Genome-wide scan for selection signatures in wild African harlequin quail (Coturnix delegorguei delegorguei) reveals candidate genes associated with immune response, morphological and production traits

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Abstract

The wild African harlequin quails (Coturnix delegorguei delegorguei) of Western Kenya suffer from incessant hunting, habitat fragmentation, and the effects of climate change. These challenges, among others, have forced them to breed under intensive pressure, disrupting normal evolutionary processes. Here, we provide the first overview of the selection signatures in wild African harlequin quails using genotyping-by-sequencing information from 76 captured individuals. Additionally, 19 domestic Japanese quails (Coturnix coturnix japonica) were incorporated for comparative signatures of selection analysis between wild and domesticated quail species that undergo different selection pressures. Composite likelihood ratio test (CLR) and integrated haplotype score (iHS) methods were used to detect selection signatures. As a result, 252 and 424 candidate genes were detected in wild African harlequin and domestic Japanese quails, respectively, through the CLR test, whereas 150 and 457 candidate genes were identified through iHS. Some of the essential candidate genes identified in the wild African harlequin quail were associated with important traits such as immune response (MAPK13, MAPK14, CREB1, ITGB3, and PPP1CA) and morphological traits (WNT5A, GRIA1, CREB1, ADCY8, and ALK) whereas, in domestic Japanese quail, primarily production-related genes such as VIPR2, DYNLL2, COL6A3, MSX2, PRF1and GNA12 were identified. Our findings provide insights into the role of selection in shaping both wild and domestic quail genomes in terms of significant immune response, growth, reproduction, and morphological and behavioral traits.

Genome-wide scan for selection signatures in wild African harlequin quail (*Coturnix delegorguei delegorguei*) reveals candidate genes associated with immune response, morphological and production traits

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ABSTRACT

The wild African harlequin quails (*Coturnix delegorguei delegorguei*) of Western Kenya suffer from incessant hunting, habitat fragmentation, and the effects of climate change. These challenges, among others, have forced them to breed under intensive pressure, disrupting normal evolutionary processes. Here, we provide the first overview of the selection signatures in wild African harlequin quails using genotyping-by-sequencing information from 76 captured individuals. Additionally, 19 domestic Japanese quails (*Coturnix coturnix japonica*) were incorporated for comparative signatures of selection analysis between wild and domesticated quail species that undergo different selection pressures. Composite likelihood ratio test (CLR) and integrated haplotype score (iHS) methods were used to detect selection signatures. As a result, 252 and 424 candidate genes were detected in wild African harlequin and domestic Japanese quails, respectively, through the CLR test, whereas 150 and 457 candidate genes were identified through iHS. Some of the essential candidate genes identified in the wild African harlequin quail were associated with important traits such as immune response (MAPK13, MAPK14, CREB1, ITGB3, and PPP1CA) and morphological traits (WNT5A, GRIA1, CREB1, ADCY8, and ALK) whereas, in domestic Japanese quail, primarily production-related genes such as VIPR2, DYNLL2, COL6A3, MSX2, PRF1and GNA12 were identified. Our findings provide insights into the role of selection in shaping both wild and domestic quail genomes in terms of significant immune response, growth, reproduction, and morphological and behavioral traits.

Keywords: Selection pressure, GBS, candidate genes,

Coturnix

INTRODUCTION

The wild African harlequin quail (*Coturnix delegorguei delegorguei*) is endemic to Eastern and Southern Africa and is commonly found in grassland areas with scattered bush cover (Lewis & Pomeroy, 1989). For generations, rural smallholder farmers in Kenya have hunted quail for consumption as a complementary source of poultry protein (Urban et al., 1986, Ogada et al., 2022). However, in addition to continuous and uncontrolled harvesting, breeding attempts by rural farmers, climate change, habitat destruction by humans, migration, population bottlenecks, and inbreeding are among the main challenges facing wild African harlequin quail in Kenya (Wamuyu et al., 2017; Ogada et al., 2021). These factors interfere with the normal evolutionary processes experienced by wild African harlequin quails and may influence natural, artificial, or sexual selection (Allendorf & Hard, 2009).

In contrast, commercial quail breeds, such as the domestic Japanese quail, have become the most commonly consumed quail species globally since their domestication in the late 19^{th} century and early 20^{th} century (Nishibori et al., 2001). The domestic Japanese quails have undergone intense selection pressure since their domestication through modern breeding methods aimed at increased egg and meat production (Mills et al., 1997; Lukanov & Pavlova, 2020). The domestication and artificial selection of the Japanese quail have brought about genetic variation changes, altering its phenotype and increasing its size and number of eggs laid (Lukanov & Pavlova, 2020).

The main differences between wild and domestic quail species lie in the morphological, behavioral, and productivity characteristics (Chang et al., 2009). In our previous study, the wild African harlequin quail meat and eggs were found to contain higher protein content and minerals (zinc, potassium, calcium, and iron) when compared to domestic Japanese quail, helmeted guinea fowl, indigenous and commercial chickens (Chepkemoi et al., 2017). Therefore, understanding the genetic architecture of the wild African harlequin quail, among other factors, could help elucidate this finding, among other observed traits.

Genomic regions affected by selection pressures tend to develop signatures such as high allele frequencies, substantial linkage disequilibrium, increased homozygous genotypes, and long haplotypes (Nielsen, 2005; Qanbari & Simianer, 2014). Signatures of selection tests are crucial for understanding genomes as they can provide an accurate and deep understanding of the processes that affect population diversity and trait selection in the genome (Oleksyk et al., 2010; Ma et al., 2015). This study used the composite likelihood ratio test (CLR) and integrated haplotype score (iHS) methods to detect selection signatures. The CLR method uses site frequency spectrum (SFS) patterns of single-nucleotide polymorphisms (Williamson et al., 2007). In contrast, the iHS test examines the homozygosity of extended haplotypes generated by a selective sweep (Voight et al., 2006).

Quails are increasingly becoming an essential source of poultry protein in developing countries, thus helping to ensure food security (Jeke et al., 2018). At present, there is no information on the impacts of selection on the wild African harlequin quail. Furthermore, wild and domestic quails are exposed to different selection pressures; thus, it is important to investigate the effects of natural and artificial selection on the quail genome. Gaining knowledge about the selection signatures in quail genomes will form the basis for comprehending the underlying mechanisms that influence their key traits.

MATERIALS AND METHODS

Sample collection and genotyping-by-sequencing data

One hundred quails were sampled for this study; 78 captured wild African harlequin quails and 22 domestic Japanese quails from Siaya and Kajiado Counties of Kenya, respectively. This comprised an equal number of male and female individuals for every visited farm. Wild African harlequin quails were captured around homesteads using traditional methods described by Wamuyu et al. (2017). DNA extracted from blood samples was sequenced using the genotyping-by-sequencing (GBS) approach and the generated sequence data was extracted from our previous publication (Ogada et al., 2021).

Sequence data processing and SNP calling

Raw reads were processed through a series of quality control procedures which involved; (i) removing reads with [?]10% unidentified nucleotides (N); (ii) reads with >50% bases with a Phred quality < 5; (iii) removing reads with >10 nucleotides alignment to the adapter; (iv) allowing [?]10% mismatches; and (v) removing reads that contain the *Hae* III enzyme sequence.

Burrows-Wheeler Aligner (BWA) version 0.7.17 was used to align the retained reads against the *Coturnix Japonica* 2.0 genome (Assembly accession number GCF_001577835.1) with the parameters mem -t 4 -k 32 -M' (Li & Durbin, 2009). Variant calling was performed using SAMtools version 1.11 *mpileup* command (Li et al., 2009) in conjunction with BCFtools version 1.11 *call* command (Li, 2011). Variant filtering was performed by restricting the dataset to biallelic SNPs found in at least 80% of samples, with a minimum depth of 2 reads, minimum Phred score of 30, and minimum minor allele frequency (MAF) of 0.01 using VCFtools version 0.1.13 (Danecek et al., 2011). Additional filtering was also done using PLINK version 1.9 (Purcell et al., 2007) to remove individuals with missing genotype data (–mind 0.1), variants with missing genotype data (–geno 0.05), minor allele frequency threshold (–maf 0.05) and Hardy–Weinberg exact test threshold (–hwe 1e6).

Signatures of selection detection

Two complementary methods (CLR and iHS) that were found to have power > 70% to detect selection signatures were applied (Ma et al., 2015). CLR values based on the variation in the site-frequency spectrum along the chromosome were computed at 1000 grids (-grid 1000) using the SweeD program version 4.0.0 (Pavlidis et al., 2013) at each SNP. To generate phased haplotypes, SHAPEIT version 2.r900 (Delaneau et al., 2013) was used to perform haplotype phasing with default settings. The ratio of extended haplotype homozygosities (EHH) associated with each allele was calculated into standardized iHS (|iHS|) values using the function "*ihh2ihs*"in *rehh* version 3.2.1 R package (Gautier et al., 2017). The iHS analysis was conducted using unpolarized alleles, which is ideal for non-model organisms that lack representative studies to allow for the correct designation of 'ancestral' or 'derived' alleles (Santos et al., 2021).

Identification of Candidate Genes Under Selection and Gene Annotation

Candidate genes under selection were determined using an outlier approach where SNPs above the cutoff value were highly considered (Wang et al., 2018). The 99th percentile of the observed genome-wide distribution of all standardized iHS values and CLR values was used as the threshold to identify outliers. SNPs that met the threshold and were located within a 250 kb window were highly considered and used to determine candidate genes under positive selection.

The annotation of the candidate regions was based on the Japanese quail genome assembly (Accession number GCF_001577835.1) from NCBI. Gene Ontology (GO) terms and KEGG (Kyoto Encyclopedia of Genes and Genomes) pathways identification was performed using the Database for Annotation, Visualization, and Integrated Discovery (DAVID) version 6.8 browser tool (Huang et al., 2009) and Metascape v3.5.20230101 (Zhou et al., 2019). The biological significance of the enriched terms and pathways was considered if $P < 0.05$.

RESULTS

After quality control, 95 individuals (76 wild African harlequin quails and 19 domestic Japanese quails) with 499,461 SNPs were retained for further analysis. The wild African harlequin and domestic Japanese quail datasets had 8,024 and 491,441 SNPs, respectively.

Signatures of selection detection using CLR approach

Genome-wide selection signatures were detected using the composite likelihood ratio statistical approach in wild African harlequin and domestic Japanese quails. Potential candidate regions under selection were identified with outliers that fell into the 99th percentile of CLR values distribution in wild African harlequin (CLR > 1.39) and domestic Japanese (CLR > 8.33) quails. Wild African harlequin quail chromosomes 1 and 2 had the highest number of significant CLR values (Figure 1). In contrast, outliers were observed in most Japanese quail chromosomes except chromosomes 10 and 12 (Figure 2). 252 and 424 potential candidate genes were identified across 28 autosomes in wild African harlequin and Japanese quails, respectively.

Figure 1. Manhattan plot showing CLR values distribution across all wild African harlequin quail autosomes. The red line indicates the 99th percentile threshold.

In wild African harlequin quails, functional analysis of the candidate genes showed an association with key biological processes, metabolic pathways, and molecular functions. Wild African harlequin quail candidate genes were implicated in melanogenesis (FZD7, WNT5A, WNT8B, LOC107320948, WNT3, WNT4), Wnt signaling pathway (PPP3R1, FZD7, WNT5A, WNT8B, WNT3, NKD1, WNT4), follicle-stimulating hormone signaling pathway (FSHB, FSHR), ear morphogenesis (SOX2, PTPN11, PROX1), positive regulation of skeletal muscle satellite cell proliferation (HGF, GPC1), among others (see Supporting Information Table S1). Enrichment analysis of the candidate genes revealed cluster groups with enriched terms such as behavior (GO:0007610), brain and sensory organ development (GO:0007420; GO:0007423), inner ear development (GO:0048839), response to growth factor (GO:0070848), regulation of MAPK cascade (GO:0043408), cell

morphogenesis (GO:0000902), gliogenesis and glial cell differentiation (GO:0042063, GO:0010001), and tissue morphogenesis (GO:0048729).

Figure 2. Manhattan plot showing CLR values distribution across all domestic Japanese quail autosomes. The red line indicates the 99th percentile threshold.

Some of the top enrichment clusters identified in domestic Japanese quail include cell morphogenesis (GO:0000902), regulation of transmembrane transport (GO:0034762), embryonic morphogenesis (GO:0048598), focal adhesion (GO:0005925), negative regulation of cellular component organization (GO:0051129), platelet activation, signaling and aggregation (GO:0030168), regulation of cell growth (GO:0001558), heart development (GO:0007507), cell-cell adhesion (GO:0098609), mesenchymal cell differentiation (GO:0048762) and brain development (GO:0007420), among others (see Supporting Information Table S2). Key domestic Japanese quail candidate genes identified include VIPR2, RAC1, COL6A3, SLC9A1, MSX2, and PRF1.

Signatures of selection detection using the iHS approach

The standardized iHS values were used to identify genomic regions that showed signatures of selection patterns. Outliers that fell into the 99th percentile in domestic Japanese ($|iHS| > 3.2$) and wild African harlequin ($|iHS| > 3.55$) quails were considered to be potential candidate regions under selection. Chromosome 2 had the highest number of outlier SNPs in wild African harlequin quail (Figure 3), whereas, in domestic Japanese quails, outlier SNPs numbers were high in all chromosomes (Figure 4). 150 and 457 potential candidate genes were detected across 28 autosomes in wild African harlequin and domestic Japanese quails, respectively.

Enrichment analysis of the wild African harlequin quail candidate genes showed their association with platelet activation (MAPK14, ITGB3, MAPK13), hematopoietic cell lineage (LOC107324620, ITGB3, LOC107317826), Th1 and Th2 cell differentiation (MAPK14, LOC107317826, MAPK13), Th17 cell differentiation (MAPK14, LOC107317826, MAPK13), adrenergic signaling in cardiomyocytes (CREB1, MAPK14, MAPK13, PPP1CA), among others. Key enrichment terms include focal adhesion (GO:0005925), regulation of secretion (GO:0051046), olfactory transduction (GO:0004984), actin binding, and cytoskeleton organization (GO:0003779; GO:0030036), Osteoclast differentiation (GO:0030316), negative regulation of transcription by competitive promoter binding (GO:0010944), and the regulation of peptidyl-tyrosine phosphorylation (GO:0050730), among others (see Supporting Information Table S3).

Figure 3. Manhattan plot showing standardized iHS values distribution across all wild African harlequin quail autosomes. The red line indicates the 99th percentile threshold.

Some of the top enriched clusters of the domestic Japanese quail candidate genes include the regulation of lipid metabolic process (GO:0019216), cholesterol transport (GO:0030301), spermatogenesis (GO:0007283), cell proliferation (GO:0008283), phagosome (GO:0045335), the intestinal immune network for IgA production (GO:0002387), antigen processing and presentation (GO:0019882), autoimmune thyroid disease (cjo05320), and Th1 and Th2 cell differentiation (GO: 0045063, GO:0045064), among others (see Supporting Information Table S4). Key candidate genes involved in crucial biological processes of the domestic Japanese quail include DYNLL2 and genes from the APOA, ABCA, G12/G13 gene families.

Figure 4. Manhattan plot showing standardized iHS values distribution across all domestic Japanese quail autosomes. The red line indicates the 99th percentile threshold.

DISCUSSION

Signatures of selection detection in both wild and domesticated species is considered a critical step toward understanding the molecular basis of adaptive evolution. This information can be used to identify genomic regions and underlying biological mechanisms affecting their essential traits. There are different methods

of detecting selection signatures. However, two complementary approaches (composite likelihood ratio test (CLR) and integrated haplotype score (iHS)) that were found to have power $> 70\%$ to detect selection signatures were applied in this study. Unfortunately, there is currently no information on the effects of selection on the wild African harlequin quail, despite the incessant harvesting by rural smallholder farmers, effects of habitat destruction, and climate change, among other challenges. Moreover, there is limited information on selection signatures detected in the domestic Japanese quail, the most common domesticated quail species reared in Kenya. It has experienced constant evolutionary and genetic changes in its phenotype and genome architecture due to modern breeding methods. Such information could have been a foundation for understanding biological pathways governing important traits in wild quails and how modern breeding methods will likely affect them if breeding initiatives were to be made.

The application of CLR and iHS in detecting selective sweeps in wild African harlequin and domestic Japanese quail genomes was successful. Several complementary methods for signatures of selection detection allow for improved testing as each statistical test captures patterns in data differently (Fariello et al., 2013). The linkage disequilibrium (LD)-based iHS approach, which requires haplotypes per individual of one population to detect selection, was anticipated to be more reliable for this study due to the single populations that were sampled and the lack of a good reference population about quail (Voight et al., 2006). In addition, the CLR method was also adopted for this study as it uses allele frequency data to compare a neutral and a selective sweep model, and it is not highly sensitive to assumptions about the underlying recombination rate or recombination hotspots (Williamson et al., 2007). Furthermore, the CLR method can detect a beneficial mutation that spread in the entire population. In contrast, methods based on extended haplotype length and high linkage disequilibrium only detect the beneficial mutation that has yet to spread throughout the entire population (Voight et al., 2006; Wang et al., 2006; Williamson et al., 2007).

Both signatures of selection detection methods identified candidate genes associated with crucial biological, molecular, and cellular processes such as immune response, growth, reproduction, and morphological and behavioral traits. Some essential candidate genes involved in various immune response processes and pathways include MAPK1, MAPK13, MAPK14, CREB1, DYNLL2, RAC1, and ITGB3. The MAPK signaling pathway genes were enriched in the wild African harlequin and domestic Japanese quail. Mitogen-activated protein kinases (MAPKs) are a group of serine/threonine protein kinases that are highly conserved and have essential roles in cellular processes, such as proliferation, stress responses, apoptosis, and immune response regulation (Liu et al., 2007). The MAPK13 and MAPK14 (p38 MAPK pathway) genes, which play an important role in inflammatory responses, were positively selected in the wild African harlequin quail. The p38 pathway participates in the innate and adaptive immune response process by controlling the production of inflammatory cytokines (TNFα, interleukin (IL)-1, IL-10, and IL-12) by specialized dendritic and macrophage cells, CD40-induced gene expression, and proliferation of B cells, antigen processing in $CD8^+$ conventional dendritic cells, and T cell homeostasis and function (Arthur & Ley, 2013; Soares-Silva et al., 2016; Han et al., 2020).

In addition to the p38 pathway, the extracellular signal-regulated kinase (ERK1/2) is also a MAPK pathway involved in positive selection and the differentiation of DP thymocytes to either CD4 or CD8 T cells (Fischer et al., 2005). The MAPK1, a key component of the ERK1/2 pathway, was positively selected in domestic Japanese quails. It was shown to participate in adaptive immune responses during bacterial infection in Nile tilapia (Wei et al., 2020). MAPK1, through the MAPK/ERK pathway, facilitates the activation and proliferation of immune cells, including T cells, B cells, and macrophages (Sun et al., 2015). Bacterial pathogens such as *Salmonella* , *Shigella* ,*Yersinia* and *Escherichia* species are known to manipulate pathways like the MAPK in their hosts to propagate infection (Krachler et al., 2011). Another positively selected candidate gene in domestic Japanese quails associated with *Salmonella* infection was the DYNLL2 gene, which is predicted to be involved in cytoskeletal motor activity and cytoskeletal protein binding. An observed increase in DYNLL2 protein in gamma delta T-lymphocytes ($\gamma\delta$ T-lymphocytes) of chickens infected with *Salmonella* Enteritidis showed its role in regulating immune response (Sekelova et al., 2017). Like commercial chicken, domestic Japanese quails are reared on farms under different housing systems such as battery cages, free-range and floor-raised systems, among others. Choice of the housing system in connection to other

production factors such as infrastructure, stocking density (farm and flock size), manure collection, disease status of the flock, and rodent and insect load does determine the risk of *Salmonella*infection (Van Hoorebeke et al., 2011).

The ITGB3 gene, which was positively selected in the wild African harlequin quail, is involved in the blood coagulation pathway through adrenergic signaling in platelet activation. ITGB3 encodes for glycoprotein IIIa (GPIIIa) and, along with the alpha IIb chain, forms the platelet adhesive protein receptor complex glycoprotein IIb/IIIa (GP IIb/IIIa), which mediates platelet aggregation by acting as a receptor for fibrinogen (Cerhan et al., 2007). It plays a critical role in many cellular processes, such as cytoskeletal organization, cell adhesion, migration, proliferation, and survival (Ridley et al., 1992; Arthur et al., 2002; Guo et al., 2008). Its immune roles in the T cell development (Luo et al., 2013), B cell development and signaling (Walmsley et al., 2003), epidermal homeostasis resulting in wound healing (Winge & Marinkovich, 2019), and phagocytosis (Lee et al., 2000; Han et al., 2019) are continuously being studied. Phagocytosis is a necessary component of the innate immune response. It plays an essential role in host-defense mechanisms by enabling the uptake and destruction of infectious pathogens through specialized cell types like macrophages, neutrophils, and monocytes (Lee et al., 2020). Similar to the ITGB3 gene, the RAC1 candidate gene that was detected in domestic Japanese quail is also associated with wound healing by regulating the innate immune response in keratinocytes (Bustelo et al., 2007; Pedersen et al., 2012; Winge & Marinkovich, 2019).

PPP1CA, WNT5A, GRIA1, CREB1 and ADCY8 candidate genes, associated with adaptation and behavior, were detected in the wild African harlequin quail. Melanogenesis and ear morphogenesis biological processes are crucial for wild African harlequin quail breeding behavior, social interactions, and survival. Melanogenesis involves melanin production, which plays a significant role in structural plumage in birds (Jeon et al., 2021). Plumage color and patterns are helpful in camouflage, mating, and differentiating between male and female wild African harlequin quails (Mason & Bowie, 2020). Melanin-based patterns are influenced by melanocyte migration, differentiation, cell death, and/or interaction with neighboring skin cells at the cellular level (Inaba & Chuong, 2020). The wild African harlequin quail songs and calls are also essential to their communication and behavior; hence, ear morphogenesis is a vital biological process for their survival and reproduction. The WNT5A gene, among other genes, was implicated in melanogenesis, ear morphogenesis, sex differentiation, and muscle development. Through activating multiple intracellular signaling cascades, the WNT gene family controls cell proliferation, differentiation, apoptosis, survival, migration, and polarity (Kikuchi et al., 2012). According to Kikuchi et al. (2012), regulating cellular functions, including migration and differentiation, makes the WNT5A gene a target for selection.

The GluA1 subunit has been implicated in the regulation of circadian rhythms and behavior (Ang et al., 2021). The Glutamate receptor 1 (GluA1), encoded by the GRIA1 gene, forms part of the AMPA receptor that mediates fast glutamate signaling in the central nervous system (synaptic plasticity). Positive selection of genes associated with behavioral response to stress and circadian entrainment (GRIA1, CREB1, ADCY8) could contribute to the observed timely seasonal migration and behavioral patterns of wild African harlequin quails (Bossu et al., 2022). The PPP1CA gene encodes for a protein that is part of the three catalytic subunits of protein phosphatase 1 (PP1). The PP1 protein was found to be a key regulator of period and light-induced resetting of the circadian clock in the common fruit fly (Fang et al., 2007) and different mammals (Eide et al., 2005; Gallego et al., 2006; Schmutz et al., 2011). It regulates the circadian period length, in counterbalance with casein kinase 1δ and ε (CK1δ/ε), through the regulation of the speed and rhythmicity of period circadian regulator 1 and 2 (PER1 and 2) phosphorylation (Lee et al., 2011; Schmutz et al., 2011).

Candidate genes associated with growth and reproduction were detected in the wild African harlequin and domestic Japanese quail. The Wnt–Hippo signaling pathway-related genes identified in wild African harlequin quails include SOX2, FZD7, WNT3, NKD1, and WNT4. The Hippo signaling pathway plays a crucial role in cellular differentiation, tissue, and organ development by controlling organ size through the regulation of cell proliferation and apoptosis (Justice et al., 1995; Xu et al., 1995; Heallen et al., 2011; Wu & Guan, 2021). It has also been implicated in other diverse roles, such as tissue homeostasis, wound healing and regeneration, immunity, tumorigenesis, and embryogenesis (Wu & Guan, 2021). The transcription factor SOX2 is involved

in osteoblast differentiation (Seo et al., 2013), inner ear development (Kiernan et al., 2005), neurogenesis, and the proliferation and/or maintenance of stem cells (Oesterle et al., 2008), among others. The positive selection of genes associated with tissue and organ size, among other factors, could contribute to how the wild African harlequin quails have managed to maintain their small body size, supporting their growth and survival in the wild. The wild African harlequin quail is known to fly longer distances during migration and at faster speeds (Wamuyu et al., 2017).

CREB1 gene is involved in growth hormone synthesis, secretion, and action. CREB1 encodes a phosphorylation-dependent transcription factor that mediates the response to various cellular processes, including regulation of transcription, signal transduction, glucose homeostasis, and growth-factor-dependent cell survival, proliferation, and memory (Kinjo et al., 2005). CREB1 stimulates transcription upon binding to the DNA cAMP response element (CRE) located in the promoter region of target genes, leading to the recruitment of transcriptional coactivators and the initiation of gene transcription (Shankar et al., 2005). In humans, the CREB/CREB1 gene is involved in immune function (Cerhan et al., 2007) as it promotes proliferation and survival and differentially regulates Th1, Th2, and Th17 responses (Wen et al., 2010). It has also been shown to be a critical driver of vaccine efficacy in non-human primates (Tomalka et al., 2021).

Several candidate genes associated with lipid and cholesterol transport and metabolism in domestic Japanese quails, such as the APOA (APOA1 and APOA4) and ABCA (ABCA2, ABCA5, ABCA7) gene families, were identified (Albrecht & Viturro, 2007; Dominiczak & Caslake, 2011). Additionally, muscle cell differentiation, tissue, and structure development genes (COL6A3, SLC9A1, SMARCD3, MSX2, and PRF1) were identified. The positively selected DYNLL2 gene, apart from its role in immune response, was also found to be a regulator of chicken myogenesis, providing insights into breast muscle development in chickens and other birds (Li et al., 2022). VIPR2, one of the positively selected cAMP signaling pathway genes identified in domestic Japanese quails, has been implicated in the regulation of egg production as it has been associated with brooding behavior in chicken and geese (Luan et al., 2014; Huang et al., 2022).

In this study, only two genes (CBFB and RET) overlapped between the CLR and iHS tests in the domestic Japanese quail, in contrast to the wild African harlequin quail, where no overlapped genes were observed. CBFB protein is mainly associated with definitive hemopoiesis (Speck et al., 1999). In contrast, RET is known for its protein kinase activity, leading to the activation of signaling pathways involved in cell growth, differentiation, and survival, such as MAPK and AKT (Schuchardt et al., 1994; Taraviras et al., 1999).

CONCLUSION

In the present study, we used genotyping-by-sequence data to detect selection signatures in wild African harlequin and domestic Japanese quails. Our results revealed candidate genes associated with immune response, growth, reproductive, morphological, and behavioral traits. The wild African harlequin candidate genes were primarily associated with morphological and behavioral traits, whereas the domestic Japanese quail candidate genes were mainly associated with growth and production traits.

Identifying true signatures can be complicated due to the likelihood of detecting false positives. Therefore, further studies are always encouraged to reaffirm and refine results from less-studied species such as the wild African harlequin quail. Nevertheless, this study was able to give a glimpse of how natural and artificial selective pressures have shaped the genomic landscape of wild and domestic quail species. Furthermore, information on the effects of artificial selection on domestic Japanese quails may inform conservation policies for wild quails, especially in regions where domestic quails have been used to restock wild quail populations.

CONFLICT OF INTEREST

The authors declare that there are no competing interests regarding the publication of this paper.

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AUTHOR CONTRIBUTIONS

Stephen Ogada: Formal analysis (lead); Methodology (lead); Software (lead); Validation (equal); Writing-original draft (lead); Writing-review & editing (equal). **Philip Murunga Panyako:**Formal analysis (supporting); Methodology (supporting); Validation (equal); Writing-review & editing (equal). **Jacqueline Lichoti:**Supervision (supporting); Validation (equal); Writing-review & editing (supporting). **Min-Sheng Peng:** Formal analysis (supporting); Validation (equal); Writing – review & editing (equal). **Sheila Cecily Ommeh:** Conceptualization (lead); Formal analysis (supporting); Validation (equal); Investigation (lead); Methodology (supporting); Resources (lead); Supervision (lead); Writing-original draft (supporting); Writing-review & editing (supporting).

ETHICAL APPROVAL

This study received ethical clearance from the Kenya Wildlife Service under permit number KWS/BRM/5001 to sample wild African harlequin quails and a "no objection for the research" from the Director of Veterinary Services, Ministry of Agriculture, Livestock and Fisheries in Kenya under permit number RES/POL/VOL.XXVII/162 to sample domestic quails.

DATA AVAILABILITY STATEMENT

The aligned GBS reads in the format of bam files were deposited in the National Centre for Biotechnology Information (NCBI) repository under project ID PRJNA748759 and PRJNA748896.

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