

## **Bioinformatic Study of Follicle Stimulating Hormone Receptor (FSHR) Gene in Different Buffalo Breeds**

**Authors :** Hamid Mustafa, Adeela Ajmal, Kim EuiSoo, Noor-ul-Ain

**Abstract :** World wild, buffalo production is considered as most important component of food industry. Efficient buffalo production is related with reproductive performance of this species. Lack of knowledge of reproductive efficiency and its related genes in buffalo species is a major constraint for sustainable buffalo production. In this study, we performed some bioinformatics analysis on Follicle Stimulating Hormone Receptor (FSHR) gene and explored the possible relationship of this gene among different buffalo breeds and with other farm animals. We also found the evolution pattern for this gene among these species. We investigate CDS lengths, Stop codon variation, homology search, signal peptide, isoelectric point, tertiary structure, motifs and phylogenetic tree. The results of this study indicate 4 different motif in this gene, which are Activin-recp, GS motif, STYKc Protein kinase and transmembrane. The results also indicate that this gene has very close relationship with cattle, bison, sheep and goat. Multiple alignment (MA) showed high conservation of motif which indicates constancy of this gene during evolution. The results of this study can be used and applied for better understanding of this gene for better characterization of Follicle Stimulating Hormone Receptor (FSHR) gene structure in different farm animals, which would be helpful for efficient breeding plans for animal's production.

**Keywords :** buffalo, FSHR gene, bioinformatics, production

**Conference Title :** ICBCSB 2015 : International Conference on Bioinformatics, Computational and Systems Biology

**Conference Location :** New York, United States

**Conference Dates :** June 04-05, 2015