East African Scholars Journal of Biotechnology and Genetics
Abbreviated Key Title: East African Scholars J Biotechnol Genet
ISSN: 2663-189X (Print) & ISSN: 2663-7286 (Online)
Published By East African Scholars Publisher, Kenya

OPEN ACCESS

Volume-1 | Issue-1 | Jan-Feb -2019 |

Research Article

Computational Molecular Analysis of Bovine Luteinizing Hormone Receptor using Predict Protein

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Abstract: The primary structure identifies a protein, determines its chemical and biological characteristics, and specifies the higher levels of protein structure. Variation in amino acid composition tend to change the structure of the obtained protein leading to the change in conformation of third structure of the protein and its function. The cellular actions of LH are mainly mediated by the luteinizing hormone/choriogonadotropin receptor (LHCGR), which has features typical of receptors that interact with G proteins, including a cellular domain, seven transmembrane domains, and an extracellular hormone-binding domain.The luteinizing hormone receptor (LHR) plays a key role in testosterone production through its interaction with the gonadotropins.. Single nucleotide polymorphisms (SNPs) in the bovine luteinizing hormone/choriogonadotropin receptor (LHCGR) gene was reported to have significant effect on super ovulation .Nucleotide sequence of Bovine luteinizing hormone receptor was retrieved from the GenBank, accession no : AF491303.1. Predict protein was used in the molecular analysis of Bovine luteinizing hormone receptor. Predict Protein integrates feature prediction for secondary structure using a comprehensive list of methods and data bases currently incorporated into the server .Findings of this study can be used to understand the physiological role of bovine luteinizing hormone receptor on Testosterone production and luteal function in pregnant Cows.

Keywords: BOVINE, LHR, PREDICTPROTEIN, PHYSICO CHEMICAL PROPERTIES.

INTRODUCTION

The luteinizing hormone receptor (LHR) is a member of the G-protein coupled receptor super family and consists of an extracellular domain, seven transmembrane domains connected by alternating intracellular and extracellular loops, and an intracellular carboxyl (C)-terminal tail. The luteinizing hormone receptor (LHR) plays a key role in testosterone production through its interaction with the gonadotropins, LH and chorionic gonadotropin (Ma, T. H. *et al.*, 2012). hCG is structurally related to LH and both hormones bind to the same LH/choriogonadotrophin receptor (Rahman, N. A., & Rao, C. V. 2009). The LHR has a pivotal role in testicular development and function (Zhang, F. P. *et al.*, 2001). The cellular actions of LH are mainly mediated by the luteinizing hormone/choriogonadotropin receptor (LHCGR), which has features typical of receptors that interact with G proteins (Dufau, M. L. *et al.*, 1995). Single nucleotide polymorphisms (SNPs) in the bovine luteinizing hormone/choriogonadotropin receptor (LHCGR) gene was reported to have significant effect on super ovulation (Mitri, F. *et al.*, 2014). The primary structure identifies a protein, determines its chemical and biological characteristics, and specifies the higher levels of protein structure (Alain, J.C. 2002). Variation in amino acid composition tend to change the structure of the obtained protein leading to the change in conformation of third structure of the protein and its function (Wang, Z., & Moult, J. 2001).

Predict Protein integrates feature prediction for secondary structure using a comprehensive list of methods and data bases currently incorporated into the server (Yachdav, G. *et al.*, 2014). Parameters evaluated include Amino acid composition, secondary structure composition, Solvent accessibility, Predicted localization, Disulfide bridges and Protein binding sites. The association of single nucleotide polymorphisms (SNPs) in Bovine luteinizing hormone receptor with super ovulation has been established. Increasing knowledge on the molecular structure of Bovine luteinizing hormone receptor can lead to insights into understanding the pathogenesis of conditions associated

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Journal homepage:
http://www.easpublisher.com/easjbg/

Article History
Received: 15.01.2019
Accepted: 12.02.2019
Published: 28.02.2019

DOI: 10.36349/easjbg.2019.v01i01.002

with polymorphism in the Luteinizing hormone receptor.

Materials and Methods

The amino acid sequence of Bovine Luteinizing Hormone Receptor was obtained from sequence database at National Center for Biotechnology Information (NCBI). Predict Protein was used to evaluate the molecular structure of bovine luteinizing hormone receptor. Predict Protein integrates feature prediction for secondary structure using a comprehensive list of methods and data bases currently incorporated into the server PROFsec predicts secondary structure elements and solvent accessibility using evolutionary information from multiple sequence alignments and a multi-level system (Rost, B. *et al.*, 2014). LocTree3 predicts the sub-cellular localization for all proteins in all domains of life. Water-soluble globular and trans-membrane proteins are predicted in one 18 classes in Eukaryota (chloroplast, chloroplast membrane, cytosol, ER, Golgi, ER membrane, Golgi membrane, extra-cellular, mitochondria, mitochondria membrane, nucleus, nucleus membrane, peroxisome membrane, plasma membrane, plastid, vacuole and vacuole membrane), 6 classes in Bacteria (cytosol, extra-cellular, fimbrium, outer membrane, periplasmic space and plasma membrane) and 3 classes in Archaea (cytosol, extra-cellular and plasma membrane). Each prediction is accompanied by a confidence score (ranging from 0=unreliable to 100=reliable) and a Gene Ontology term of the predicted localization class (Goldberg, T. *et al.*, 2012). DISULFIND tool was used for the automatic prediction of disulfide bridges (Ceroni, A. *et al.*, 2006). Protein binding sites was predicted using ISIS2 (protein-protein binding sites) and SomeNA (polynucleotide binding sites), (Ofran, Y., & Rost, B. 2007).

RESULTS

The three-dimensional structure and biological activity of proteins depend on the physicochemical properties of their constituent amino acids. The result indicate a sequence length 0f 701 and 62 aligned proteins. Three states of secondary structure are predicted: helix (H; includes alpha-, pi- and 3_10-helix), (beta-) strand (E = extended strand in beta-sheet conformation of at least two residues length) and loop (L). Secondary structure is predicted by a system of neural networks with an expected average accuracy of more than 72%. The sub-cellular localization for all proteins in all domains of life was predicted with a confidence score of 100, indicating high level of accuracy of prediction.

DISULFIND tool was used for the automatic prediction of disulfide bridges DISULFIND uses a combination of machine learning algorithms to predict intra chain bridges from sequence alone. Similar to many other tools of this kind, it solves the prediction problem in two steps. First, the disulfide bonding state of each cysteine is predicted by a binary classifier; second, cysteines that are known to participate in the formation of bridges are paired to obtain a connectivity pattern. Disulfide bridges are covalent bonds that happen between cysteine (C) residues only. Disulfide bridges play a major role in the stabilization of the folding process and, consequently, in studies related to structural and functional properties of specific proteins. In addition, knowledge about the disulfide bonding state of cysteines may help the experimental structure determination process and may be useful in other genomic annotation tasks. Protein binding sites was predicted using ISIS2 (protein-protein binding sites) and SomeNA (polynucleotide binding sites)..

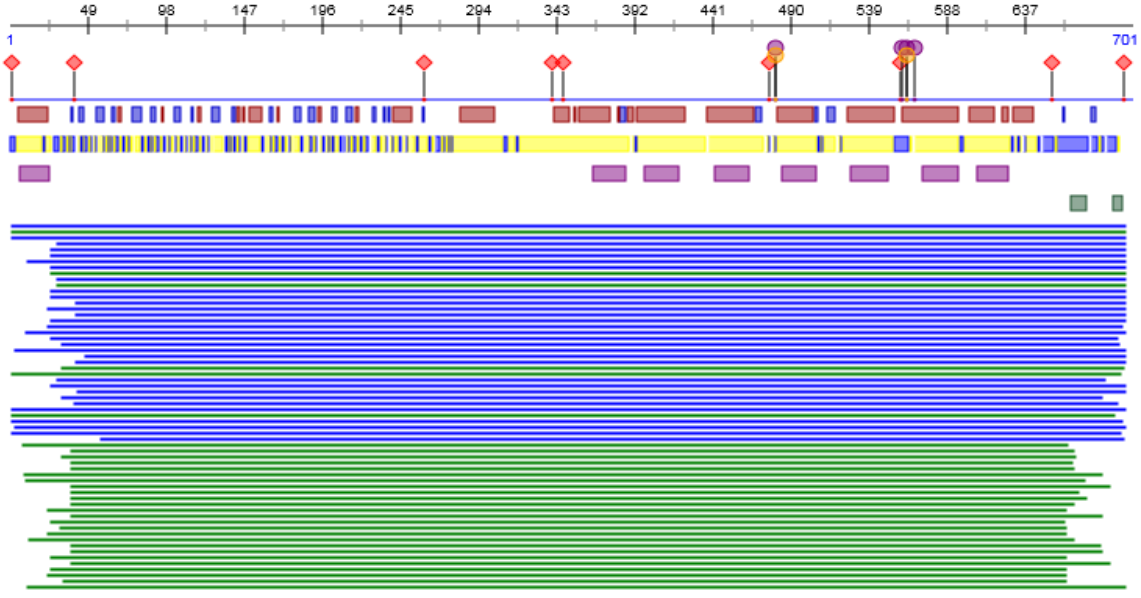


Fig 1; Sequence Alignment of Bovine luteinizing hormone receptor

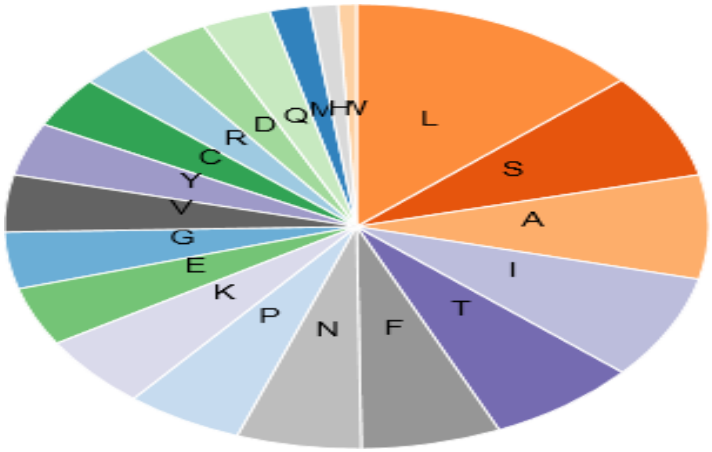


Fig. 2; Amino Acid compositio of bovine Luteinizing hormone receptor

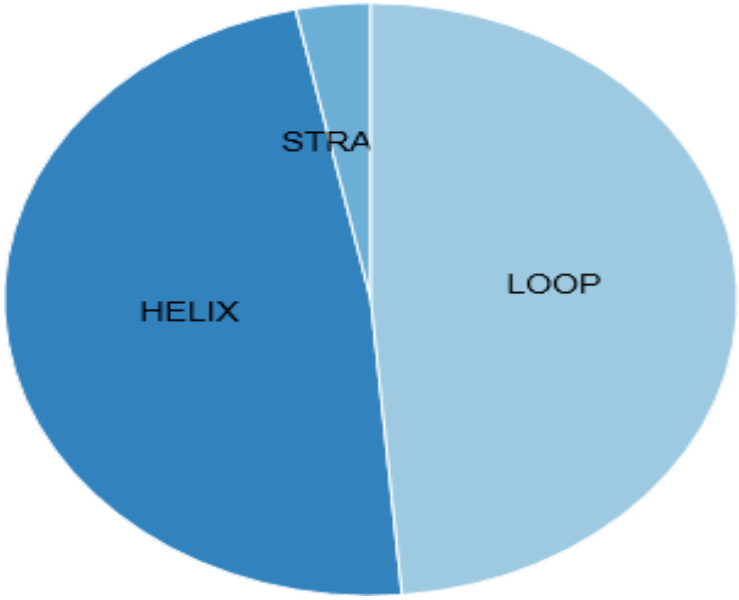


Fig. 3; Secondary structure composition

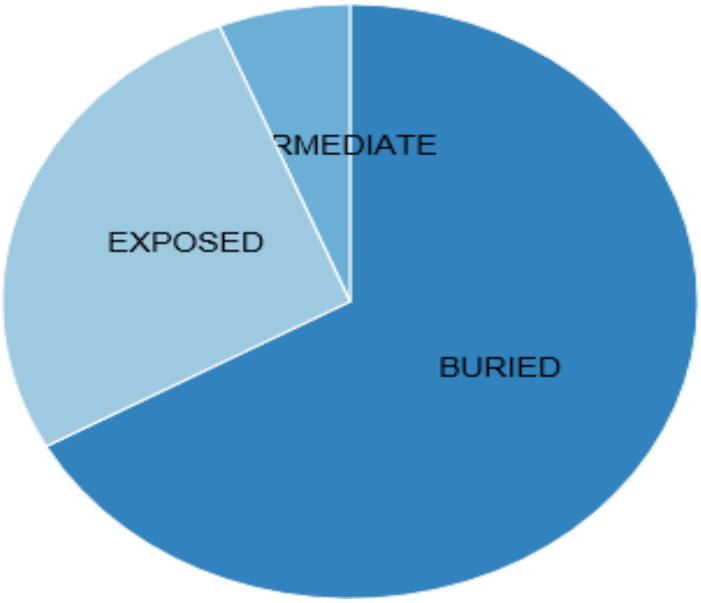
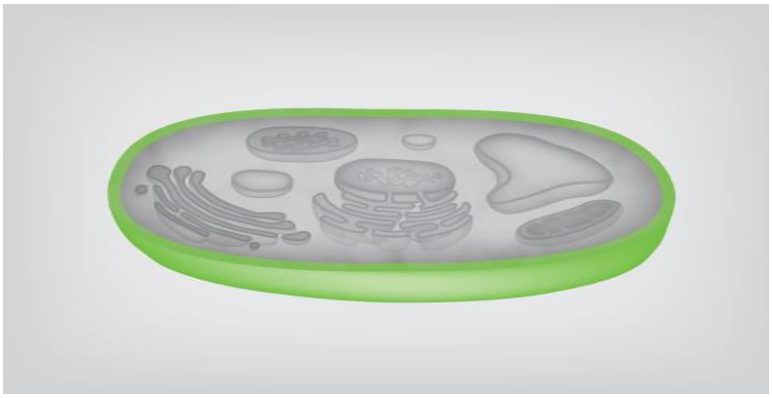
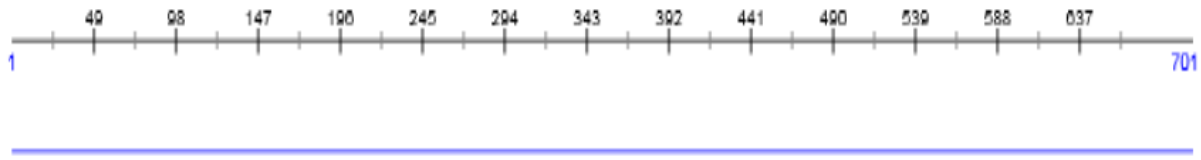


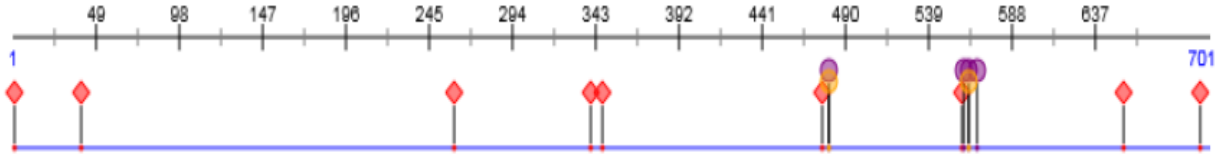
Fig. 4; solvent accessibility



Fiq 5; Predicted localization for the Eukarya domain: Plasma Membrane (GO term ID: GO:0005886) Prediction confidence 100



Fiq 6; Disulfide Bridges



Fiq 7; Binding sites

DISCUSSION AND CONCLUSION

The cellular actions of LH are mainly mediated by the luteinizing hormone/choriogonadotropin receptor (LHCGR), which has features typical of receptors that interact with G proteins, including a cellular domain, seven transmembrane domains, and an extracellular hormone-binding domain (Dufau, M. L. *et al.*, 1995). Both LH and human chorionic gonadotropin (hCG) are endogenous ligands for LHR (Hearn, M. T., & Gomme, P. T. 2000). Prior to ovulation, FSH and estradiol both increase pituitary production of LH and induce LHR expression in the ovaries where LHR functions in promoting follicular maturation, lutenization and ovulation (Ascoli, M. *et al.*, 2002). Three single nucleotide polymorphisms (SNPs) in the *luteinizing hormone/choriogonadotropin receptor* gene of cattle (*Bos taurus*) were significantly associated with variations in cattle fertility and production traits, most notably on calving interval, days to first service and production index (Hastings, N. *et al.*, 2006). Earlier reports have indicated that *LHCGR* gene is a potential marker for super ovulation response and can be used to predict the most appropriate dose of FSH for super ovulation in Chinese Holstein cows (Mitri, F. *et al.*, 2014). Steroidogenesis is also dependent on LH activity for androgen production in the theca cells, a substrate for estrogen production, and for estrogen and progesterone production by the corpus luteum (Mitri, F. *et al.*, 2014) LH stimulates androgen production in theca cells, thus providing substrate for granulosa cell estrogen production. LH also triggers ovulation, and thereafter maintains the progesterone production of corpus luteum. The role of LH is to stimulate Leydig cell androgen production and thereby to maintain the endocrine (extratesticular) and paracrine (spermatogenic) effects of androgens. Increasing information on the molecular structure of luteinizing hormone receptor would be relevant for understanding the pathogenesis of conditions associated with polymorphism of luteinizing hormone receptor conflict of interest- The author declare that there is no conflict of interest.

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