BIOINFORMATICS

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Tardigrade's possible genes of interest

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1   Abstract

Tardigrades are the first known animal to survive in space. Thus we are trying to predict genes, responsible for utterly good DNA reparation, processing results of a TMS (Tandem Mass Spectrometry), looking for proteins that are most likely in a nucleus.

2   Introduction

Tardigrades, fascinatingly resilient microscopic animals also known as water bears or moss piglets, exhibit an unparalleled ability to endure extreme environmental conditions, ranging from the high altitudes of the Himalayas to the abyssal depths of the deep sea. Classified as "extremophiles," they can endure freezing temperatures, complete dehydration, high pressures exceeding 1,200 atmospheres, and radiation levels far surpassing those tolerated by other animals. Notably, tardigrades became the first known animals to survive the harsh conditions of space during the "Tardigrades In Space" (TARDIS) project in September 2007 [1].

This research not only expands our understanding of extremophiles but also holds potential implications for fields such as radiation biology and genetic engineering. Unlocking the secrets encoded in the tardigrade genome may pave the way for innovative strategies to enhance stress resistance in other organisms and even shed light on mechanisms relevant to human health and longevity.

3   Methods

To process our TMS data we create a local database consisting from our short peptides. Then we use local alignment-based search with diamond [2] utility. Diamond blasting showed only 2 genes: g4106.t1 and g12510.t1. Niether of these genes were predicted to be in a nucleus by both TargetP [3] and WoLF PSORT [4]. Also blast with Protein-Protein BLAST 2.5.0 was made, that found 5412 unique genes. The results of blast were sorted by e-value and top 5000 unique genes were filtered out (as TargetP doesn't accept more than 5000 sequences in one query).

4   Results

Results text

5   Discussion

Discussion text

6   Bibliography

References

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[2] B. Buchfink, C. Xie, and D. H. Huson, "Fast and sensitive protein alignment using DIAMOND," *Nature Methods*, vol. 12, pp. 59–60, Jan. 2015.

[3] J. J. A. Armenteros, M. Salvatore, O. Emanuelsson, O. Winther, G. v. Heijne, A. Elofsson, and H. Nielsen, "Detecting sequence signals in targeting peptides using deep learning," *Life Science Alliance*, vol. 2, Oct. 2019. Publisher: Life Science Alliance Section: Methods.

[4] "WoLF PSORT: Protein Subcellular Localization Prediction."