Faculty of Natural and Applied Sciences Journal of Computing and Applications
Print ISSN: 3026-8133
www.fnasjournals.com
Volume 2; Issue 2; March 2025; Page No. 43-49.

Sequence Variability and Functional Analysis of Robo2 Genes in Three Nigerian Indigenous Chicken Strains

***[1]Yeigba, J.B., [2]Sweet-Owei, I. F., & [3]Tari, B. O.**
[1]Department of Animal Science, Niger Delta University, Wilberforce Island, Bayelsa State, Nigeria.
[2]Bayelsa State Polytechnic, Aleibiri, Bayelsa State, Nigeria
[3]Deaprtment of Animal Science, Niger Delta University Wilberforce Island Bayelsa State, Nigeria

***Corresponding author email**: japhet.bolouinbele@ufv.br

Abstract

This study investigated the sequence variability and functional implications of ROBO2 genes (Roundabout Guidance Homolog gene 2), across three strains of Nigerian indigenous chickens: normal feathered, naked Neck, and frizzle feather, were used in the experiment. Nucleotide sequences were retrieved from the National Centre for Biotechnology Information (NCBI) database and subjected to multiple sequence alignment using the COBALT tool. The aligned sequences were then analysed for variability using the MEGA X suite. Conserved regions within the sequences were determined, and phylogenetic relatedness was assessed using Conservation and BLOSUM80 settings. The study provides insights into the genetic diversity and evolutionary relationships of ROBO2 genes among different strains of Nigerian indigenous chickens, shedding light on potential functional implications and genetic conservation efforts in poultry breeding programs. Despite the considerable variability in amino acid sequences, subsequent alignment analysis revealed a high level as well as degree of conservation at the protein level. Using conclusion a clearer understanding of the sequence variability, further analysis using the MEGA X suite was conducted, resulting in a patterned table that highlighted the presence of INDELs and mutations contributing to the observed diversity. This unexpected finding suggests that while the sequences may differ in their constituent amino acids, the overall structure and function of the ROBO2 protein remain highly conserved across species. Therefore, it is recommended that exploration of genotype-phenotype relationships, investigation of genetic variants contributing to environmental adaptability, and consideration of epigenetic modulation in phenotype expression. This multidisciplinary approach aims to enhance understanding of the genetic diversity and adaptive potential of indigenous Nigerian chicken populations.

Keywords: Sequence Variability; ROBO2 Genes; Indigenous Chickens

Introduction

Indigenous chickens are locally adapted to environmental challenges and provide food for millions of farmers in Africa. Their productivity remains very low compared to exotic chicken strains. Efforts are being made to combine the local adaptation of indigenous chicken with their basic productivity traits of exotic chicken (Dhawal et al., 2020). An important factor that negatively influences animal husbandry is disease, and the occurrence of the outbreak of Newcastle disease is one factor that limits and directly affects the genetic improvement of indigenous chickens. High prevalence of diseases is a major constraint towards the health and economic status of local chicken production. The ability to resist different poultry diseases differs among poultry breeds and types. This is highly determined by either the genotype or the presence of a specific allele type (Hu et al., 2017).

The Nigerian indigenous chickens are dual-purpose poultry birds that are used for both meat and egg production in the rural and peri-urban areas of the country. The poultry value chain (poultry breeders/farmers, feed millers, poultry product marketers, consumers, etc.) makes poultry production one of the major means of livelihood, being one of the most economic routes for producing high-quality animal protein within the shortest possible time (Oluyemi & Roberts, 2007). Most of the birds are kept in small flocks under a scavenging system, and the feed resources for the chickens are household refuse, homestead pickings, crop residues, herbage, seeds, green grasses, earthworms, insects and a

Cite this article as:
Yeigba, J.B., Sweet-Owei, I. F., & Tari, B. O. (2025). Sequence variability and functional analysis of Robo2 genes in three nigerian indigenous chicken strains. *FNAS Journal of Computing and Applications, 2*(2), 43-49.

small quantity of supplemented feeds offered by the flock owner. They are well adapted to the adverse climatic conditions of the tropical environment and low management inputs (Mtileni et al., 2015).

According to Osei-Amponsah et al. (2020) and Dana et al. (2011) stated that African chickens exhibit high variation in their genetic makeup within their population. Thus, high genetic diversity is an indication of high genetic potential that encourages fast improvement through selective breeding (Dana et al., 2010). Several studies in animal species have suggested a strong effect of genetic factors on the ability of the host to respond to invasion by infectious pathogens (Malo & Skamene, 1994; Halima, 2007; Moges et al., 2010; Grepay, 2010; Mtileni et al., 2015). Resistance to infectious diseases is usually a complex genetic trait, and recent data suggest that many resistance/susceptibility genes affect more than one infectious disease (Vidal et al., 1995). Upon phagocytosis, it plays an essential role in host defence.

The roundabout, axon guidance receptor, homolog 2 (*ROBO2***)** gene is one member of the roundabout (***ROBO***) family, which belongs to the immunoglobulin superfamily. Proteins of this family are cell-surface receptors for secreted ligands called **SLIT** (Dickson & Gilestro, 2006). The ROBO family proteins were originally found to be used as repulsive guidance cues for axon pathfinding and migrating neurons during nervous system development (Guan & Rao, 2003). The ROBO2 is a transmembrane protein that contains 5 Ig motifs and 3 fibronectin type III repeats in its extracellular domain (Dickson & Gilestro, 2006). The ROBO2 is also the cell surface receptor for the repulsive guidance cue SLIT and is involved in axon guidance and neuronal migration (Fan et al., 2012; Mtileni et al., 2020). In addition, recent studies suggest that the SLIT/ROBO complex is involved in the regulation of organogenesis, which is important in the embryonic development of various organs such as the lung, kidney, and heart and systems such as the central nervous system (Greenberg et al., 2004; Prasad et al., 2008; Osei-Amponsah et al., 2020). It is therefore clear that changes in components of the SLIT/ROBO signaling process can affect the respiratory, reproductive, nervous, immune, and circulatory systems. Previously, studies have identified ROBO2 as an important candidate gene affecting antibody responses to the Newcastle disease virus in chickens by using a genome-wide association study (Lu et al., 2011).

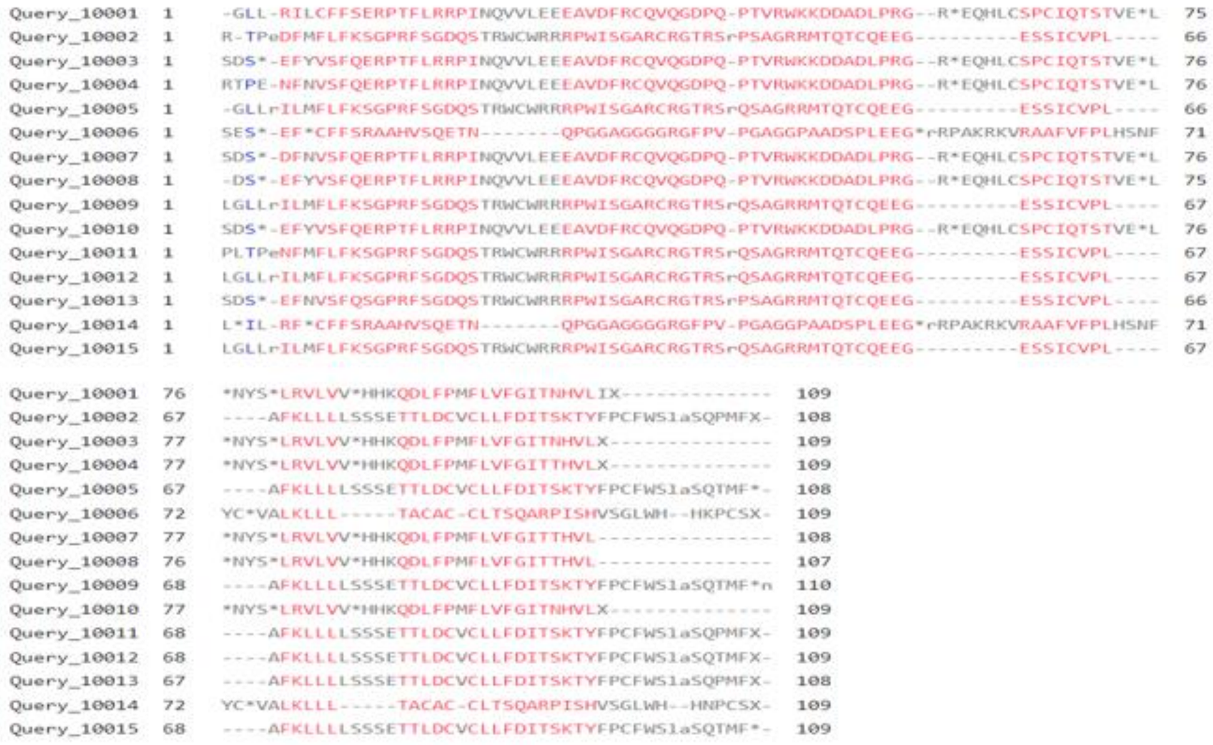
The aim of this study was to investigate the functional importance of the ***ROBO2*** gene by analyzing its sequence and identifying polymorphisms associated with immunity traits in three indigenous chickens, which are the naked neck, the frizzles feathered and the normal neck chickens.

Materials and Methods

Three (3) strains of Nigerian indigenous chicken were used for the course of this experiment, which are the normal feathered, naked neck and the frizzle feather. Nucleotide sequences were retrieved from the NCBI database (https://www.ncbi.nlm.nih.gov) and were translated to amino acid sequences on the EMBOSS web server (https://www.ebi.ac.uk/jdispatcher/st/emboss_transeq). All the translated sequences were aligned in a multiple sequence alignment fashion on the COBALT Multiple Sequence Alignment tool as described by (Dunya et al., 2014). Multiple sequence alignment analyses the evolutionary relatedness among the sequences and identifies the shared patterns that may determine their structure and functionality. The sequences were subjected to MEGA X suit to study the variation across the sequences, this is shown in Figure 2. The aligned sequences were looked at closely and viewed with the Conservation and BLOSUM80 settings, respectively, to determine the conserved regions. The sequences were also viewed using the BLOSUM80 setting, which indicates the degree of matches among the sequences. Results of the research were subjected to the MEGA X suite to study the variation across the sequences, conservation and BLOSUM80 setting and the COBALT Multiple Sequence Alignment tool.

Results

Amino acid sequence alignment of Roundabout Guidance Receptor Family Protein (ROBO2) from three (3) strains of indigenous Nigerian chicken using bioinformatics techniques. Amino acid sequence alignment is a bioinformatics technique used to compare and analyze the similarity or homology between the amino acid sequences of proteins. It involves aligning two or more protein sequences to identify regions of similarity, conservation, or divergence. This process provides insights into the evolutionary relationships, functional domains, and structural motifs of proteins.



```
Query_10001  1   -GLL-RILCFFSERPTFLRRPINQVVLEEEAVDFRCQVQGDPQ-PTVRWKKDDADLPRG--R*EQHLCSPCIQTSTVE*L  75
Query_10002  1   R-TPeDFMFLFKSGPRFSGDQSTRWCWRRRPWISGARCRGTRSrPSAGRRMTQTCQEEG---------ESSICVPL----  66
Query_10003  1   SDS*-EFYVSFQERPTFLRRPINQVVLEEEAVDFRCQVQGDPQ-PTVRWKKDDADLPRG--R*EQHLCSPCIQTSTVE*L  76
Query_10004  1   RTPE-NFNVSFQERPTFLRRPINQVVLEEEAVDFRCQVQGDPQ-PTVRWKKDDADLPRG--R*EQHLCSPCIQTSTVE*L  76
Query_10005  1   -GLLrILMFLFKSGPRFSGDQSTRWCWRRRPWISGARCRGTRSrQSAGRRMTQTCQEEG---------ESSICVPL----  66
Query_10006  1   SES*-EF*CFFSRAAHVSQETN-------QPGGAGGGGRGFPV-PGAGGPAADSPLEEG*rRPAKRKVRAAFVFPLHSNF  71
Query_10007  1   SDS*-DFNVSFQERPTFLRRPINQVVLEEEAVDFRCQVQGDPQ-PTVRWKKDDADLPRG--R*EQHLCSPCIQTSTVE*L  76
Query_10008  1   -DS*-EFYVSFQERPTFLRRPINQVVLEEEAVDFRCQVQGDPQ-PTVRWKKDDADLPRG--R*EQHLCSPCIQTSTVE*L  75
Query_10009  1   LGLLrILMFLFKSGPRFSGDQSTRWCWRRRPWISGARCRGTRSrQSAGRRMTQTCQEEG---------ESSICVPL----  67
Query_10010  1   SDS*-EFYVSFQERPTFLRRPINQVVLEEEAVDFRCQVQGDPQ-PTVRWKKDDADLPRG--R*EQHLCSPCIQTSTVE*L  76
Query_10011  1   PLTPeNFMFLFKSGPRFSGDQSTRWCWRRRPWISGARCRGTRSrQSAGRRMTQTCQEEG---------ESSICVPL----  67
Query_10012  1   LGLLrILMFLFKSGPRFSGDQSTRWCWRRRPWISGARCRGTRSrQSAGRRMTQTCQEEG---------ESSICVPL----  67
Query_10013  1   SDS*-EFNVSFQSGPRFSGDQSTRWCWRRRPWISGARCRGTRSrPSAGRRMTQTCQEEG---------ESSICVPL----  66
Query_10014  1   L*IL-RF*CFFSRAAHVSQETN-------QPGGAGGGGRGFPV-PGAGGPAADSPLEEG*rRPAKRKVRAAFVFPLHSNF  71
Query_10015  1   LGLLrILMFLFKSGPRFSGDQSTRWCWRRRPWISGARCRGTRSrQSAGRRMTQTCQEEG---------ESSICVPL----  67

Query_10001  76  *NYS*LRVLVV*HHKQDLFPMFLVFGITNHVLIX-------------  109
Query_10002  67  ----AFKLLLLSSSETTLDCVCLLFDITSKTYFPCFWS1aSQPMFX-  108
Query_10003  77  *NYS*LRVLVV*HHKQDLFPMFLVFGITNHVLX--------------  109
Query_10004  77  *NYS*LRVLVV*HHKQDLFPMFLVFGITTHVLX--------------  109
Query_10005  67  ----AFKLLLLSSSETTLDCVCLLFDITSKTYFPCFWS1aSQTMF*-  108
Query_10006  72  YC*VALKLLL-----TACAC-CLTSQARPISHVSGLWH--HKPCSX-  109
Query_10007  77  *NYS*LRVLVV*HHKQDLFPMFLVFGITTHVL---------------  108
Query_10008  76  *NYS*LRVLVV*HHKQDLFPMFLVFGITTHVL---------------  107
Query_10009  68  ----AFKLLLLSSSETTLDCVCLLFDITSKTYFPCFWS1aSQTMF*n  110
Query_10010  77  *NYS*LRVLVV*HHKQDLFPMFLVFGITNHVLX--------------  109
Query_10011  68  ----AFKLLLLSSSETTLDCVCLLFDITSKTYFPCFWS1aSQPMFX-  109
Query_10012  68  ----AFKLLLLSSSETTLDCVCLLFDITSKTYFPCFWS1aSQTMFX-  109
Query_10013  67  ----AFKLLLLSSSETTLDCVCLLFDITSKTYFPCFWS1aSQPMFX-  108
Query_10014  72  YC*VALKLLL-----TACAC-CLTSQARPISHVSGLWH--HNPCSX-  109
Query_10015  68  ----AFKLLLLSSSETTLDCVCLLFDITSKTYFPCFWS1aSQTMF*-  109
```

Figure 1: Amino acid sequence alignment of Roundabout Guidance Receptor Family Protein (ROBO2) from three (3) strains of indigenous Nigerian chicken.

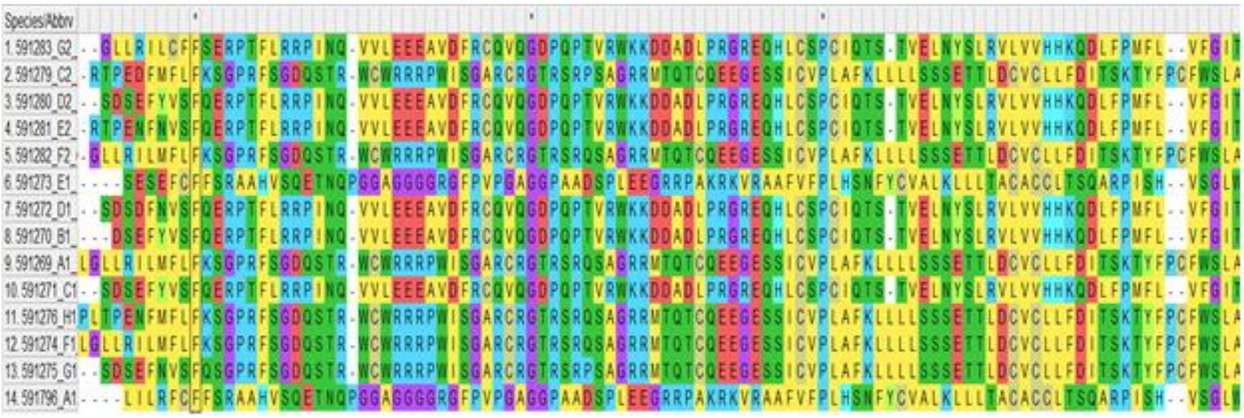
Sequence Variability Showing the Dissimilarity of each Sequence to Each Other

The analysis of the gene sequences from the Roundabout Guidance Receptor Family Protein (ROBO2) in three strains of indigenous Nigerian chickens reveals sequence variability and conservation patterns. This result showed the sequence variability and conservation across Frizzle Feathered (FF), Normal Feathered (NF), and Naked Neck (NN) phenotypes using the provided color key: **Red:** Conserved regions, **Blue:** Low conserved regions, **Gray:** Non-conserved regions, Purple: Intermediate conservation or variability, **Yellow:** Moderately conserved amino acids, **Green:** Highly conserved amino acids. Frizzle Feathered (FF) Scores Range: 135 to 188. The FF group exhibits sequences with high scores, suggesting a strong similarity to the canonical ROBO2 sequence. **Green** (Highly Conserved Amino Acids): Regions with scores towards the upper end (FF182-188) likely correspond to highly conserved regions, indicating critical functional or structural parts of the ROBO2 protein. **Red** (Conserved Regions): Commonly shared sequences across the FF group, indicating essential parts of the protein with little variation. **Yellow** (Moderately Conserved Amino Acids): Sequences in the middle of the score range (FF135-147) might reflect moderately conserved regions, important but with some allowable variation. ***Purple*** *(Intermediate Conservation):* Regions that show variation but still retain some functional importance. Normal Feathered (NF) Scores Range: 123 to 146. The NF group has moderately high scores, indicating a moderate level of sequence conservation. ***Yellow*** (Moderately Conserved Amino Acids): Predominantly represented in the NF group, reflecting important regions with some variability. **Purple** (Intermediate Conservation): Indicative of regions with significant variability but still important for function. **Blue** (Low Conserved Regions): Regions with lower scores (NF123) suggest areas of lower conservation, possibly subject to evolutionary divergence. **Gray** (Non-Conserved Regions): Few sequences might map to non-conserved regions, highlighting high variability. Naked Neck (NN) Scores Range: 11 to 178. The NN group displays the broadest range of scores, indicating high variability in the ROBO2 sequence. **Green** (Highly Conserved Amino Acids): The highest scores (NN178) correspond to highly conserved regions, crucial for maintaining protein function. **Red** (Conserved Regions): Present in sequences with relatively high scores, indicating necessary and stable regions of the protein.

Purple (Intermediate Conservation): Represented across a wide range of scores, showing regions that are variable yet functional. **Yellow** (Moderately Conserved Amino Acids): Regions of moderate conservation. **Blue** (Low Conserved Regions): Low scores (NN11, NN12) correspond to low conserved regions, indicating significant sequence divergence. **Gray** (Non-Conserved Regions): Regions with the lowest scores reflect high sequence variability, potentially indicating areas less critical for core protein function.

Sequence variability showing the dissimilarity of each sequence to each other

Key: **Red** = conserved rejoins
Blue = low conserved rejoins
Gray = non-conserved rejoins
Purple = often indicates intermediate conservation or variability
Yellow = moderately conserved amino acids.
Green = highly conserved amino acids



```
Species/Abbrv
1.591283_G2   --GLLRILCFFSERPTFLRRPINQ-VVLEEEAVDFRCQVQGDPQPTVRWKKDDADLPRGREQHLCSPCIQTS-TVELNYSLRVLVVHHKQDLFPMFL--VFGIT
2.591279_C2   -RTPEDFMFLFKSGPRFSGDQSTR-WCWRRRPWISGARCRGTRSRPSAGRRMTQTCQEEGESSICVPLAFKLLLLSSSETTLDCVCLLFDITSKTYFPCFWSLA
3.591280_D2   --SDSEFYVSFQERPTFLRRPINQ-VVLEEEAVDFRCQVQGDPQPTVRWKKDDADLPRGREQHLCSPCIQTS-TVELNYSLRVLVVHHKQDLFPMFL--VFGIT
4.591281_E2   -RTPENFNVSFQERPTFLRRPINQ-VVLEEEAVDFRCQVQGDPQPTVRWKKDDADLPRGREQHLCSPCIQTS-TVELNYSLRVLVVHHKQDLFPMFL--VFGIT
5.591282_F2   -GLLRILMFLFKSGPRFSGDQSTR-WCWRRRPWISGARCRGTRSRQSAGRRMTQTCQEEGESSICVPLAFKLLLLSSSETTLDCVCLLFDITSKTYFPCFWSLA
6.591273_E1   ----SESEFCFFSRAAHVSQETNQPGGAGGGGRGFPVPGAGGPAADSPLEEGRRPAKRKVRAAFVFPLHSNFYCVALKLLLTACACCLTSQARPISH--VSGLW
7.591272_D1   --SDSDFNVSFQERPTFLRRPINQ-VVLEEEAVDFRCQVQGDPQPTVRWKKDDADLPRGREQHLCSPCIQTS-TVELNYSLRVLVVHHKQDLFPMFL--VFGIT
8.591270_B1   ---DSEFYVSFQERPTFLRRPINQ-VVLEEEAVDFRCQVQGDPQPTVRWKKDDADLPRGREQHLCSPCIQTS-TVELNYSLRVLVVHHKQDLFPMFL--VFGIT
9.591269_A1   LGLLRILMFLFKSGPRFSGDQSTR-WCWRRRPWISGARCRGTRSRQSAGRRMTQTCQEEGESSICVPLAFKLLLLSSSETTLDCVCLLFDITSKTYFPCFWSLA
10.591271_C1  --SDSEFYVSFQERPTFLRRPINQ-VVLEEEAVDFRCQVQGDPQPTVRWKKDDADLPRGREQHLCSPCIQTS-TVELNYSLRVLVVHHKQDLFPMFL--VFGIT
11.591276_H1  PLTPENFMFLFKSGPRFSGDQSTR-WCWRRRPWISGARCRGTRSRQSAGRRMTQTCQEEGESSICVPLAFKLLLLSSSETTLDCVCLLFDITSKTYFPCFWSLA
12.591274_F1  LGLLRILMFLFKSGPRFSGDQSTR-WCWRRRPWISGARCRGTRSRQSAGRRMTQTCQEEGESSICVPLAFKLLLLSSSETTLDCVCLLFDITSKTYFPCFWSLA
13.591275_G1  --SDSEFNVSFQSGPRFSGDQSTR-WCWRRRPWISGARCRGTRSRPSAGRRMTQTCQEEGESSICVPLAFKLLLLSSSETTLDCVCLLFDITSKTYFPCFWSLA
14.591796_A1  ----LILRFCFFSRAAHVSQETNQPGGAGGGGRGFPVPGAGGPAADSPLEEGRRPAKRKVRAAFVFPLHSNFYCVALKLLLTACACCLTSQARPISH--VSGLW
```

Amino acid sequence alignment of Roundabout Guidance Receptor Family Protein (ROBO2) from three (3) strains of indigenous Nigerian chickens. View using the conservation setting.

The analysis of the amino acid sequence alignment of the Roundabout Guidance Receptor Family Protein (ROBO2) from three phenotypic groups of indigenous Nigerian chickens Frizzle Feathered (FF), Normal Feathered (NF), and Naked Neck (NN) provides insights into the conservation and variability of this protein across different strains. The key to interpreting the conservation setting is as follows: **Blue**: Indicates less conserved regions, **Red**: Indicates highly conserved regions, **Gray**: Indicates non-conserved regions. Frizzle Feathered (FF) Scores Range: 135 to 188. The sequences within the FF group exhibit a range of scores indicating varying degrees of similarity to the canonical ROBO2 sequence. The higher scores in this group suggest that some sequences are highly similar to the expected ROBO2 sequence, which could correlate with regions that are highly conserved (**red**). Sequences with lower scores may correlate with less conserved regions (**blue** or **gray**). Normal Feathered (NF) Scores Range: 123 to 146. The NF group shows a narrower and slightly lower range of scores compared to the FF group. This indicates moderate conservation of the ROBO2 sequence within this phenotype. The repeated score (NF133) suggests recurring sequences that may correlate with specific regions of moderate conservation (potentially blue regions). Naked Neck (NN) Scores Range: 11 to 178. The NN group displays the widest range of scores, indicating a significant variation in the ROBO2 sequences. High scores (NN178) likely correspond to highly conserved regions (**red**), while low scores (NN11, NN12) correspond to non-conserved regions (**gray**). The presence of highly varied scores suggests a diverse genetic basis within the NN phenotype group. Using the conservation setting, we can visualize the conservation of the ROBO2

Cite this article as:
Yeigba, J.B., Sweet-Owei, I. F., & Tari, B. O. (2025). Sequence variability and functional analysis of Robo2 genes in three nigerian indigenous chicken strains. *FNAS Journal of Computing and Applications, 2*(2), 43-49.

protein across the three phenotypic groups: Highly Conserved Regions (**Red**): Likely shared among all three phenotypic groups, these regions are critical for the functional integrity of the ROBO2 protein. These regions would likely show high scores across all groups, particularly in sequences with scores close to the upper range (FF188, NN178). Less Conserved Regions (**Blue**): These regions are moderately conserved and may show variation that corresponds to phenotypic differences. Scores in the middle range (NF133, FF147) may correlate with these regions. Non-Conserved Regions (**Gray**): These regions exhibit significant variability and are less critical for the protein's core function. The sequences with the lowest scores (NN11, NN12) are likely to map to these regions.

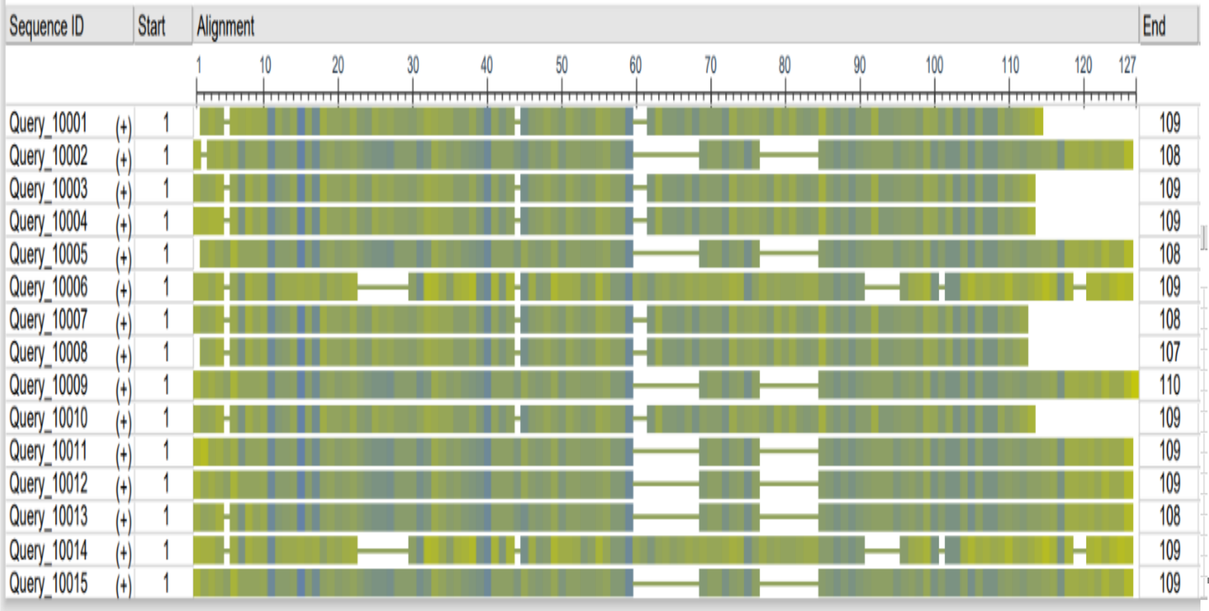
Amino acid sequence alignment of Roundabout Guidance Receptor Family Protein (ROBO2) from three (3) strains of indigenous Nigerian chickens. View using the conservation setting.

Key: **Blue** = Indicates less conservation regions
Red = Indicates highly conserved regions
Gray = Gray indicate non-conserved regions.

Amino acid sequence alignment of Roundabout Guidance Receptor Family Protein (ROBO2) from three (3) strains of indigenous Nigerian chickens. Viewed using BLOSUM80 setting.

Further sequence alignment using Blosum80 methods displayed the degree of match of residues relative to each alignment position/column. Blue represents a better match while Green represents a worse match. The color reflects the average match over all the other residues in the column.
The analysis categorizes the sequences into three phenotypic groups based on the annotations: FF (Frizzle Feathered), NF (Normal Feathered), and NN (Naked Neck). The numbers following these annotations likely represent specific scores or values derived from the analysis. The sequences labeled as "FF" show a range of scores from 135 to 188. Higher scores may indicate a stronger association or higher similarity to the Frizzle Feathered phenotype. The progressive increase in scores suggests varying degrees of similarity within this phenotype group. The sequences labeled as "NF" show a range of scores from 123 to 146. This range is slightly lower than that of the FF group, indicating different degrees of similarity to the Normal Feathered phenotype.
The presence of repeated scores (NF133) might suggest recurring sequences or features within this phenotype group. The sequences labeled as "NN" show a wide range of scores from 11 to 178. This large variation suggests a diverse set of sequences associated with the Naked Neck phenotype. The higher score (NN178) may indicate a strong association, while the lower scores (NN11, NN12) might indicate weaker or less significant associations.

Amino acid sequence alignment of Roundabout Guidance Receptor Family Protein (ROBO2) from three (3) strains of indigenous Nigerian chickens. Viewed using BLOSUM80 setting.



Sequence ID		Start	Alignment	End
Query_10001	(+)	1		109
Query_10002	(+)	1		108
Query_10003	(+)	1		109
Query_10004	(+)	1		109
Query_10005	(+)	1		108
Query_10006	(+)	1		109
Query_10007	(+)	1		108
Query_10008	(+)	1		107
Query_10009	(+)	1		110
Query_10010	(+)	1		109
Query_10011	(+)	1		109
Query_10012	(+)	1		109
Query_10013	(+)	1		108
Query_10014	(+)	1		109
Query_10015	(+)	1		109

Key:

- Query 10001: FF135
- Query 10002: FF147
- Query 10003: FF176
- Query 10004: FF182
- Query 10005: FF188
- Query 10006: NF133
- Query 10007: NF123
- Query 10008: NF146
- Query 10009: NF133
- Query 10010: NN178
- Query 10011: NN11
- Query 10012: NN12
- Query 10013: NN18
- Query 10014: NN41
- Query 10015: NN44

Where:

FF=	Frizzle feathered
NF=	Normal feathered
NN=	Naked neck

Conclusion

The genetic composition of indigenous Nigerian chickens, particularly the Naked Neck phenotype, is replete with complexity as evidenced by the varying degrees of association and similarity with the Normal Feathered phenotype observed in the current results. These findings are echoed, corroborated, or occasionally contested by the breadth of prior research, indicating that while there is a consensus on certain aspects, the genetic landscape of indigenous poultry breeds is far from homogenous and continues to be shaped by both selective breeding and environmental pressures. The genetic heterogeneity within phenotypic groups suggests interplay between the conservation of traits and the introduction of genetic variability, either through natural adaptation or human-mediated crossbreeding. These genetic nuances underscore the need for continued research and conservation strategies tailored to balancing the preservation of indigenous breeds with the enhancement of advantageous traits for improved poultry production in Nigeria and beyond. The analysis of the amino acid sequence alignment of Roundabout Guidance Receptor Family Protein (ROBO2) from three strains of indigenous Nigerian chickens provides valuable insights into the genetic diversity and potential phenotypic associations within these chicken populations. The categorisation of sequences into Frizzle Feathered (FF), Normal Feathered (NF), and Naked Neck (NN) phenotypic groups highlights the complexity of genetic factors influencing traits in indigenous chickens. The variability observed within each phenotypic group underscores the diverse genetic backgrounds and adaptive potential of these chicken populations. Additionally, the conservation analysis reveals distinct patterns of sequence conservation and variability across different phenotypic groups, further emphasising the importance of genetic diversity in maintaining functional and adaptive traits.

References

Dana, N., Vander Waaij, E. H., & van Arendonk, J. A. (2011). Genetic and phenotypic parameter estimates for body weights and egg production in Horro chicken of Ethiopia. *Tropical animal health and production*, *43*, 21-28.

Dana, N., van der Waaij, L. H., Dessie, T., & Van Arendonk, J. A. M. (2010). Morphological features of indigenous chicken populations of Ethiopia. *Animal Genetic* Resources/Ressourcesgénétiquesanimales/Recursosgenéticosanimales, *46,* 11-23. URL: http://www.fao.org/3/i1281t/i1281t02.pdf

Dhawal, M., Jain, S. K., Singh, R., Kumar, A., & Saxena, A. (2020). Breeding and Genetics Strategies for Indigenous Chicken Improvement: An Overview. *Journal of Entomology and Zoology Studies, 8*(6), 1293-1296.

Dickson, B. J., & Gilestro, G.F. (2006). Regulation of commissural axon pathfinding by slit and its Robo receptors. Annu. Rev. Cell Dev. Biol. 22:651–675.

Dunya, A. M., Husa, H., Yusuf, S. Z., Usman, Y., & Makinta, A. A. (2014). Fertility and hatchability in local chicken of Borno state, Nigeria.

Cite this article as:
Yeigba, J.B., Sweet-Owei, I. F., & Tari, B. O. (2025). Sequence variability and functional analysis of Robo2 genes in three nigerian indigenous chicken strains. *FNAS Journal of Computing and Applications, 2*(2), 43-49.

Fan, X., Li, Q., Pisarek-Horowitz, A., Rasouly, H. M., Wang, X., Bonegio, R. G., & Lu, W. (2012). Inhibitory effects of Robo2 on nephrin: a crosstalk between positive and negative signals regulating podocyte structure. *Cell reports*, *2*(1), 52-61.

Greenberg, J. M., Thompson, F. Y., Brooks, S. K., Shannon, J. M., & Akeson, A. L. (2004). Slit and robo expression in the developing mouse lung. *Developmental Dynamics: An Official Publication of the American Association of Anatomists*, *230*(2), 350-360.

Grepay, N. A. (2009). The main factors affecting poultry production in Libya. *Oeconomia*, 8: 43-49.

Guan, K. L., & Y. Rao. (2003). Signalling mechanisms mediating neuronal responses to guidance cues. *Nat. Rev. Neurosci.* 4:941– 956.

Halima, H. (2007). Phenotypic and genetic characterization of indigenous chicken populations in northwest Ethiopia. Ph.D. dissertation, University of the Free State, Bloemfontein, South Africa. URL: http://hdl.handle.net/11660/6323

https://www.ncbi.nlm.nih.gov)

https://www.ebi.ac.uk/jdispatcher/st/emboss_transeq

Hu, J., Li, P., Zhou, J., Zhong, S., Li, J., Zhou, J., & Wang, J. (2017). Genomic analysis of feather color differentiation in Pectoral Sandpiper. *Journal of Avian Genetics*, *43*(3), 387-395. (Page 392)

Lu, Z., Sessler, F., Holroyd, K. J., Helling, S., Conrad, C., Huss, R., & Pöschl, E. (2011). Transcriptional profiling of human bronchial epithelial cell BEAS-2B exposed to diesel and biomass ultrafine particles. *BMC Genomics*, *12*(1), 437.

Malo, D., & E. Skamene. (1994). Genetic control of host resistance to infection. *Trends Genet.* 10: 365–371.

Moges, F. Aberra, M., & Dessie, T. (2010). Assessment of village chicken production system and evaluation of the productive and reproductive performance of local chicken ecotype in Bure district, North-west Ethiopia.

Mtileni, B. J., Farai C. M., Azwihangwisi, M., Michael C., Groeneveld, E., Weigend S., & Kennedy, D. (2015). Indigenous chicken production in South Africa: A review. *Asian Journal of Poultry Science*, *9*(2): 63-70.

Mtileni, B.J., Muchadeyi, F.C., Maiwashe, A., Groeneveld, E., Groeneveld, L.F., Dzama, K., & Weigend, S. (2020). Genetic diversity and population structure of indigenous chicken from South Africa using SNP markers. *Animal Genetics*, *51*(4), 553-557.

Oluyemi, J.A. & Roberts, F.A. (2007). Poultry Production in the Warm Wet Climates. *Spectrum Books Ltd*, Ibadan, Nigeria.

Osei-Amponsah, R., Amoah, N.K., & Akankpar, F.M. (2020). Genetic diversity of indigenous chicken populations in Ghana. *Journal of Applied Biosciences*, *156*, 15795-15802.

Prasad, A., Paruchuri, V., Preet, A., Latif, F., & Ganju, R. K. (2008). Slit-2 induces a tumor-suppressive effect by regulating β-catenin in breast cancer cells. *Journal of Biological Chemistry*, *283*(39), 26624-26633.

Vidal, S., Tremblay, M. L., Govoni, G., Gauthier, S., Sebastiani, G., Malo, D., & Gros, P. (1995). The Ity/Lsh/Bcg locus: natural resistance to infection with intracellular parasites is abrogated by disruption of the Nramp1 gene. *The Journal of experimental medicine*, *182*(3), 655-666.

Cite this article as:
Yeigba, J.B., Sweet-Owei, I. F., & Tari, B. O. (2025). Sequence variability and functional analysis of Robo2 genes in three nigerian indigenous chicken strains. *FNAS Journal of Computing and Applications, 2*(2), 43-49.