad}	61.06±2.14^{fgh}	19.11±0.40^{a}	42.33±0.63^{ab}	16.36±0.76^{a}	31.36±1.48^{abc}	81.21±4.68^{ae}
K	5.17±0.17^{d}	66.93±2.56^{cf}	18.22±0.11^{abc}	37.63±0.74^{de}	13.87±0.30^{cf}	27.49±0.49^{cd}	73.87±1.30^{e}
D	5.55±0.22^{cd}	70.74±3.10^{abc}	19.44±0.29^{a}	39.02±1.06^{cd}	14.60±0.65^{ad}	29.74±1.50^{bc}	77.32±1.74^{cde}
Crosses							
H×S	5.83±0.44^{bcd}	67.03±1.92^{cf}	16.89±0.78^{cd}	35.92±0.36^{e}	15.99±0.39^{ab}	32.78±1.07^{ab}	79.28±3.25^{ae}
H×K	7.00±0.58^{ab}	55.91±1.09^{h}	15.94±0.44^{d}	34.98±0.34^{e}	14.03±0.56^{be}	27.47±1.08^{cd}	85.97±3.40^{abc}
H×D	6.93±0.47^{ab}	75.97±0.53^{a}	15.97±0.41^{d}	35.43±1.14^{e}	12.24±0.26^{ef}	24.30±0.49^{de}	85.88±2.85^{ad}
S×K	6.22±0.59^{ad}	67.53±1.71^{cde}	18.33±0.33^{abc}	39.88±0.16^{bcd}	14.77±0.95^{ad}	27.67±2.06^{cd}	80.11±3.97^{ae}
S×D	5.72±0.15^{bcd}	66.20±1.75^{cf}	18.89±0.40^{a}	41.22±0.75^{abc}	15.41±0.65^{abc}	30.31±1.31^{bc}	77.93±1.07^{be}
K×D	6.10±0.10^{ad}	68.32±0.97^{cde}	16.89±0.22^{cd}	35.59±1.43^{e}	12.55±0.43^{ef}	25.05±0.77^{de}	80.85±0.73^{ae}
RE							
S×H	6.28±0.50^{ad}	63.94±0.77^{d-g}	17.27±0.06^{bcd}	36.13±0.60^{e}	13.13±0.72^{def}	24.62±1.25^{de}	80.67±3.33^{ae}
K×H	7.28±0.15^{a}	62.22±1.73^{efg}	16.94±0.53^{cd}	35.06±0.37^{e}	13.21±1.11^{def}	25.60±2.25^{de}	87.67±0.90^{a}
D×H	6.83±0.10^{abc}	59.84±1.88^{gh}	16.56±0.87^{d}	35.36±1.27^{e}	12.30±0.46^{ef}	25.61±0.99^{de}	86.21± 0.54^{ab}
K×S	5.83±0.17^{bcd}	69.33±1.26^{bcd}	19.33±0.33^{a}	40.85±0.45^{abc}	15.39±0.47^{abc}	27.93±0.79^{cd}	77.12±1.27^{de}
D×S	6.06±0.47^{ad}	64.46±1.16^{dg}	18.78±0.49^{ab}	42.69±0.66^{a}	15.05±0.23^{ad}	27.93±0.59^{cd}	78.94±3.32^{ae}
D×K	6.22±0.11^{ad}	74.08±0.84^{ab}	17.00±0.88^{cd}	35.53±0.29^{e}	11.99±0.45^{f}	22.80±0.95^{e}	80.77±0.72^{ae}
P-value	*	***	***	***	***	***	*
CV	10.69	4.80	4.78	3.62	7.37	7.66	5.50

[a-h] Means with the same letter in a column are not significantly different (P > 0.05); *P ≤ 0.05; ***P ≤ 0.001; AH, albumen height; AW, albumen width; YH, yolk height; YW, yolk width; YWT, yolk weight; YR, yolk ratio; HU, hugh unit.

4.6. Crossbreeding Effects

4.6.1. Heterosis effects (H^e)

Heterosis effect on body weight

Heterosis (%) estimated based on mid-parent for BW of all crossbred genetic groups are presented in Figure 2 and Figure 3, respectively. The results showed that the H×S, H×K, H×D, S×K, and S×D crossbreds had positive H^e (ranged from 0.20 – 15.93%) on BW from hatch to WK 14. The highest estimates for H^e were observed in S×D (15.93%) cross followed by S×K (14.86%) at WK 4. The H×S and H×D crossbreds exhibited positive and high H^e while, crossbred H×K showed positive but low H^e for BW throughout all age measurements. On the other hand, the crossbred K×D exhibited negative H^e (ranged from -2.55 to -8.55%) throughout the experimental period.

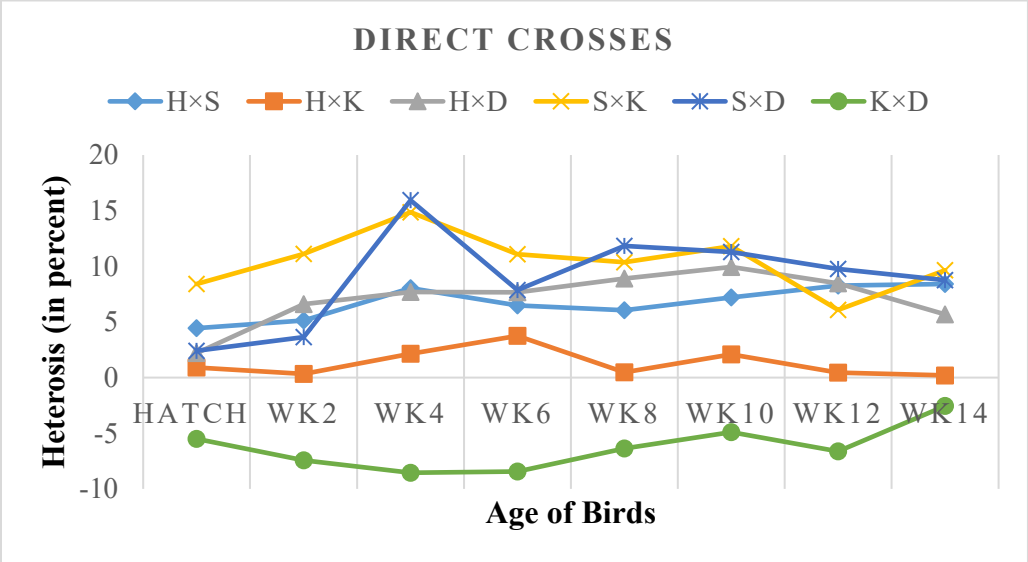

Figure 2. Heterosis effect on body weight for direct crosses

Reciprocal crosses also showed positive H^e (ranged from 0.41 – 9.31%) on BW from hatch to WK 14 (Figure 3). From the reciprocal crosses the highest estimates of H^e for BW was observed from D×S (9.31%) cross combination, followed by K×S (9.23%) at WK 4. The S×H cross also showed positive and high H^e but lower compared to D×S and K×S at all age measurements. Similarly, K×H and D×K crossbreds showed positive but much lower

estimates compared to other crossbreds. However, estimate of D×K crossbred was better compared to its direct cross K×D, which was negative starting from hatch – WK 14.

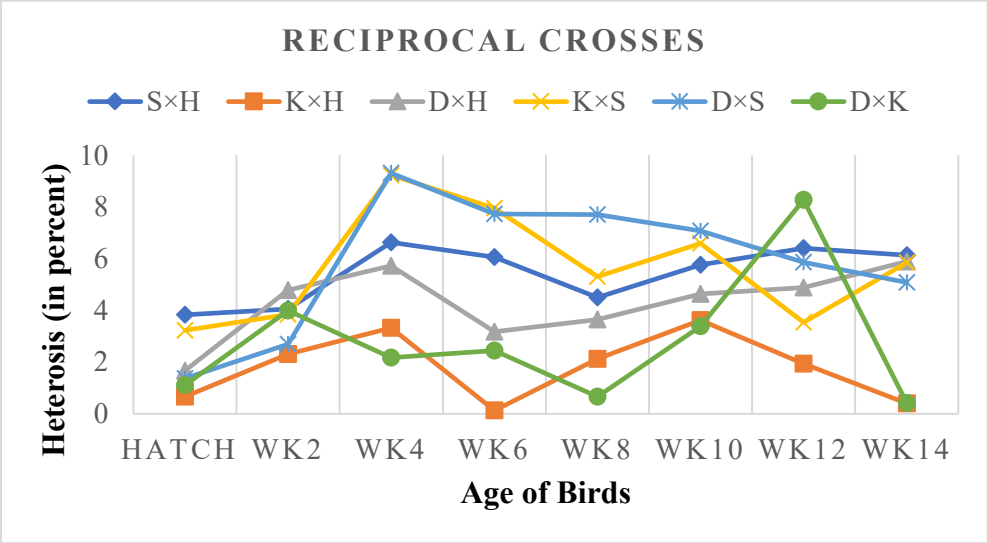

Figure 3. Heterosis effect on body weight for reciprocal crosses

Heterosis effect on feed intake and feed conversion ratio

Table 14 presents the heterosis percentages for average daily feed intake (ADFI) and feed conversion ratio (FCR) across different genotypes and growth stages. The heterosis values vary widely, reflecting both positive and negative deviations from the mid-parent averages, depending on the cross and trait assessed.

For ADFI, the highest positive H^e was observed in the D×H cross during WK 0–4 (8.09%) and in K×H during WK 5–8 (7.57%). Other crosses showing consistently positive H^e across all periods included H×S, H×K, and H×D, all exhibiting moderate heterotic gains in feed intake, with values such as 6.92%, 3.90%, and 6.27% during WK 0–4, respectively. Reciprocal crosses like S×H and K×H also reflected similar trends with values exceeding 5% in early periods. In contrast, some crosses exhibited negative H^e for ADFI in specific periods, notably D×S and D×K, with values like –3.83% and –5.92% in WK 0–4.

For FCR, negative H^e values were prevalent, indicating improved feed efficiency (since lower FCR is better). The most substantial improvements were observed in S×H and K×S, with H^e values reaching –36.54% and –36.12% in WK 5–8, respectively. H×D also

exhibited strong negative H^e in the early stage (–36.36%). These suggest significant feed efficiency improvements through crossbreeding. However, some crosses like K×D and D×K showed positive H^e in FCR during certain periods, such as +27.94% (K×D, WK 9–12) and +25.37% (D×K, WK 5–8), indicating reduced efficiency.

Table 14. Estimates of heterosis (%) for ADFI and FCR among different genotypes

Genotype	Traits							
	ADFI (Ages in week)				FCR (Ages in week)			
	0-4	5-8	9-12	13-16	0-4	5-8	9-12	13-16
Cross								
H×S	6.92	4.83	2.99	7.59	-9.13	-11.67	-8.89	-3.81
H×K	3.90	5.38	3.08	5.48	-3.59	-29.93	-10.65	-8.97
H×D	6.27	2.24	2.27	7.99	-36.36	14.04	2.88	-7.44
S×K	3.81	2.79	0.21	2.37	-24.74	-4.48	-14.91	-14.14
S×D	-1.15	3.05	1.10	3.13	-20.40	-13.03	0.39	2.74
K×D	0.67	5.30	0.66	3.45	13.84	-10.91	27.94	5.09
RE								
S×H	4.25	5.67	0.70	7.27	-33.41	-36.54	-11.98	-9.42
K×H	4.37	7.57	2.69	7.76	-2.63	-27.96	-7.04	-12.04
D×H	8.09	6.10	4.01	3.89	-18.32	-3.82	11.72	-15.30
K×S	3.87	3.51	0.22	2.44	-24.88	-36.12	-34.33	-10.36
D×S	-3.83	3.75	1.07	3.20	-19.31	2.61	6.49	-2.23
D×K	-5.92	0.66	0.13	1.42	10.84	25.37	-0.55	-0.22

H, Improved Horro; S, Sasso; K, Potchefstroom Koekoek; D, Dz-white; ADFI, average daily feed intake; FCR, feed conversion ratio.

Heterosis effect on meat and carcass traits

The estimates of heterosis (%) for carcass characteristics traits among different chicken genotypes and sexes are presented in Table 15. The results revealed considerable variability in the magnitude and direction (positive or negative) of heterosis across traits, crosses, and between sexes.

Slaughter weight (SW) exhibited positive H^e in most male crosses, notably in H×S (12.05%), S×K (4.90%), and S×D (8.86%). On the other hand, negative H^e was observed in H×K (-2.00%), H×D (-4.51%), and K×D (-10.04%). For females, the highest positive H^e occurred in H×K (14.59%), while negative H^e was evident in crosses like S×D (-20.25%). Dressed weight (DW) followed a similar pattern. Positive H^e estimates were recorded in H×S (14.77%), S×K (11.71%), and S×D (15.84%) for males. H×K (13.58%)

and D×S (6.28%) showed favorable heterosis in females. Eviscerated weight (EV) showed moderate positive H^e, particularly in males of S×D (12.53%) and S×K (6.31%), and in females of H×K (19.02%) and D×S (11.90%).

Thigh weight (TWT) heterosis was mostly positive, especially in males of S×K (14.58%) and D×K (20.99%), and in females of H×K (21.43%) and D×K (17.89%). Drumstick weight (DWT) showed mixed H^e. Males of S×D (12.05%) and D×S (15.66%) had higher positive values, while several crosses displayed negative or low H^e. Breast weight (BWT) heterosis estimates were highly positive in males for S×K (14.93%) and S×D (17.08%), and even higher in females, notably H×K (32.57%).

For wing and back weights, results varied. The S×K males (33.49%) exhibited strong positive H^e for wing weight, whereas in females, the highest heterosis was in D×K (21.74%). Gizzard, heart, and liver weights presented variable heterosis estimates, with some high positive values such as H×K (48.46%) for male liver weight and H×K (20.74%) for female heart weight, while other crosses showed marked negative heterosis, especially in internal organ traits.

Table 15. Estimates of heterosis (%) for carcass characteristics traits

Traits	Sex	Genotypes											
		Crosses						Reciprocals					
		H×S	H×K	H×D	S×K	S×D	K×D	S×H	K×H	D×H	K×S	D×S	D×K
SW	M	12.05	-2.00	-4.51	4.90	8.86	-10.04	10.10	-3.88	6.59	4.26	7.88	3.09
	F	5.31	14.59	3.90	-7.66	-20.25	5.68	-5.91	4.55	-8.72	10.58	5.04	-9.18
DW	M	14.77	-0.98	-5.75	11.71	15.84	-11.58	10.61	-5.27	4.28	10.87	3.96	2.32
	F	8.44	13.58	3.09	-6.65	-17.94	4.88	-4.96	6.65	-9.55	14.91	6.28	-9.51
EV	M	7.50	-8.03	1.39	6.31	12.53	-13.53	8.03	-11.19	10.31	16.09	8.66	0.97
	F	6.10	19.02	4.84	-11.04	-23.60	4.93	-7.46	-1.02	-2.29	16.95	11.90	-10.17
TWT	M	2.30	-11.71	5.56	14.58	10.11	-8.64	8.05	-5.06	16.67	3.13	12.92	20.99
	F	9.09	21.43	12.94	-6.42	-20.00	5.26	-5.05	2.38	-3.53	15.60	17.27	17.89
DWT	M	0.63	-5.66	-2.16	8.60	12.05	-16.87	11.95	-10.69	12.23	-4.30	15.66	8.43
	F	-15.60	18.10	7.83	-18.18	-29.09	4.65	-17.57	0.13	-5.01	3.64	8.18	16.28
BWT	M	13.31	-3.49	-2.59	14.93	17.08	6.30	11.51	-6.98	6.03	-0.67	9.49	0.39
	F	9.01	32.57	11.49	-9.70	-21.19	6.88	-7.21	2.86	-1.15	8.02	5.51	4.76
Wing	M	1.42	-9.44	-13.51	33.49	15.67	-24.32	-5.66	11.11	-8.11	13.21	-3.22	-8.11
	F	15.38	4.35	0.00	4.00	-15.38	4.35	-7.69	4.35	-8.33	20.00	26.92	21.74
Back	M	6.00	-2.44	-0.87	9.39	3.69	-8.20	-4.91	-10.57	6.09	-0.96	-1.02	-1.64
	F	5.88	10.26	2.56	-9.47	-22.11	-2.27	-1.18	2.56	-15.38	3.16	0.00	-4.55
Gizzard	M	0.18	-12.38	-13.01	2.23	1.84	-22.21	-4.90	-22.62	-8.07	-3.88	-20.82	-4.68
	F	4.33	9.04	-17.81	-26.55	-20.43	0.35	-0.20	-6.21	-36.46	11.77	-16.13	-22.84
Heart	M	-3.60	-16.23	-13.32	14.44	6.33	-14.07	7.81	7.47	-8.26	-9.54	17.02	7.11
	F	-5.68	20.74	-2.37	-6.98	-34.98	-18.32	-0.74	9.60	-4.49	14.88	24.28	-7.92
Liver	M	34.95	48.46	-49.92	6.08	-30.81	-7.17	-6.05	25.92	-21.56	36.26	-40.09	-14.44
	F	15.12	3.44	-19.54	-11.57	-16.71	-1.02	-25.83	31.64	-27.86	10.24	-14.58	-24.86

H, Improved Horro; S, Sasso; K, Potchefstroom Koekoek; D, Dz-white; SW= slaughter weight; DW= dressed weight; EV= eviscerated weight; TWT= Tigh weight; DWT= dream steak weight; BWT= breast weight.

Table 16 presents the estimates of heterosis (%) for instrumental color (L*, a*, b*) and water holding capacity (WHC) in breast meat from the four pure breeds and their crossbreds. The results indicate notable variation in H^e across traits and genotypic combinations.

For meat color, substantial H^e was observed across the L*, a*, and b* color values. Lightness (L*) H^e ranged from -22.92% in D×K to 13.17% in H×K. Positive H^e for L*, as seen in H×K and K×H, suggest brighter meat in these crosses, a desirable trait for many consumers. On the other hand, significant negative H^e in crosses such as D×K and D×H indicates darker meat, which may be less appealing in certain markets. Redness (a*) displayed particularly high heterosis variation, with estimates ranging from 39.88% in H×K to -68.79% in D×H. High positive H^e values in H×K and H×S crosses reflect an enhancement of the red hue in breast meat, which is often associated with freshness and quality. However, several reciprocal crosses, notably D×H, K×S, and S×H, demonstrated large negative H^e values for redness, highlighting the significant influence of maternal effects and the direction of the cross on this color attribute. Yellowness (b*) heterosis was similarly variable, with notable positive values observed in S×D (29.54%), S×K (22.49%), and D×K (47.28%). On the other hand, crosses such as H×S (-30.61%) and K×H (-17.45%) exhibited negative H^e, suggesting a reduction in yellowness relative to their mid-parent values.

In evaluating heterosis for water holding capacity (WHC) in chicken breast meat, the estimates varied across different genotypic crosses. Positive H^e was observed in several crosses, indicating an improvement in WHC over the average of the parent genotypes. Among these, the S×K cross exhibited the highest positive H^e at 1.98%, followed by K×D (1.15%), H×S (1.11%), and S×D (0.24%). On the other hand, negative H^e was recorded in several reciprocal crosses, notably S×H (-2.92%), K×H (-2.52%), and D×H (-2.44%), suggesting a reduction in WHC compared to the mid-parent values. Other combinations like H×K (-1.51%), H×D (-1.29%), and K×S (-1.22%) also demonstrated modest negative H^e.

Table 16. Estimates of heterosis (%) for meat color and WHC

Genotypes	Traits			
	Meat color			WHC
	L*	a*	b*	
Crosses				
H×S	3.10	20.84	-30.61	1.11
H×K	13.17	39.88	-5.03	-1.51
H×D	-13.37	-13.61	13.77	-1.29
S×K	-9.77	2.64	22.49	1.98
S×D	-9.92	-23.64	29.54	0.24
K×D	-5.25	11.32	0.00	1.15
RE				
S×H	-5.34	-57.82	-3.55	-2.92
K×H	12.36	-40.37	-17.45	-2.52
D×H	-11.95	-68.79	-36.33	-2.44
K×S	15.16	-63.49	15.03	-1.22
D×S	-15.18	4.50	-16.00	-0.71
D×K	-22.92	-22.40	47.28	0.55

H, Improved Horro; S, Sasso; K, Potchefstroom Koekoek; D, Dz-white; L*, Lightness; a*, redness; b*, yellowness; WHC, water holding capacity.

The estimates of H^e for the proximate composition of breast meat revealed considerable variability across different genotypic crosses and reciprocals (Table 17). For moisture content (MO), the crosses generally exhibited negative H^e values, with the most significant being observed in S×H (-2.47%) and D×H (-2.53%), suggesting a decrease in moisture relative to mid-parent values in these combinations. The H×S cross also displayed a small negative heterosis of -1.22%, while other crosses like H×K (0.37%) and K×D (0.42%) had slightly positive heterosis, indicating no substantial improvement in moisture content.

Regarding crude protein (CP), positive H^e was evident in many crosses, particularly in S×K (12.34%) and S×D (12.47%), indicating enhanced protein content in these combinations. However, some crosses like H×K (-5.69%) and K×D (-1.53%) exhibited negative H^e, suggesting reduced protein levels compared to mid-parent values, which could affect meat nutritional quality. The highest H^e for CP was observed in the reciprocal cross S×H (18.43%), reflecting a considerable increase in protein content in these offspring.

Crude fat (CF) exhibited negative H^e across several crosses. The most pronounced decrease was seen in S×K (-56.30%) and S×D (-52.01%), indicating a substantial reduction in fat content for these combinations, which could be seen as desirable for leaner meat. The H×S

cross (-10.85%) also showed a decrease, while other crosses like H×K (27.02%) and K×S (5.00%) displayed positive H^e, indicating a higher fat content in these combinations.

For ash content (CA), H^e varied widely, with some crosses showing negative values (e.g., H×S -20.78%, S×K -17.47%, and S×D -7.31%) suggesting lower mineral content in these crosses, while others like K×D (13.60%) and D×H (33.12%) showed positive H^e, reflecting an increase in ash content in these genotypes. The largest increase was seen in the reciprocal cross K×H (54.15%), which indicated a significant rise in the mineral content of the meat.

Energy content of the meat showed limited variation, with most crosses displaying small positive or negative H^e. The H×S cross (2.73%) exhibited the highest positive H^e, suggesting slightly more energy in this meat compared to the mid-parent values, while D×K (-10.59%) showed the largest negative H^e, indicating lower energy content.

Table 17. Estimates of heterosis (%) for proximate composition of breast meat

Genotype	Traits				
	MO	CP	CF	CA	Energy
Crosses					
H×S	-1.22	7.95	-10.85	-20.78	2.73
H×K	0.37	-5.69	27.02	11.12	2.20
H×D	0.73	-1.84	-5.63	2.07	-2.75
S×K	-0.71	12.34	-56.30	-17.47	-5.20
S×D	-1.15	12.47	-52.01	-7.31	-3.94
K×D	0.42	-1.53	-4.35	13.60	-2.15
RE					
S×H	-2.47	18.43	-50.34	-5.80	-0.68
K×H	-1.93	11.13	-51.75	54.15	-4.03
D×H	-2.53	10.84	-27.39	33.12	1.67
K×S	-0.63	5.00	-7.46	-22.93	1.81
D×S	1.38	-9.59	27.60	7.32	-0.12
D×K	3.27	-7.47	-21.72	-8.53	-10.59

H, Improved Horro; S, Sasso; K, Potchefstroom Koekoek; D, Dz-white; MO, moisture content; CP, crude protein; CF, crude fat; CA, crude ash.

Heterosis estimates for fertility and hatchability traits

The estimates of H^e for fertility and hatchability traits, presented in Table 18, highlight the variation in performance across different genotypic crosses and reciprocals. The crosses showed a range of positive and negative H^e for the fertility trait. Notably, the H×K cross displayed a significant positive heterosis of 8.82%, indicating a notable increase in fertility. On the other hand, the H×S cross showed a slight negative H^e of -1.20%, suggesting a decrease in fertility compared to the mid-parent values. Other crosses, such as H×D (5.21%) and S×K (1.77%), exhibited moderate positive H^e, while S×D (-0.13%) showed minimal negative H^e.

When it comes to hatchability of total eggs set (HTES), the H×S cross had the most significant positive H^e (11.69%), suggesting a considerable improvement in hatchability for this cross. The K×H reciprocal cross also displayed a high positive H^e of 13.68%, reflecting a notable enhancement in hatchability. Crosses like H×K (10.74%) and D×S (10.20%) also showed moderate positive H^e, indicating better hatchability in these combinations compared to mid-parent values. In contrast, the reciprocal crosses, such as S×H (-1.93%) and D×H (-1.50%) showed negative H^e, indicating lower hatchability for these reciprocal crosses. For hatchability of fertile eggs (HFE), heterosis estimates were generally positive but more modest compared to HTES. The H×S cross again showed a significant positive H^e of 13.20%, while the K×H reciprocal cross had a smaller but still notable positive H^e of 5.84%. Other crosses like D×S (6.14%) and S×D (2.73%) also showed improvements, albeit at a lower level. However, several crosses, including H×D (0.41%) and K×D (0.08%), exhibited minimal or negligible positive H^e, indicating almost no improvement in hatchability of fertile eggs compared to mid-parent values.

Table 18. Estimates of heterosis (%) for fertility and hatchability traits

Genotype	Fertility	HTES	HFE
Crosses			
H×S	-1.20	11.69	13.20
H×K	8.82	10.74	2.10
H×D	5.21	5.38	0.41
S×K	1.77	3.24	1.43
S×D	-0.13	2.60	2.73
K×D	2.72	2.79	0.08
RE			
S×H	0.03	-1.93	-1.69
K×H	7.75	13.68	5.84
D×H	0.45	-1.50	-1.70
K×S	0.89	3.56	2.67
D×S	3.81	10.20	6.14
D×K	2.47	-5.05	-7.35

H, Improved Horro; S, Sasso; K, Potchefstroom Koekoek; D, Dz-white; HTES, hatchability from total egg set; HFE, hatchability from fertile egg.

Heterosis estimates for egg production traits

Estimates of H^e on egg production traits was analyzed, with heterosis (%) calculated based on mid-parent values are detailed Table 19. Positive H^e was observed for BWSM, and EM in crosses like H×S, H×K, H×D, S×K, and K×D, with heterosis ranging from 0.63% to 20%. AFE showed negative H^e across all crossbreds, similarly except for H×S (1.39%) and H×D (0.11%) all crosses showed negative H^e on EWAFE. On the other hand, HHEP, HDEP, and EN exhibited positive H^e, except for S×K and S×D. Reciprocal crosses demonstrated positive H^e for BWSM, EWAFE, HHEP, HDEP, EM, and EN (ranging from 1.46% to 40.88%), while AFE remained the sole trait with negative H^e across all genetic groups.

Table 19. Estimates of heterosis (%) for egg production traits

Genotype	Traits						
	AFE	BWSM	EWAFE	HHEP	HDEP	EM	EN
Crosses							
H×S	-2.51	11.64	1.39	14.02	7.04	20.33	11.69
H×K	-5.92	15.13	-2.09	0.65	2.71	11.45	3.31
H×D	-3.82	8.24	0.11	4.63	6.13	12.66	5.92
S×K	-1.42	12.84	-0.44	-1.47	2.52	3.32	-4.63
S×D	-1.50	7.78	-2.40	-1.77	-0.52	4.69	1.06
K×D	-5.10	0.63	-0.52	10.62	13.60	10.09	12.19
RE							
S×H	-4.14	10.56	10.89	15.92	13.07	13.58	14.22
K×H	-9.14	16.49	9.47	26.85	29.44	40.88	28.27
D×H	-6.40	10.43	10.99	25.16	17.20	32.58	24.6
K×S	-2.16	17.37	7.38	22.60	26.37	33.89	19.90
D×S	-3.32	9.25	9.85	14.12	13.65	24.25	9.48
D×K	-5.83	1.46	10.03	7.82	10.72	19.94	9.64

AFE, age at first egg; BWSM, body weight at sexual maturity; EWAFE, egg weight at first egg; HHEP, hen housed egg production; HDEP, hen day egg production; EM, egg mass; EN, total egg number.

Heterosis estimates for egg quality traits

Heterosis effects varied significantly for egg quality traits across different crossbred genotypes Table 20. EWT displayed positive H^e for most crosses and their reciprocals, ranging from 0.42% to 8.54%, with the exception of H×S cross. For EL, majority of H^e estimates were negative, except H×S (1.64%), H×K (3.82%), H×D (1.49%), K×H (2.83%), and K×S (0.37%). Similarly, EW predominantly exhibited negative H^e, with the exception of H×K (0.56%), H×D (1.04%), K×S (2.58%), and D×K (3.24%). In terms of SWT, H^e was negative across all genetic groups except for H×K (4.54%). On the other hand, ST showed high and positive H^e on most groups, excluding S×K (-2.97%) and its reciprocal K×S (-1.98%). However, SR demonstrated negative H^e across all crosses and reciprocals. AH exhibited strong positive H^e in the majority of crosses, except for H×S, S×D, and S×H. Similarly, AW also displayed positive H^e in most crosses. In contrast, YH showed negative H^e across all crosses and reciprocals, with the exception of K×S. YW and YWT also had negative H^e, except for S×D, K×S, and D×S. For HU, most heterosis estimates were positive but relatively low, except for the crossbreds H×S, S×D, S×H, K×S, and D×S. On the other hand, YR predominantly exhibited high and negative H^e.

Table 20. Estimates of heterosis (%) for external and internal egg quality traits

Traits	Genotypes											
	Crosses						Reciprocals					
	H×S	H×K	H×D	S×K	S×D	K×D	S×H	K×H	D×H	K×S	D×S	D×K
EWT	-0.65	5.82	5.83	4.22	0.42	0.65	8.54	6.98	0.93	7.41	6.45	5.68
EL	1.64	3.82	1.49	-1.40	-15.02	-6.25	-2.38	2.83	-3.59	0.37	-20.31	0.00
EW	-2.81	0.56	1.04	-0.84	-18.23	-6.12	-1.88	-0.85	-5.38	2.58	-23.73	3.24
SWT	-9.58	4.54	-9.86	-1.57	-0.35	-0.63	-7.56	-6.03	-13.39	-3.21	-3.25	-6.94
ST	27.12	27.55	13.89	-2.97	40.10	35.18	16.67	39.12	22.81	-1.98	9.82	32.41
SR	-8.88	-1.51	-14.92	-5.35	-0.76	-1.39	-14.85	-12.40	-14.23	-9.80	-9.01	-12.05
AH	-7.87	21.77	16.69	8.17	-3.70	13.81	-0.87	26.59	15.01	1.45	1.91	16.04
AW	8.59	-13.53	14.13	5.52	0.46	-0.74	3.57	-3.78	-10.11	8.33	-2.19	7.63
YH	-10.58	-13.56	-16.17	-1.79	-2.01	-10.31	-8.55	-8.13	-13.11	3.58	-2.58	-9.74
YW	-13.26	-10.46	-10.91	-0.24	1.33	-7.14	-12.78	-10.26	-11.09	2.18	4.95	-7.29
YWT	-0.53	-5.40	-19.42	-2.28	-0.42	-11.80	-18.28	-10.90	-19.02	1.84	-2.75	-15.74
YR	-0.10	-11.04	-24.06	-5.99	-0.78	-12.46	-24.95	-17.07	-19.97	-5.09	-8.57	-20.30
HU	-3.78	9.21	6.75	3.32	-1.69	6.94	-2.09	11.37	7.17	-0.54	-0.41	6.84

EWT, egg weight; EL, egg length; EW, egg width; SWT, shell weight; ST, shell thickness; SR, shell ratio; AH, albumen height; AW, albumen width; YH, yolk height; YW, yolk width; YWT, yolk weight; YR, yolk ratio; HU, hugh unit.

4.6.2. Combining abilities and reciprocal effects

Combining abilities for body weight

The general combining ability (GCA), specific combining ability (SCA), and reciprocal effect (RE) for BW across purebred and crossbred genetic groups from hatch up to WK 14 are presented in Table 21. GCA effects were high ($P < 0.0001$) for BW among purebreds. From the results, it was observed that the S breed gave the highest GCA values at all studied ages. On the other hand, GCA estimates for K chickens were positive except for hatch, WK 2, and WK 6. On the other hand, H and D chicken breeds exhibited the lowest negative additive effects for BW.

Estimates of SCA ranged from -34.13 g up to 58.19 g across crossbreds. The cross with the best SCA for BW was found in the cross combination of S×K at all age measurement. The H×D and S×D crosses also exhibited the highest positive SCA estimates for BW compared with other crosses. Similarly, except for WK 4 and WK 8, the cross H×S also had the highest positive estimates of SCA for BW. On the other hand, the H×K crossbred recorded the lowest negative estimates of SCA for BW, except for WK 4 and WK 10. However, SCA estimates were negative for all weight measurement for the K×D crossbred.

Reciprocal effects (RE) were not significant on most of the growing stages, except for hatch ($P < 0.002$), WK 2 ($P < 0.0001$), and WK 10 ($P < 0.036$). Estimates of RE for BW in the crossbreds were equally positive and negative ranging from -28.57 g up to 21.07 g. For the D×K and S×H crossbreds estimate of RE were positive at all WK studied. RE were all negative for the crossbred K×H except hatch and WK 6. On the other hand, for the cross D×K the effects were negative for all measurement taken.

Table 21. Estimates (±SE) of combining ability for body weight for different genotypes at different growing period

Genotype	Age (weeks)							
	Hatch	WK 2	WK 4	WK 6	WK 8	WK 10	WK 12	WK 14
GCA								
g^{H}	-1.38±0.15^{e}	-8.41±0.32^{g}	-29.46±3.56^{d}	-35.69±0.86^{f}	-40.57±3.51^{d}	-78.01±2.95^{e}	-88.49±21.79^{c}	-118.34±7.54^{c}
g^{S}	1.58±0.51^{a}	13.66±1.05^{a}	43.79±11.62^{a}	54.84±2.82^{a}	71.32±11.45^{a}	93.47±9.64^{a}	93.69±15.41^{a}	120.46±24.63^{a}
g^{K}	-0.11±0.51^{bcd}	-0.28±0.74^{be}	2.55±11.62^{bc}	7.23±2.82^{be}	-4.61±11.45^{bcd}	0.90±9.64^{bcd}	18.58±21.79^{ab}	1.26±24.63^{b}
g^{D}	-0.08±0.25^{bcd}	-4.96±0.74^{efg}	-16.89±5.81^{cd}	-26.38±1.41^{ef}	-26.15±5.72^{cd}	-16.35±4.82^{bcd}	-23.78±6.67^{bc}	-3.37±12.31^{b}
SCA								
$s^{H\times S}$	0.29±0.38^{bc}	0.55±0.79^{be}	-0.37±8.72^{bc}	2.07±2.11^{bf}	-1.28±8.58^{bcd}	2.73±7.23^{bcd}	17.53±18.87^{ab}	22.96±18.47^{ab}
$s^{H\times K}$	-0.15±0.28^{bcd}	-0.94±0.59^{cf}	0.77±6.50^{bc}	-0.83±1.57^{bf}	-0.37±6.40^{bcd}	0.73±5.39^{bcd}	-2.53±24.36^{abc}	-19.02±13.77^{bc}
$s^{H\times D}$	0.40±0.35^{bc}	3.51±0.74^{bc}	7.67±8.22^{bc}	12.47±1.99^{bcd}	19.63±8.09^{bc}	26.87±6.82^{bcd}	30.28±16.34^{ab}	36.96±17.42^{ab}
$s^{S\times K}$	1.04±0.56^{ab}	5.30±1.18^{b}	18.93±13.00^{ab}	26.29±3.15^{ab}	29.31±12.80^{ab}	42.31±10.78^{ab}	26.36±24.36^{ab}	58.19±27.54^{ab}
$s^{S\times D}$	0.03±0.44^{bcd}	0.24±0.91^{be}	16.06±10.06^{b}	14.01±2.44^{bc}	30.16±9.91^{ab}	31.97±8.35^{bc}	36.83±15.40^{ab}	30.29±21.33^{ab}
$s^{K\times D}$	-0.66±0.15^{cde}	-2.93±1.05^{def}	-15.20±3.56^{cd}	-19.93±0.86^{cf}	-29.17±5.51^{cd}	-28.76±2.95^{cde}	-38.53±12.18^{bc}	-34.13±7.54^{bc}
RE								
$r^{S\times H}$	0.09±0.25^{bcd}	0.60±0.52^{be}	2.01±5.81	0.99±1.41	5.40±5.72	6.27±4.82^{bcd}	10.27±16.34	15.53±12.31
$r^{K\times H}$	0.03±0.44^{bcd}	-0.99±0.91^{cf}	-1.55±10.06	8.18±2.44	-5.36±9.91	-6.27±8.35^{bcd}	-7.97±15.41	-1.41±21.33
$r^{D\times H}$	0.08±0.38^{bcd}	0.87±0.32^{bcd}	2.32±8.72	9.35±2.11	16.33±8.58	20.80±7.23^{bcd}	18.06±10.89	-1.37±18.47
$r^{K\times S}$	0.81±0.35^{ab}	4.41±0.74^{bc}	8.99±8.22	8.27±1.99	18.81±8.09	24.90±6.82^{bcd}	15.70±12.18	28.57±17.42
$r^{D\times S}$	0.16±0.28^{bcd}	0.55±0.79^{be}	9.86±6.50	0.29±1.57	14.72±6.40	19.58±5.39^{bcd}	22.86±10.89	27.30±13.77
$r^{D\times K}$	-1.01±0.35^{de}	-5.99±0.59^{fg}	-14.58±8.22	-25.24±1.99	-23.33±8.09	-36.13±6.82^{de}	-44.27±18.87	-21.07±17.42
P-values								
GCA	***	***	***	***	***	***	***	***
SCA	***	***	***	***	***	***	**	**
RE	**	***	ns	ns	ns	*	ns	ns
GCA/SCA	1.73	4.22	2.26	2.39	1.71	2.05	2.51	2.41

[a-g]Means with the same letter in a column are not significantly different (P > 0.05); ns= non-significant; *P ≤ 0.05; **P ≤ 0.01; ***P ≤ 0.001; H, Improved Horro; S, Commercial Sasso; D, Dz-white; K, Potchefstroom Koekoek; Males are listed first in the cross; GCA, general combining ability; SCA, specific combining ability; RE, reciprocal effect.

Combining ability for feed intake and feed conversion ratio

Table 22 presents the estimates of combining ability for average daily feed intake (ADFI) and feed conversion ratio (FCR) across different genotypes and growth stages. General Combining Ability (GCA) and Specific Combining Ability (SCA) values provide insight into the additive and non-additive genetic contributions to feed intake and efficiency. For ADFI, genotype S consistently displayed positive GCA estimates across all periods, peaking at +1.14 g/bird/day in WK 13–16, indicating that it contributes favorably to feed intake when used as a parent. In contrast, genotype H had consistently negative GCA estimates, most notably –1.58 in WK 13–16, indicating its limited additive contribution to feed intake.

For FCR, genotype S again showed favorable GCA estimates, with significant negative values across all periods (e.g., –0.54 in WK 0–4), indicating its strong contribution to feed efficiency. On the other hand, genotype H showed consistently positive FCR GCA values (e.g., +0.35 in WK 0–4), implying that it tends to increase FCR and reduce efficiency. K and D displayed variable, mostly mildly positive GCA effects.

For ADFI, most SCA values were positive and not significantly different from each other. The highest values were detected in H×S (+1.86 in WK 13–16) and H×K (+1.55), suggesting synergistic effects in increasing feed intake. Some crosses showed negative SCA values, such as K×D (–0.66 in WK 0–4), suggesting lower-than-expected intake. For FCR, several crosses displayed negative SCA values, indicating improved efficiency. Notably, D×H had a strong negative SCA (–0.60 in WK 0–4), followed by K×S (–0.49 in WK 9–12), suggesting superior feed efficiency due to non-additive genetic interactions. Some crosses such as D×K showed positive SCA values.

Highly significant GCA and SCA effects ($P < 0.0001$) across nearly all periods for both traits suggest that both additive and non-additive gene actions are important. The GCA/SCA ratios ranged from 0.18 to 0.84, indicating that non-additive effects (SCA) dominate in later growth stages for FCR, whereas additive effects are more prominent in early feed intake.

Table 22. Estimates (±SE) of combining ability for feed intake and feed conversion ratio among different genotypes

Genotype	Traits							
	ADFI				FCR			
	WK 0-4	WK 5-8	WK 9-12	WK 13-16	WK 0-4	WK 5-8	WK 9-12	WK 13-16
g^{H}	-0.53±0.18^{b}	-0.55±0.66^{a}	-0.64±0.32^{a}	-1.58±0.22^{h}	0.35±0.13^{abc}	0.29±0.16^{abc}	0.22±0.29^{ab}	0.34±0.15^{a}
g^{S}	0.57±0.09^{ab}	0.86±0.33^{a}	0.47±0.16^{a}	1.14±0.11^{abc}	-0.54±0.07^{ef}	-0.31±0.08^{cde}	-0.44±0.14^{d}	-0.29±0.08^{bc}
g^{K}	0.02±0.18^{ab}	0.15±0.66^{a}	0.40±0.32^{a}	0.50±0.22^{cd}	0.13±0.13^{abc}	-0.24±0.16^{b-e}	-0.10±0.29^{a-d}	0.28±0.15^{bc}
g^{D}	-0.06±0.06^{ab}	-0.46±0.20^{a}	-0.24±0.10^{a}	-0.06±0.07^{def}	0.05±0.04^{a-d}	0.26±0.05^{abc}	0.33±0.09^{ab}	0.24±0.05^{ab}
$s^{H\times S}$	0.31±0.16^{ab}	0.63±0.57^{a}	0.18±0.28^{a}	1.86±0.19^{a}	-0.10±0.11^{b-e}	-0.29±0.14^{cde}	-0.08±0.25^{a-d}	0.01±0.13^{abc}
$s^{H\times K}$	0.09±0.20^{ab}	1.02±0.74^{a}	0.75±0.36^{a}	1.55±0.25^{ab}	0.11±0.15^{abc}	-0.50±0.18^{e}	-0.15±0.32^{bcd}	-0.16±0.17^{abc}
$s^{H\times D}$	0.17±0.09^{ab}	0.77±0.33^{a}	0.52±0.16^{a}	-1.40±0.11^{gh}	0.34±0.07^{abc}	-0.31±0.08^{cde}	0.18±0.14^{ab}	-0.21±0.08^{abc}
$s^{S\times K}$	0.01±0.13^{ab}	0.15±0.47^{a}	0.00±0.23^{a}	0.03±0.16^{de}	0.00±0.09^{a-d}	-0.43±0.11^{de}	-0.34±0.20^{cd}	0.08±0.11^{abc}
$s^{S\times D}$	-0.28±0.14^{ab}	0.15±0.50^{a}	-0.01±0.24^{a}	0.03±0.17^{de}	0.02±0.10^{a-d}	0.22±0.12^{abc}	0.11±0.21^{abc}	-0.11±0.12^{abc}
$s^{K\times D}$	-0.66±0.16^{b}	-0.95±0.57^{a}	-0.16±0.28^{a}	-0.73±0.19^{efg}	-0.05±0.11^{a-e}	0.52±0.14^{a}	-0.54±0.25^{d}	-0.12±0.13^{abc}
$r^{S\times H}$	0.26±0.10	-0.17±0.37	0.70±0.18	0.11±0.12^{d}	0.41±0.07^{ab}	0.41±0.09^{ab}	0.06±0.16^{abc}	0.14±0.09
$r^{K\times H}$	-0.04±0.13	-0.44±0.47	0.12±0.23	-0.79±0.16^{fg}	-0.02±0.09^{a-d}	-0.03±0.11^{a-e}	-0.07±0.20^{a-d}	0.08±0.11
$r^{D\times H}$	0.85±0.14	0.28±0.50	0.72±0.24	1.04±0.17^{bc}	-0.60±0.10^{f}	0.26±0.12^{abc}	0.09±0.21^{abc}	-0.35±0.12
$r^{K\times S}$	0.56±0.06	0.11±0.20	-0.15±0.10	-0.12±0.07^{def}	-0.43±0.04^{def}	-0.11±0.05^{a-e}	-0.49±0.09^{d}	-0.30±0.05
$r^{D\times S}$	-0.56±0.13	0.42±0.47	0.21±0.23	0.41±0.16^{cd}	-0.12±0.09^{cde}	-0.09±0.11^{a-e}	0.09±0.20^{abc}	0.11±0.11
$r^{D\times K}$	-0.50±0.10	0.16±0.37	-0.26±0.18	0.15±0.12^{d}	0.46±0.07^{a}	0.22±0.09^{a-d}	0.37±0.16^{a}	0.23±0.09
P-value								
GCA	***	**	***	***	***	***	***	***
SCA	***	**	***	***	***	***	***	***
RE	ns	ns	ns	***	**	***	***	ns
GCA/SCA	0.26	0.28	0.34	0.18	0.36	0.37	0.52	0.84

$^{a-g}$Means with the same letter in a column are not significantly different (P > 0.05); ns= non-significant; **P ≤ 0.01; ***P ≤ 0.001; H, Improved Horro; S, Commercial Sasso; D, Dz-white; K, Potchefstroom Koekoek; Males are listed first in the cross; GCA, general combining ability; SCA, specific combining ability; RE, reciprocal effect.

Combining ability for meat and carcass traits

Table 23 provides the estimates of combining ability for Slaughter Weight (SW), Dressed Carcass Weight (DW), and Eviscerated Weight (EW) for various genotypes and sexes, including both purebred and crossbred chickens. According to the results, GCA, SCA, and RE were significant ($P < 0.05$), demonstrating that these effects contributed meaningfully to the variation in weight traits.

For SW, the S breed exhibited the highest positive GCA for both males and females, with values of 225.94 g and 187.60 g, respectively, indicating substantial increases in weight compared to other genotypes. In contrast, the H breed showed negative values for both sexes, with males at -190.94 g and females at -156.77 g. The other genotypes, such as K and D, exhibited moderate or negative GCA values for SW. For DW, S again performed better, with males showing 215.83 g and females at 155.21 g. In comparison, H exhibited negative estimates, with males at -158.33 g and females at -118.54 g. The other genotypes displayed a range of values, but none surpassed the performance of S in either sex. In terms of EW, S also showed the highest GCA, with males at 226.60 g and females at 141.27 g. H again had negative combining abilities for both sexes, with males at -140.06 g and females at -87.06 g.

The cross between K×D showed the highest positive SCA estimates for SW in males (148.33 g) among the crossbreds, but negative estimates in females (-120.00 g). Similarly, crosses between Improved Horro and Sasso yielded positive estimates for SW in males (107.81 g), but negative estimates in females (-5.10 g). For DW, the H×S cross performed well in males (86.67 g) but again showed negative SCA for females (4.38 g). Estimates of EW for H×S were 25.10 g in males, but negative in females (-13.77 g). For other crossbreds such as H×K, S×K, and S×D, the estimates of SCA varied widely. Some crosses, like S×K, displayed high positive estimates for DW and EW in both males and females, indicating substantial improvements for those traits in crossbreeding. However, other crosses, like H×D, showed negative estimates in certain combinations, such as SW in females (-91.67 g) and DW in males (-75.00 g).

Reciprocal crossbreeding effects for various genetic groups (e.g., S×H, K×H, D×S) were statistically significant. For SW, the S×H cross showed positive effects in males (21.67 g), while the K×S cross had significant positive estimates for DW (103.33 g). Negative effects were observed in several reciprocal combinations, particularly in EW for some crosses.

Table 24 presents an estimate of combining ability for thigh, drumstick, breast, and wing traits across different genotypes and sexes. From the results, GCA was significant for all traits in both sexes, except for breast in females (P = 2.187). Variation due to SCA varied, with thigh, breast, and wing weights showing significant effects ($P < 0.05$), while drumstick weight did not reach significance in males. On the other hand, the RE were significant ($P < 0.05$) for most traits except drumstick and breast in males and for wing in females.

For thigh weight, the S breed showed the highest positive GCA for males (40.36 g) and a moderate value for females (18.44 g). In contrast, the H breed had negative values for both sexes (-30.78 g for males and -18.85 g for females), suggesting lower thigh weights. The other genotypes, K and D, showed moderate values, with K showing close to zero effects for both sexes. For drumstick weight, S again showed the best performance for both sexes, with males at 30.00 g and females at 22.21 g. Other genotypes, like H, exhibited negative estimates for both sexes, indicating lower drumstick weights.

Genotypes like K and D also displayed more varied results, with K showing slightly positive estimates for both sexes and D showing negative values, especially for males (-9.17 g). In terms of breast weight, S exhibited significantly higher estimates compared to other genotypes, with males at 64.44 g and females at 50.94 g. In contrast, H had negative estimates for both sexes, with males at -33.60 g and females at -27.19 g. Other genotypes showed a range of values, with K and D showing moderate negative or low positive estimates.

For wing weight, S had the highest estimate for males at 12.04 g, followed by K and H, which had smaller estimates but were still positive for males. The female data for wing weight exhibited more variation across the genotypes, with no significant pattern across the genotypes, except for S, which showed better performance.

In crossbreeds, the H×S combination showed relatively small positive SCA estimates for thigh weight in males (3.07 g) and negative estimates in females (-13.38 g). For drumstick weight, the H×S cross showed lower estimates for both sexes, but the S×D cross exhibited higher positive estimates in females (34.17 g). Breast weight for S×K and S×D crosses showed some positive estimates in both males and females, especially for the females in S×D (52.50 g). However, the wing weight for many crosses like H×K and S×K showed lower or negative estimates.

Reciprocal effects (RE) were also significant for many of the traits, with the K×S cross showing positive estimates for thigh weight (15.57 g in males) and drumstick weight (6.67 g). The D×S cross demonstrated higher positive estimates for breast weight (20.85 g in males), but wing weight did not show much variance across the reciprocal crosses.

Table 23. Estimates (±SE) of combining ability for slaughter, dressed carcass, and eviscerated weight of different genotype and sex

Genotype	Slaughter Weight (g)		Dressed Carcass Weight (g)		Eviscerated Weight (g)	
	Male	Female	Male	Female	Male	Female
Purebred						
g^{H}	-190.94±14.87^{f}	-156.77±21.56^{h}	-158.33±18.28^{g}	-118.54±39.05^{i}	-140.06±56.72^{h}	-87.06±14.57^{h}
g^{S}	225.94±7.43^{a}	187.60±10.78^{a}	215.83±9.41^{a}	155.21±19.53^{a}	226.60±28.36^{a}	141.27±7.29^{a}
g^{K}	36.98±14.87^{cde}	14.48±21.56^{cde}	26.67±18.28^{be}	2.71±39.05^{cf}	21.73±17.37^{be}	2.52±14.57^{def}
g^{D}	-71.98±4.55^{e}	-45.31±6.60^{efg}	-84.17±5.60^{efg}	-39.38±11.96^{eh}	-108.27±42.54^{gh}	-56.73±4.46^{fgh}
Crossbred						
$s^{H\times S}$	107.81±12.87^{bc}	-5.10±18.67^{def}	86.67±15.83^{bc}	4.38±33.82^{cf}	25.10±49.12^{be}	-13.77±12.62^{dg}
$s^{H\times K}$	-51.56±16.62^{e}	73.02±24.10^{cd}	-54.17±20.43^{dg}	60.21±43.66^{bc}	-97.85±63.42^{fgh}	36.65±16.29^{bcd}
$s^{H\times D}$	110.00±7.43^{bc}	-91.67±10.78^{fgh}	80.00±9.14^{bc}	-75.00±19.53^{ghi}	53.33±28.36^{bcd}	-28.33±7.29^{eh}
$s^{S\times K}$	-8.33±10.51^{de}	166.67±15.24^{ab}	-8.33±12.92^{cf}	156.67±27.61^{a}	80.00±40.11^{bc}	150.00±10.30^{a}
$s^{S\times D}$	-10.83±11.15^{de}	234.17±16.17^{a}	-110.00±13.71^{fg}	180.00±29.29^{a}	-28.33±17.37^{dg}	186.67±10.93^{a}
$s^{K\times D}$	148.33±12.87^{ab}	-120.00±18.67^{gh}	125.00±15.83^{ab}	-93.33±33.82^{hi}	100.00±49.12^{b}	-66.67±12.62^{gh}
RE						
$r^{S\times H}$	21.67±8.31^{cde}	93.33±12.05^{bc}	36.67±10.22^{be}	90.00±21.83^{b}	-3.83±42.54^{cf}	66.67±8.15^{bc}
$r^{K\times H}$	20.00±10.51^{cde}	71.67±15.24^{cd}	36.67±12.92^{be}	40.00±27.61^{bcd}	21.67±17.37^{be}	81.67±10.30^{b}
$r^{D\times H}$	-9.27±11.15^{de}	-13.85±16.17^{def}	-13.33±13.71^{cf}	-19.36±29.29^{dg}	60.48±42.54^{bcd}	12.56±10.93^{cde}
$r^{K\times S}$	36.56±4.55^{cde}	16.98±6.60^{cde}	103.33±5.60^{bc}	29.79±11.96^{be}	117.15±56.72^{b}	23.31±4.46^{be}
$r^{D\times S}$	76.35±10.51^{bcd}	-65.73±15.24^{efg}	64.17±12.92^{bcd}	-41.46±27.61^{fgh}	45.48±40.11^{bcd}	-30.77±10.30^{eh}
$r^{D\times K}$	-52.19±8.31^{e}	-16.77±12.05^{def}	-66.67±10.22^{efg}	-22.29±21.83^{dg}	-74.65±31.71^{eh}	-22.02±8.15^{dg}
P-values						
GCA	***	***	***	***	***	***
SCA	***	***	***	***	***	***
RE	***	***	***	***	***	***
GCA/SCA	1.92	3.35	1.35	3.16	1.59	6.13

[a-i] Means with the same letter in a column are not significantly different (P > 0.05); ***P ≤ 0.001; H, Improved Horro; S, Commercial Sasso; D, Dz-white; K, Potchefstroom Koekoek; Males are listed first in the cross; GCA, general combining ability; SCA, specific combining ability; RE, reciprocal effect.

Table 24. Estimates (±SE) of combining ability for thigh, drumstick, breast, and wing traits of different genotype and sex

Genotype	Thigh (g)		Drumstick (g)		Breast (g)		Wing (g)
	Male	Female	Male	Female	Male	Female	Male
Pure							
g^H	-30.78±4.07^{c}	-18.85±7.98^{c}	-28.75±3.63^{b}	-19.75±28.79	-33.60±22.82^{bc}	-27.19±46.12	-5.42±5.23^{ab}
g^S	40.36±2.03^{a}	18.44±3.99^{abc}	30.00±1.82^{a}	22.21±14.40	64.44±11.41^{a}	50.94±23.06	12.04±2.61^{a}
g^K	0.05±4.07^{abc}	1.98±7.98^{abc}	7.92±3.63^{ab}	0.75±28.79	-0.52±22.82^{bc}	-3.02±46.12	-1.75±5.23^{ab}
g^D	-9.64±1.25^{bc}	-1.56±2.44^{abc}	-9.17±1.11^{ab}	-3.21±8.82	-30.31±6.99^{bc}	-20.73±14.12	-4.88±1.60^{ab}
Cross							
$s^{H\times S}$	3.07±3.52^{abc}	0.73±6.91^{abc}	4.58±3.15^{ab}	-13.38±24.93	27.65±19.77^{ab}	0.31±39.94	-4.04±4.53^{ab}
$s^{H\times K}$	-20.36±4.55^{bc}	5.52±8.92^{abc}	-11.67±4.06^{ab}	8.08±32.19	-20.73±25.52^{bc}	24.27±51.57	1.08±5.85^{ab}
$s^{H\times D}$	13.33±2.03^{abc}	-11.67±3.99^{bc}	16.67±1.82^{ab}	-8.33±14.40	16.67±11.41^{abc}	-18.33±23.06	1.67±2.61^{ab}
$s^{S\times K}$	-18.33±2.88^{bc}	20.00±5.64^{ab}	-20.00±2.57^{ab}	20.00±20.36	-39.00±16.14^{c}	35.00±32.61	-7.17±3.70^{b}
$s^{S\times D}$	4.17±3.05^{abc}	34.17±5.99^{a}	5.00±2.72^{ab}	34.17±21.59	-17.33±17.12^{bc}	52.50±34.59	-6.83±3.92^{b}
$s^{K\times D}$	40.00±3.52^{a}	10.00±6.91^{abc}	35.00±3.15^{a}	8.33±24.93	-12.50±19.77^{bc}	-3.33±39.94	5.00±4.53^{ab}
RE							
$r^{S\times H}$	-8.33±2.27^{bc}	11.67±4.46^{abc}	-15.00±2.03^{ab}	1.67±16.10	4.17±12.76^{abc}	30.00±25.78	2.50±2.92^{ab}
$r^{K\times H}$	-8.75±2.88^{bc}	13.33±5.64^{abc}	6.67±2.57^{ab}	11.67±20.36	7.50±16.14^{abc}	43.33±32.61	-6.17±3.70^{ab}
$r^{D\times H}$	14.74±3.05^{abc}	0.73±5.99^{abc}	5.42±2.72^{ab}	2.04±21.59	-5.10±17.12^{bc}	3.65±34.59	-1.29±3.92^{ab}
$r^{K\times S}$	15.57±1.25^{ab}	1.56±2.44^{abc}	2.92±1.11^{ab}	-5.54±8.82	9.40±6.99^{abc}	-5.52±14.12	10.29±1.60^{ab}
$r^{D\times S}$	7.76±2.88^{abc}	-4.06±5.64^{bc}	18.33±2.57^{ab}	-7.42±20.36	20.85±16.14^{abc}	-16.98±32.61	3.08±3.70^{ab}
$r^{D\times K}$	3.91±2.27^{abc}	8.23±4.46^{abc}	-9.58±2.03^{ab}	8.21±16.10	5.98±12.76^{abc}	7.81±25.78	-8.29±2.92^{b}
P-values							
GCA	***	***	***	***	***	ns	***
SCA	*	ns	ns	ns	*	ns	**
RE	**	***	*	ns	ns	ns	ns
GCA/SCA	2.32	-6.86	4.35	-10.92	2.32	-7.19	0.98

[a-c] Means with the same letter in a column are not significantly different (P > 0.05); ns= non-significant; *P ≤ 0.05; **P ≤ 0.01; ***P ≤ 0.001; H, Improved Horro; S, Commercial Sasso; D, Dz-white; K, Potchefstroom Koekoek; Males are listed first in the cross; GCA, general combining ability; SCA, specific combining ability; RE, reciprocal effect.

Table 25 presents estimate of combining ability for gizzard, heart, and liver weights in different chicken genotypes and sexes, including both purebred and crossbred combinations. Statistical significance was evident for GCA across all traits ($P < 0.001$), particularly strong for gizzard and heart weights. SCA showed significance influenced for gizzard weight ($P = 0.0448$) in males and for liver weight ($P < 0.0001$) in both sexes, but no significance for heart weight ($P = 0.5802$) in for both sexes. On the other hand, effects of RE showed difference ($P < 0.0001$) only for liver weight in both sexes.

Among the purebred genotypes, H consistently showed negative GCA effects on gizzard, heart, and liver weights for both sexes, indicating lower organ weights compared to other genotypes. In contrast, S and K exhibited generally positive estimates for both sexes, with S particularly enhancing heart and liver weights in both males and females, and K showing moderate improvements, especially in male gizzard weight.

For crossbred genotypes, performance varied widely. Notably, the S×K cross demonstrated outstanding positive SCA effects, especially for heart and liver weights, achieving the highest estimates among all crosses 14.30 g and 23.00 g, respectively in males and females. Similarly, the K×D cross yielded significant positive SCA effects on male gizzard weight (2.97 g) but showed negative values for liver weight in females. Other crossbred combinations like H×S and H×D also enhanced heart weights, though to a lesser extent than S×K.

The S×H and K×S reciprocal crosses notably improved heart and liver weights in both sexes, with values like 10.37 g and 11.18 g in S×H males and females, respectively. However, some crosses like D×H and D×S consistently showed negative estimates across most traits, indicating weak combining ability.

The GCA/SCA ratio indicated that additive genetic effects were more pronounced for gizzard weight in males (1.34) but less important for other traits, suggesting dominance and non-additive effects played a larger role in heart and liver weight determination. In general, crosses like S×K, S×H, and K×S exhibited superior combining ability for heart and liver traits, while purebreds like S and K performed moderately well, and H consistently underperformed.

Table 25. Estimates (±SE) of combining ability for gizzard, heart, and liver traits of different genotype and sex

Genotype	Gizzard wt. (g)		Heart wt. (g)	Liver wt. (g)	
	Male	Female	Male	Male	Female
Purebred					
g^H	-3.60±1.23^{b}	-3.87±1.30^{ab}	-1.29±0.56	-4.02±2.69^{cd}	-4.70±6.35^{cd}
g^S	1.75±0.62^{ab}	0.56±0.65^{ab}	1.48±0.28	3.70±1.35^{bc}	4.24±3.18^{bcd}
g^K	2.28±1.23^{ab}	0.81±1.30^{ab}	0.04±0.56	1.96±2.69^{bc}	-0.85±6.35^{bcd}
g^D	-0.43±0.38^{ab}	2.49±0.40^{ab}	-0.23±0.17	-1.64±0.82^{cd}	1.31±1.94^{bcd}
Crossbred					
$s^{H\times S}$	0.45±1.07^{ab}	1.85±1.13^{ab}	0.08±0.48	5.02±2.33^{bc}	1.11±5.50^{bcd}
$s^{H\times K}$	-2.64±1.38^{ab}	1.12±1.46^{ab}	0.01±0.62	2.23±3.01^{bc}	2.77±7.10^{bcd}
$s^{H\times D}$	0.68±0.62^{ab}	-2.75±0.65^{ab}	0.25±0.28	4.35±1.35^{bc}	-1.68±3.18^{bcd}
$s^{S\times K}$	-1.05±0.87^{ab}	5.62±0.92^{a}	-1.47±0.39	14.30±1.50^{a}	23.00±4.49^{a}
$s^{S\times D}$	-3.60±0.93^{b}	0.73±0.98^{ab}	0.63±0.42	-1.72±0.82^{cd}	0.45±4.46^{bcd}
$s^{K\times D}$	2.97±1.07^{a}	-3.92±1.13^{ab}	1.17±0.48	-1.20±2.33^{cd}	-9.50±5.50^{d}
RE					
$r^{S\times H}$	0.72±0.69^{ab}	0.57±0.73^{ab}	-0.63±0.31	10.37±2.02^{ab}	11.18±3.55^{ab}
$r^{K\times H}$	1.55±0.87^{ab}	1.88±0.92^{ab}	-1.22±0.39	2.50±1.90^{bc}	-3.62±4.49^{bcd}
$r^{D\times H}$	-0.17±0.93^{ab}	-4.13±0.98^{b}	-0.73±0.42	-4.89±2.02^{cd}	-8.66±4.76^{d}
$r^{K\times S}$	1.15±0.38^{ab}	-1.21±0.40^{ab}	-0.04±0.17	8.61±0.82^{ab}	11.01±1.94^{abc}
$r^{D\times S}$	-1.50±0.87^{ab}	-2.17±0.92^{ab}	0.92±0.39	-8.45±1.90^{d}	-2.79±4.49^{bcd}
$r^{D\times K}$	-1.49±0.69^{ab}	-0.30±0.73^{ab}	-0.23±0.31	-1.16±1.50^{cd}	-5.52±3.55^{d}
P-values					
GCA	***	***	ns	***	**
SCA	*	ns	ns	***	***
RE	*	*	ns	***	***
GCA/SCA	1.34	0.69	-6.50	0.10	0.08

[a-d] Means with the same letter in a column are not significantly different (P > 0.05); ns= non-significant; *P ≤ 0.05; **P ≤ 0.01; ***P ≤ 0.001; H, Improved Horro; S, Commercial Sasso; D, Dz-white; K, Potchefstroom Koekoek; Males are listed first in the cross; GCA, general combining ability; SCA, specific combining ability; RE, reciprocal effect.

Table 26 provides estimates of combining ability for breast meat quality traits, including meat color (L*, a*, b*) and water holding capacity (WHC). The results revealed notable differences among genotypes and crosses. The GCA effects were not significant for all color traits, except for b* (P = 0.0043). Whereas the SCA effects were significant (P < 0.005) for L*, a*, and b*, highlighting the importance of specific cross combinations for improving meat color. Reciprocal effects were highly significant (P < 0.0001) for a* and b*, confirming the influence of maternal factors in determining these traits.

The K breed demonstrated the most positive GCA effect on lightness (L*) with an estimate of 1.37, while S showed a negative effect (-1.15), suggesting paler meat in K and darker

meat in S birds. Regarding redness (a*), K (0.08) and S (0.01) had slight positive contributions, while H and D had minimal or negative effects. For yellowness (b*), S positively influenced this trait (0.26), while H was negative (-0.21), indicating a tendency for S to produce brighter meat.

Specific combining ability (SCA) effects were especially pronounced for meat color traits. Notably, the S×K cross produced the highest positive effect on L* (5.19), followed closely by H×K (4.08), implying brighter breast meat in these cross combinations. On the other hand, K×D showed a large negative effect on L* (-4.02), associated with darker meat. For redness, S×D (0.20) and H×K (0.15) displayed positive effects, while S×K had the lowest estimate (-0.48). The K×D cross positively affected b* (0.65), outperforming other crosses, while H×D and S×D had notably negative b* values (-0.79 and -0.74, respectively).

The S×H and K×H both showed high positive RE on meat color. For b*, K×H (0.19) and K×S (0.32) demonstrated the highest effect compared to other reciprocals, while S×H (-0.47) exhibited the poorest. The GCA/SCA ratios, particularly low for most traits, indicated that non-additive genetic effects (dominance and interaction effects) played a larger role in determining breast meat quality, especially for meat color. In general, crosses like S×K, K×D and H×K crossbreds showed superior performance in meat color. Among purebreds, K and S exhibited favorable combining ability for meat color.

The estimates of general combining ability (GCA) for water holding capacity (WHC) in chicken breast meat also varied considerably among genotypes. The pure genotype H showed the highest positive GCA effect at 1.76%, indicating its strong potential to pass favorable alleles for WHC to offspring. The reciprocal cross S×H also showed similarly high positive effect (1.68%). In contrast, the pure genotype K had the lowest GCA value of -1.04%, suggesting a tendency to reduce WHC when used as a parent. Other pure lines such as S and D had near-zero or slightly negative GCA effects.

For specific combining ability (SCA), most crosses had negative or near-zero values. The S×K cross exhibited the lowest SCA effect at -1.27%, indicating this particular combination performs poorly for improving WHC. Crosses like H×K (-0.89%) and H×D (-0.48%) also showed negative effects. However, some reciprocal crosses like D×K

(0.71%) and K×H (0.42%) had positive SCA values, suggesting that certain specific parental combinations could slightly enhance WHC.

All effects showed high statistical significance ($P < 0.0001$), and the ratio of GCA to SCA was 1.72, indicating that additive genetic effects (GCA) had a stronger influence on WHC than non-additive effects (SCA).

Table 26. Estimates (±SE) of combining ability for instrumental color and WHC

Genotypes	Traits			
	Meat color			WHC
	L*	a*	b*	
GCA				
g^{H}	0.26±0.63	-0.10±0.15	-0.21±0.12^{bcd}	1.76±0.27^{a}
g^{S}	-1.15±0.32	0.01±0.08	0.26±0.06^{ab}	0.04±0.13^{b-e}
g^{K}	1.37±0.63	0.08±0.15	-0.06±0.12^{a-d}	-1.04±0.27^{ef}
g^{D}	-0.48±0.19	0.01±0.05	0.01±0.04^{a-d}	-0.76±0.08^{c-f}
SCA				
$s^{H\times S}$	-0.50±0.55	-0.02±0.13	-0.30±0.10^{bcd}	0.00±0.23^{b-e}
$s^{H\times K}$	4.08±0.71	0.15±0.17	-0.22±0.13^{bcd}	-0.89±0.30^{def}
$s^{H\times D}$	0.32±0.32	-0.37±0.08	-0.79±0.06^{d}	-0.48±0.13b^{c-f}
$s^{S\times K}$	5.19±0.45	-0.48±0.11	-0.12±0.08^{a-d}	-1.27±0.19^{f}
$s^{S\times D}$	-1.16±0.47	0.20±0.11	-0.74±0.09^{cd}	-0.38±0.20^{b-f}
$s^{K\times D}$	-4.02±0.55	-0.24±0.13	0.65±0.10^{a}	-0.24±0.23^{b-f}
RE				
$r^{S\times H}$	1.72±0.35	0.53±0.08^{a}	-0.47±0.07^{bcd}	1.68±0.15^{a}
$r^{K\times H}$	0.17±0.45	0.54±0.11^{a}	0.19±0.08^{ab}	0.42±0.19^{bc}
$r^{D\times H}$	-2.51±0.47	-0.34±0.11^{cd}	-0.14±0.09^{a-d}	-0.68±0.20^{c-f}
$r^{K\times S}$	0.88±0.19	-0.29±0.05^{bcd}	0.32±0.04^{ab}	0.24±0.08^{b-d}
$r^{D\times S}$	-1.38±0.45	0.08±0.11^{abc}	0.06±0.08^{abc}	-0.16±0.19^{b-f}
$r^{D\times K}$	-3.47±0.35	0.06±0.08^{abc}	0.32±0.07^{ab}	0.71±0.15^{ab}
P-value				
GCA	ns	ns	**	***
SCA	ns	**	**	***
RE	ns	***	***	***
GCA/SCA	0.01	0.03	0.18	1.72

$^{a-f}$ Means with the same letter in a column are not significantly different ($P > 0.05$); ns= non-significant; **$P \leq 0.01$; ***$P \leq 0.001$; H, Improved Horro; S, Commercial Sasso; D, Dz-white; K, Potchefstroom Koekoek; Males are listed first in the cross; GCA, general combining ability; SCA, specific combining ability; RE, reciprocal effect.

Table 27 presents the estimates of combining ability for the proximate composition of breast meat, focusing on moisture (MO), crude protein (CP), crude fat (CF), crude ash (CA), and energy content (kcal). The analysis shows a marked influence of genotype, the significant GCA effects for CP ($P = 0.0256$) and CA ($P = 0.0093$), indicating these traits

were moderately influenced by additive genetic effects. SCA was significant for MO ($P = 0.0161$), CP ($P < 0.0001$), and CF ($P = 0.0458$), emphasizing the importance of specific cross combinations for these meat quality attributes. RE were highly significant ($P < 0.0001$) for most traits, particularly reflecting maternal or cross-directional influences on MO, CP, CF, and CA. Energy content, however, was less influenced by both genetic and reciprocal effects.

For GCA, S exhibited the highest positive estimate for MO (0.25%), while K (-0.17%) and D (-0.14%) contributed negatively, though none of these effects reached high magnitudes. In terms of CP, K (0.33%) and D (0.15%) showed positive contributions, while S had a negative effect (-0.41%), suggesting possible differences in the lean content of their progeny. CF estimates showed S contributing positively (0.08%), while K (-0.12%) slightly reduced fat content. For CA, only minor variations existed, but S again had a positive estimate (0.08%), while others remained near zero or negative. Energy content estimates were generally minimal among purebreds.

SCA effects were much more prominent. Notably, the S×D cross demonstrated the highest positive effect for CF (1.27%), suggesting greater intramuscular fat deposition in this combination. It was followed by S×K (0.78%), whereas crosses like H×S (-0.41%) and K×D (-0.24%) negatively influenced fat content. For CP, H×D (1.36%) exhibited the strongest positive contribution, while S×D (-2.32%) had the largest negative impact. The H×K cross stood out for its notable positive effect on CA content (0.26%), while H×S (-0.15%) reduced ash content.

Reciprocal crossbreeding effects were significant across nearly all traits. K×H (0.86%) and D×K (0.88%) showed high positive estimates for MO, with K×H also contributing strongly to CF (1.19%) and energy (3.51 kcal). In contrast, K×S (-0.43%) lowered CF content substantially. CP showed the highest positive influence in K×S (0.94%), and the most negative in K×H (-1.80%). CA estimates followed a similar pattern, with K×H (-0.25%) and K×S (-0.19%) reducing ash content, while other combinations such as D×H (0.06%) had small positive effects.

Table 27. Estimates (±SE) of combining ability for proximate composition of meat

Genotype	MO (%)	CP (%)	CF (%)	CA (%)	Energy (kcal)
GCA					
g^H	0.06±1.24	-0.07±1.14^{abc}	0.04±0.13	-0.03±0.02^{b-e}	0.10±5.65
g^S	0.25±0.62	-0.41±0.57^{bcd}	0.08±0.07	0.08±0.01^{a-d}	-0.94±2.82
g^K	-0.17±1.24	0.33±1.14^{abc}	-0.12±0.13	-0.04±0.02^{b-e}	0.22±5.65
g^D	-0.14±0.38	0.15±0.35^{abc}	0.00±0.04	-0.01±0.01^{b-e}	0.62±1.73
SCA					
$s^{H\times S}$	-0.49±1.07^{ab}	1.05±0.98^{ab}	-0.41±0.12^{bc}	-0.15±0.02^{de}	0.51±4.89
$s^{H\times K}$	-0.20±1.38^{ab}	-0.15±1.27^{abc}	0.08±0.15^{bc}	0.26±0.02^{a}	0.16±6.31
$s^{H\times D}$	-1.21±0.62^{b}	1.36±0.57^{a}	-0.33±0.07^{bc}	0.18±0.01^{ab}	2.50±2.82
$s^{S\times K}$	0.03±0.87^{ab}	-0.77±0.80^{cd}	0.78±0.09^{ab}	-0.04±0.02^{b-e}	3.94±3.99
$s^{S\times D}$	0.94±0.93^{a}	-2.32±0.85^{e}	1.27±0.10^{a}	0.11±0.02^{abc}	2.15±4.23
$s^{K\times D}$	1.05±1.07^{a}	-0.67±0.98^{cd}	-0.24±0.12^{bc}	-0.13±0.02^{de}	-4.88±4.89
RE					
$r^{S\times H}$	0.47±0.69^{ab}	-1.04±0.63^{cde}	0.67±0.07^{abc}	-0.11±0.01^{cde}	1.87±3.16
$r^{K\times H}$	0.86±0.87^{a}	-1.80±0.80^{de}	1.19±0.09^{a}	-0.25±0.02^{e}	3.51±3.99
$r^{D\times H}$	-0.41±0.93^{ab}	0.52±0.85^{abc}	-0.17±0.10^{bc}	0.06±0.02^{a-d}	0.58±4.23
$r^{K\times S}$	-0.33±0.38^{ab}	0.94±0.35^{ab}	-0.43±0.04^{c}	-0.19±0.01^{e}	-0.07±1.73
$r^{D\times S}$	0.13±0.87^{ab}	-0.29±0.80^{bcd}	0.08±0.09^{bc}	0.08±0.02^{a-d}	-0.46±3.99
$r^{D\times K}$	0.88±0.69^{a}	-0.77±0.63^{cd}	-0.07±0.07^{bc}	-0.04±0.01^{b-e}	-3.74±3.16
P-value					
GCA	ns	*	ns	**	ns
SCA	**	***	*	***	ns
RE	***	***	***	***	ns
GCA/SCA	0.01	0.04	-0.04	0.04	1.23

[a-e] Means with the same letter in a column are not significantly different (P > 0.05); ns= non-significant; *P ≤ 0.05; **P ≤ 0.01; ***P ≤ 0.001; H, Improved Horro; S, Commercial Sasso; D, Dz-white; K, Potchefstroom Koekoek; Males are listed first in the cross; GCA, general combining ability; SCA, specific combining ability; RE, reciprocal effect.

Combining ability for fertility and hatchability

Table 28 provides the estimates of combining ability for fertility and hatchability traits, including fertility percentage, hatchability of total eggs set (HTES), and hatchability of fertile eggs (HFE). The GCA effects were highly significant (P < 0.0001) for fertility and HTES, and moderately significant for HFE (P < 0.05). SCA effects were also significant for fertility and HTES (P < 0.0001), while non-significant for HFE (P > 0.05). RE were significant for all traits, particularly HTES (P < 0.01) and HFE (P < 0.05).

Among the parents, genotype K exhibited the highest positive GCA effects for fertility (2.13%), HTES (2.75%), and HFE (1.14%), indicating its superior additive genetic

contribution to reproductive performance. In contrast, genotype H recorded consistently negative GCA estimates for fertility (-3.50%), HTES (-4.43%), and HFE (-1.82%), suggesting its poor general combining ability for these traits. Genotype S showed moderate positive GCA effects across the three traits, while D exhibited low to slightly negative estimates, particularly for HFE (-0.17%).

The cross H×K exhibited the highest positive SCA values for fertility (3.89%), HTES (5.06%), and HFE (2.15%), making it the most promising combination for enhancing reproductive traits through non-additive gene actions. Another notable combination was S×D, which exhibited favorable SCA estimates, especially for HTES (2.81%) and HFE (1.41%). On the other hand, negative SCA values were recorded in combinations such as K×D, which showed particularly low performance for HFE (-3.16%) alongside reduced fertility (-0.11%) and HTES (-2.96%).

Reciprocal effects (RE) were also significant across the evaluated traits, underscoring the importance of maternal and egg cytoplasmic influences on reproductive efficiency. The cross direction had a pronounced impact, with the reciprocal combination S×H displaying the highest positive effects for HTES (4.58%) and an outstanding value for HFE (5.91%). Similarly, D×S demonstrated favorable reciprocal effects for HTES (3.22%) and HFE (2.37%). On the other hand, negative reciprocal estimates were observed in crosses such as D×K, which exhibited consistently negative values across all traits, particularly HFE (-2.38%).

Table 28. Estimates (±SE) of combining ability for fertility and hatchability traits

Genotype	Fertility (%)	HTES (%)	HFE (%)
GCA			
g^H	-3.50±2.98^{e}	-4.43±3.43^{f}	-1.82±1.03^{b}
g^S	0.72±1.49^{bcd}	1.30±1.71^{a-e}	0.85±0.52^{ab}
g^K	2.13±2.98^{ab}	2.75±3.43^{a-d}	1.14±1.03^{ab}
g^D	0.65±0.91^{bcd}	0.37±1.05^{a-f}	-0.17±0.32^{ab}
SCA			
$s^{H\times S}$	-1.54±2.58^{cde}	-0.18±2.97^{b-f}	1.46±0.90
$s^{H\times K}$	3.89±3.33^{a}	5.06±3.83^{a}	2.15±1.16
$s^{H\times D}$	-1.99±1.49^{de}	-2.33±1.71^{def}	-0.85±0.52
$s^{S\times K}$	-0.40±2.11^{bcd}	0.12±2.42^{a-f}	0.52±0.73
$s^{S\times D}$	1.76±2.23^{ab}	2.81±2.57^{a-d}	1.41±0.78
$s^{K\times D}$	-0.11±2.58^{bcd}	-2.96±2.97^{ef}	-3.16±0.90
RE			
$r^{S\times H}$	-0.52±1.66^{bcd}	4.58±1.92^{ab}	5.91±0.58^{a}
$r^{K\times H}$	0.45±2.11^{bcd}	-1.01±2.42^{c-f}	-1.52±0.73^{b}
$r^{D\times H}$	0.32±2.23^{bcd}	-0.81±2.57^{c-f}	-1.16±0.78^{ab}
$r^{K\times S}$	-0.26±0.91^{bcd}	-0.18±1.05^{b-f}	-0.04±0.32^{ab}
$r^{D\times S}$	1.23±2.11^{abc}	3.22±2.42^{abc}	2.37±0.73^{ab}
$r^{D\times K}$	-0.14±1.66^{bcd}	-2.25±1.92^{def}	-2.38±0.58^{b}
P-value			
GCA	***	***	*
SCA	***	***	ns
RE	**	***	**
GCA/SCA	0.63	0.56	0.22

$^{a-g}$Means with the same letter in a column are not significantly different (P > 0.05); ns= non-significant; *P ≤ 0.05; **P ≤ 0.01; ***P ≤ 0.001; H, Improved Horro; S, Sasso; D, Dz-white; K, Potchefstroom Koekoek; Males are listed first in the cross; GCA, general combining ability; SCA, specific combining ability; RE, reciprocal effect.

Combining ability for egg production traits

Estimates of combining ability and reciprocal effect for egg production traits are detailed in Table 29. For all the studied egg production traits, GCA effects were significantly different (P < 0.0001) among purebred genotypes. The K breed showed the highest positive GCA values for most traits, except AFE, while the S breed had moderately positive GCA value, except for HHEP, HDEP, and EN. The D breed displayed moderate positive GCA values for most egg production traits, excluding AFE, BWSM, and EWAFE, and the H breed exhibited predominantly negative GCA values, except for AFE.

Variation due to SCA were high ($P < 0.0001$) for all egg production traits, with positive values observed across genetic groups, except for AFE. The H×K crossbred had the highest SCA for BWSM, followed by S×K, H×D, S×D, and H×S. On the other hand, the S×D crossbred showed the highest SCA for EWAFE, while S×K had the highest value for HHEP, HDEP, EM, and EN. However, the K×D crossbred recorded the lowest SCA for BWSM, HHEP, HDEP, and EN.

The RE values were significantly different ($P < 0.0001$) for EWAFE, HHEP, HDEP, EM, and EN among genetic groups. The D×K crossbred had the highest positive RE for EWAFE, while D×H showed the highest RE for HHEP and HDEP. The K×S crossbred showed the highest RE for EM, and D×H for EN. Negative RE were observed in S×H and K×H for EWAFE, and for D×S, S×H, and K×H for EN. The GCA/SCA ratios varied, with EWAFE having the highest ratio (1.51), indicating a strong GCA influence. HHEP, HDEP, EM, and EN showed moderate ratios, while AFE and BWSM had the lowest.

Table 29. Estimates (±SE) of combining ability for egg production traits

Genotype	Egg production traits						
	AFE	BWSM	EWAFE	HHEP	HDEP	EM	EN
g^{H}	0.63±1.68^{ab}	-111.38±6.61^{g}	-1.76±0.35^{f}	-3.17±0.58^{h}	-3.45±0.28^{de}	-336.71±19.47^{f}	-3.83±0.22^{e}
g^{S}	2.24±0.84^{ab}	99.73±4.67^{ab}	1.57±0.18^{abc}	-1.48±0.50^{gh}	-0.50±0.14^{cd}	10.28±9.73^{e}	-0.89±0.11^{de}
g^{K}	-1.66±1.68^{abc}	36.09±6.61^{cd}	0.64±0.35^{b-e}	3.79±0.58^{abc}	3.39±0.28^{b}	324.37±19.47^{ab}	4.20±0.22^{bc}
g^{D}	-1.21±0.51^{abc}	-24.45±2.02^{ef}	-0.44±0.11^{e}	0.86±0.18^{efg}	0.56±0.09^{bc}	2.06±5.96^{e}	0.53±0.07^{d}
$s^{H\times S}$	-1.03±1.45^{abc}	12.50±5.72^{cde}	0.85±0.30^{b-e}	1.72±0.50^{c-f}	1.09±0.24^{bc}	37.75±16.86^{e}	2.06±0.19^{bcd}
$s^{H\times K}$	-4.71±1.87^{c}	94.75±7.39^{ab}	0.09±0.39^{e}	1.41±0.65^{c-f}	1.26±0.31^{bc}	240.29±21.76^{bcd}	2.70±0.25^{bcd}
$s^{H\times D}$	-1.98±0.84^{abc}	16.67±3.30^{cde}	1.83±0.18^{ab}	4.22±0.29^{ab}	3.70±0.14^{b}	243.88±9.73^{bcd}	5.11±0.11^{ab}
$s^{S\times K}$	-0.57±1.19^{abc}	39.22±4.67^{cd}	1.50±0.25^{a-d}	5.57±0.41^{a}	6.50±0.20^{a}	474.75±13.76^{a}	7.72±0.16^{a}
$s^{S\times D}$	-1.38±1.26^{abc}	12.67±4.95^{cde}	2.27±0.26^{a}	3.49±0.43^{a-d}	3.05±0.21^{b}	279.87±14.60^{bc}	2.52±0.17^{bcd}
$s^{K\times D}$	-0.55 ±1.45^{abc}	7.00±5.72^{cde}	1.92±0.30^{ab}	-0.68±0.50^{fg}	-0.68±0.24^{cd}	152.25±16.86^{b-e}	-0.81±0.19^{de}
$r^{S\times H}$	1.27±0.94	8.569±3.60^{cde}	-1.70±0.20^{f}	-0.38±0.32^{efg}	-0.50±0.16^{cd}	83.15±10.88^{de}	-0.68±0.12^{de}
$r^{K\times H}$	2.48±1.19	-10.39±4.67^{de}	-2.02±0.25^{f}	-5.70±0.41^{i}	-5.70±0.20^{e}	-396.15±13.76^{f}	-7.19±0.16^{f}
$r^{D\times H}$	-1.67±1.26	48.80±4.95^{b}	0.51±0.26^{cde}	2.06±0.43^{b-e}	2.33±0.21^{bc}	168.31±14.60^{b-e}	2.54±0.17^{bcd}
$r^{K\times S}$	0.90±0.51	108.59±2.02^{a}	0.24±0.11^{de}	1.45±0.18^{c-f}	1.77±0.09^{bc}	180.35±5.96^{b-e}	0.77±0.07^{cd}
$r^{D\times S}$	-0.74±1.19	47.46±4.67^{bc}	0.14±0.25^{e}	-0.22±0.41^{efg}	-0.13±0.20^{c}	95.15±13.76^{cde}	-0.27±0.16^{d}
$r^{D\times K}$	-2.57±0.94	-66.12±3.69^{fg}	0.62±0.20^{b-e}	1.07±0.32^{def}	0.94±0.16^{bc}	61.15±10.88^{de}	2.03±0.12^{bcd}
P-values							
GCA	***	***	***	***	***	***	***
SCA	***	***	***	***	***	***	***
RE	ns	*	***	***	***	***	***
GCA/SCA	0.100	0.370	1.507	0.670	0.638	0.494	0.447

[a-g]Means with the same letter in a column are not significantly different (P > 0.05); ns= non-significant; *P ≤ 0.05; ***P ≤ 0.001; H, Improved Horro; S, Sasso; K, Potchefstroom Koekoek; D, Dz-white; g, General Combining Ability; s, Specific Combining Ability; r, Reciprocal Effect; Males are listed first in the cross.

Combining ability for egg quality traits

Estimates of GCA, SCA, and RE for egg quality traits are presented in Table 30. From the results, GCA effects were highly significant ($P < 0.001$) for EWT, EL, EW, AW, YW, YWT, and YR, but not for ST. The S breed showed the highest positive GCA estimates for EWT, followed by K breed, while the D and H breeds had negative values. Positive GCA estimate for EL was observed in H and K breeds, while S and D breeds showed negative estimates. The D breed exhibited the highest positive GCA value for AW, followed by K, with S and H breeds, showing negative values. Only the S breed recorded positive GCA value for YW and YWT, while D, K, and H breeds showed negative estimates. For YR, similarly the S breed showed the highest positive GCA estimate, followed by H, while D and K had small negative estimates.

The SCA variations were highly significant ($P < 0.001$) for all traits. The S×D crossbred had the highest positive SCA estimate for EWT, followed by K×D, H×K, S×K, and H×S, while H×D recorded a negative SCA estimate. The K×D crossbred showed the highest positive SCA value for EL, followed by H×S, S×K, and H×K, while H×D and S×D had negative estimates. For ST, the H×K crossbred had the highest positive SCA estimate, while K×D and S×D exhibited small negative SCA values. Positive SCA estimates for AW were observed in K×D, H×S, and S×K, while S×D, H×K, and H×D showed negative estimates. Most SCA estimates for YW were negative, except for S×D and S×K. By contrast, S×K showed the highest positive SCA values for YWT, while H×S gave the highest negative estimate. For YR, only H×D and S×K exhibited positive SCA estimates, while the remaining crosses showed negative values.

The RE value was significantly different ($P < 0.05$) for EWT, EW, ST, AW, and YR, but not for EL, YW, and YWT. From the present study, the K×S crossbred had the highest positive RE for EWT, followed by D×S, D×H, and D×K, while K×H and S×H showed negative values. For EW, estimates of RE was positive for most crosses, except S×H and D×S. However, D×S had the highest positive estimate for ST. The K×S crossbred exhibited the highest positive estimate for AW but negative estimate for YR. On the other hand, the S×H crossbred exhibited the highest positive estimate for YR.

Table 30. Estimates (±SE) of combining ability for egg quality traits

Genotypes	EWT (g)	EL (mm)	EW (mm)	ST (mm)	AW (mm)	YW (mm)	YWT (g)	YR (%)
GCA	***	**	*	ns	***	***	***	***
g^{H}	-1.64^{hi}±0.27	0.89^{a}±0.36	0.45^{a}±0.36	0.01±0.01	-2.29^{abc}±0.12	-1.27^{cd}±0.58	-0.11^{abc}±0.58	0.80^{ab}±1.25
g^{S}	1.40^{ab}±0.13	-0.66^{ab}±0.18	-0.29^{ab}±0.18	-0.01±0.01	-0.92^{ab}±0.06	2.16^{a}±0.29	1.14^{ab}±0.29	1.44^{ab}±0.62
g^{K}	0.79^{ad}±0.27	0.67^{ab}±0.36	0.53^{a}±0.36	0.00±0.01	0.41^{ab}±0.12	-0.87^{bcd}±0.58	-0.46^{abc}±0.58	-1.37^{b}±1.25
g^{D}	-0.55^{fg}±0.08	-0.90^{ab}±0.11	-0.68^{ab}±0.11	0.00±0.00	2.80^{a}±0.04	-0.03^{abc}±0.18	-0.57^{abc}±0.18	-0.87^{b}±0.38
SCA	***	***	***	***	***	***	***	***
$s^{H\times S}$	0.23^{cf}±0.23	0.75^{a}±0.31	0.50^{a}±0.31	0.03^{ad}±0.01	2.69^{a}±0.10	-2.87^{d}±0.50	-0.64^{abc}±0.50	-1.35^{b}±1.08
$s^{H\times K}$	1.13^{abc}±0.30	0.21^{ab}±0.40	-0.87^{ab}±0.40	0.05^{a}±0.01	-5.06^{bc}±0.13	-0.85^{bcd}±0.65	0.02^{abc}±0.65	-0.71^{b}±1.40
$s^{H\times D}$	-1.17^{gh}±0.13	-1.33^{ab}±0.18	-1.30^{ab}±0.18	0.01^{ad}±0.01	-8.07^{c}±0.06	-0.04^{abc}±0.29	0.03^{abc}±0.29	0.65^{ab}±0.62
$s^{S\times K}$	0.82^{ad}±0.19	0.46^{ab}±0.25	0.69^{a}±0.25	0.00^{af}±0.01	0.90^{ab}±0.08	0.48^{abc}±0.41	0.31^{abc}±0.41	0.13^{ab}±0.88
$s^{S\times D}$	1.53^{a}±0.20	-1.42^{ab}±0.27	-1.15^{ab}±0.27	-0.05^{f}±0.01	-0.87^{ab}±0.09	0.74^{abc}±0.44	-0.18^{abc}±0.44	-1.19^{b}±0.94
$s^{K\times D}$	1.25^{abc}±0.23	1.64^{a}±0.31	1.88^{a}±0.31	-0.01^{bf}±0.01	2.88^{a}±0.10	-0.03^{abc}±0.50	-0.28^{abc}±0.50	-1.12^{b}±1.08
RE	***	ns	*	**	***	ns	ns	**
$r^{S\times H}$	-2.26^{i}±0.15	1.05±0.20	-0.19^{ab}±0.20	0.02^{ad}±0.01	1.55^{a}±0.06	-0.10±0.33	1.43±0.33	4.08^{a}±0.70
$r^{K\times H}$	-0.28^{efg}±0.19	0.25±0.25	0.28^{ab}±60.25	-0.02^{def}±0.01	-3.15^{abc}±0.08	-0.04±0.41	0.41±0.41	0.93^{ab}±0.88
$r^{D\times H}$	0.34^{cf}±0.20	0.82±0.27	0.79^{a}±0.27	-0.01^{cf}±0.01	1.40^{a}±0.09	-1.32±0.44	-1.21±0.44	-2.79^{b}±0.94
$r^{K\times S}$	1.02^{ad}±0.08	0.96±0.11	1.40^{a}±0.11	-0.04^{ef}±0.00	2.94^{a}±0.04	1.06±0.18	0.23±0.18	-0.08^{b}±0.38
$r^{D\times S}$	0.46^{be}±0.19	-5.38±0.25	-5.21^{b}±0.25	0.04^{abc}±0.01	-2.54^{abc}±0.08	1.81±0.41	0.50±0.41	0.75^{ab}±0.88
$r^{D\times K}$	0.05^{def}±0.15	0.02±0.20	0.68^{a}±0.20	0.05^{ab}±0.01	2.00^{a}±0.06	-1.56±0.33	-0.86±0.33	-1.64^{b}±0.70
GCA/SCA	0.681	0.044	0.016	0.002	0.259	0.227	0.345	0.158

$^{a\text{-}g}$Means with the same letter in a column are not significantly different (P > 0.05); ns= non-significant; *P ≤ 0.05; **P ≤ 0.01; ***P ≤ 0.001; H, Improved Horro; S, Commercial Sasso; D, Dz-white; K, Potchefstroom Koekoek; Males are listed first in the cross; GCA, general combining ability; SCA, specific combining ability; RE, reciprocal effect.

4.6.3. Maternal effects (M^e)

Maternal effects on meat and carcass traits

Table 31 depict the M^e on various carcass characteristics across different genotypes. For slaughter weight (SW), the M^e ranged widely, with the cross K×D showing a significantly negative M^e (-148.33, P = 0.030), while other combinations such as H×K (20.00, P = 0.401) and H×S (21.67, P = 0.184) recorded non-significant positive effects. A similar trend was observed for dressed carcass weight (DW), where H×S had a significant positive M^e (36.67, P = 0.043), while H×D exhibited a significantly negative M^e (-80.00, P < 0.01). The S×D also recorded a significant positive M^e for DW (110.00, P < 0.05), suggesting notable M^e contributions from the S dam line when crossed with D.

In terms of eviscerated weight (EW), the M^e was markedly negative and highly significant in S×K (-80.00, P < 0.001), indicating a detrimental maternal influence on this trait in that cross. Though other combinations exhibited varying effects, none were statistically significant. For thigh weight (TWT), the K×D cross demonstrated a significantly negative M^e (-40.00, P = 0.012), while other combinations did not show significant differences, though H×K approached significance (P = 0.078). Regarding dream steak weight (DWT), no significant M^e were observed across the combinations. Breast weight (BWT) also showed no significant M^e, although S×K presented a numerically higher value (39.00, P = 0.136), albeit non-significant.

For wing, back, and gizzard weights, no M^e reached significance, although S×D showed a significant positive M^e for gizzard weight (3.60, P = 0.020). A significant negative M^e was detected for heart weight in the K×D cross (-1.17, P = 0.042), indicating that the K dam line reduced heart weight when crossed with D. However, liver weight presented notable M^e in several combinations. A positive and significant M^e was observed in H×S (10.37, P = 0.026), while a negative effect was recorded in H×D (-4.35, P = 0.044) and S×K (-14.30, P = 0.005).

Table 31. Estimates (±SE) of maternal effect on carcass characteristics traits

Traits	H×K		H×S		H×D		S×K		S×D		K×D	
	M^e	P	M^e	P	M^e	P	M^e	P	M^e	P	M^e	P
SW	20.00±22.91	0.401	21.67±15.28	0.184	-110.00±31.22	0.005	8.33±25.17	0.747	10.83±31.46	0.737	-148.33±59.65	0.030
DW	36.67±75.72	0.638	36.67±16.07	0.043	-80.00±21.80	0.004	8.33±28.43	0.775	110.0±45.00	0.033	-125.00±77.62	0.136
EV	21.67±62.52	0.735	-3.83±22.67	0.869	-53.33±63.71	0.420	-80.0±5.00	0.000	28.33±14.43	0.075	-100.0±65.57	0.155
TWT	-8.75±4.51	0.078	-8.33±10.41	0.440	-13.33±20.21	0.523	18.33±12.6	0.173	-4.17±12.83	0.751	-40.00±13.23	0.012
DWT	6.67±15.28	0.671	-15.0±21.79	0.506	-16.67±27.54	0.557	20.0±18.03	0.291	-5.00±5.00	0.339	35.00±21.79	0.137
BWT	7.50±10.90	0.506	4.17±5.75	0.484	-16.67±17.56	0.363	39.0±24.25	0.136	17.33±16.62	0.319	12.50±46.30	0.792
Wing	-6.17±7.69	0.439	2.50±2.50	0.339	-1.67±7.64	0.831	7.17±6.05	0.261	6.83±5.01	0.200	-5.00±5.00	0.339
Back	8.33±17.56	0.644	11.67±10.41	0.286	-6.67±29.30	0.824	11.67±10.41	0.286	5.00±18.03	0.787	-6.67±16.07	0.686
Gizzard	1.55±1.96	0.445	0.72±1.67	0.675	-0.68±4.09	0.870	1.05±2.21	0.644	3.60±1.32	0.020	-2.97±3.47	0.410
Heart	-1.22±1.73	0.497	-0.63±1.30	0.635	-0.25±0.96	0.803	1.47±1.53	0.359	-0.63±1.16	0.596	-1.17±0.51	0.042
Liver	2.50±4.90	0.620	10.37±4.03	0.026	-4.35±1.91	0.044	-14.30±4.04	0.005	1.72±2.28	0.466	1.20±4.12	0.776

M^e= Maternal effect; P = P -values; SW= slaughter weight; DW= dressed carcass weight; EV= eviscerated weight; TWT= Tigh weight; DWT= dream steak weight; BWT= breast weight

Maternal effects on fertility and hatchability traits

The estimates of M^e on fertility and hatchability traits revealed varying degrees of influence among the genotype combinations (Table 32). For fertility, the M^e was highly significant and positive in the H×D cross (1.99, $P < 0.001$), indicating a strong positive contribution from the H dam line when crossed with D. On the other hand, a significant negative M^e was recorded in the S×D combination (-1.76, $P < 0.001$), suggesting a detrimental effect from the S dam line in this pairing. The other genotype combinations did not show significant maternal effects on fertility.

In terms of hatchability of total eggs set (HTES), significant positive M^e were noted in H×D (2.33, $P = 0.009$) and K×D (2.96, $P = 0.001$) crossbreds, indicating beneficial maternal contributions from H and K dams in these combinations. Other crosses, although showing both positive and negative effects, were not statistically significant.

Regarding hatchability of fertile eggs (HFE), a significant positive M^e was observed in the K×D combination (3.16, $P = 0.030$), highlighting a favorable maternal influence of the K dam line on this trait when crossed with D. No other combinations showed significant M^e for HFE, though numerically higher estimates were seen in H×S (5.91, $P = 0.303$), albeit without statistical significance.

Table 32. Estimates (±SE) of maternal effect on fertility and hatchability traits

Genotypes	Fertility		HTES		HFE	
	M^e	P-value	M^e	P-value	M^e	P-value
H×K	0.45±1.03	0.672	-1.01±1.71	0.567	-1.53±2.24	0.510
H×S	-0.52±2.42	0.835	4.58±2.76	0.126	5.91±5.47	0.303
H×D	1.99±0.13	0.000	2.33±0.73	0.009	0.85±0.93	0.378
S×K	0.40±1.03	0.708	-0.12±1.06	0.910	-0.52±2.13	0.812
S×D	-1.76±0.11	0.000	-2.81±1.84	0.155	-1.41±1.95	0.483
K×D	0.11±0.55	0.849	2.96±0.68	0.001	3.16±1.27	0.030

M^e= Maternal effect; HTES, hatchability from total egg set; HFE, hatchability from fertile egg

Maternal effects on egg production and egg quality traits

Table 33 presents estimate of the M^e on egg production traits, showing varying magnitudes with both positive and negative values. Most egg production traits exhibited positive M^e. The H×S cross combination had a positive M^e on AFE, whereas H×K, H×D, S×K, S×D, and K×D displayed negative effects. Positive M^e values were observed for BWSM and EM across all cross combinations. For EWAFE, all combinations except H×S showed positive estimate. EN had positive M^e for H×K, H×D, S×K, and S×D, but negative for H×S and K×D crossbreds.

Estimates of M^e for the studied egg quality traits also varied, displaying both positive and negative values with low to moderate to high magnitudes (Table 34). With the exception of the H×D, all other crosses displayed negative M^e on EWT. In terms of EL, the S×K and K×D crossbred showed negative estimates, while the remaining crosses exhibited positive estimates. For EW, the estimates were positive for the H×K, H×S, and S×D, whereas the other three cross combination exhibited negative estimates. Regarding SWT and SR, the H×S and H×D cross combinations demonstrated negative M^e, while the H×K, S×K, S×D, and K×D showed positive estimates. However, for ST, the H×K, H×D, and S×K crosses exhibited negative estimates, whereas the H×S, S×D, and K×D displayed positive estimates.

For AH, all crosses except H×D and S×D exhibited negative estimates. In contrast, only the S×D and K×D showed negative estimates for AW. Similarly, YH displayed negative estimates for all crosses except S×K. For YW, only the H×K and H×S showed negative estimates, while the others exhibited positive values. On the other hand, YWT and YR displayed positive M^e for all cross combinations except H×D and S×D.

Table 33. Estimates (±SE) of maternal effect on egg production traits

Genotypes	AFE		BWSM		EWAFE		EM		EN	
	M^e	P-value	M^e	P-value	M^e	P-value	M^e	P-value	M^e	P-value
H×K	-2.48±0.00	0.448	10.39±10.09	0.325	2.02±0.39	<0.001	396.1±48.08	<0.001	7.19±0.86	<0.001
H×S	1.27±1.01	0.235	8.44±17.79	0.644	-1.53±0.18	<0.001	83.15±81.97	0.322	-0.68±1.56	0.669
H×D	-1.98±0.46	0.001	16.67±19.97	0.421	1.83±0.65	0.017	243.8±47.99	<0.001	5.11±1.02	<0.001
S×K	-0.57±1.74	0.751	39.22±9.46	0.002	1.49±0.57	0.025	474.8±54.2	<0.001	7.72±1.36	<0.001
S×D	-1.38±1.83	0.467	12.70±15.56	0.432	2.27±0.26	<0.001	279.9±57.1	<0.001	2.52±1.07	0.039
K×D	-0.55±1.35	0.692	7.00±30.64	0.823	1.92±0.23	<0.001	152.2±33.8	0.001	-0.81±1.02	0.443

M^e= Maternal effect; AFE, age at first egg; BWSM, body weight at sexual maturity; egg weight at first egg; EM, egg mass; EN, total egg number.

Table 34. Estimates (±SE) of maternal effect on egg quality traits

Traits	H×K		H×S		H×D		S×K		S×D		K×D	
	M^e	P	M^e	P	M^e	P	M^e	P	M^e	P	M^e	P
EWT	-0.28±0.03	<0.001	-2.25±0.58	0.002	1.17±0.29	0.002	-0.82±0.44	0.939	-1.53±0.27	<0.001	-1.25±0.28	0.001
EL	0.25±1.23	0.840	1.05±1.47	0.492	1.33±0.73	0.094	-0.46±2.05	0825	1.42±2.17	0.526	-1.64±1.34	0.246
EW	0.28±0.72	0.710	-0.19±0.59	0.757	1.30±0.62	0.060	-0.69±0.27	0.025	1.14±2.45	0.649	-1.88±2.05	0.379
SWT	0.27±0.24	0.273	-0.05±0.31	0.860	0.09±0.27	0.727	0.05±0.26	0.868	0.08±0.51	0.873	0.17±0.41	0.694
ST	-0.02±0.02	0.318	0.01±0.02	0.444	-0.01±0.02	0.463	-0.00±0.02	0.915	0.05±0.02	0.037	0.01±0.01	0.626
SR	0.58±0.46	0.234	0.34±0.63	0.597	-0.04±0.47	0.934	0.24±0.58	0.689	0.47±1.02	0.653	0.57±0.82	0.503
AH	-0.14±0.63	0.829	-0.22±0.05	<0.001	0.05±0.33	0.883	-0.19±0.50	0.707	0.17±0.52	0.754	-0.06±0.09	0.524
AW	-3.15±1.98	0.141	1.54±2.21	0.498	8.07±2.08	0.002	0.89±2.49	0.725	-0.87±0.99	0.400	-2.88±0.34	<0.001
YH	-0.50±0.83	0.561	-0.19±0.70	0.789	-0.29±0.69	0.678	0.50±0.29	0.108	-0.05±0.75	0.943	-0.05±0.75	0.944
YW	-0.04±0.41	0.926	-0.10±0.69	0.888	0.04±1.63	0.983	0.48±0.28	0.116	0.74±1.19	0.549	0.03±1.43	0.983
YWT	0.41±1.10	0.706	1.43±0.57	0.029	-0.03±0.41	0.942	0.31±1.11	0.783	-0.18±0.63	0.779	0.28±0.36	0.457
YR	0.93±2.05	0.658	4.08±1.18	0.005	-0.65±0.72	0.378	0.13±2.24	0.954	-1.19±1.34	0.393	1.12±0.81	0.196

M^e= Maternal effect; P = P -values; EWT, egg weight; EL, egg length; EW, egg width; SWT, shell weight; ST, shell thickness; SR, shell ratio; AH, albumen height; AW, albumen width; YH, yolk height; YW, yolk width; YWT, yolk weight; YR, yolk ratio; HU, hugh unit.

5. DISCUSSION

5.1. Growth Performance and Feed Efficiency

Breed effect on body weight

The BW trait in chickens is of paramount importance in poultry production for several reasons, as it directly affects both economic profitability and production efficiency (Zhong *et al*., 2024). Therefore, in the present study the crossbreeding effects on BW from a full diallel cross involving four (H, S, K, and D) chicken breeds were evaluated.

Results from Table 2 indicated that purebred effects differed significantly across all ages. While these differences can primarily be attributed to the genetic variation among breeds, environmental factors (e.g., feed quality, temperature variability) and genotype-by-environment interactions may also contribute to the observed performance trends. Throughout the study, the S breed exhibited superior BW, followed by K, D, and H chickens. This aligns with multiple studies conducted under varying environmental and management conditions, where the S breed consistently outperformed other breeds in BW (Tolasa *et al*., 2020; Itafa *et al*., 2021; Fikrineh *et al*., 2023a). Similarly, our findings agree with Abdullah (2021), who reported that commercial chickens surpassed local breeds and their reciprocals. However, discrepancies in BW for the K breed compared to the report by Shambel *et al*. (2022) and higher performance of D and H breeds in this study relative to prior research by Samrawit *et al*. (2020) could reflect differences in breed generations, management practices, or local environmental conditions. For instance, the 26.42 % and 36.46 % increase in BW for D and H breeds, respectively, compared to earlier findings at the same location (Werer Agricultural Research Center), suggests that improved husbandry or genetic selection over time may have played a role.

In this study, most crossbred groups (except K×D) exhibited significantly higher BW than at least one parental purebred, suggesting the presence of H^e. The underperformance of K×D crossbreds agreed with the report by Saadey *et al*. (2008) and Siwendu *et al*. (2013), while the general superiority of crossbreds supports findings by Khalil *et al*. (2018), Tolasa *et al*. (2020), and Shambel *et al*. (2022). Nevertheless, the absence of explicit environmental and additional pedigree (phenotype) data limits our ability to fully

disentangle genetics from environmental contributions. Future studies may incorporate detailed environmental covariates to better assess genotype-by-environment interactions in Ethiopian poultry production systems. However, a different result was reported by Itafa *et al*. (2021), that the purebred S outperformed the crossbred S×K and K×S throughout the growing period. On the other hand, similar results were reported by Tolasa *et al*. (2020) for the crossbred S×K (820.00 g) at the 8th WK. The same author reported heavier BW for the reciprocal cross K×S compared to the current result at WK 8. Following K×S, the crossbreds resulting from crossing S×D, D×S, H×S, and S×H also exhibited the heaviest weights throughout the measurement period, which could be linked to the enhanced genetic makeup of the S chicken breed. Similar results were recorded with breeds having the S chicken as one of the parents (Alemneh *et al*., 2021; Bilalissi *et al*., 2022; Dzungwe *et al*., 2022; Mancinelli *et al*., 2023). On the other hand, compared to the other crossbreds, K×D, H×D, H×K, and their reciprocal crosses performed poorly. The crossbred mean BW observed in the present study was less than the BW reported by Shambel *et al*. (2022) for crosses H×K and K×H. They observed BW of 1256.9 g and 1253.9 g at wk 12, respectively.

Breed effect on feed intake and feed conversion ratio

Results from Table 3 showed the significant influence of crossbreeding on feed intake and feed conversion efficiency, reflecting both the genetic potential of parent lines and the synergistic effects of heterosis.

Among the purebred genotypes, H birds exhibited the lowest feed intake and the poorest feed conversion across all stages, with FCR values as high as 5.70 in WK 13–16. In contrast, genotype S consistently showed higher feed intake and significantly better FCR values, such as 2.52 in WK 0–4 and 4.12 in WK 13–16. These results suggest inherent genetic differences in metabolic rate, growth potential, and nutrient utilization between the breeds. In line with the present finding, Samrawit *et al*. (2020) and Shambel, *et al*. (2022) also reported the lowest ADFI and FCR values for H chickens across all stages they studied.

Crossbreeding significantly enhanced performance, as evidenced by the improved ADFI and markedly lower FCRs in many crossbreds. For example, K×S birds demonstrated exceptional feed efficiency with FCR values as low as 1.75 in WK 5–8 and 2.31 in WK 9–12, while maintaining one of the highest feed intakes (e.g., 74.75 g/day in WK 13–16). This

superior performance can largely be attributed to heterosis, where offspring outperform the average of their parents in key traits. Similar findings were reported by Yosef *et al.* (2022) in their evaluation of Koekoek × White Leghorn crosses, where reciprocal hybrids displayed significantly better feed efficiency than their purebred parents.

Moreover, the performance of S×K, S×H, and K×H crosses align with results from Zhao *et al.* (2022), who observed that White Leghorn × Beijing-You hybrids had enhanced feed efficiency compared to pure lines, which was attributed to a favorable combination of growth genes and improved digestive efficiency. In the current study, crossbreds involving genotype S repeatedly showed lower FCRs, suggesting that S likely carries dominant genes for efficient nutrient conversion.

Crossbreds like H×D and D×H improved upon the performance of pure H, their FCRs (e.g., 4.96 and 4.54, respectively, in WK 13–16) were still higher compared to other crosses, indicating that the benefits of crossbreeding are genotype-specific and not uniformly expressed across all combinations. This observation is consistent with research by Shambel *et al.* (2022), who noted that crosses between indigenous Ethiopian breeds and exotic lines yielded varying results depending on the compatibility and adaptability of the breeds involved.

Environmental adaptability and maternal effects may also have played roles in the performance differences among reciprocal crosses. For example, K×S and S×K performed similarly, but slight differences in FCR across periods suggest possible maternal influences, as supported by earlier findings from Shambel *et al.* (2022), who reported that crossbreds with K×H and H×K showed marginally better growth and feed efficiency.

5.2. Meat and Carcass Characteristics

Chicken meat quality is influenced by a combination of genetic, environmental, and processing factors that determine its texture, flavor, color, and safety. Key elements such as breed selection, feed composition, pre-slaughter handling, slaughter techniques, and post-processing storage, all play crucial roles in delivering high-quality poultry products to consumers (Kralik *et al.*, 2018; Marchewka *et al.*, 2023; Yue *et al.*, 2024). Understanding

these factors is essential for producers to optimize meat quality and for consumers to make informed choices.

The results from the present study (Table 4), highlight significant influences of both genotype and sex on carcass, cut types, and organ weights, with crossbreeding combinations exhibiting diverse performance trends compared to pure lines. Generally, crossbred genotypes tended to outperform purebreds in key economic traits, supporting the well-documented concept of heterosis, where crossbreeding can improve growth performance, carcass yield, and organ development due to complementary genetic effects.

Genotype and sex significantly ($P < 0.05$) influenced slaughter weight (SW), dressed weight (DW), and eviscerated weight (EW) in both purebred and crossbred chickens. The findings highlight a clear advantage of crossbreeding over pure breeding for enhancing carcass traits, with crossbred genotypes consistently outperforming their purebred counterparts across all measurements. This aligns with previous studies by Khawaja *et al*. (2012) and Keambou, (2015), who also reported superior performance in crossbred genotypes for SW, DW, and EW. Notably, specific crosses (e.g. K×S, S×K, and S×D) achieved the highest values for these traits. Dzungwe *et al*. (2024) observed that the pure Sasso genotype still surpassed other purebred and crossbred genotypes in certain comparisons, suggesting nuanced genetic advantages worth further exploration.

Sex played a significant role in carcass traits, with males consistently outperforming females across all genotypes. This difference was especially pronounced in heavier genotypes such as S and K, as well as their crossbred counterparts. These findings underscore the need to account for sex-based variations when designing crossbreeding programs for targeted production goals. Shambel and Atsbaha (2025) also documented significant sex-related differences in SW, DW, and EW, reinforcing the broader implications of sex selection in poultry breeding strategies for these traits. The difference in growth between sexes is mainly due to the presence of male sex hormones which contribute to the more weight for males at the same age.

The observed performance differences between reciprocal crosses (S×K vs. K×S) indicate potential maternal or cytoplasmic effects and possible sex-linked genetic influences on carcass yield traits. Notably, Dzungwe *et al*. (2024) found that the Wassachie × Sasso cross

underperformed compared to its reciprocal counterpart in both slaughter and carcass weight measurements. These results have significant implications for breeding programs, demonstrating that cross direction matters. Breeders should carefully consider parental line placement in crossbreeding strategies to maximize carcass yield potential.

The study demonstrates that crossbreeding high-growth genotypes (S and K) yields superior carcass performance, while crosses involving lower-growth genotypes (H and D) result in comparatively reduced weights. These findings align with recent research by Shambel and Atsbaha, (2025), who highlighted the strong performance of the K breed, and Dzungwe *et al.* (2022), who reported optimal results for the S breed. This reinforces the importance of genetic complementarity in crossbreeding, and strategically pairing high-performing, compatible breeds enhances both production efficiency and carcass yield.

As shown in Table 5, genotype and sex significantly influenced ($P < 0.05$) thigh, drumstick, breast, and wing weights, except for female wing weight, where differences were non-significant ($P > 0.05$). Mirroring trends in total carcass weight, crossbred genotypes consistently outperformed purebreds in these key cuts. This aligns with findings from multiple studies (Cassandro *et al*., 2015; Arslan *et al*., 2023; Dzungwe *et al*., 2024; Shambel and Atsbaha, 2025), reinforcing the well-documented advantage of crossbreeding in enhancing primal cut yields.

Among the pure breeds, genotype S demonstrated the highest individual cut weights, especially in males, reaffirming its well-established superiority in growth and carcass traits. Notably, crossbreeding enhanced these characteristics even further, with combinations involving the S and K genotypes producing the most favorable results. This finding is consistent with the report by Alemneh *et al.* (2021), who also observed superior carcass potential in F_1 crosses of Sasso, supporting the outcomes of the present study.

Notably, the S×K, D×S, and K×S crosses exhibited significantly higher weights in commercially valuable cuts such as the breast and drumstick. The exceptional breast weight observed in the S×K cross is likely attributed to the complementary effects of S's strong breast muscle deposition capacity and K's well-balanced carcass traits. Additionally, the marked improvements in thigh and drumstick weights in crosses like D×S and K×S may be driven by enhanced musculoskeletal development and structural strength, traits

potentially inherited from D and K genotypes. Crossbred birds often benefit from improved nutrient utilization efficiency and a balanced frame size, contributing to a more uniform and desirable muscle distribution. On the other hand, the relatively minor variation in wing weights with non-significant differences noted in females suggests that this trait may be less responsive to genetic interactions or might require more specific gene combinations to elicit heterotic effects. This observation aligns with findings from several studies (Khawaja *et al*., 2012; Keambou, 2015; Alene *et al*., 2024).

Reciprocal cross effects were evident as well. Differences between crosses like S×H and H×S, as well as between K×S and S×K, indicate the potential influence of maternal and cytoplasmic inheritance or sex-linked genes on muscle development in different carcass regions. Consistent with this study, Itafa *et al*. (2021) also reported a similar trend, highlighting the superiority of S×K and its reciprocal cross in terms of growth performance and carcass characteristics. This underlines the importance of considering not just which breeds to cross, but also the direction of the cross, in optimizing carcass part yields.

The observed differences in back, gizzard, heart, and liver weights across genotypes and sexes in Table 6 can largely be attributed to the genetic potential of the parental breeds and the heterotic effects arising from crossbreeding. The K×S cross displayed the highest liver weight among both males and females. This could be due to complementary gene action from both parents: K, known for its robustness and organ development, and S, noted for meat production potential. The improved organ size may also reflect enhanced metabolic activity necessary for faster growth in these crosses. Similarly, the S×K and H×S crosses achieved relatively high gizzard and heart weights, likely benefiting from additive genetic effects where favorable alleles from both parents combine to improve these traits.

Proximate composition and physicochemical properties of meat

The proximate composition of breast meat showed significant differences ($P < 0.0001$) among the genetic groups (Table 7), with marked variations resulting from both purebred performance and crossbreeding combinations. This finding is consistent with the report by Khawaja *et al*. (2012).

Moisture is an essential physiochemical attribute in meat due to its fundamental role in determining palatability. Moisture content ranged from 72.46% in D×H to 75.79% in D×K, with significant differences (P = 0.0037) among groups. Castellini *et al*. (2002) observed differences in meat maturity, protein, and moisture content among Ross, Kabir, and Robusta maculate chickens of the same age, suggesting that genotype affects meat's chemical composition. Generally, crosses involving D with K or S tended to retain higher moisture levels. This could be due to the influence of D's genetic background in maintaining muscle water-holding capacity, especially when combined with genotypes characterized by moderate to fast growth. The MO value is inversely related to fat and protein content in meat (Mohammed, 2018), so the observed pattern can also be partially explained by the corresponding protein and fat levels in these crosses.

Notably, the S×K, S×D, and K×H crosses recorded higher CP content, reflecting synergistic interactions between breeds with inherently strong protein deposition capabilities. This improvement in protein content among crossbreds is likely driven by heterosis for muscle accretion and enhanced feed efficiency, resulting in greater protein synthesis compared to their purebred counterparts. In agreement with this pattern, Dzungwe *et al*. (2024) reported that crosses between Wassachie and Sasso yielded higher protein content than pure Sasso. These findings reaffirm the concept that crossbreeding can optimize muscle growth by effectively blending diverse genetic resources. Interestingly, not all crossbreds followed this trend, for instance, the D×S group exhibited comparatively lower protein content.

The crude fat (CF) content showed significant variation (P < 0.0001), ranging from 1.39% in the S×K cross to 4.07% in D×S. Among the pure breeds, breast meat from S (3.56%) and H (3.22%) recorded the highest CF levels, while K (2.82%) and D (2.82%) exhibited the lowest. The CF content in breast meat from the H and K breeds was higher than the values previously reported by Atsbaha *et al*. (2022). Notably, crosses like S×K and S×H demonstrated lower fat levels, which might be attributed to improved feed efficiency and faster metabolic rates characteristic of these combinations. Crosses with higher fat percentages, such as D×S and H×K, may be benefiting from D's genetic tendency for fat deposition, enhanced by the growth performance or metabolic traits of S or H. Supporting this, Ullengala *et al*. (2020) reported similar CF values for five Aseel crosses. On the other

hand, the leaner profiles observed in the S×K and S×D crosses could reflect the additive effect of S and K's genetic inclination toward lower intramuscular fat, making them promising options for lean meat production.

The ash content, which reflects the mineral concentration of breast muscle, displayed significant variation ($P < 0.0001$) across the genetic groups. Among them, the K×H cross and purebred S recorded the highest values, suggesting potential additive or complementary effects in traits related to mineral deposition. The elevated ash content in K×H might be attributed to enhanced skeletal development and muscle mineralization, combining K's balanced carcass conformation with H's superior growth performance. The ash content observed for K, H, and their crossbreds aligned with the findings of Atsbaha *et al*. (2022), though the values remained lower than those reported by Ullengala *et al*. (2020). Additionally, differences in moisture and ash content pointed to variations in water-holding capacity and mineral retention, likely inherited from their respective parental lines.

Energy content did not differ significantly among the groups ($P > 0.05$). Nonetheless, purebred D and crosses such as H×K and D×H showed numerically higher energy values. In contrast, Atsbaha *et al*. (2022) reported significant differences in energy content for H, K, and Cosmopolitan chicken breeds and their crosses. This relative consistency in energy values, despite noticeable fluctuations in proximate components, suggests a compensatory mechanism where variations in fat and protein levels balance each other to maintain a stable overall caloric density. Such patterns are common in crossbreeding programs, where differing genetic potentials for muscle composition interact but often equalize in terms of final energy output.

Meat pH, WHC, Texture and color characteristics

The pH and instrumental color characteristics of breast meat were influenced by genetic group, with distinct patterns emerging among both purebreds and crossbreds (Table 8). Although pH values measured at 45 minutes and 24 hours postmortem did not differ significantly, notable variations were observed in instrumental color parameters (L*, a*, b*), with significant differences ($P < 0.05$) across genetic groups. These differences highlight the impact of genotype combinations on meat quality traits, likely driven by heterosis, additive genetic effects, and physiological variations in muscle metabolism.

These findings are consistent with reports from Funaro *et al*. (2014); Ullengala *et al*. (2020); Lee *et al*. (2022) and Dzungwe *et al*. (2024), all of them documented significant differences in breast meat color attributes between genetic groups, while pH remained unaffected. Similarly, Fletcher (1999) reported significant variation in meat lightness and redness across different appearance groups. By in contrast to the present study, the same authors observed significant differences in pH values but no significant variation in yellowness.

Although pH values at both 45 minutes and 24 hours postmortem showed no significant differences across most genotypes, minor variations could be attributed to differences in muscle glycogen reserves and postmortem metabolic activity. The slightly higher initial pH observed in crosses such as H×D and S×K may suggest lower glycogen content at slaughter, resulting in reduced lactic acid production and a slower pH decline. This overall consistency in pH values implies that crossbreeding did not markedly alter postmortem muscle acidification patterns, likely because the parental lines (H, K, S, and D) shared relatively similar muscle glycolytic capacities and stress responses at slaughter. In line with the present finding similar trends were reported by Atsbaha *et al*. (2022) for local, H, K, and Cosmopolitan chicken breeds and their crosses.

Breast meat color traits varied significantly, emphasizing the influence of genetic interactions on pigment concentration, pH decline dynamics, and water-holding capacity. Crosses such as H×K and K×S exhibited higher L* values (lightness), which could be attributed to breed-specific differences in muscle fiber type composition and intramuscular fat levels. These results suggest that crossing high-yielding lines like H, K, and S enhances meat lightness, likely due to improved muscle structure, lower myoglobin content, and better water-holding capacity. Supporting this, Atsbaha *et al*. (2022) also observed significant variation in color traits, although with slightly higher values for H and K breeds.

On the other hand, the darker breast meat seen in D×K and D×S crosses may be explained by higher myoglobin concentrations from the D genotype or slower postmortem glycolysis, resulting in tighter muscle structures with reduced light reflectance. Additionally, the increased redness (a*) in H×K and greater yellowness (b*) in S×D further highlight how

genetic background influences both muscle pigment content and the deposition of fat-soluble pigments, shaping the final appearance and quality of the meat.

Water holding capacity and shear force in chicken breast meat across various genotypes reveals significant genetic influences on these meat quality traits. In this context, the purebred H exhibited the highest WHC at 85.85%, while the purebred K genotype had the lowest at 78.61%. In line with the present result, Atsbaha *et al.* (2022) reported similar WHC value for H breed in same study location. However, in contrast, Kim *et al.* (2020) reported much lower WHC for meats collected from different farms.

Among crossbred genotypes, H×S maintained a high WHC of 84.21%, suggesting that crossbreeding can preserve favorable traits from purebred lines. On the other hand, crosses involving K, such as K×S (78.70%) and D×K (79.42%), exhibited lower WHC values, indicating that the K genotype's characteristics may be dominant in these crosses. These findings align with previous studies that have reported variations in WHC among different chicken genotypes. For instance, a study by Guan *et al.* (2013) comparing Chinese indigenous chicken breeds and commercial broilers found that indigenous breeds had lower drip loss, indicating higher WHC, compared to fast-growing broilers, which had higher drip loss and lower WHC, which align with the present finding.

Regarding shear force, which is inversely related to meat tenderness, the highest values were observed in the S×D (23.83 N) and K×D (23.70 N) crosses, suggesting these genotypes produce tougher meat. In contrast, the D×S cross had the lowest shear force at 19.53 N, indicating a more tender meat texture. These results are consistent with findings from other studies. For example, a study conducted by Petracci *et al.* (2013) on commercial chicken hybrids reported that fast-growing genotypes had higher shear force values, indicating tougher meat, compared to slower-growing genotypes, which had lower shear force and thus more tender meat.

5.3. Egg Production Performance

Age at first egg is a vital trait in poultry production, influencing economic returns, egg production, and flock management (Liu *et al*., 2019). Consequently, AFE is also a critical indicator of reproductive performance in hens (Tan *et al*., 2021).

In the present study (Table 9), the K×H crossbred showed the earliest AFE, suggesting that this crossbred combination accelerates sexual maturity compared to both purebreds and crossbreds, highlighting the presence of hybrid vigor in the K×H cross. Similar results were obtained by Shambel *et al*. (2022), in which the crossbred K×H reached early at sexual maturity compared with other crosses evaluated together. Among purebreds, the D breed reached early at sexual maturity, followed by K, S, and H. This indicates that the D and K breeds have genetic traits favoring earlier at sexual maturity compared to S and H. AFE for D and K breeds in the current study was higher than the report of Samrawit (2020) and Shambel, *et al*. (2022), respectively. However, Fikrineh *et al*. (2023b), reported high AFE, for K chicken breed (166.50 days) compared to the present result. The AFE of S breed obtained in the current study was in line with the result reported by Guni *et al*. (2021). Similar to current result, Wondmeneh (2015) and Shambel *et al*. (2022), reported 156.6 days and 156 days of AFE for H chicken breed, respectively. In contrast, early AFE for H had been reported by several researchers such as (Kedija *et al*., 2020; Samrawit, 2020; Shambel and Atsbaha, 2024). However, the present finding for H, was much higher than reported by Nigussie (2011). The K×D crossbred group also showed early maturity, suggesting that the K and D breeds complement each other well in terms of reducing AFE. Reciprocal crosses (e.g., K×H vs. H×K) showed variability, indicating that the maternal or paternal lineage may influence AFE.

In the present study, the highest Body Weight at Sexual Maturity (BWSM) was recorded for crossbred chickens. The K×S and S×K crossbreds consistently showed high BWSM, indicating that this combination results in larger birds at sexual maturity. This could be advantageous for meat production or overall robustness. The superiority of crossbreds over purebreds in BWSM has been reported by several researchers such as (Iraqi *et al*., 2012; Debes, 2017; Bassey *et al*., 2021). Among purebreds, S had the heaviest BWSM followed by K, while H had the lowest. Similarly, Osei *et al*. (2012) reported that Sasso excided by having the heaviest BWSM compared with Forest and Savannah chicken breeds. In addition, Fikrineh *et al*. (2023b) also reported that the highest BWSM when Fayoumi crossed with Koekoek. On the other hand, studies on crossbreeding indigenous breeds with exotic breeds, Kedija *et al*. (2020) showed that lowest BWSM for H chickens. The D×H

and H×D crossbreds exhibited the lowest BWSM, this could be due to that H breed may dilute BW when crossed with D.

Among purebreds, S laid the heaviest eggs, followed by K, D, and H. The increase EWT observed in S chickens could be attributed to the positive correlation between BW and EWT (Du Plessis and Erasmus, 1972). In line with the current result, Fikrineh *et al*. (2023b) reported similar EWAFE results for K breed. The present EWAFE result for D breed was in line with the finding reported by Habtamu *et al*. (2023). In contrast, Kedija *et al*. (2020) reported heavier EWAFE for H compared to the current result. The K×S crossbred group laid the heaviest eggs, indicating that this combination is favourable for producing larger eggs early in the laying cycle. Similarly, the D×S and D×K crossbreds also performed well in terms of EWAFE, indicating the use of D breed contributes positively to egg size when crossed with S and K. In agreement with the current study several research showed that crossbred's superiority in terms of EWAFE compared with their purebred counter parts (Balcha *et al*., 2021; Wang *et al*., 2022).

Among purebreds, K had the highest EN, HHEP, and HDEP followed by D and S, while H performed the poorest (Table 10). The EN, HHEP, and HDEP values for K in this study were higher than those reported by Fikrineh *et al*. (2023b). However, Shambel and Atsbaha (2024) reported similar results of HHEP for K breeds, but higher HHEP value for H. In contrast, Mekete and Ayano (2023) found higher egg production for K breed compared with the current findings, while their results for the S breed aligned with those of this study. Additionally, under farmer management conditions, Habtamu *et al*. (2023) reported lower HHEP and HDEP values for the D breed.

The crossbreds, K×S and K×H recorded the highest EN, HHEP, and HDEP, indicating superior egg laying performance. This is likely due to heterosis, where the combination of K with H or S results in improved productivity. The EN, HHEP, and HDEP values observed in the present study were slightly higher than the values reported by Shambel *et al*. (2022) for crossbreds H×K and K×H. In the present study, K×S, K×H, K×D, D×K, D×H, and D×S crossbreds outperformed their purebred counter parts in EN, HHEP, and HDEP. In crossbreeding experiment involving Fayoumi and Rhode Island Red, Basant *et al*. (2013) reported that the superiority of crossbreds over their purebred counter parts in HHEP and

HDEP. Emad (2014) also reported high egg production for Sasso and Mandarah crossbred compared with the purebred Sasso. Similarly, Waleed and Shaheen (2011) reported superiority of crossbreds over purebreds on egg production for crosses involving Iraqi local, White Leghorn, and New Hampshire chicken breeds.

EM is a critical metric for commercial egg production, as it reflects both egg size and laying frequency. The result of this study showed that, the K×S, K×H, and D×K crossbreds recorded the highest EM. The same trend with the current results was observed by Soliman *et al*. (2020) when local and commercial strains crossed the crossbreds outperform the local but not the commercial strains.

5.4. Fertility and Hatchability

Fertility and hatchability are essential components of sustainable poultry production, and notable improvements were observed in several crossbred groups. As presented in Table 11, significant differences ($P < 0.05$) were noticed in fertility, hatchability from total eggs sets (HTES), and hatchability from fertile eggs (HFE) across the genetic groups, underscoring the considerable impact of genotype and crossbreeding combinations on reproductive performance. These findings are consistent with the reports of Adeleke *et al*. (2012), Ahmed *et al*. (2012), Ajayi and Agaviezor (2016), and Ebegbulem *et al*. (2017), who similarly documented the influence of genetic makeup and crossbreeding strategies on fertility and hatchability traits in poultry.

Among the purebred groups, H recorded the lowest fertility rates, while S, K, and D maintained comparatively higher values, reflecting inherent breed differences in reproductive efficiency. Supporting these observations, Samrawit (2020) reported similar fertility rates for D (87.73%) and H (78.77%) chickens. Likewise, Shambel and Atsbaha (2024) noted a comparable fertility rate for the K breed but reported higher fertility in H chickens than observed in the present study. Additionally, the fertility rate for the S breed reported by Bilalissi *et al*. (2022) closely aligns with the current findings. However, in contrast, Dzungwe *et al*. (2024) documented a higher fertility rate for the S breed (97.10%) compared to the result obtained here. The relatively lower fertility observed in the H genotype may be attributed to genetic limitations in reproductive traits, a characteristic

commonly associated with improved broiler strains where selection pressure has traditionally prioritized rapid growth and carcass yield over reproductive performance.

Crossbreeding substantially enhanced fertility in several combinations, with D×S and S×K crosses achieving the highest fertility and hatchability rates. These improvements likely reflect heterosis effects on key reproductive traits such as egg viability and embryonic survival. Notably, crosses like H×K (91.40%), S×K (91.42%), K×S (90.63%), and K×H (90.51%) also recorded significantly higher fertility rates compared to their purebred counterparts. Similar patterns have been reported by Bilalissi *et al*. (2022) and Shambel and Atsbaha (2024), who consistently found that crossbreds outperformed purebreds in fertility. These outcomes suggest that genotypes such as K, S, and D possess favorable combining abilities when mated with other lines. This advantage could be attributed to improved mating behavior, enhanced sperm viability, and better reproductive synchronization between males and females from genetically diverse backgrounds.

The HTES and HFE values in this study displayed similar patterns, both benefiting from crossbreeding. Pure H consistently showed the lowest performance for both traits, with HTES at 60.93% and HFE at 77.36%, likely due to a combination of lower fertility and possible embryonic mortality associated with genetic backgrounds. In line with the present result, Samrawit (2020) reported similar HTES and HFE value for D and H breeds. In contrast, crossbreeding significantly improved these reproductive traits across most combinations. The D×S cross recorded the highest HTES (81.56%) and one of the highest HFE values (87.91%), highlighting the superior maternal effects and heterotic advantages of this pairing in enhancing embryonic survival and hatchability.

Notably, crosses involving K also demonstrated substantial improvements, with HTES values; 78.24% (K×H), 77.83% (K×S), and 77.68% (K×D), alongside corresponding HFE increases. These enhancements are likely attributable to K's robust reproductive traits and favorable gene combinations that reduce embryonic losses. Supporting this, Shambel and Atsbaha (2024) also reported improvements in both HTES and HFE when K and H lines were crossed with Cosmopolitan breeds. Interestingly, although pure H exhibited poor reproductive performance, it's cross with S (H×S) produced the highest HFE value (89.85%), suggesting that while H struggles in pure form, it responds well to crossbreeding,

particularly with S breed due to heterotic effects that improve embryonic viability and reduce mortality. Purebred lines like K (85.99%) and D (84.27%) maintained relatively high HFE, yet these too were surpassed by their crossbred counterparts.

The overall increase in both HTES and HFE among crossbreds can be explained by enhanced egg quality, improved fertility, and higher embryonic viability resulting from genetic diversity and heterozygosity. These factors likely promote better nutrient deposition in eggs and more compatible male-female genetic interactions, reducing the expression of deleterious gene combinations. Consistent with these findings, previous studies by Shambel and Atsbaha (2024) and Dzungwe *et al*. (2024) reported similar improvements in hatchability traits through crossbreeding. Collectively, these results reaffirm the value of crossbreeding as a powerful strategy for genetic improvement of reproductive performance in poultry.

5.5. Egg Quality Traits

Egg weight (EWT) shows significant variation across genotypes, highlighting the strong influence of genetics on this trait. Purebred S had the highest EWT at 32 WK of age, followed by K and D. The EWT of S chicken in this study was consistence with findings by Yonas *et al*. (2019) and Wolde *et al*. (2021). In contrast, Beyene *et al*. (2022) reported a higher EWT for S breed, however their observed EWT for the K breed aligned with the present result. The EWT for D breed reported by Samrawit (2020)was slightly higher than that found in this study. However, the same author reported similar EWT values for H with the present findings. Table 12 shows that the H×K, H×D, S×H, K×H, S×K, K×S, D×S, and D×K crossbreds exhibited higher EWT compared with their purebred counter parts, suggesting hybrid vigor. Indicating that crossing K and D with S improves EWT compared to purebreds. H chickens recorded the lowest EWT, indicating possible genetic constraints for this trait within the breed. However, crossbreeding H with S and K led to notable improvements in EWT. These findings align with Kedija *et al*. (2019) and Atsbaha *et al*. (2023), they reported significant gains in EWT through crossbreeding H with exotic breeds, further supporting the heterosis effects observed in this study, particularly in H×S, S×H, H×K, and K×H crossbreds. However, the reciprocal cross D×H performed poorly, suggesting that the maternal or paternal influence of H may negatively impact EWT.

Purebreds D and S had the longest eggs, indicating that these breeds inherently contribute to increased EL. The EL observed in this study for D and H agreed with findings reported by Samrawit (2020). In contrast, Beyene *et al.* (2022) and Kefelegn and Ashenafi (2024), reported slightly longer EL for purebred S. The EL of the K breed in this study was consistent with finding of Yesihak *et al.* (2024). Crossbred H×D also performed well, suggesting that combining H and D can enhance this trait. D×S had the smallest EL, given that both D and S purebreds performed well, this suggests a potential negative interaction or dominance effect when S is used as the dam in this cross.

The egg width (EW) values exhibited significant differences ($P < 0.05$) among genotypes (Table 12). The difference for EW in consensus to this study had also been reported by (Kedija *et al*., 2019; Udoh *et al*., 2020; Fikrineh *et al*., 2023c). The S chicken showed the widest eggs, followed by the D×K and D, suggesting that both S and D breeds positively influence EW. This observation was consistent with the result reported by Wolde *et al.* (2021). On the other hand, the D×S crossbred had the smallest EW, which corresponds to its poor performance in EL. This further reinforces the notion of negative interaction in the D×S cross.

Significant differences ($P < 0.05$) in SWT were observed across genetic groups, though the variations were minimal. This suggests that genetic influences on this trait are limited or that environmental factors play a more substantial role. From the current result, the purebred S exhibited the heaviest shell, followed by S×D and D×S, indicating that S breed positively contributes to SWT. Similar SWT value for the S breed was reported by Wolde *et al.* (2021), though Samrawit (2020) reported higher SWT values for D and H breeds compared with the current study. The D×H crossbred showed the lowest SWT, consistent with its low performance on other traits. In contrast, the S×D crossbred displayed the thickest shell, followed by K×H and K×D, suggesting that specific combinations can enhance ST, potentially due to complementary genetic effects. These findings align with previous studies by Sola and Ayorinde (2011) and Khalil *et al.* (2013), who also demonstrated that crossbreeding improved ST. The K and D had the thinnest shells, indicating possible genetic limitations for this trait. Similarly, Samrawit (2020) observed that breed D exhibited lower performance in terms of ST compared to H. Differences ($P <$

0.03) were noted in SR across groups, although the variations were minimal. The S chicken demonstrated the highest SR. On the other hand, the K×H and D×K recorded the lowest SR, indicating that these combinations may not be effective for enhancing shell quality.

Table 13 showed that, significant differences in AH ($P < 0.036$) and AW ($P < 0.0001$) were observed across genotypes. The K×H and H×K crossbreds demonstrated the highest AH, reflecting strong heterosis in these combinations. From the results, H×K, H×D, K×D, K×H, D×H, and D×K crossbreds displayed higher AH compared to their purebred counter parts, indicating hybrid vigor. The superiority of crossbred over purebreds has been supported by previous studies (Sola and Ayorinde, 2011; Sinha *et al*., 2018; Kedija *et al*., 2019). Purebred K and crossbred S×D recorded the lowest AH, while H×K had the narrowest AW, implying that certain combinations, particularly those involving K and S, may not be optimal for enhancing albumen quality. The H breed performed well in AH and AW when crossed with K and D, highlighting its potential to positively influence albumen quality in crossbreds. The S breed showed moderate performance in AH and AW, suggesting that while S is a robust breed overall, its contribution to albumen quality may be limited in specific crosses. Udoh *et al*. (2020) reported results consistent with the present study regarding AH for the S breed, although their reported AW value was lower. On the other hand, the K breed underperformed in AH, but showed promise in crosses such as K×H. In contrast with the current result, Fikrineh *et al*. (2023c) reported a slightly higher AH value for K breed. However, the same author noted that K performed moderately relative to Fayoumi and White Leghorn but underperformed compared to its reciprocal cross with Fayoumi, aligning with the current result.

The purebred D and crossbred K×S exhibited the highest YH, while crossbred D×S and purebred S demonstrated the widest YW. This suggests that both D and S breeds positively influence yolk size. In contrast, the crossbred H×K had the smallest YH and YW, indicating that this combination may not be optimal for enhancing yolk characteristics. The present findings align with Samrawit (2020), who reported similar values for the D breed in terms of YH and YWT, though the YWT value was lower than that reported by Tewodros *et al*. (2022). However, H showed mixed results, with some crosses (H×D) performing well in YH but others (H×K) underperforming. The K breed underperformed in YH and YW,

particularly in its purebred form. The YH and YW values for the S breed in the present study were higher than those reported by Yonas *et al*. (2019).

The S breed consistently excelled in YWT and YR, both in purebred form and in crosses, while the H breed showed strong performance in YR, particularly in purebred form. For YR, the purebred H, S, and crossbred H×S achieved the highest percentages, indicating that both H and S positively influence yolk size and proportion. Similar findings were reported by Wolde *et al*. (2021), where S crossed with local chickens, S outperformed the local breed and their F1 cross in YWT, while the local breed and the F1 cross outperformed S in YR. The purebred D underperformed in YWT and YR, particularly in crosses like H×D and D×K. Samrawit (2020) also noted that D breed underperformed in YR compared to H breed. Meanwhile, the K breed showed mixed results, with some crosses (K×S) performing well in YWT but other (K×D) underperforming. The crossbred K×H had the highest HU, indicating superior egg quality, closely followed by D×H and H×K. This suggests that crosses involving H and K can enhance egg quality. Results from the present study are consistent with Tewodros *et al*. (2022), who reported similar HU values for the D breed.

5.6. Cross Breeding Effects

5.6.1. Heterosis effects (H^e)

Heterosis effect on body weight

Estimates of heterosis (%) on BW for different breed groups are presented in Figure 2 and Figure 3. Generally, there is an agreement that crossbreeding improves growth rate and adult BW in chicken. In this study, the crosses showed varying level of H^e for BW during different age intervals from hatch to WK 14. The variations in the magnitude of heterotic effects are caused by difference in the genotype of breeds, strains, population, and their size (Verma *et al*., 1985).

In the present study, most H^e were positive and ranged from 0.20% to 15.93% for BW. The high and positive H^e for BW on most of the crossbreds shows that hybrid offsprings grew faster and reached higher BW on the mid-parent value. This indicates that the non-additive genetic effects, particularly dominance, are contributing to the observed heterosis. The H^e found that in the early stage of growth (WK 2 - WK 6), thereafter it was in a declining

trend up to the end of the studied period. Results from the current study align with the findings of Iraqi *et al*. (2021), which indicates that the magnitude of heterosis is dependent on age.

Figure 2 indicated that crossing between S male and K female was the best combination for BW at hatch, 2nd, 6, 10, and 14th WK of age. The cross S×D recorded the best estimate of H^e for BW at the 4th, 8, and 12th WK of age. Similarly, the reciprocals (K×S and D×S) (Figure 3) showed high and positive H^e, however, it was lesser compared to their direct crosses. The BW of S×K and its reciprocal counterpart K×S showed significant increase over both parental averages. This indicates the overdominance effect could be contributing to the high and positive heterosis value observed. The result obtained in this study was much higher than that reported by Itafa *et al*. (2021) for K×S crossbred and its reciprocal cross. Itafa recorded for crosses K×S and S×K, heterosis estimates of 0.046% and 0.045% at initial BW, respectively.

Crossbreds produced by mating commercial exotic and locally improved breeds (H×S and S×H) exhibited significant and high levels of H^e at various ages. The crossbred H×S, S×D, and their reciprocals exhibited significantly higher and positive heterosis estimates for BW, suggesting the presence of a dominant allele from S chicken bred that contributes to the large body size. The non-additive (dominance) effect likely accounts for the increased body size. Similar to the present finding, Mancinelli *et al*. (2023) reported that crossing between two locals (Bionda Piemontese and Robusta Maculate) with Sasso chicken breed showed 7.10 and 5.06% heterosis value at adult BW, respectively. The cross H×D also had high and positive heterosis value at all age measurements compared to its reciprocal. The magnitude of the heterosis value from these results reflect the level of genetic resemblance between the parental populations and the extent of heterozygosity of the crosses. Different studies indicated that the BW of crossbred chickens at various ages was positively associated with H^e for BW (Siwendu *et al*., 2013; Tyasi *et al*., 2019; Atsbaha *et al*., 2023). Findings of the current study also showed that the H×K and its reciprocal K×H had positive, but low H^e at all ages. Similarly to the present study, Shambel (2022) reported positive estimates of H^e for BW when H crossed with K breed. On the contrary, the

estimates of H^e reported by Kedija *et al*. (2018) for Horro and Dominant Red Barred were positive and higher compared to the present result.

On the other hand, the crossing between K×D exhibited negative H^e at all ages, while its reciprocal D×K had positive but low estimates of heterosis at all age measurements. The difference in H^e between the reciprocal crosses (K×D and D×K) suggests that non-additive genetic effects, such as maternal effects and dominance interactions, could be influencing the outcome. The D×K cross shows positive heterosis likely due to favorable dominance effects, whereas the K×D cross results in negative heterosis, possibly due to antagonistic dominance, epistatic, or maternal effects that suppress growth in this combination. Williams *et al*. (2002) found that the magnitude of heterosis for BW varies and can be either positive or negative, depending on the cross. In line with the present finding, Saadey *et al*. (2008) and Siwendu *et al*. (2013) also reported negative heterosis estimates for BW of different crossbred chickens.

Heterosis effect on feed intake and feed conversion ratio

Heterosis estimates presented in Table 14 underscore the powerful role of crossbreeding in influencing feed intake and efficiency in poultry. The predominantly positive H^e values for ADFI suggest that most crossbreds benefited from hybrid vigor, leading to increased appetite or growth-related metabolic activity. Particularly, crosses like D×H, K×H, and H×S demonstrated consistent and strong H^e for feed intake across multiple stages, indicating that these genetic combinations enhance nutrient consumption and possibly growth rate, especially during early development. This aligns with findings from Yosef *et al*. (2022), who observed increased feed intake in Koekoek × White Leghorn hybrids compared to their parental lines, attributing the improvement to a combination of metabolic complementarity and dominance of alleles controlling appetite and growth. Similarly, Zhao *et al*. (2022) reported enhanced feed intake in Beijing You × White Leghorn crosses, noting that such crosses often benefit from the additive genetic effects of both parents.

The FCR heterosis values reveal a more nuanced but encouraging picture. Strong negative heterosis, such as in S×H (–36.54%) and K×S (–36.12%), indicates significant improvement in feed efficiency. These values suggest that crossbred birds required

substantially less feed per unit of weight gain than predicted by the mid-parent averages. The benefits of such improvements are widely documented. For instance, Balcha *et al*. (2024) observed improvement in FCR among White Leghorn crossed with Fayoumi and their reciprocals, driven by both enhanced digestive efficiency and better nutrient absorption under crossbred physiology.

Interestingly, crosses involving D showed mixed results for FCR. For example, D×K showed positive heterosis (+25.37% in WK 5–8), which implies a decrease in efficiency. This may stem from physiological mismatches between the parent breeds, such as growth rate disparities or differing nutrient assimilation profiles. This finding echoes observations by Balcha *et al*. (2024), who highlighted that not all crosses yield desirable heterosis due to incompatibilities in growth dynamics or stress tolerance.

Negative H^e in ADFI, observed in D×S and D×K in WK 0–4, may suggest early-stage metabolic limitations or slower adaptation to feeding regimes, which is often seen in slower-growing lines crossed with faster-growing breeds. Nevertheless, the corresponding FCR H^e in these crosses was not consistently negative, suggesting that although feed intake was reduced, efficiency was not necessarily compromised, an important point for systems aiming at cost-effective production.

Heterosis estimates for meat and carcass traits

The study on heterosis for carcass characteristics among different genotypes and sexes reveals insightful trends regarding the potential benefits and challenges of crossbreeding in poultry (Table 15). The observed heterosis values for carcass and meat traits such as slaughter weight (SW), dressed weight (DW), eviscerated weight (EV), thigh weight (TWT), breast weight (BWT), and organ weights in this study reflect the complex genetic interactions resulting from crossbreeding among the four chicken breeds in a full diallel mating design.

For SW, positive H^e values predominated in males, with particularly high estimates in the H×S (12.05%) and S×D (8.86%) crosses, suggesting favorable non-additive genetic effects. These results align with the findings of Khalil *et al*. (2018) and Sungkhapreecha *et al*. (2022), who reported positive H^e for live weight in crossbred chickens, but contrast with

reports by Keambou, (2015), who observed inconsistent and sometimes negative H^e for BW traits in their crossbreeding experiments. Interestingly, females displayed greater variability, with heterosis estimates ranging from -20.25% (S×D) to 14.59% (H×K), highlighting possible sex-linked differences in heterotic response.

Dressed weight (DW) and eviscerated weight (EV) followed comparable trends, with most male crosses yielding positive H^e, especially H×S and S×D, supporting the suggestion that crossing can enhance carcass yield, a conclusion previously supported by Itafa *et al.* (2021). However, the inconsistent and sometimes negative H^e in female crosses, as seen in S×D for DW (-17.94%) and EV (-23.60%), might indicate maternal effects or sex-linked inheritance, as noted by Yakubu and Ari (2018).

For both TWT and BWT, which are particularly valuable for consumers and producers due to their desirability as meat cuts, crossbreeding resulted in significant positive heterosis. TWT and BWT showed high H^e in both sexes for certain crosses, such as TWT in D×K males (20.99%) and BWT in H×K females (32.57%), suggesting a strong potential for improving these commercially valuable parts through strategic crossbreeding. In males, the S×K and K×S crosses also displayed substantial improvements in thigh weight, with heterosis values of 14.58% and 12.92%, respectively. The crossbreeding of S and K likely led to an enhanced muscle mass, particularly in the thigh region, which is beneficial for both meat yield and market demand. Comparable positive H^e for these traits was reported by Akinsola *et al.* (2019), though some studies, like that of Horst (1989), have noted limited benefits for cut-up parts heterosis, particularly in highly selected commercial broiler lines.

Organ weights exhibited more erratic H^e, with liver weight (notably 48.46% in H×K males) showing exceptionally high positive H^e in some crosses, while most other organs, such as gizzard and heart, displayed predominantly negative or low heterosis values. Such findings mirror those of Adeleke *et al.* (2011), who reported inconsistent organ weight heterosis in Nigerian indigenous × exotic crosses, but contrast with reports by Nwachukwu *et al.* (2006), who found uniformly positive heterotic effects for organ weights in their crossbred broilers. The variation could be due to differential inheritance patterns or metabolic stress responses in crosses, as suggested by Horst (1989). The notable sex-dependent differences observed across nearly all traits suggest that males tend to exhibit higher heterosis for

growth and carcass yield traits than females. This pattern is consistent with earlier findings by Yakubu and Ari (2018), who attributed such disparities to differential hormonal influences and sex-linked genetic factors.

Heterosis estimates for WHC and color characteristics

The heterosis estimates for various meat quality traits, including meat WHC and instrumental color, reveal valuable insights into the effects of crossbreeding between different genetic groups (Table 16). These traits are crucial for evaluating the quality of poultry meat, as they directly influence tenderness, color, and shelf life. Understanding how crossbreeding affects these attributes can provide practical recommendations for improving meat quality in poultry production.

The instrumental color parameters showed highly variable heterosis estimates, highlighting the complexity of pigment deposition and myoglobin oxidation dynamics in different crossbreds. For L* (lightness), heterosis ranged from 15.16% (K×S) to -22.92% (D×K). The high positive heterosis in K×S (15.16%) implies brighter breast meat, which could be linked to reduced myoglobin content or higher pH, leading to reduced light absorption. Negative heterosis in D×K (-22.92%) may indicate darker meat, often a result of slower pH declines or higher pigment concentration, outcomes aligned with findings by Cheng *et al*. (2008) who demonstrated breed effects on breast meat color due to differences in muscle biochemistry.

For a* (redness), extreme positive heterosis was seen in H×K (39.88%) and moderate negative values in several reciprocal crosses, such as -68.79% in D×H. High positive heterosis might reflect increased myoglobin concentration or altered oxidation states favoring redder meat, as suggested by Rizzi *et al*. (2009), who linked genetic background to variations in redness intensity. Negative heterosis in reciprocals could result from maternal inheritance effects or sex-linked genetic factors influencing myoglobin stability, an idea supported by Duclos *et al*. (2007) who reported maternal effects on poultry meat quality.

The b* (yellowness) values showed heterosis estimates ranging from 47.28% (D×K) to -36.33% (D×H). Positive heterosis, as in D×K (47.28%), indicates enhanced yellowness,

possibly due to increased carotenoid deposition or lipid oxidation byproducts. Negative heterosis in D×H (-36.33%) suggests lower yellowness, perhaps reflecting differences in lipid content or antioxidant capacity, as noted by Zerehdaran *et al*. (2004) in studies linking crossbreeding to meat color through differences in fat deposition and oxidative stability.

Reciprocal effects, as shown by contrasting values in cross vs. reciprocal pairs (e.g., H×K vs. K×H), emphasize the role of maternal inheritance and sex-linked genes, consistent with findings by Fairfull *et al*. (1983) who highlighted the importance of reciprocal crosses in poultry breeding programs. The variable direction and magnitude of heterosis across traits and combinations affirm the complex, non-additive genetic architecture underlying meat quality, necessitating tailored breeding strategies to optimize carcass and meat traits through strategic crossbreeding.

These heterosis estimates offer insight into the potential of crossbreeding strategies to enhance or compromise breast meat quality, specifically in terms of WHC. Positive heterosis in crosses like S×K (1.98%) and K×D (1.15%) suggests that combining specific genetic lines can lead to synergistic effects, improving meat's ability to retain moisture. This aligns with the concept that crossbreeding can exploit non-additive genetic effects, such as dominance or epistasis, to enhance desirable traits. However, several studies have explored the impact of crossbreeding on meat quality in chickens. For instance, research by Mikulski *et al*. (2011) observed that slower-growing chicken genotypes exhibited better meat quality attributes, such as tenderness and juiciness, compared to fast-growing broilers. Similarly, Franco *et al*. (2012) highlighted that native meat-type chickens, despite slower growth rates, produced meat with desirable quality characteristics, including flavor and texture.

On the other hand, the negative heterosis seen in S×H (-2.92%), K×H (-2.52%), and D×H (-2.44%) points to less favorable combinations where the genetic interplay may not support improvements in WHC. This could be due to antagonistic gene interactions or dominance of less favorable alleles for WHC, echoing findings from Zerehdaran *et al*. (2004), who emphasized that not all crossbreeding leads to heterotic gains, especially when the parental lines are closely related or lack complementary traits. Importantly, the asymmetry in

heterosis between direct and reciprocal crosses (e.g., H×S = +1.11% vs S×H = -2.92%) highlights potential maternal or sex-linked effects.

Heterosis estimates for proximate composition

The heterosis estimates for the proximate composition of breast meat (MO, CP, CF, CA, and energy) demonstrate the influence of crossbreeding on these nutritional and chemical attributes (Table 17). These traits are essential for determining the quality of poultry meat from both a nutritional and consumer perspective. The results highlight both positive and negative heterosis in different crosses, providing insights into the potential benefits or drawbacks of specific genetic combinations for improving meat composition.

The heterosis estimates for MO were relatively modest, ranging from -2.53% in D×H to 3.27% in D×K. The slight positive H^e in crosses like D×K (3.27%) could indicate improved water-holding capacity, possibly due to favorable heterozygous effects on muscle fiber integrity and interstitial space fluid retention. On the other hand, negative H^e, as seen in crosses like S×H (-2.47%), might suggest increased protein or fat content at the expense of moisture, given the inverse relationship often observed between moisture and other meat components. This pattern aligns with findings from Wattanachant *et al*. (2004), who reported that crossbreeding could influence water content in poultry meat through changes in muscle structure and postmortem metabolism.

In terms of CP, heterosis values were notably positive in several crosses, with the highest observed in S×H (18.43%) and substantial values in S×K (12.34%), S×D (12.47%), and K×H (11.13%). These results indicate a pronounced positive H^e on protein content, likely due to complementary gene actions affecting muscle growth and protein deposition. The superior protein content in these crosses may reflect enhanced muscle fiber hypertrophy or increased myofibrillar protein synthesis. This observation is consistent with the work of Faria *et al*. (2009), who demonstrated that crossbreeding can improve carcass protein content through heterotic effects on muscle accretion pathways.

Crude fat (CF) heterosis showed remarkable variability, ranging from highly negative values like -56.30% in S×K to positive values like 27.60% in D×S. The marked negative H^e for fat content in most crosses, particularly in combinations involving S×K, S×D, and

their reciprocals, suggests a reduction in intramuscular fat deposition in crossbreds compared to purebreds. This could be attributed to heterosis-driven improvements in feed efficiency and lean tissue growth, resulting in leaner carcasses. Interestingly, positive heterosis values in H×K (27.02%) and D×S (27.60%) suggest certain crosses favor lipid accumulation, potentially due to genetic background effects on lipid metabolism and storage. Similar patterns were reported by Zerehdaran *et al*. (2004), who noted that crossbreeding can lead to both increased or decreased fat deposition depending on the genetic makeup of the parental lines.

For crude ash (CA), which reflects mineral content, heterosis estimates were highly variable. Positive heterosis was most pronounced in K×H (54.15%) and D×H (33.12%), indicating significant non-additive genetic effects improving mineral content in these crossbreds. Such high positive heterosis may result from maternal influences or sex-linked inheritance affecting bone mineralization and mineral content in muscle tissues. On the other hand, negative heterosis in combinations like K×S (-22.93%) and H×S (-20.78%) implies unfavorable genetic interactions for mineral retention. The importance of genotype and cross direction in determining ash content was also highlighted by Cheng *et al*. (2008), who found considerable breed and cross-specific variation in mineral deposition traits in poultry.

Finally, for gross energy content, heterosis estimates showed moderate fluctuations, ranging from -10.59% in D×K to 2.73% in H×S. The modest positive heterosis in H×S (2.73%) and K×S (1.81%) might reflect a balanced increase in energy-contributing nutrients like fat and protein. Negative heterosis, particularly in D×K (-10.59%), could be linked to lower fat content or leaner carcasses, which naturally have reduced caloric density. Similar findings were noted by Faria *et al*. (2009), where crossbreeding strategies influenced meat energy value through correlated changes in proximate components, particularly fat.

In general, the observed heterosis values for proximate composition traits demonstrate considerable variation among different cross combinations and reciprocals, underscoring the complex, non-additive inheritance of these traits. Strategic selection of parental lines

and cross directions could thus optimize specific meat quality attributes in commercial poultry breeding programs.

Heterosis estimates for fertility and hatchability traits

Table 18 presents estimate of heterosis for reproductive traits (fertility, HTES, and HFE), from crosses and reciprocal crosses. These reproductive traits are economically important in poultry breeding programs as they directly influence chick output and overall flock productivity. The heterosis values highlight the degree of non-additive genetic effects, maternal contributions, and potential cytoplasmic inheritance influencing these parameters.

Heterosis estimates for fertility ranged from -1.20% in H×S to 8.82% in H×K among the crosses, and from -1.93% in S×H to 7.75% in K×H among the reciprocals. Positive H^e in crosses like H×K (8.82%) and K×H (7.75%) suggests beneficial gene combinations enhancing reproductive efficiency, possibly through improved semen quality, ovum viability, or fertilization success. The favorable H^e observed here may be due to heterozygosity at loci affecting reproductive hormones, gamete function, or immune response, as highlighted by Fathi *et al.* (2013), who reported increased fertility rates in certain crossbred chickens due to enhanced genetic diversity and robustness. On the other hand, negative or low heterosis estimates in some crosses, such as H×S (-1.20%), could reflect genetic incompatibilities or less effective mating behaviors between specific breed combinations, a phenomenon also noted by Fairfull *et al.* (1983) in studies examining diallel crosses in poultry.

For HTES, heterosis estimates were mostly positive across the crosses, ranging from 2.60% in S×D to 11.69% in H×S. The highest heterosis in H×S (11.69%) and K×H (13.68%) suggests a strong non-additive genetic advantage in embryo survival and hatch success when certain genotypes are combined. These favorable heterosis values may be attributed to complementary maternal and paternal genetic contributions that enhance egg quality, shell integrity, or embryonic viability. In agreement, El-Safty (2012) demonstrated that crossbreeding improved hatchability by optimizing both maternal environment and genetic makeup. Negative heterosis values, as seen in D×K (-5.05%), suggest suboptimal genetic combinations, possibly due to incompatibility in embryonic development-related genes or maternal factors such as brooding behavior and egg handling.

The HFE also exhibited a predominance of positive H^e in most crosses, peaking at 13.20% in H×S and 6.14% in D×S. The high H^e in H×S for both HTES and HFE implies particularly advantageous gene interactions between these two genotypes, possibly enhancing embryo viability post-fertilization. This is consistent with findings from Fathi *et al.* (2013) and Abdullah (2021), who reported significant improvements in hatchability traits in crossbred chickens, attributing the effects to improved genetic vigor and balanced contributions of maternal and paternal genes influencing embryogenesis. On the other hand, negative H^e like -7.35% in D×K crossbred may result from detrimental epistatic interactions or cytoplasmic-nuclear incompatibility affecting embryonic metabolism and survival.

Reciprocal differences were evident in several trait combinations, underscoring the importance of maternal effects and sex-linked genes. For instance, while H×K showed a positive H^e of 8.82% for fertility, its reciprocal K×H was similarly high at 7.75%, but for HTES, K×H (13.68%) markedly outperformed H×K (10.74%). Such differences could be explained by the maternal influence on egg formation, shell quality, and early embryonic conditions, as suggested by El-Safty (2012) and Cheng *et al.* (2008), who emphasized the pivotal role of maternal genotype in determining hatchability outcomes through both genetic and egg microenvironmental factors.

Heterosis effect for egg production and quality traits

The level of heterosis grows as the genetic distance between parental lines increases, and measuring it is crucial for assessing the enhancement of crossbred characteristics relative to their parents (Mancinelli *et al.,* 2023).

As detailed on Table 19, all crosses exhibited negative, H^e for AFE, indicating that crossbred birds achieved sexual maturity earlier than the mid-parent average. This finding aligns with previous research (Hristakieva *et al*., 2014; Lalev *et al*., 2014; El-Tahawy and Habashy, 2021; Atsbaha *et al*., 2023). However, Ni *et al.* (2023) reported low but positive H^e for AFE.

BWSM are generally beneficial for dual-purpose breeds, as they can boost both meat and egg production. For egg production, it positively impacts egg weight, overall productivity, and breeding success (Jesuyon, 2024). In this study, all genotypes displayed positive H^e for

BWSM, ranging from 0.63% to 17.37%. Crosses involving H and S or K breeds showed particularly promising results. Combinations such as K×S, K×H, H×K, S×K, H×S, S×H, D×H, D×S, H×D, and S×D demonstrated high positive H^e for BWSM. While most crosses exhibited negative, H^e, the H×S and H×D crosses showed positive H^e for EWAFE, suggesting their potential for improving early egg weight. The overall positive H^e observed in these crosses highlights the significant role of non-additive genetic effects, such as dominance, overdominance, and epistasis, in enhancing these traits. These findings are consistent with previous studies reporting positive hybrid vigor for BWSM (Iraqi, 2008; Assefa *et al*., 2021; Fikrineh *et al*., 2023b).

For HHEP, HDEP, EN, and EM, most crosses displayed positive H^e. However, specific combinations like S×K and S×D showed negative H^e for HHEP, HDEP, and EN. Similar results were reported by Saadey *et al*. (2008) in a 4×4 diallel cross involving Fayoumi, Sinai, Rhode Island Red, and White Leghorn breeds, where positive H^e was observed for egg production and EN. The positive H^e in most crosses underscores the potential of crossbreeding to enhance egg production.

Most crosses and their reciprocals exhibited positive H^e for EWT, except for H×S. However, its reciprocal, S×H, displayed the highest positive H^e. The negative H^e observed in H×S suggests that this particular cross may not be ideal for improving EWT. In agreement, Saadey *et al*. (2008) reported positive H^e for EWT in a direct cross between White Leghorn and Rhode Island Red but negative H^e in its reciprocal cross.

Crossbreds H×S, H×K, H×D, K×H, K×S, and D×K demonstrated positive H^e values for EL and EW. Similarly, Atsbaha *et al*. (2023) reported positive H^e for EL and EW. The occurrence of both positive and negative H^e highlights the role of non-additive genetic effects in determining egg dimensions. Specific combinations, such as H×K and K×S, which exhibit positive H^e, suggest that certain parental lines (H, K, S) could possess complementary alleles or genetic backgrounds that interact favorably to enhance egg size. These crosses are particularly promising for breeding programs focused on improving egg dimensions, as they demonstrate potential hybrid vigor. Negative H^e was observed for SWT in all crosses except H×K. On the other hand, positive H^e was noted ST in most crosses, except S×K and K×S. In agreement, Santosh and Raj (2023) reported the highest positive

H^e values for ST. Similarly, Atsbaha *et al*. (2023) also documented positive H^e for ST. However, in contrast, the same authors reported positive H^e for SWT. The positive H^e for ST in most crosses is advantageous for enhancing shell quality, which is critical for reducing breakage and improving hatchability. The positive H^e for AH and AW observed in most crosses indicates that crossbreeding can improve albumen quality, which is important for egg grading and consumer preference. These results are supported by Atsbaha *et al*. (2023), who reported positive H^e values for AH.

5.6.2. Combining ability and reciprocal effects

Combining ability and reciprocal effects on body weight

General combining ability (GCA) is often used in breeding programs to predict how the offspring of a particular individual will perform on average, based on the genetic potential passed on by that individual. In this study, GCA effects were highly significant ($P < 0.0001$) among purebreds for BW at all age studied Table 21.

The significance of GCA indicates the paramount importance of additive genetic effect for inheritance of BW. The variance ratio of GCA to SCA also indicated that, the additive genetic effect are the main drivers of BW variation. The dominance of additive genetic variance in the inheritance of BW indicates that the individual contributions of parental alleles are key for BW improvement. Significantly high and positive GCA was found in S breed throughout the growing period, which had higher additive effects on BW than the average effects of other parental lines. Therefore, selection within S parental line followed by crossbreeding may be advocated to utilize both additive and non-additive genetic variance. In simpler terms, when crossing S with the other breed, the offspring are likely to inherit favorable growth genes from the fast-growing parent, regardless of the other parent's specific genetic makeup. Hence, exploitation of additive genetic variance on BW by using S chickens as a parent would be much useful. These results were similar with Emad *et al*. (2017), who found high and positive GCA estimates for S chicken breed. In addition, Mekki *et al*. (2005) and Adebambo *et al*. (2011) also found that exotic commercial chickens had higher GCA values than the indigenous. This indicates that the exotic breeds exhibit lower gene variation for BW. Following S chickens, except for hatch, 2^{nd} and 8^{th} WK the GCA for K breeds was high and positive than the average effects of other parental

lines. This agrees with the result obtained by Tyasi *et al.* (2019) who reported that K chicken got encouraging effects of GCA at all age measurement except for hatch and 8th WK of age. In line with the current study, Fikrineh *et al.* (2023a), also reported the GCA estimates of S chicken breed high and positive, similarly negative GCA for K breeds at hatch, 2nd and 8th WK of age. On the other hand, D and H had the lowest (negative) additive effect on BW, therefore, use of H chicken breeds as a parent line would not be desirable. Significant GCA for BW in consensus to this study has also been reported by several studies (Mekki *et al*., 2005; Adebambo *et al*., 2011; Sungkhapreecha *et al*., 2022).

SCA involves interaction between specific alleles from both parents. It focuses on the synergistic effects when these genes combine in offspring. The concept of SCA is often tied to the idea of heterosis, where two genetically distinct parents combine traits that are beneficial when present together in the offspring. Result presented in Table 21 indicated that variation due to SCA was high ($P < 0.001$) for BW. Significant SCA effect indicated the importance of non-additive genetic variance (dominance) in the heritance of BW. The crosses with high and positive SCA values for BW was found in combination of S×K, H×D, S×D, and H×S at all ages measurements, accordingly. The high and positive SCA indicates that the combination of alleles from these specific parents results in favorable gene interactions, leading to improved traits in the offspring. However, H×K and K×D crosses exhibited low and negative SCA values throughout the measurement period. Similar findings of significant SCA for BW at different ages were reported in diallel experiments by (Musa *et al*., 2015; Tyasi *et al*., 2019; Sungkhapreecha *et al*., 2022). On the other hand, Fikrineh *et al.* (2023a) reported that high and positive SCA value for Fayoumi and Koekoek, low and negative SCA for Fayoumi and Sasso crosses.

The reciprocal crossbreeding effect is the difference in offspring performance based on the direction of the cross, where one parent is the sire, and the other is the dam. This effect can be due to maternal influences, paternal effects, or genetic factors like sex-linked traits. In this study, RE were not significant throughout the growing ages except for hatch ($P < 0.002$), WK2 ($P < 0.0001$), and WK10 ($P < 0.0361$). Similar results were reported by Fikrineh *et al.* (2023a), in which no significant variation was observed on the reciprocal crosses except at hatch. In contrast with this finding Siwendu *et al.* (2013), reported that

RE effect were significant source of variation except hatch. Generally, based on these results, the low RE could indicates that there were no significant maternal or paternal effects influencing BW.

Combining ability and reciprocal effects on ADFI and FCR

The estimates of combining ability provided in Table 22 illustrate the complex genetic architecture underlying feed intake and feed conversion efficiency in poultry. Both GCA and SCA effects are crucial in determining the performance of crosses, and their relative importance shifts with developmental stage and trait.

Genotype S emerged as the most valuable general combiner, contributing positively to both high feed intake and low FCR across all periods. These traits are likely under additive genetic control in S, making it an ideal candidate for recurrent selection or as a base for developing elite lines. These findings are in line with Zhao *et al*. (2022), who reported that White Leghorn-type lines with strong additive effects contributed to lower FCR in hybrid layers.

On the other hand, genotype H consistently exhibited poor GCA values for both traits. Its negative contribution to feed intake and positive FCR suggests that H carries alleles unfavorable for growth and efficiency, likely due to slower metabolism or lower growth potential. This result agrees with Shambel *et al*. (2022), who reported that certain indigenous Ethiopian genotypes added little to hybrid vigor in crossbreeding programs.

Strong negative SCA estimates for FCR in crosses such as D×H, H×K, and K×S indicate that hybrid vigor plays a critical role in improving feed efficiency. These combinations likely involve complementary gene interactions that enhance nutrient utilization or growth rates. For example, the cross D×H, with SCA values of –0.60 in early stages, showed superior efficiency, likely due to the combination of fast-growing exotic traits from D and robustness or stress tolerance from H.

However, certain crosses like K×D and D×K showed poor SCA for FCR (+0.52 and +0.37, respectively), indicating suboptimal genetic compatibility. These results reinforce the idea that not all crosses result in positive heterosis, and careful matching based on physiological and metabolic traits is essential.

The GCA/SCA ratio for FCR rose over time, reaching 0.84 in weeks 13–16, suggesting a stronger additive component in late-stage feed efficiency. This implies that long-term selection programs could successfully improve FCR through additive selection. However, the lower GCA/SCA ratio in earlier stages (e.g., 0.36) indicates that early growth and intake benefit more from hybrid vigor.

Combining ability and reciprocal effects for meat and carcass traits

Table 23 presents estimate of combining ability for slaughter weight, dressed carcass weight, and eviscerated weight of four chicken genotypes (H, S, K, and D) and their crosses, separated by sex. The significance of general combining ability (GCA), specific combining ability (SCA), and reciprocal effects (RE) was also tested, revealing highly significant ($P < 0.0001$) differences across traits, underscoring the crucial roles of additive, non-additive, and maternal effects in carcass performance.

Among purebreds, S exhibited the highest and most favorable GCA effects for all three carcass traits in both sexes. This aligns with Sasso's commercial meat-type breeding background, which emphasizes rapid growth, superior feed conversion, and carcass yield traits. Similar findings have been documented by Yakubu *et al*. (2020), who reported higher body and carcass weights in commercial broiler genotypes compared to indigenous or dual-purpose breeds. In contrast, H and D showed consistently negative GCA effects, particularly for eviscerated weight. These results suggest that these breeds contribute less favorably to carcass traits when used as purebreds, possibly due to slower growth rates and lower muscling capacity, characteristics typically observed in local and dual-purpose chickens (Bettridge *et al*., 2018). The relatively modest GCA values for K indicate an intermediate performance, consistent with its dual-purpose classification.

Looking at specific combining ability (SCA), several crossbreds demonstrated strong positive effects. Notably, K×D males had high SCA estimates for slaughter weight (148.33 g), dressed weight (125.00 g), and eviscerated weight (100.00 g), implying substantial non-additive genetic effects such as heterosis and dominance in this cross. This indicates that certain breed combinations benefit from complementary gene actions, enhancing carcass traits beyond what is predicted by additive effects alone. These observations are in agreement with Fathi *et al*. (2013) who reported significant SCA effects in diallel crossbred

chickens for carcass yield traits. Another standout was the S×D female cross, which recorded exceptionally high positive SCA estimates, for eviscerated weight, reflecting strong sex-dependent hybrid vigor. The favorable interaction between Sasso (as sire) and Dz-white (as dam) could be attributed to enhanced maternal effects from Dz-white, known for relatively good reproductive performance and adaptability, and the superior growth potential of Sasso sires.

The analysis also revealed notable reciprocal effects (RE), with significant maternal influences on carcass traits. For example, S×H females had positive RE values for all traits, for eviscerated weight, suggesting that using Sasso as the dam and Improved Horro as the sire positively influences carcass yield. This could be due to the superior egg quality and maternal care traits from Sasso hens, which improve early chick growth and subsequent carcass yield, a phenomenon well-documented by El-Safty (2012) and Fairfull *et al.* (1983).

The GCA/SCA ratios for the traits ranged from 1.35 to 6.13, with eviscerated weight in females showing the highest ratio, suggesting a greater importance of additive genetic variance for this trait in females. In contrast, lower ratios for other traits indicate substantial contributions of non-additive effects (dominance and epistasis) in influencing carcass performance, echoing findings from Yakubu *et al.* (2020) in indigenous and crossbred chicken populations.

The estimates of combining ability for carcass traits presented in Table 24 reveal clear genotype and sex-based variations in both GCA and SCA effects for thigh, drumstick, breast, and wing weights in chickens. Notably, the S genotype demonstrated the highest positive GCA values across nearly all traits and both sexes, particularly for breast weight (64.44 g in males and 50.94 g in females) and thigh weight (40.36 g in males), indicating its superior genetic potential as a parent for meat yield traits. This is consistent with findings by Nigussie *et al.* (2010), who reported that exotic commercial broilers like Sasso exhibit enhanced growth and carcass performance when compared to indigenous or dual-purpose breeds, likely due to their selection history for high meat yield.

On the other hand, the H genotype consistently recorded negative GCA values across most traits, with the lowest estimates for breast and thigh weights. This may be attributed to its

origin as an improved local breed, primarily selected for adaptability rather than rapid growth or high carcass yield, a trend similarly observed in studies by Tadelle *et al*. (2013), where Ethiopian indigenous chickens showed lower carcass weights relative to commercial strains. The relatively modest performance of K and D genotypes suggests intermediate combining abilities, possibly reflecting their dual-purpose selection histories.

Among the crosses, K×D exhibited notably high positive SCA effects, particularly for thigh and drumstick weights in males (40.00 g and 35.00 g, respectively). This indicates a favorable specific genetic interaction between these two genotypes for these traits, possibly due to complementary allelic effects or heterotic advantage. Such crossbred performance enhancement has been reported by Okeno *et al*. (2012), who noted that crosses between genetically diverse chickens often exhibit improved carcass traits due to heterosis.

Reciprocal effects (RE) were significant for several traits, with values suggesting maternal influence or sex-linked inheritance. For instance, K×S and S×H displayed positive reciprocal effects on breast weight, particularly in females. This could be attributed to maternal effects related to egg size, early chick vigor, or mitochondrial inheritance, as highlighted by Fairfull *et al*. (1983) in their studies on maternal effects in poultry breeding.

The significance of GCA effects ($P < 0.0001$ for most traits) indicates that additive genetic variance predominantly governs the inheritance of these carcass traits, aligning with previous diallel cross studies by crossbreeding programs in tropical environments by Yakubu *et al*. (2020). The relatively lower and often non-significant SCA effects, except for thigh and breast weights, suggest that non-additive gene action plays a lesser, though trait-specific, role. The GCA/SCA ratios further confirm this, with values above 1 for most traits, underscoring the preeminence of additive gene effects. However, for traits like drumstick and female-specific carcass parts, negative GCA/SCA ratios hint at more complex inheritance patterns, potentially involving sex-linked or epistatic interactions.

The combining ability estimates for gizzard, heart, and liver weights presented in Table 25 reveal significant variability across different purebred and crossbred genotypes, as well as between sexes. The significant GCA effects for nearly all traits ($P < 0.05$) suggest that additive genetic effects play a notable role in determining these organ weights, while the

significance of SCA and RE for several traits indicates the presence of non-additive gene actions, including dominance and maternal or reciprocal influences.

For gizzard weight, the purebred genotype K exhibited relatively high positive GCA estimates in both sexes, while H had consistently negative values. This suggests that K possesses favorable additive genes for increased gizzard weight, while H may carry alleles associated with reduced gizzard development. The significant SCA effects ($P = 0.0448$) and RE ($P < 0.05$) further underscore the influence of specific cross combinations and maternal effects on this trait. Of particular note, the cross K×D displayed the highest positive SCA value (2.97 g) for male gizzard weight, pointing to possible heterotic effects in this combination. Similar observations were reported by Nwachukwu *et al*. (2006) and Yakubu *et al*. (2010), who emphasized the importance of specific crosses in enhancing visceral organ development in chickens, attributing it to complementary gene action and maternal contributions to early organogenesis.

Heart weight estimates revealed significant GCA effects ($P < 0.0001$) but non-significant SCA effects ($P = 0.5802$), suggesting that heart size is predominantly controlled by additive genetic effects. Notably, S had the highest positive GCA in males (1.48 g), which could be associated with its genetic predisposition for enhanced cardiovascular capacity, possibly linked to higher metabolic rates in certain indigenous or dual-purpose breeds as suggested by Oluyemi, (2000). Among crossbreds, the combination S×K showed a notable negative value (-1.47 g), indicating potential incompatibilities or less favorable non-additive interactions for heart weight between these genotypes.

Liver weight displayed some of the most pronounced combining ability estimates and significant effects across GCA, SCA, and RE (all $P < 0.05$). The highest SCA estimates were observed in the cross S×K, with values of 14.30 g in males and 23.00 g in females, indicating strong heterotic effects in this particular cross. This could be due to enhanced feed conversion efficiency or improved metabolic capacity resulting from favorable gene interactions, as liver size is closely related to nutrient metabolism and detoxification capacity in poultry. Additionally, significant reciprocal effects were observed, with combinations such as S×H and K×S displaying high positive values, pointing to maternal influences on liver development.

In terms of sex-specific differences, several crosses showed pronounced variation between males and females. For instance, S×K had a notably higher liver weight in females (23.00 g) compared to males (14.30 g), suggesting potential sex-linked genetic effects or hormonal influences on organ growth. This pattern aligns with the observations of Zerehdaran *et al*. (2004), who reported sex-related differences in organ weights attributable to differential hormonal regulation and growth trajectories in male and female chickens.

The GCA/SCA ratios further clarify the nature of gene action for these traits. Gizzard weight in males (1.34) had a ratio greater than one, indicating the predominance of additive genetic effects, while liver weight in both sexes exhibited ratios well below one (0.10 and 0.08), reinforcing the major role of non-additive effects and specific cross combinations in influencing liver size.

Combining ability and reciprocal effects for WHC and color

Table 26 presents estimate of combining ability for meat WHC and instrumental color traits (L*, a*, b*) of breast meat across different chicken genotypes and their crosses. The results reveal notable variation in both GCA and SCA effects, suggesting the relative importance of additive and non-additive genetic effects in determining meat quality characteristics.

Among the GCA effects, genotype K showed a positive effect on L* (lightness) value, while S exhibited a notable negative effect, indicating that K tends to produce lighter breast meat, whereas S contributes to darker meat color. This aligns with findings by Bihan *et al*. (2001) and Zerehdaran *et al*. (2004), who reported significant genetic influences on meat color traits, largely attributed to differences in muscle fiber composition and myoglobin content between genotypes. Regarding a* (redness) values, most GCA effects were modest, though K recorded a slightly higher value, while H showed a slightly negative effect. The significant P-value for GCA (0.0043) in b* (yellowness) suggests that additive genetic effects play a significant role in this color trait. Notably, S demonstrated a positive effect, implying that it contributes to more yellowish meat. This is consistent with Rondelli *et al*. (2003), who highlighted breed differences in breast meat yellowness due to genetic variations in fat deposition and carotenoid storage capacity.

In terms of SCA effects, crosses like S×K and H×K exhibited substantial positive effects on L*, indicating these combinations produce markedly lighter meat. The significant P-value for SCA in L* (0.0249) reflects the importance of non-additive genetic interactions, such as dominance or epistasis, in determining breast meat lightness in these crosses. These results resonate with findings from Duclos *et al*. (2007), who emphasized the significance of heterotic effects in improving meat quality traits through crossbreeding.

For a* values, RE were highly significant ($P < 0.0001$), particularly in combinations like S×H and K×H. This suggests maternal effects or sex-linked genetic contributions may influence redness intensity, a finding supported by Debut *et al*. (2003), who noted maternal lineage impacts on meat quality, especially traits sensitive to stress response and metabolic rate differences in offspring.

The combining ability analysis reveals valuable insights for designing crossbreeding programs aimed at improving water holding capacity (WHC) in chicken breast meat. The strong positive general combining ability of the H genotype (1.76) emphasizes its potential as a superior parent for enhancing WHC. On the other hand, the consistently negative GCA values for K and its involvement in several crosses with low SCA effects (e.g., S×K = -1.27) indicate that K may carry alleles unfavorable for WHC. This reflects that not all parental lines contribute positively, careful parental selection is essential in crossbreeding to avoid dilution or loss of desirable meat quality traits.

The significance of reciprocal crosses like S×H (1.68) and D×K (0.71) having positive SCA effects also highlights the importance of maternal or reciprocal effects in crossbreeding. With a GCA/SCA ratio greater than 1, the data imply that additive gene action predominates in controlling WHC, meaning that breeding strategies emphasizing selection of parents with high GCA (like H) would be more effective than relying on specific hybrid combinations. However, the non-negligible SCA effects in some reciprocal crosses suggest that exploiting specific cross combinations could further optimize WHC.

Combining ability and reciprocal effects for proximate composition

The estimates of GCA, SCA, and RE for the proximate composition traits of chicken breast meat presented in Table 27 reveal insightful patterns into the genetic control of meat quality

traits in diallel cross combinations. Starting with moisture, the GCA effects were not significant (P = 0.3272), suggesting additive gene action played a limited role in determining moisture content in the breast meat. However, SCA (P = 0.0161) and RE (P = 0.0004) were significant, indicating that non-additive gene actions such as dominance and epistasis, along with maternal and cytoplasmic influences, substantially affected moisture content. Notably, the highest positive RE for moisture was observed in the K×H cross, while D×S and K×D also showed considerable positive values, possibly due to favorable dominance interactions between these genotype pairs. This aligns with the findings of Muhlisin *et al*. (2013), who reported that reciprocal effects and maternal influences can significantly impact meat water-holding capacity and related traits in broiler crossbreds.

For crude protein (CP), both SCA (P < 0.0001) and RE (P < 0.0001) effects were highly significant, while GCA was marginally significant (P = 0.0256). This pattern suggests that while some additive genetic contributions exist, dominance and reciprocal (possibly maternal or sex-linked) effects are more decisive for protein content. The highest positive SCA estimate for CP was in the H×D cross, implying a synergistic interaction between these genotypes for enhancing breast meat protein content. The importance of dominance effect in meat protein content is supported by Nwachukwu *et al*. (2006), who emphasized the role of specific gene combinations in improving protein levels in crossbred broilers. Interestingly, reciprocal crosses such as K×S and D×H also displayed positive values, underlining the maternal and/or cytoplasmic inheritance influence in protein deposition.

Crude fat (CF) presented significant SCA (P = 0.0458) and RE (P < 0.0001) effects, with GCA remaining non-significant (P > 0.05). This finding suggests that fat deposition is predominantly controlled by non-additive gene action and influenced by maternal effects. The highest SCA estimate was observed in the S×D cross, suggesting a strong complementary effect between these lines for increased fat content in breast meat. This is consistent with results by Bihan *et al*. (2001), who indicated that specific cross combinations could exhibit increased intramuscular fat due to heterotic effects. Moreover, reciprocal effects such as K×H and S×H suggest the maternal genotype also modulates fat deposition, potentially through differences in yolk-derived lipids or early post-hatch metabolic programming.

Regarding crude ash (CA), both SCA ($P < 0.0001$) and RE ($P < 0.0001$) effects were highly significant, whereas GCA ($P = 0.0093$) was also significant, indicating that both additive and non-additive gene actions contribute to ash content in breast meat. The highest SCA estimate was recorded in the H×K cross, implying a favorable interaction between these genotypes for increasing mineral content. The importance of both additive and dominance variance in mineral deposition has been previously noted by Havenstein *et al*. (2003), who observed that mineral content is responsive to both direct genetic selection and specific cross combinations in broilers. Reciprocal effects were particularly notable, with K×H indicating that direction of crossing can significantly alter mineral content, potentially through maternal provisioning or sex-linked inheritance.

For energy content, none of the combining ability sources reached statistical significance ($P > 0.05$). This suggests that energy content in breast meat may be more influenced by environmental or residual factors not accounted for by the genetic components tested here. This finding aligns with Zerehdaran *et al*. (2004), who noted that while proximate components like fat and protein are genetically regulated, overall energy content often shows higher environmental variance due to its composite nature.

The GCA/SCA ratio provides further insight, with values near zero or negative for most traits, reaffirming the preponderance of non-additive genetic effects, except for energy (1.23), which indicates a greater additive genetic influence for this trait, although not statistically significant. These findings collectively suggest that, in this study, proximate meat composition traits in chickens are largely influenced by specific combining ability and reciprocal effects rather than general combining ability, underlining the importance of exploiting heterosis and maternal effects in breeding programs aimed at improving meat quality.

Combining ability and reciprocal effects for fertility and hatchability

The combining ability analysis for fertility and hatchability traits presented in Table 28 offers valuable insights into the genetic contributions of the four genotypes and their crosses. For fertility, genotype K exhibited the highest positive GCA estimate, suggesting it is a good general combiner for fertility, while H had a notably negative value, indicating poor general performance. This pattern could be attributed to inherent reproductive characteristics and gamete viability differences among the breeds. Similar trends were reported by Yakubu *et al*. (2020), who found that local chicken ecotypes showed variable fertility rates due to genetic makeup and maternal effects. The SCA effects showed that the H×K cross had the highest positive effect, while H×D and K×D performed poorly. The outstanding performance of H×K could be due to complementary gene action or non-additive genetic interactions enhancing fertility, as suggested by Ajayi and Agaviezor (2016), who highlighted the significance of heterotic effects in improving reproductive traits in chicken crosses.

For hatchability traits (HTES and HFE), similar patterns emerged. Genotype K again had the highest GCA for HTES, reinforcing its role as a good general combiner for reproductive efficiency. On the other hand, H had a negative GCA for both HTES and HFE, confirming its generally poor reproductive potential. In terms of SCA, the H×K cross excelled in both HTES and HFE, underscoring the value of this specific combination in breeding programs aimed at improving hatchability. The poor SCA effects in crosses like K×D, particularly in HFE, may result from genetic incompatibilities or deleterious interactions affecting embryo viability, consistent with the findings of Nwachukwu *et al*. (2006), who observed similar challenges in certain crossbred chicken combinations.

Reciprocal effects (RE) further highlighted the maternal influence on these traits. Notably, S×H had the highest positive reciprocal effect for HTES and HFE, suggesting that when S is used as a dam and H as a sire, hatchability is significantly enhanced. This maternal advantage might be attributed to better egg quality, incubation behavior, or maternal environment. The GCA/SCA ratio was highest for fertility (0.63) and lowest for HFE (0.22), indicating that additive genetic variance is more influential in fertility, while non-additive effects predominate in hatchability on a fertile egg basis. The highly significant P-

values for GCA in all traits, particularly for fertility and HTES ($P < 0.0001$), underscore the critical role of additive genetic effects in determining reproductive performance in this population.

Combining ability and reciprocal effects for egg production and quality traits

GCA effects were highly significant ($P < 0.0001$) among purebreds for egg production traits Table 29. The variation underscores the importance of additive genetic effects in the inheritance of egg production traits. The K breed showed the highest positive GCA values for HHEP, HDEP, EM, and EN, while S exhibited the highest positive GCA values for AFE, BWSM, and EWAFE. On the other hand, D showed moderate positive GCA values for some traits (HHEP, HDEP, EM, EN) but negative GCA for AFE, BWSM, and EWAFE. This indicates that D may not be ideal for improving early maturity or body weight. However, H predominantly showed negative GCA values, except for AFE, where it had a positive GCA. This suggests that H breed may not contribute strongly to most production traits but could be useful for reducing the AFE. Breeds with high additive genetic effects (K and S) should be prioritized as parents in crossbreeding programs to ensure consistent improvement in key traits. While its GCA of H chicken breed is generally low, its positive GCA for AFE suggests it could be useful in crosses aimed at reducing the age at sexual maturity.

SCA reflects non-additive genetic effects, such as dominance and epistasis, which are specific to particular breed combinations. High SCA values indicate that certain crosses perform better than expected based on the GCA of the parent breeds. H×K recorded the highest positive SCA for BWSM, indicating strong heterosis for BWSM. This cross also showed moderate SCA for EWAFE, HHEP, HDEP, EM, and EN. S×K showed the highest positive SCA for HHEP, HDEP, EM, and EN, making it a promising combination for improving egg production traits. S×D cross had the highest positive SCA for EWAFE, suggesting that this combination is particularly effective for improving EWAFE. On the other hand, H×D cross showed moderate positive SCA for BWSM, HHEP, and HDEP, indicating potential for improving BWSM and egg production. Crosses with high SCA (e.g., H×K, S×K, S×D) should be prioritized in breeding programs to exploit heterosis and

dominance effects. Specific combinations like S×K for egg production and S×D for EWAFE can be used to address specific breeding goals.

The GCA/SCA ratio provides insights into the relative contributions of additive and non-additive genetic effects. The GCA/SCA ratios for various traits reveal distinct genetic influences: AFE has a very low ratio, indicating dominance or epistatic interactions are more significant than additive effects, making crossbreeding or selection ideal for improvement. On the other hand, EWAFE has a high ratio, highlighting the dominance of additive effects, making purebred selection highly effective. BWSM, HHEP, and HDEP showed a moderate ratio, with both additive and non-additive effects playing roles, suggesting a combination of purebred selection and crossbreeding. EM and EN also show moderate ratios, with non-additive effects slightly more significant, suggesting hybrid strategies to leverage heterosis alongside purebred selection for optimal results.

Reciprocal effects reflect the influence of maternal or paternal effects on trait expression. The direction of crossing should be carefully considered to optimize outcomes. D×K and D×H showed the highest positive RE for EWAFE, HHEP, and HDEP, indicating that using D as the maternal parent and K and H as the paternal parent improves EWAFE and enhances egg production. K×S cross had the highest positive RE for EM, indicating that using K as the maternal parent and S as the paternal parent improves EM. Some crosses (e.g., S×H, K×H) showed negative RE for traits like EWAFE, EM, and EN, suggesting that the direction of crossing can negatively impact performance. Crosses with negative RE (e.g., S×H, K×H) should be avoided or used cautiously.

GCA effects were significantly different ($P < 0.001$) for egg quality traits across purebreds Table 30. The significance of GCA underscores the critical role of additive genetic effects in the inheritance of egg quality traits (Khalil *et al*., 2018). S breed showed the highest positive GCA for EWT, YW, and YWT, making it a strong contributor to egg quality. K had positive GCA for EWT, EL, EW, ST and AW, indicating its potential for improving these traits, however the breed exhibited negative value for YWT, YW, and YR. In agreement, positive GCA value for K on EWT and EW was reported by Fikrineh *et al*. (2023c). However, in contrast, the same author reported negative value for EL and ST and positive value for YWT.

SCA refers to situations where certain genetic combinations perform either better or worse than predicted based on the average performance of the parent lines involved (Emad *et al*., 2017). It highlights the non-additive genetic interactions that influence the performance of specific crosses. Table 30 indicated that variation due to SCA was high ($P < 0.001$) for all traits. The S×D cross exhibited the highest positive SCA for EWT, demonstrating significant heterosis. Meanwhile, the K×D cross displayed the highest positive SCA for EL, EW, and AW, indicating its potential to enhance these characteristics. The H×K cross showed the highest positive SCA for ST and YR, positioning it as a promising combination for improving shell and yolk quality. Similar findings were reported by Singh *et al*. (2016) and Santosh and Raj (2023) in their studies.

RE showed significant variations for various traits, except EL, YW, and YWT. K×S showed the highest positive RE for EWT and AW, indicating that using K as the maternal parent and S as the paternal parent improves EWT and AW. D×S cross had the highest positive RE for ST, suggesting that using D as the maternal parent and S as the paternal parent improves ST. Crosses like S×D and K×D should be prioritized for improving EWT and EL, while H×K can be used to enhance ST. The direction of crossing should be considered to optimize egg quality traits, as seen in the positive RE for K×S and D×S. Similarly, Fikrineh *et al*. (2023c) reported, except for EL, other studied traits aligned with this study showed variation in RE. Singh *et al*. (2016) also reported significant RE for EWT.

The GCA/SCA ratio is used to assess the relative importance of additive genetic effects versus non-additive genetic effects in the expression of a trait. A high GCA/SCA ratio suggests that additive genetic effects are more important, while a low ratio indicates that non-additive genetic effects (dominance or epistasis) play a more significant role. Traits like EWT (0.681) and YWT (0.345) were primarily influenced by additive genetic effects, suggesting selection-based breeding (such as recurrent selection) would be more effective. On the other hand, traits like EL (0.044), EW (0.016), ST (0.002), and YR (0.158) were dominated by non-additive effects, making hybrid breeding or specific crosses to exploit heterosis more suitable. For traits with moderate ratios like AW (0.259) and YW (0.227), a combined approach of selection and hybrid breeding is recommended.

5.6.3. Maternal effects (M^e)

Maternal effects on meat and carcass traits

The maternal effects on carcass characteristics of different chicken genotypes presented in Table 31 reveal notable trends and variations, with a few statistically significant findings that warrant interpretation. Maternal effects, which include genetic contributions from the dam as well as maternal influences during embryonic development and early growth, are well-documented to affect carcass traits in poultry (Fairfull *et al*., 1983; Wei and van der Werf, 1994).

For slaughter weight (SW), significant negative maternal effects were observed when D was the dam breed in H×D (-110.00; P = 0.005) and K×D (-148.33; P = 0.030) crosses, suggesting that using D as the maternal line may negatively impact final body weight. This could be attributed to maternal genetic factors or lower maternal provisioning such as egg nutrient content or brooding behavior. Similar findings were reported by Yakubu *et al*. (2020), who noted that maternal line differences significantly influenced growth performance traits in indigenous and crossbred chickens.

For dressed carcass weight (DW), H×S (36.67; P = 0.043) and S×D (110.00; P = 0.033) showed significant positive maternal effects, indicating the potential of S as a dam breed to improve carcass yield when crossed with other lines. This positive maternal influence could be due to superior egg composition or better early chick vitality associated with S hens. On the other hand, D dams in H×D (-80.00; P = 0.004) again showed a negative effect, reinforcing the earlier observation for SW.

For eviscerated weight (EV), a highly significant negative maternal effect was recorded in the S×K cross (-80.00; P < 0.001). The small standard error suggests consistency in this negative effect, possibly indicating incompatibility or suboptimal maternal genetic contribution when S hens are mated with K males for this trait. Although the biological reasoning might involve maternal factors affecting organ development or fat deposition patterns, similar findings on cross-specific maternal effects have been noted by Nigussie *et al*. (2010), emphasizing the need to consider specific combinations rather than assuming uniform maternal influence.

In terms of thigh weight (TWT), only K×D (-40.00; P = 0.012) showed a significant negative maternal effect. This aligns with the pattern observed for SW and DW, further suggesting D's limitations as a dam breed for carcass-related traits. Maternal effects on muscling traits like thigh weight may reflect both genetic and early nutritional influences, as noted by Goliomytis *et al.* (2015), who highlighted maternal line differences affecting muscle deposition in broilers.

Organ weights also presented interesting patterns. Gizzard weight showed a significant positive maternal effect in S×D (3.60; P = 0.020), implying potential maternal influence from S hens in organ development. For heart weight, a small but significant negative maternal effect appeared in K×D (-1.17; P = 0.042). This observation mirrors the general negative maternal effect pattern associated with D as a dam breed, indicating possibly inherited limitations in organ size or early development.

Liver weight, where both positive (H×S: 10.37; P = 0.026) and negative (H×D: -4.35; P = 0.044; S×K: -14.30; P = 0.005) maternal effects were observed. The strong negative effect in S×K highlights again that maternal line influences may act differently depending on the trait and cross combination. Liver size can be an indirect indicator of metabolic capacity and fat deposition, traits known to be maternally influenced (Goliomytis *et al*., 2015).

Maternal effects on fertility and hatchability traits

Table 32 presents estimate of maternal breed effects on fertility and hatchability traits, specifically fertility percentage, HTES, and HFE, in various genotype combinations derived from crosses among four chicken breeds. Notably, significant maternal effects were observed in some genotype combinations, suggesting that the maternal genetic background plays a critical role in reproductive performance in chickens.

For fertility, significant positive maternal effects were recorded in the H×D cross, whereas a significant negative effect was observed in the S×D cross. The superior maternal contribution of the D breed when crossed with H and the reduced maternal effect when crossed with S might be attributed to inherent breed differences in reproductive physiology and maternal qualities such as egg production, yolk formation, and egg viability. Previous studies by Yakubu *et al.* (2020) and Nwachukwu *et al.* (2006) similarly reported that

maternal effects significantly influence fertility in crossbred chickens, with certain indigenous breeds known to enhance reproductive traits in crosses due to better brooding and nurturing abilities.

In terms HTES, significant maternal effects were evident in the H×D and K×D crosses. The D breed as a dam appears to contribute positively to this trait in both crosses, possibly due to improved egg quality traits such as shell thickness, albumen quality, and reduced embryonic mortality during incubation. According to Shanawany (1993), maternal factors such as egg size, shell integrity, and internal egg quality have direct effects on hatchability rates, further supporting the positive contributions observed here.

For HFE, only the K×D cross showed a significant positive maternal effect. This suggests that, aside from fertility and HTES, the D breed as a dam also enhances the likelihood of fertile eggs successfully hatching, perhaps through genetic influences on embryo viability and maternal investment during egg formation. The absence of significant maternal effects in other crosses for HFE could indicate that while maternal genetic factors influence early reproductive traits, post-fertilization development may be more influenced by additive genetic effects from both parents or specific combining abilities.

Interestingly, non-significant maternal effects in most other crosses across the three traits suggest that in these cases, either the maternal breed contributes little to variation in these traits or that environmental and paternal effects may be more dominant. This aligns with the findings of Kingori *et al*. (2010), who noted that hatchability and fertility traits are complex and influenced by multiple interacting factors, including management, incubation conditions, and genetic background.

Maternal effects on egg production and quality Traits

The M^e exhibited variation across most egg production traits, as detailed in Table 33. The H×D cross combination demonstrated a significant M^e, indicating a strong negative influence of the H×D cross combination on AFE. However, other crossbred combinations did not show differences. Low and negative estimates for AFE were similarly reported by Lalev *et al*. (2014) and Kedija *et al*. (2020). However, the S×K cross combination displayed a significant M^e, suggesting a strong positive influence of the S×K interaction on BWSM,

while other interactions were not significant. Consistent with the current findings, Shambel *et al.* (2022) observed a positive and significant M^e on BWSM in H and K crosses. However, the same author reported a positive and significant M^e on AFE for the cross combinations, which contrasts with the present results. Additionally, crossbred combinations H×K, H×D, S×K, S×D, and K×D showed significant M^e ($P < 0.05$) on EWAFE, with the H×S combination exhibiting a significant negative M^e ($P < 0.001$). In line with the present findings, Iraqi (2008) also reported significant M^e on EWAFE. For EM, the H×K, H×D, S×K, S×D, and K×D cross combinations displayed highly significant M^e ($P < 0.001$), whereas the H×S combination was not significant ($P = 0.322$). The highest estimates of M^e on EM observed in this study align with those reported by Kedija *et al.* (2020), however, unlike the present findings, the effect in their study was not significant. Regarding EN, the H×S and K×D cross combinations were not significant ($P > 0.05$), while the H×K, H×D, S×K, and S×D combinations showed significant M^e ($P < 0.05$). Overall, the substantial variation on M^e observed across most egg production traits highlights the significant role of maternal additive and dominance gene effects in driving differences in egg production performance among breeds.

The M^e exhibited significant variation for egg quality across most traits Table 34. Significant M^e observed on EWT in crosses H×K, H×S, H×D, S×D, and K×D ($P < 0.05$). Notably, H×S displayed a strong negative M^e, whereas H×D exhibited a positive effect. This highlights the substantial impact of maternal breed selection on EWT. Crossbreeding also significantly influenced traits such as AW and YWT, with H×D showing positive M^e for EWT and AW, and H×S for YWT, reflecting enhanced performance. However, negative M^e were observed in H×S, S×D, and K×D for EWT, as well as in K×D for AW, indicating these combinations may be less favorable. Traits like EL and SWT showed no significant M^e, suggesting limited crossbreeding influence. These findings underscore the need for strategic crossbreeding to harness heterosis and improve key traits, while avoiding combinations with detrimental M^e in targeted breeding programs.

6. CONCLUSION AND RECOMONDATION

6.1 Conclusions

This study underscores the effectiveness of crossbreeding as a powerful genetic improvement strategy, enhancing key poultry production traits such as carcass yield, meat quality, feed efficiency, and egg production potential. The consistent superiority of crossbred chickens over purebreds highlights the significant role of heterosis (hybrid vigor) and genetic complementarity in optimizing poultry performance.

Crossbred genotypes demonstrated notable improvements across all evaluated slaughter traits, particularly when genetically distinct breeds were combined. For instance, crosses involving genotype S (known for high growth potential) exhibited enhanced muscle development and carcass yield, reinforcing that strategic breed pairing maximizes heterosis benefits.

Beyond quantitative gains, crossbreeding also improved meat composition. Crosses such as K×H and D×H achieved higher protein content, while D×K maintained optimal moisture levels. Additionally, S×K produced leaner carcasses with reduced fat, demonstrating that such crossbreeding can be tailored to meet specific consumer and market demands for healthier, high-quality poultry meat.

Feed efficiency (critical economic factor) was also positively influenced by crossbreeding. Genotype S played a key role in improving feed conversion ratio (FCR) and average daily feed intake (ADFI) when crossed with other breeds, such as in H×S, S×H, and K×S combinations. This reflects the synergistic effects of additive and non-additive genetic factors, maternal influence, and hybrid vigor, making crossbreeding a viable strategy for boosting productivity without compromising growth performance.

On the other hand, the observed genetic interactions also suggest potential benefits for egg production. Crossbreeding has been shown to enhance egg number, egg weight, and early maturity in laying hens, particularly when breeds with strong general combining ability (GCA), like genotype S, are paired with complementary lines. This opens opportunities for developing dual-purpose poultry that excel in both meat and egg production, a valuable

asset for Ethiopian smallholder farmers who rely on multifunctional birds for nutrition and income.

In summary, crossbreeding remains a versatile and impactful tool for poultry genetic improvement. By integrating growth performance, carcass quality, feed efficiency, and reproductive potential, well-designed crossbreeding programs can drive sustainable productivity gains; especially in Ethiopia, where adaptable, high-performing poultry is essential for food security and economic resilience.

6.2 Recommendations

To enhance poultry productivity in Ethiopia; where adaptability, efficiency, and market preferences are crucial, the following strategies are recommended within the limit of the current research:

- Adopt targeted crossbreeding programs that combine high-growth genotypes (e.g., S) with locally adapted breeds to optimize carcass yield, meat quality, and feed efficiency.
- Promote high-performing crosses such as S×H, K×S, and H×K, which have demonstrated superior performance across multiple traits, for wider adoption in breeding initiatives.
- Implement reciprocal crossing strategies for selected crosses based on the present findings and consider sex-linked performance differences to maximize heterosis effects.
- Integrate meat quality traits (e.g., protein content, leanness) into breeding objectives to meet rising consumer demand for nutritious poultry products.
- Strengthen farmer-researcher partnerships through training and extension services to facilitate the adoption of improved crossbreeding techniques across diverse agro-ecological zones.

6.2.1 Scope for future research

While this study provides valuable insights, further research is needed to:

- ✓ Conduct genomic studies to identify genetic markers linked to heterosis for growth, yield, and meat quality.
- ✓ Analyze market acceptance and economic viability of crossbred poultry in both rural and urban Ethiopian markets.
- ✓ Investigate crossbreeding's impact on disease resistance, animal welfare, and environmental sustainability in various production systems.

By addressing these gaps, future research can further refine crossbreeding strategies, ensuring they meet the evolving needs of Ethiopia's poultry sector while enhancing food security and farmer livelihoods.

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8. APPENDICES

Appendix A. Statistical analyses

Appendix A 1. Analysis of variance table for body weight at different growth stages

Variables	Age in week	Source of variation	DF	Type III SS	Mean Square	F- value	Pr > F	CV
Body weight	Hatch	GSA	3	35.56	11.85	95.33	***	1.99
		SCA	6	5.80	0.96	7.77	***	
		RE	6	3.43	0.57	4.59	**	
		Error	30	3.73	0.12			
	WK 2	GSA	3	2257.02	752.34	268.15	***	2.60
		SCA	6	149.89	24.98	8.90	***	
		RE	6	115.48	19.25	6.86	***	
		Error	30	84.17	2.81			
	WK 4	GSA	3	24622.60	8207.50	105.54	***	5.21
		SCA	6	3170.40	528.40	6.79	***	
		RE	6	805.70	134.30	1.72	ns	
		Error	30	2332.80	77.80			
	WK 6	GSA	3	40237.00	13412.30	103.50	***	4.02
		SCA	6	4947.00	824.40	6.36	***	
		RE	6	1721.00	286.90	2.21	ns	
		Error	30	3887.00	129.60			
	WK 8	GSA	3	59504.00	19834.80	75.30	***	3.98
		SCA	6	10147.00	1691.10	6.42	***	
		RE	6	2880.00	479.90	1.82	ns	
		Error	30	7901.00	263.40			
	WK 10	GSA	3	120720.00	40240.00	112.49	***	3.61
		SCA	6	16703.00	2784.00	7.78	***	
		RE	6	5641.00	940.00	2.62	*	
		Error	30	10731.00	358.00			
	WK 12	GSA	3	140159.00	46720.00	51.26	***	4.52
		SCA	6	19130.00	3188.00	3.49	**	
		RE	6	6448.00	1075.00	1.17	ns	
		Error	30	27338.00	911.00			
	WK 14	GSA	3	228234.00	76078.00	61.98	***	4.21
		SCA	6	30664.00	5111.00	4.16	**	
		RE	6	4501.00	750.00	0.61	ns	
		Error	30	36824.00	1227.00			

ns= non-significant; *p≤0.05; **p≤0.01; ***p≤0.001; GCA, general combining ability; SCA, specific combining ability; RE, reciprocal effect.

Appendix A 2. Analysis of variance table for average daily feed intake (ADFI)

Variables	Age in week	Source of variation	DF	Type III SS	Mean Square	F- value	Pr > F	CV
ADFI	WK 0-4	GSA	3	4.84	1.61	10.27	***	3.42
		SCA	6	5.08	0.84	5.39	***	
		RE	6	1.22	0.20	1.29	ns	
		Error	30	4.71	0.15			
	WK 5-8	GSA	3	10.13	3.37	5.96	**	3.07
		SCA	6	10.85	1.80	3.19	*	
		RE	6	3.56	0.59	1.04	ns	
		Error	30	16.98	0.56			
	WK 9-12	GSA	3	6.77	2.25	10.74	***	1.29
		SCA	6	5.82	0.97	4.62	**	
		RE	6	1.58	0.26	1.26	ns	
		Error	30	6.30	0.21			
	WK 13-16	GSA	3	32.18	10.72	187.97	***	0.57
		SCA	6	43.87	7.31	128.15	***	
		RE	6	6.28	1.04	18.34	***	
		Error	30	1.71	0.05			

ns= non-significant; *p≤0.05; **p≤0.01; ***p≤0.001; GCA, general combining ability; SCA, specific combining ability; RE, reciprocal effect.

Appendix A 3. Analysis of variance table for feed conversion ratio (FCR)

Variables	Age in week	Source of variation	DF	Type III SS	Mean Square	F- value	Pr > F	CV
FCR	WK 0-4	GSA	3	3.45	1.15	48.84	***	9.08
		SCA	6	2.45	0.40	17.39	***	
		RE	6	0.57	0.09	4.04	**	
		Error	30	0.70	0.02			
	WK 5-8	GSA	3	2.40	0.80	21.24	***	11.85
		SCA	6	1.77	0.29	7.83	***	
		RE	6	1.54	0.25	6.85	***	
		Error	30	1.13	0.03			
	WK 9-12	GSA	3	2.87	0.95	45.58	***	6.82
		SCA	6	1.47	0.24	11.70	***	
		RE	6	0.91	0.15	7.22	***	
		Error	30	0.63	0.02			
	WK 13-16	GSA	3	2.70	0.90	31.49	***	6.46
		SCA	6	0.95	0.15	5.54	***	
		RE	6	0.20	0.03	1.20	ns	
		Error	30	0.85	0.02			

ns= non-significant; *p≤0.05; **p≤0.01; ***p≤0.001; GCA, general combining ability; SCA, specific combining ability; RE, reciprocal effect.

Appendix A 4. Analysis of variance table for thigh, drumstick, and breast weights

Sex	Variables	Source of variation	DF	Type III SS	Mean Square	F- value	Pr > F	CV
Male	TWT	GSA	3	21357.00	7119.00	39.55	***	7.83
		SCA	6	3320.70	553.50	3.07	*	
		RE	6	4554.50	759.10	4.21	**	
		Error	30	5398.90	180.00			
	DWT	GSA	3	14986.10	4995.40	18.28	***	10.22
		SCA	6	2452.80	408.80	1.49	ns	
		RE	6	4394.40	732.40	2.68	*	
		Error	30	8195.80	273.20			
	BWT	GSA	3	49604.00	16534.80	45.26	***	7.04
		SCA	6	7414.00	1235.70	3.38	*	
		RE	6	4658.00	776.40	2.12	ns	
		Error	30	10958.00	365.30			
Female	TWT	GSA	3	5614.20	1871.41	15.21	***	11.37
		SCA	6	546.70	91.12	0.74	ns	
		RE	6	4234.70	705.79	5.73	***	
		Error	30	3689.20	122.97			
	DWT	GSA	3	7153.00	2384.34	8.06	***	20.68
		SCA	6	1630.60	271.76	0.91	ns	
		RE	6	3690.30	615.05	2.08	ns	
		Error	30	8870.10	295.67			
	BWT	GSA	3	30180.90	10060.30	12.18	***	14.77
		SCA	6	3989.80	665.00	0.80	ns	
		RE	6	14212.50	2368.80	2.86	*	
		Error	30	24762.20	825.40			

ns= non-significant; *p≤0.05; **p≤0.01; ***p≤0.001; GCA, general combining ability; SCA, specific combining ability; RE, reciprocal effect; TWT, thigh weight; DWT, drumstick weight; BWT, breast weight.

Appendix A 5. Analysis of variance table for proximate composition of breast meat

Variables	Source of variation	DF	Type III SS	Mean Square	F- value	Pr > F	CV
MO	GSA	3	0.92	0.30	1.19	ns	1.31
	SCA	6	4.89	0.81	3.15	*	
	RE	6	8.82	1.47	5.68	***	
	Error	30	7.75	0.25			
CP	GSA	3	2.41	0.80	3.56	*	4.11
	SCA	6	11.13	1.85	8.21	***	
	RE	6	25.18	4.19	18.58	***	
	Error	30	6.77	0.22			
CF	GSA	3	0.17	0.05	0.48	ns	22.65
	SCA	6	1.82	0.30	2.47	*	
	RE	6	8.50	1.41	11.56	***	
	Error	30	3.67	0.12			
CA	GSA	3	0.06	0.02	4.58	**	9.14
	SCA	6	0.38	0.06	12.88	***	
	RE	6	0.26	0.04	8.92	***	
	Error	30	0.14	0.01			

ns= non-significant; *p≤0.05; **p≤0.01; ***p≤0.001; GCA, general combining ability; SCA, specific combining ability; RE, reciprocal effect; MO, moisture content; CP, crude protein; CF, crude fat; CA, crude ash.

Appendix A 6. Analysis of variance table for egg production

Variables	Source of variation	DF	Type III SS	Mean Square	F- value	Pr > F	CV
AFE	GSA	3	76.86	25.62	12.40	***	1.67
	SCA	6	189.52	31.58	15.30	***	
	RE	6	28.48	4.74	2.29	ns	
	Error	30	61.93	2.06			
BWSM	GSA	3	194018.00	64673.00	225.22	***	1.68
	SCA	6	132362.00	22060.00	76.82	***	
	RE	6	4413.00	736.00	2.56	*	
	Error	30	8614.00	287.00			
EWAFE	GSA	3	49.15	16.38	105.14	***	1.84
	SCA	6	9.01	1.50	9.63	***	
	RE	6	42.70	7.11	45.67	***	
	Error	30	4.67	0.15			
HHEP	GSA	3	219.19	73.06	123.06	***	2.81
	SCA	6	84.71	14.12	23.78	***	
	RE	6	188.16	31.36	52.82	***	
	Error	30	17.81	0.59			
HDEP	GSA	3	191.69	63.89	71.66	***	3.39
	SCA	6	79.42	13.23	14.84	***	
	RE	6	196.84	32.80	36.79	***	
	Error	30	26.75	0.89			

ns= non-significant; *p≤0.05; **p≤0.01; ***p≤0.001; GCA, general combining ability; SCA, specific combining ability; RE, reciprocal effect; AFE, age at first egg; BWSM, body weight at sexual maturity; EWAFE, egg weight at first egg; HHEP, hen housed egg production; HDEP, hen day egg production.

Appendix A 7. Analysis of variance table for fertility and hatchability of eggs

Variables	Source of variation	DF	Type III SS	Mean Square	F- value	Pr > F	CV
Fertility	GSA	3	141.55	47.18	61.67	***	1.71
	SCA	6	59.92	9.98	13.05	***	
	RE	6	15.39	2.56	3.35	*	
	Error	30	22.95	0.76			
HTES	GSA	3	231.74	77.25	32.51	***	3.62
	SCA	6	115.06	19.17	8.07	***	
	RE	6	88.27	14.71	6.19	***	
	Error	30	71.26	2.37			
HFE	GSA	3	42.93	14.31	3.26	*	4.35
	SCA	6	60.43	10.07	2.29	ns	
	RE	6	100.44	16.74	3.81	**	
	Error	30	131.48	4.38			

ns= non-significant; *p≤0.05; **p≤0.01; ***p≤0.001; GCA, general combining ability; SCA, specific combining ability; RE, reciprocal effect; HTES, hatchability from total egg set; HFE, hatchability from fertile egg.

Appendix A 8. Analysis of variance table for external egg quality traits

Variables	Source of variation	DF	Type III SS	Mean Square	F- value	Pr > F	CV
EWT	GSA	3	44.60	14.86	155.07	***	1.05
	SCA	6	16.84	2.80	29.28	***	
	RE	6	22.22	3.70	38.62	***	
	Error	30	2.87	0.09			
EL	GSA	3	19.78	6.59	5.97	**	3.56
	SCA	6	101.00	16.83	15.24	***	
	RE	6	15.75	2.62	2.37	ns	
	Error	30	33.11	1.10			
EW	GSA	3	8.24	2.74	2.96	*	4.27
	SCA	6	88.98	14.83	16.00	***	
	RE	6	14.26	2.37	2.56	*	
	Error	30	27.80	0.92			
SWT	GSA	3	0.99	0.33	5.73	**	7.93
	SCA	6	0.59	0.09	1.72	ns	
	RE	6	0.24	0.04	0.70	ns	
	Error	30	1.73	0.05			
ST	GSA	3	0.00	0.00	1.29	ns	7.12
	SCA	6	0.03	0.01	20.66	***	
	RE	6	0.01	0.00	4.64	**	
	Residuals	30	0.01	0.00			
SR	GSA	3	1.56	0.52	2.27	ns	8.07
	SCA	6	4.09	0.68	2.97	*	
	RE	6	2.10	0.35	1.52	ns	
	Error	30	6.88	0.22			

ns= non-significant; *p≤0.05; **p≤0.01; ***p≤0.001; GCA, general combining ability; SCA, specific combining ability; RE, reciprocal effect; EWT, egg weight; EL, egg length; EW, egg width; SWT, shell weight; ST, shell thickness; SR, shell ratio.

Appendix A 9. Analysis of variance table for internal egg quality traits

Variables	Source of variation	DF	Type III SS	Mean Square	F- value	Pr > F	CV
AH	GSA	3	1.47	0.49	3.33	*	10.69
	SCA	6	3.01	0.50	3.39	*	
	RE	6	0.27	0.04	0.31	ns	
	Error	30	4.43	0.14			
AW	GSA	3	112.45	37.48	11.21	***	4.80
	SCA	6	119.02	19.83	5.93	***	
	RE	6	174.51	29.08	8.69	***	
	Error	30	100.30	3.34			
YH	GSA	3	7.58	2.52	10.52	***	4.78
	SCA	6	12.90	2.15	8.94	***	
	RE	6	1.25	0.21	0.87	ns	
	Error	30	7.21	0.24			
YW	GSA	3	56.16	18.72	29.69	***	3.62
	SCA	6	63.46	10.57	16.77	***	
	RE	6	1.57	0.26	0.41	ns	
	Error	30	18.91	0.63			
YWT	GSA	3	14.78	4.92	13.55	***	7.37
	SCA	6	12.11	2.01	5.54	***	
	RE	6	4.82	0.80	2.21	ns	
	Error	30	10.91	0.36			
YR	GSA	3	42.86	14.28	9.43	***	7.66
	SCA	6	69.92	11.65	7.69	***	
	RE	6	41.22	6.87	4.53	**	
	Error	30	45.41	1.51			

ns= non-significant; *p≤0.05; **p≤0.01; ***p≤0.001; GCA, general combining ability; SCA, specific combining ability; RE, reciprocal effect; AH, albumen height; AW, albumen width; YH, yolk height; YW, yolk width; YWT, yolk weight; YR, yolk ratio.

Appendix B. Pictures during research works

Pic 1: Dz♂ x Dz♀

Pic 2: K♂ x K♀

Pic 3: S♂ x S♀

Pic 4: H♂ x H♀

Pic 5: H♂ x S♀

Pic 6: H♂ x K♀

Pic 7: H♂ x Dz♀

Pic 8: S♂ x K♀

Pic 9: S♂ x Dz♀

Pic 10: K♂ x Dz♀

Pic 11: S♂ x H♀

Pic 12: K♂ x H♀

Pic 13: D♂ x H♀

Pic 14: K♂ x S♀

Pic 15: D♂ x S♀

Pic 16: D♂ x K ♀

Appendix B 1. Picture of F1 (Pure, crosses and their reciprocals) progenies, management and data collection at the age of 24th weeks






Appendix B 2. Picture of slaughtering process at BARC for carcass evaluation and further meat quality traits analysis

Appendix B 3. Picture of Meat pH measurement after 45 min of post-Slaughter

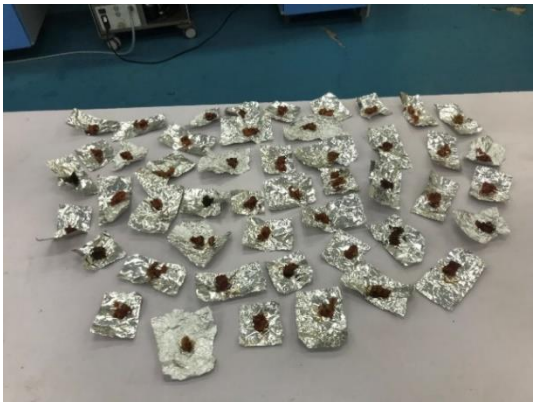
Appendix B 4. Picture of Meat pH measurement after 24 hours of post-Slaughter

Appendix B 5. Picture of Meat color testing at BARC Food and Nutrition Lab

Appendix B 6. Picture of Water Holding Capacity (WHC) determination of meat using Centrifugal method




Appendix B 7. Picture of Meat Texture (Tenderness) test at AASTU Food Science Lab




Appendix B 8. Picture of Meat Proximate Analysis (Moister and ASH) at AASTU Food Science Lab





Appendix B 9. Picture of Meat Sample preparation for Proximate Analysis (Crude protein and Fat) and Fatty acid profiling at EIAR Food and Quality Laboratory






Appendix B 10. Picture of Meat Sample Drying, grinding, and packing for Proximate Analysis (Crude protein and Fat) and Fatty acid profiling at EIAR Food and Quality Laboratory

Appendix C. List of Publications

Appendix C1. Philimon Teshome, Gebeyehu Goshu, Wondmeneh Esatu, Tadelle Dessie, Estimation of heterosis, combining ability and reciprocal effects for body weight in four genetic groups of chicken from a full diallel cross, ***Poultry Science***, Volume **104**, Issue **8**, 2025, 105232, ISSN 0032-5791, Available at https://doi.org/10.1016/j.psj.2025.105232.

Appendix C2. Philimon Teshome, Gebeyehu Goshu, Wondmeneh Esatu, Tadelle Dessie, Genetic analysis of egg production traits in four chicken breeds using a full diallel cross, ***Poultry Science***, Volume **104**, Issue **9**, 2025, 105459, ISSN 0032-5791, Available at https://doi.org/10.1016/j.psj.2025.105459.

Appendix C3. Philimon Teshome, Gebeyehu Goshu, Wondmeneh Esatu, Tadelle Dessie. 2025. Genetic parameters estimation for egg quality traits of four chicken breeds using a full diallel cross. ***Tropical Animal Health and Production***. 2025 Aug 8; ***57***(**7**):353. Available at https://doi.org/10.1007/s11250-025-04612-3.