

PHYLOGENETIC RELATIONSHIP OF GROWTH HORMONE, INSULIN-LIKE GROWTH FACTOR 1 AND MYOSTATIN GENE SEQUENCES IN CHICKEN, RABBIT AND SHEEP

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ABSTRACT

The gene sequences of Growth hormone (GH), Insulin-like Growth Factor 1 (IGF-1) and Myostatin (MSTN) were downloaded from National Centre for Biotechnology Information (NCBI) database, in FASTA format, using respective accession numbers (Table 1) of the genes in the GenBank to access the necessary gene information. The phylogenetic trees were drawn to reveal evolutionary relationships between the genes of the three species by submitting the genes respective sequences in FASTA format to MEGA7 tool. Results indicated that; Chicken GH gene had nucleotides substitution of 0.15 in the gene sequence, and rabbit GH gene had nucleotide substitution of 0.17 in the gene sequence. While, the sheep GH gene had nucleotide substitution of 0.25 in the gene sequence. Rabbit myostatin gene had nucleotides substitution of 0.14 in the gene sequence, and sheep myostatin gene had nucleotide substitution of 0.12 in the gene sequence. While, the chicken myostatin gene had nucleotide substitution of 0.38 in the gene sequence. Rabbit IGF-1 gene had nucleotides substitution of 0.18 in the gene sequence, and sheep IGF-1 gene had nucleotide substitution of 0.17 in the gene sequence. While, the chicken IGF-1 gene had nucleotide substitution of 0.57 in the gene sequence. It is concluded that; the higher the rate of substitution in phylogenetic relationship among the three genes of the three species indicate the more the chance/advantage for the gene or specie to improve more over time through research/selection while the lesser the rate of substitution indicates the genes are reaching a bottle neck in selection.

Key words: Phylogenetic, Genes, Sequences, Substitution, Variations.

INTRODUCTION

A biological database is a collection of information, or data from a biological system, stored in a computer readable format. Sharing of data between scientists accelerates the speed of discoveries and has the potential to greatly advance a scientific field as a whole (Hey *et al.*, 2009).

Phylogenetic trees reveal evolutionary relationships between organisms or sequences (e.g. genes or proteins) (Dutilh and Keşmir, 2016). Phylogeny study a set of sequences that are likely to have evolved from a common ancestor to find out how the species or sequences diverged from each other, in which order and at what time. This procedure that allow information of the evolutionary relationship between organisms, individuals, genes, prediction functions and structures, among others (Junqueira *et al.*, 2014). Often it is not possible to reliably estimate divergence times from molecular data. If the data set does not allow for such an estimate, the final tree branches do no longer represent Million years (Ma). The branch lengths can again be drawn to scale, to represent evolutionary distance (e.g. the number of nucleotides that have been substituted) instead of Ma (Dutilh and Keşmir, 2016). Most of the variations in a gene are single nucleotide polymorphisms (SNPs) arising from substitution, deletion, or insertion of a single nucleotide. A single SNP can greatly affect performance traits of an animal (Zhang *et al.*, 2002).

GH plays important functions in animal growth and development and several studies have analyzed the GH gene as a candidate for economic traits in livestock species. Mutations of this gene have been described in sheep (Marques Mdo *et al.*, 2006), and poultry (Feng *et al.*, 1997) to affect important production traits. Myostatin is expressed specifically in developing an adult skeletal muscle and functions as a negative regulator of skeletal muscle mass in mice (McPherron *et al.*, 1997). Myostatin null mice generated by gene targeting shows a dramatic and widespread increase in skeletal muscle mass. Insulin-like growth factors one and two (somatomedins- IGF-I and IGF-2) are structurally related proteins that have a key role in cell differentiation, embryogenesis, growth and regulation of metabolism (Siadkowska *et al.*, 2006).

Objectives of the Study

To determine the evolutionary nucleotide substitution and relationship of GH, IGF-1 and MSTN genes in chicken, rabbit and sheep.

MATERIALS AND METHODS

Evolutionary Phylogenetic Tree Using MEGA7 Computational Tool

This Phylogenetic Analysis study was conducted at A.B.U. ICT/Digital Centre, Animal Science Department, Faculty of Agriculture, Ahmadu Bello University Zaria, Kaduna State, Nigeria. The gene sequences of GH, IGF-1 and MSTN were downloaded from National Centre for Biotechnology Information (NCBI) database (2017), in FASTA format, using respective accession numbers (Table 1) of the genes in the GenBank to access the necessary gene information. The phylogenetic trees were drawn to reveal evolutionary relationships between the genes of the three species by submitting the genes respective sequences in FASTA format to MEGA7 tool, MEGA7.0.26. (Kumar *et al.*, 2016).

Table 1: Accession numbers of GH, IGF-1 and Myostatin Genes of Chicken, Rabbit and Sheep

Specie	GH gene Accession	IGF-1 gene Accession	Myostatin gene Accession
Chicken	NC_006114.4	NC_006088.4	NC_006094.4
Rabbit	NC_030827.1	NC_013672.1	NC_013675.1
Sheep	NC_019468.2	NC_019460.2	NC_019459.2

Source: GenBank, National Center for Biotechnology Information (NCBI) database (2017)

Results and Discussion

Phylogenetic Analysis Result of Growth Hormone Gene of Chicken, Rabbit and Sheep

The branch leading to rabbit GH gene is longer than to chicken GH gene, meaning that the rate of evolution has been faster in rabbit GH gene than to chicken GH gene because, more nucleotides have changed in rabbit GH gene than in chicken GH gene since their last common ancestor. The sheep GH gene has never share a common ancestor, even though the rate of evolution has been faster than that of chicken GH gene but at the same rate with rabbit GH gene, but does not tell us the precise time of speciation. According to Jin, (2006) by studying the evolutionary relationships of genes and other biological macromolecules, by analyzing mutations at various positions in their sequences and developing hypotheses about the evolutionary relatedness of the biomolecules. Based on the sequence similarity of the molecules, evolutionary relationships between the organisms can often be inferred.

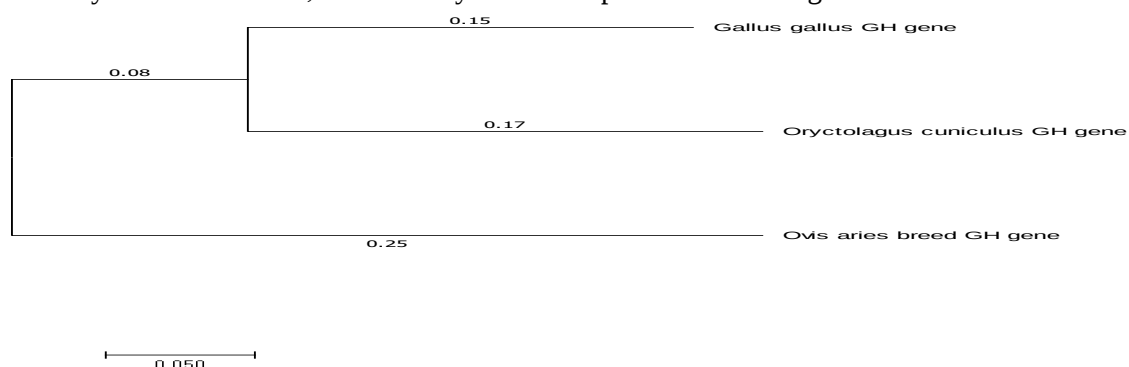


Figure 1: Phylogenetic Analysis Result of Growth Hormone Gene of Chicken, Rabbit and Sheep

Phylogenetic Analysis Result of Myostatin Gene of Chicken, Rabbit and Sheep

The branch leading to rabbit Myostatin gene is longer than to sheep Myostatin gene, meaning that the rate of evolution has been faster in rabbit Myostatin gene than to sheep Myostatin gene because, more nucleotides have changed in rabbit Myostatin gene than in sheep Myostatin gene since their last common ancestor. The chicken Myostatin gene has never share a common ancestor, even though the rate of evolution has been faster than that of sheep Myostatin gene and rabbit Myostatin gene. Mutations in the coding sequence of the gene may lead to changes in the protein structure and consequently its enzymatic function, or also by mutations in the upstream or downstream regions of the gene, leading to differential gene regulation without actually changing the structure and function of the protein (Dutilh and Keşmir, 2016).

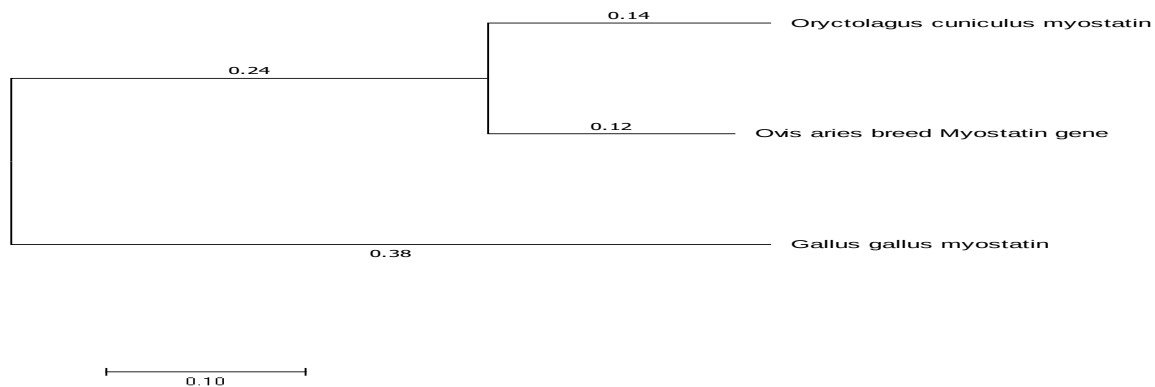


Figure 2: Phylogenetic Analysis Result of Myostatin Gene of Chicken, Rabbit And Sheep

Phylogenetic Analysis Result of Insulin-Like Growth Factor-1 Gene of Chicken, Rabbit and Sheep. The branch leading to rabbit IGF-1 gene is longer than to sheep IGF-1 gene, meaning that the rate of Evolution has been faster in rabbit IGF-1 gene than to sheep IGF-1 gene because, more nucleotides have changed in rabbit IGF-1 gene than in sheep IGF-1 gene since their last common ancestor. The chicken IGF-1 gene has never share a common ancestor, even though the rate of evolution has been faster than that of sheep IGF-1 gene and a little fast than that of rabbit IGF-1 gene, but does not tell us the precise time of speciation. Alignment techniques are necessary to whole genome analysis, in which the comparison between different genomes or from the same species allows us to identify variations in the sequences and associate them with specific phenotypes (Junqueira *et al.*, 2014).

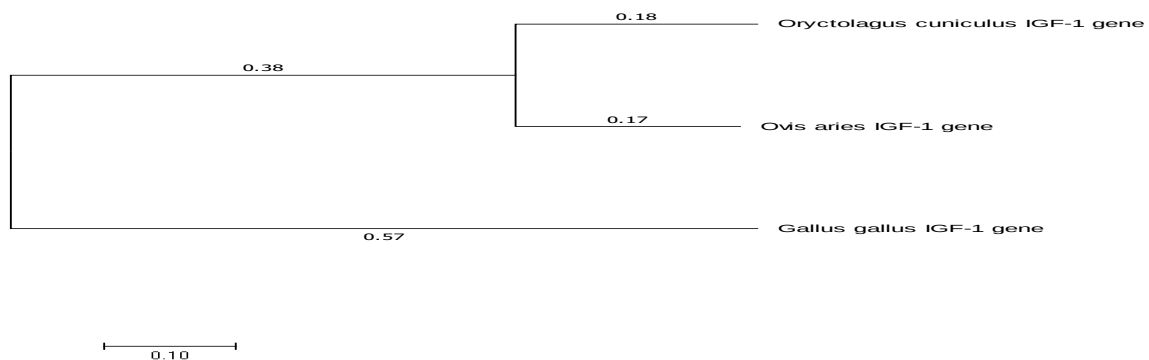


Figure 3: Phylogenetic analysis result of Insulin-like Growth Factor-1 Gene of Chicken, Rabbit and Sheep.

Conclusion

The higher/faster the rate of substitution in phylogenetic relationship/analysis among the three genes of the chicken, rabbit and sheep genomes indicate the more the chance/advantage for the gene or specie to improve/develop more over time through research or selection while the lesser the rate of substitution indicates the genes are reaching a bottle neck for selection in the genome of the three species.

Recommendation

More researches should be done to apply the knowledge and problems solved through bioinformatics analysis and procedure.

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