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IN SILICO ANALYSIS OF SINGLE NUCLEOTIDE POLYMORPHISM (SNPs) IN RABBIT GROWTH HORMONE

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ABSTRACT

The main objectives of this research were to evaluate the molecular structure and predict the effect of single nucleotide polymorphism in rabbit growth hormone. Analysis using protparam server indicated molecular weight of 24433.06, estimated half life of 30 hours, instability index of 36.04 and aliphatic index of 86.39. Secondary structure prediction showed 30% disordered , 69%alpha helix and 0% beta strand. Analysis of single nucleotide polymorphism indicate that substitution of leucin for valine at position 36 has adverse effect on the fuction of rabbit growth hormone. It can be concluded that single nucleotide polymorphism can be used as genetic markers for selection in rabbit breeding.

KEY WORDS: Growth hormone, Rabbit, Polymorphism, Prediction, In silico

INTRODUCTION

Production traits have been associated with mutation in growth hormones of various livestock species. The growth hormone is therefore an important candidate gene in selection for desirable traits (Fontanesi et al., 2016). It serves a critical role in regulation of somatic cell growth and development. The rabbit is characterize by early sexual maturity, high prolificacy and rapid growth rate. It is therefore a good alternative source of protein and could contribute to solving the problem of animal protein deficiency (Makhlout et al., 2017). The growth hormone gene has direct effect on synthesis and secretion of growth hormone which regulate protein, carbohydrate and lipid metabolism in animal tissues. The growth hormone also play regulatory role in proliferation, growth and differentiation of reproductive organs(Fontanesi et al., 2008).

Responses to growth hormone involve induction of insulin like growth factor 1, a protein hormone secreted by the liver and other growth target tissues (David and Caitlin,2006). The amino acid chains of proteins fold into a structure and perform biological functions by binding to various chemicals. Understanding protein binding sites is useful in drug design and disease diagnosis (Premarathna and Ellingson, 2021). The rabbit growth hormone is a potential biomarker for selection of desirable traits in rabbit. The objective of this study is to evaluate the molecular structure and effect of amino acid substitution on rabbit growth hormone using computational methods.

MATERIALS AND METHODS

Data Retrieval

Data on Rabbit growth hormone with accession no: >NP_001076105.1 was obtained from Gen bank of National Center for Biotechnology information (NCBI) for molecular analysis using computational methods.

Prediction of secondary structure and binding sites using C-I-TASSER Sever

The C-I-Tasser (content guided iterative threading assembly Refinement) is a new method developed from I-Tasser for high accuracy protein structure and function prediction. The system generate

content maps using deep neural networks predictions. It identifies structural templates from Protein Data Bank by multiple threading approach (Wei et al., 2021)

Predicting effect of single nucleotide polymorphism using panther

Protein analysis through evolutionary relationship (Version 15.0) is a resource for gene analysis based on evolutionary history and functions (Huaiya et al., 2019). The sever uses gene ontology tool for functional classification. Panther estimates the likelihood that a non synonymous coding SNP will cause a functional impact in the protein as described by Tang and Thomas, 2016.

RESULTS AND DISCUSSION

The secondary structure of Rabbit growth hormone is as shown in Table 1. The result indicate 30% disordered structure, 69% alpha helix and 0% beta strand.

Table 1: Predicted secondary structure of Rabbit growth hormone

Parameters(Structure)	Values(%)
Disordered	30
Alpha helix	69
Beta strand	0

Table 2: Prediction of effect of single nucleotide polymorphism using Panthe

substitution	preservation time	Message	Pdel
L36V	455	probably damaging	0.57

Pdel -probability of deleterious effect, probably damaging (time > 450my, corresponding to a false positive rate of ~0.2 as tested on HumVar),

Table 2 shows the predictive effect of single nucleotide polymorphism using Panther. The result indicate that substitution of leucine with valine at position 36 of the protein sequence lead to adverse effect on the functionality of rabbit growth hormone. The potential role of growth hormone as a biomarker for growth and carcass traits has been documented (Migdal et al., 2019).

CONCLUSION

It can be concluded that substitution of leucine for valine at position 36 has adverse effect on the function of rabbit growth hormone. Single nucleotide polymorphism in rabbit growth hormone is a potential biomarker for selection in rabbit breeding.

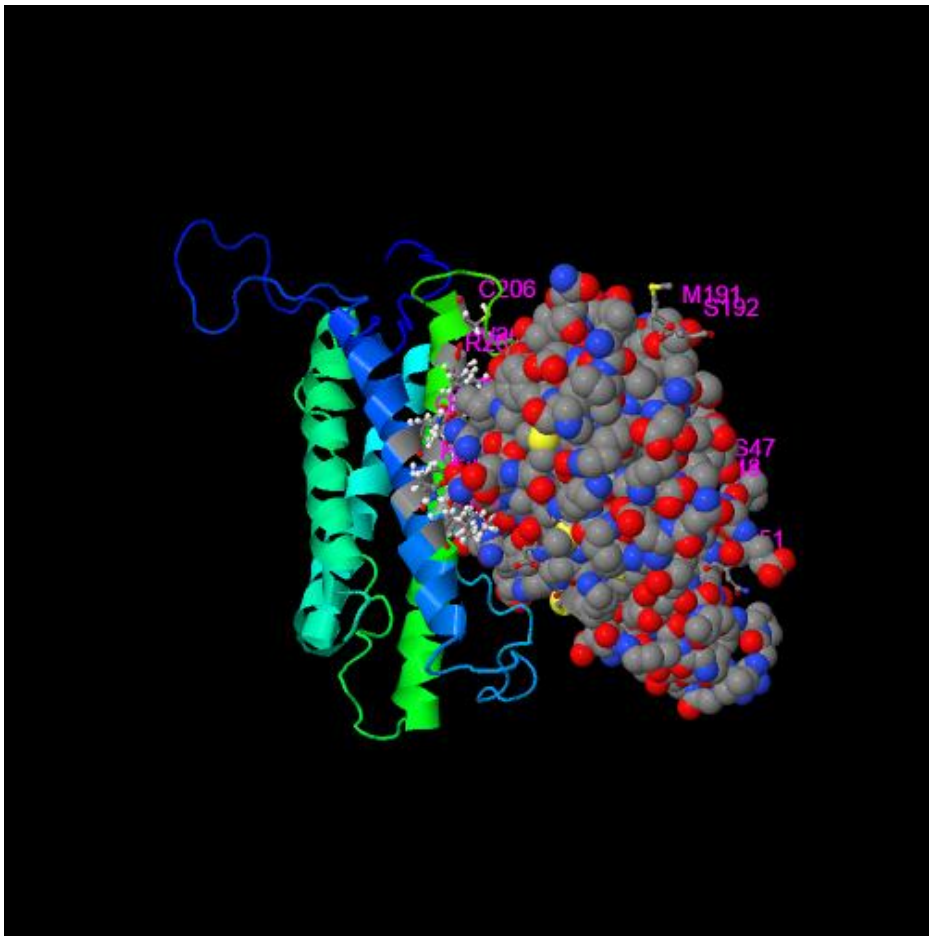

Figure 1: Binding sites of Rabbit growth hormone

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