Structural analysis of thermodynamically stable human seleno-insulin analog

Chandanapriya Vedula and Ravikiran S. Yedidi*

The Center for Advanced-Applied Biological Sciences & Entrepreneurship (TCABS-E), Visakhapatnam, Andhra Pradesh, India. 530002.

*Correspondence to RSY: tcabse.india@gmail.com

INTRODUCTION

An insulin (hormone) analog is an altered form of insulin, different from any occuring in nature, but still available to the human body for performing the same action as human insulin in terms of controlling blood glucose levels in diabetes. Through genetic enginering of the underlying dna , the aminoacid sequence of insulin can be changed to alter its charecterstics. these are often refered to as insulin receptor ligands also.. Insulin analogs mainstays in the modern treatment of diabetes mellitus exemplify the utility of protien engineering in molecular pharmacology.The chemical synthesis of these chains was achieved in 1960s which was inefficient due to disulfide pairing.to overcome this an alternative approach was substitution of cystiene residues with selenocystiene.This synthetic insulin can enhance the lifetime of insulin without impairing harmonal function.It is more resistant to reduction and internal blood rotation in the presence of insulin degrading enzyme.

EXPERIMENTALS

This structure was taken from PDB (PDB ID 6H3M) and analysed using pymol. This structure helps us to know how insulin is made and its importance in monitoring blood glucose levels. The structure quality of the structure is determined before analysing it in pymol through the following.The R workvalue(0.184) should be roughly equal to 1/10 th of the resolution(1.8A).In this case it is roughly equal(1.8/10=0.18)The difference between R work and and R free values (0.221) should be less than or equal to 0.05 (in this case-0.221-0.184=0.037). The secondary structure analysis through pymol helped us to know that there are 2 macromolecules of insulin (24 alpha helices and 4 beta strands and no small molecules and only1 H bond

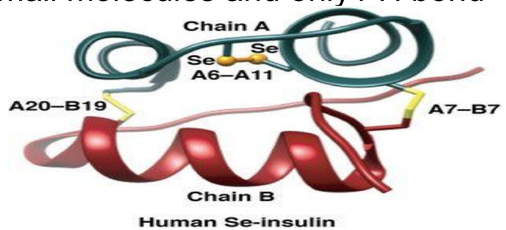

FIGURE 1 diselenocystiene bridge between intra chains.

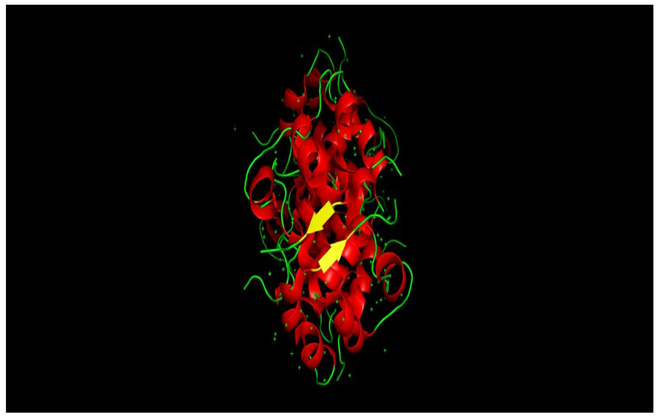

Figure 2 secondary structure of human insulin seleno analog

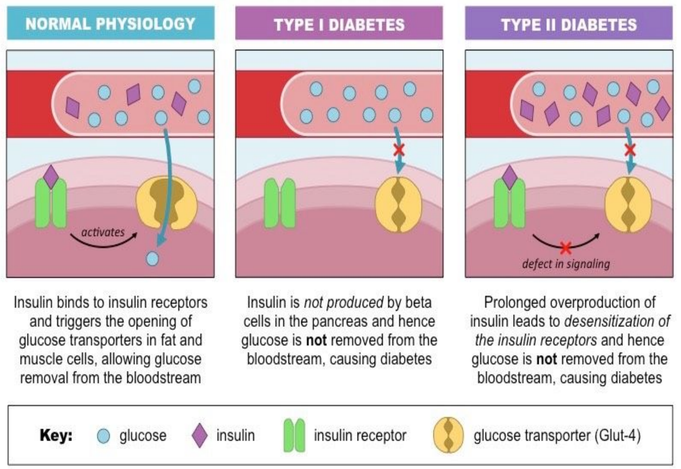

figure 3 Action of insulin in diabetes mellitus

RESULTS & DISCUSSION

This structure is good to study as its R work value is equal to 1/10th of the resolution and the difference between R work and R free values is less than 5%(0.05). Hence this structure is determined to have a good quality and further carried to anaklyse its secondary structure in pymol.This analysis shows how the diseleno bridge replaces the cystiene atoms and disulfide bridge.This structure is published in PDB in 2019 by Lansky et all.

REFERENCES

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2. secondary structure of seleno insulin analog from pymol.

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