# EAS Journal of Veterinary Medical Science

Abbreviated kev title: EAS J Vet Med Sci ISSN: 2663-1881 (Print) & 2663-7316 (Online)

Published By East African Scholars Publisher, Kenya



DOI: 10.36349/EASJVMS.2019.v01i05.004

### **Research Article**

Volume-1 | Issue-5 | Sept-Oct-2019 |

# Molecular Analysis of Heat Shock Protein 70 of Camelus Dromadarius - In **Silico**

Department of Animal Science, Faculty of Agriculture, Nasarawa State, University, Keffi., Nigeria

\*Corresponding Author Musa, S.I

**Abstract:** The molecular characteristics of heat shock protein 70 of Camelus dromedarius was analyzed using computational methods. The two domesticated Camel species, one humped dromedary and two humped. Bactrian camel live in extreme desert environments. Cells survive heat stress by thermo tolerant gene expression and elevated levels of heat shock protein. The cellular response to heat stress is mediated by heat shock factors. Which are regulated by heat shock factor genes. Protein sequence of heat shock protein 70 of Camelus dromedarius (Accession no: JF837187.1) was obtained from the GENBANK (NCBI). The secondary and tertiary structure of the protein was predicted using Phyre2 server. The result indicate 38% alpha helix, 28% beta strands and 18% disordered. Studies of molecular structure of heat shock protein will lead to better understanding of the genetic factors of heat tolerance in Camels. Heat shock proteins are important genetic markers that can be utilized in breeding programs to select thermo talerant animals.

Keywords: Camels, Heat shock protein, In silico, Molecular analysis.

#### INTRODUCTION

The two domesticated camel species, one humped Dromedary and two humped Bactrian camel live in extreme desert environments of Africa and Asia (Huiquang et al., 2015). The Camels represent an important source of meat and milk in hotter and drier regions of the world. Their exposure to varying environmental temperatures resulted in variable breed dependent physiological responses. The ability of dromedary camel (Camelus dromedarius) to survive harsh desert conditions is well documented (Al-Haidary et al., 2013). The camel is well adapted to extreme conditions and its response to heat is associated with elevated whole body temperature (David et al., 2011). Synthesis of Heat shock proteins is induced by stress factors, they act to limit cell damage and facilitate cellular recovery (Helen, 2004).Biochemical response to heat stress involve changes in proteins and metabolic rate (Bowler, 2008). Heat shock protein 70 is the most abundant heat shock protein playing a significant role in thermal adaptation, acting as first line of defense against conditions that affect protein homeostasis and stability. Expression of heat shock proteins increases when cells are exposed to elevated temperatures or other stress factors. HSP are important biomarkers that can be utilized in breeding programmes to select thermo tolerant animals. The amino acid sequences determine the higher structural levels of proteins (secondary, tertiary and quaternary) and specify their biological properties.(Branden &Tooze 1991). Most genetic variation is considered neutral but single base changes in and around a gene can affect its expression or the function of its protein products Collins et al., 1997). Evaluation of molecular structures of proteins involve in regulation of thermo tolerant ability of camels is of great significance in understanding environmental adaptations.

# MATERIALS AND METHODS

## **Prediction of Secondary and Tertiary Structures:**

Protein sequence of heat shock protein 70 of Camelus dromedarius (Accession no: JF837187.1) was obtained from the GENBANK (NCBI). The Phyre2 server was used to predict the secondary and 3D structures of the heat shock protein. The server predicts the three-dimensional structure of a protein sequence using the principles and techniques of homology modeling (Kelley & Sternberg, 2009). Phyre2 uses the alignment of hidden Markov models via HHsearch to significantly improve accuracy of alignment and

Quick Response Code

Journal homepage:

http://www.easpublisher.com/easjvms/

Article History

Received: 24.09.2019 Accepted: 12.10.2019 Published: 26.10.2019 Copyright @ 2019: This is an open-access article distributed under the terms of the Creative Commons Attribution license which permits unrestricted use, distribution, and reproduction in any medium for non commercial use (NonCommercial, or CC-BY-NC) provided the original author and source are credited.

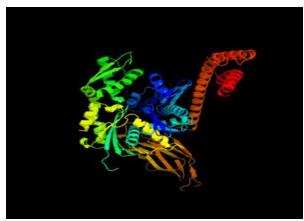
detection rate (Soding, 2005). Phyre2 also incorporates a new *ab initio* folding simulation called Poing to model regions of proteins with no detectable homology to known structures. Poing is also used to combine multiple templates. Distance constraints from individual models are treated as linear elastic springs (Jeffereys *et al.*, 2010).

# RESULTS AND DISCUSSION:

The amino acid sequences determine the higher structural levels of proteins (secondary, tertiary and quaternary) and specify their biological properties.(Branden andTooze 1991). Cellular thermo tolerance is associated with elevated HSP expression which decline with continuous stress exposure resulting in apoptosis leading to cell death(Sadder *et al.*, 2015). The genetic factors responsible for adaptation of desert animals to their environment is largely unknown (Huiquang etal.,2015). A positive correlation between characteristics temperature of the environment of a specie and the amount of HSP 70 like proteins in the cell has been established (Evgen *et al.*, 2007).

Table 1. Prediction of secondary structures 0f heat shock protein

Alpha helix (%)	Beta strand (%)	Disordered (%)
38	28	12



Fiq 1: 3D Structure of heat shock protein 70 of Camelus dromedarus

#### CONCLUSSION

Biochemical responses to heat stress involve changes in proteins and metabolic rate. Thermo tolerant gene expression and elevated heat shock protein are essential for cells to survive the impact of heat stress making it an important biomarker for heat stress. Studies of the structure of heat shock protein will provide insight in the genetic factors involve in adaptation of camels to the desert environment.

### **REFERNCES**

1. Al-Haidary, A. A., Samara, E. M., Okab, A. B., & Abdoun, K. A. (2013). Thermophysiological responses and heat tolerance of Saudi camel breeds. *Int. J. Chem. Env. Biol. Sci*, 1, 173-176.

- 2. Bowler, K. (2008). Acclimation, Heat shock and hardening. Journal of Thermo Biology, 30(2),125-130.
- 3. Branden, C., & Tooze, J. (1991). Introduction to Protein Structure. New York: Garland Publishing
- 4. Collins FS, Guyer,MS and CharkravartiA(1997). Variations on a theme: cataloging humanDNA sequence variation. *Science* 278,1580–81.
- Garbuz, D. G., Astakhova, L. N., Zatsepina, O. G., Arkhipova, I. R., Nudler, E., & Evgen'ev, M. B. (2011). Functional organization of hsp70 cluster in camel (Camelus dromedarius) and other mammals. *PLoS One*, 6(11), e27205.
- 6. Evgen'ev, M. B., Garbuz, D. G., Shilova, V. Y., & Zatsepina, O. G. (2007). Molecular mechanisms underlying thermal adaptation of xeric animals. *Journal of biosciences*, *32*(3), 489-499.
- 7. Helen, M.B. (2004). The stress of dying: The role of heat shock proteins in the regulation of apoptosis. Journal of Cell Science, 117:2641-2651.
- 8. Huiquang W., Xuanmin G. and JunW(2015). Camelid genomes reveal evolution and adaptation of desert environments. Nature Communication, 5, 5188.
- 9. Jefferys, B.R., Kelley, L.A., & Sternberg, M.J.E. (2010). Protein Folding Requires Crowd Control in a Simulated Cell Journal of Molecular Biology. 397(5), 1329-1338.
- Jones, D.T. (1999). Protein secondary structure prediction based on position-specific scoring matrices. J. Mol. Biol. 292, 195-202
- 11. Kelley, L.A., & Sternberg, M.J.E. (2009). Protein structure prediction on the Web: case study using the Phyre server. *Nature Protocols*, 4 (3), 363–371.
- 12. Sadder, M. T., Migdadi, H. M., Zakri, A. M., Abdoun, K. A., Samara, E. M., Okab, A. B., & Al-Haidary, A. A. (2015). Expression analysis of heat shock proteins in dromedary camel (Camelus dromedarius). *J. Camel Pract. Res*, 22, 19.
- 13. Söding, J. (2005). Protein homology detection by HMM-HMM comparison. Bioinformatics 21, 951-960.