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Research Article

A COMPARATIVE STUDY OF REPRESSOR ELEMENT 1-SILENCING TRANSCRIPTION FACTOR OF TELEOST FISHES

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ABSTRACT

Objective: Repressor element 1 (RE1)-silencing transcription factor (REST) is a zinc-finger transcription factor or else can be called as neuron-restrictive silencer factor primarily described as a negative regulator of nuclear differentiation at present known to play key function in neuronal cells.

Methods: With this initial note the aim of this study was to determination of protein sequence level characteristics of REST of Japanese pufferfish (*Takifugu rubripes*) and channel catfish (*Ictalurus punctatus*) with the help of different bioinformatical research tools.

Results: There was no instance of any signal signature present within the amino acid sequence of studied REST molecules. In the present research work protein multiple sequence alignment represented in polarity coloring scheme demonstrates variable sites and as well as conserved sites of proteins in Japanese pufferfish and channel catfish.

Conclusion: The current research analysis clearly manifests that protein evolution occurred within the REST of Japanese pufferfish (*Takifugu rubripes*) and channel catfish (*Ictalurus punctatus*).

Keywords: Repressor element 1-silencing transcription factor, Teleost fishes, Japanese pufferfish, Channel catfish, Sequence analysis.

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INTRODUCTION

In the recent 21st century, the maintenance of cognitive ability throughout the entire lifespan has been emerged as one of the greatest medical challenges. The development of Alzheimer's diseases (AD) was facing some fundamental quest. Why some particular individual's age with an intact cognitive ability, but in others, the cognitive ability decorated and promoted to the development of AD. Previously, a study has been suggested that the neuronal loss was an integral characteristic of senescence brain. In recent advancement of stereological neuronal quantification technique, it became intelligible that neuronal cell volume and neuronal quantity mostly maintained in the hippocampus and neocortex of the aging human brain. The normal status declined in the onset of neurodegenerative disease [1-4]. For preservation of neurons and cognitive function throughout lifetime, resilient stress response mechanisms must have evolved [5,6]. Repressor element 1 (RE1)-silencing transcription factor (REST) is a repressor of neuronal genes. REST throughout embryonic development is downregulated once terminal neuronal differentiation has occurred [7-9].

REST was found in the regulatory regions of target genes, and it was attached with the 17-33 base pair RE1 regulatory regions of target genes [10-12]. About 2000 genes within the mouse and human genomes have been recognized as direct targets of REST [11,13].

Modern state of the art bioinformatics research practices makes it attainable to address complicated research queries in biological science and medical science [14-17]. With this initial note, the aim of this study was to determination of protein sequence level characteristics of REST of Japanese pufferfish (*Takifugu rubripes*) and channel catfish with the help of different bioinformatical tools.

METHODS

The primary amino acid sequences of REST proteins were obtained from the National Centre for Biotechnology Information (NCBI) (http://ncbi/nlm/nih.gov) [18]. SignalP 4.1 server was used for the detection of signal peptide within protein sequences (http://www.cbs.dtu.dk/services/SignalP/) [19]. Amino acid sequence characterization of REST including number of amino acids, amino acid composition (%) profile, and a number of positively charged (Arg+Lys) and negatively charged (Asp+Glu) amino acid residues were calculated upon the FASTA sequences of mature protein molecules. Multiple sequence alignment was performed with the help of Clustal X program, followed by manual inspection for errors [20]. Protein aligned sequence sets were represented in polarity coloring scheme using Jalview tool [21].

RESULTS AND DISCUSSION

REST is a zinc-finger transcription factor or else can be called as neuron-restrictive silencer factor primarily described as a negative regulator of nuclear differentiation at present known to play a key function in neuronal cells [7,22-24].

The factors on which the REST target genes depend are as follows:

1. Accessibility of the specific DNA binding sequences
2. The binding affinity
3. The competition and cooperation with other transcription factors [25,26].

After binding with DNA, REST function is to assemble and position the complex that consists of important enzymes such as demethylase lysine-specific demethylase 1 and histone deacetylases. These complexes are capable to inhibit the transcription of many genes by changing vital sites of DNA and the histones [27,28]. In the entire life span of humans, these neurons are operative; however, the mechanism that protects against degradation of neurons during aging are still unidentified. Chromatin immunoprecipitation with deep sequencing and study of REST show that it promotes cell death and AD pathology which leads to the appearance of nervous tension of gene. In addition to this, REST protects neurons from toxicity of amyloid protein, oxidative stress, and deletion of REST from the brain

of mouse leading to age-related neurodegeneration [4]. The activity of REST is lost in small cell lung cancer and colon cancer and is well-known to initiate anchorage-independent development in human mammary epithelial cells [12].

There was no instance of any signal signature present within the amino acid sequence of studied REST molecules. The amino acid composition of REST present in Japanese pufferfish (*T. rubripes*) was analyzed (Fig. 1).

The amino acid composition (%) was found to be as: Alanine - 7.1%, cysteine - 2.7%, aspartate - 6.7%, glutamate - 6.8%, phenylalanine - 2.1%, glycine - 6.3%, histidine - 4.2%, isoleucine - 2.0%, lysine - 8.5%, leucine - 5.2%, methionine - 1.7%, asparagine - 5.0%, proline - 8.6%, glutamine - 4.4%, arginine - 6.5%, serine - 8.9%, threonine - 6.2%, valine - 4.7%, tryptophan - 0.1%, and tyrosine - 2.2%. The total number of amino acids that were identified was 954.

The amino acid composition of REST presents in channel catfish (*Ictalurus punctatus*) was analyzed (Fig. 1). The amino acid composition (%) was found to be as: Alanine - 5.9%, cysteine - 3.0%, aspartate - 4.9%, glutamate - 13.1%, phenylalanine - 1.7%, glycine - 3.9%, histidine - 3.2%, isoleucine - 2.4%, lysine - 12.1%, leucine - 4.8%, methionine - 1.2%, asparagine - 4.0%, proline - 4.9%, glutamine - 4.8%, arginine - 7.5%, serine - 8.3%, threonine - 5.9%, valine - 5.8%, tryptophan - 0.2%, and tyrosine - 2.2%.

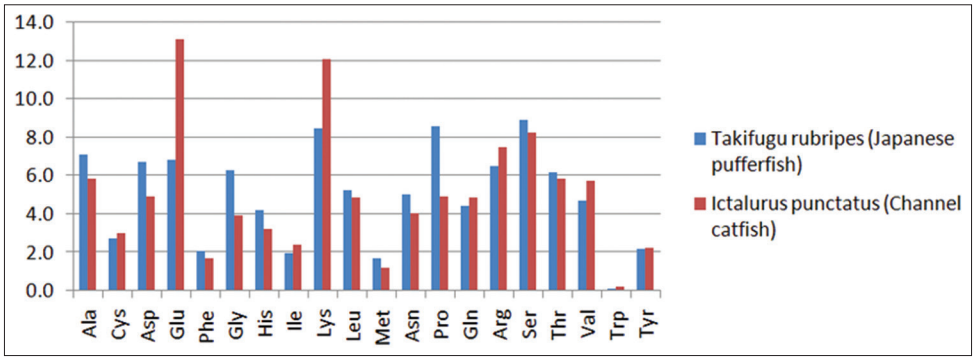

Fig. 1: Amino acid characterization (%) of repressor element 1-silencing transcription factor of teleost fishes

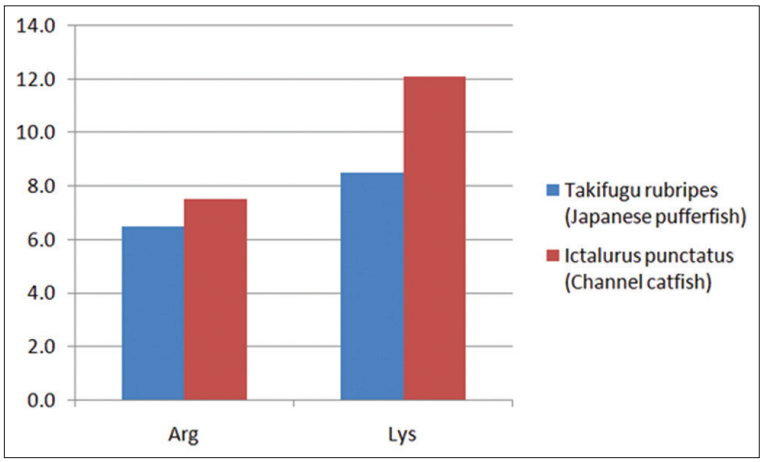

Fig. 2: Positively charged amino acid (%) of repressor element 1-silencing transcription factor of teleost fishes

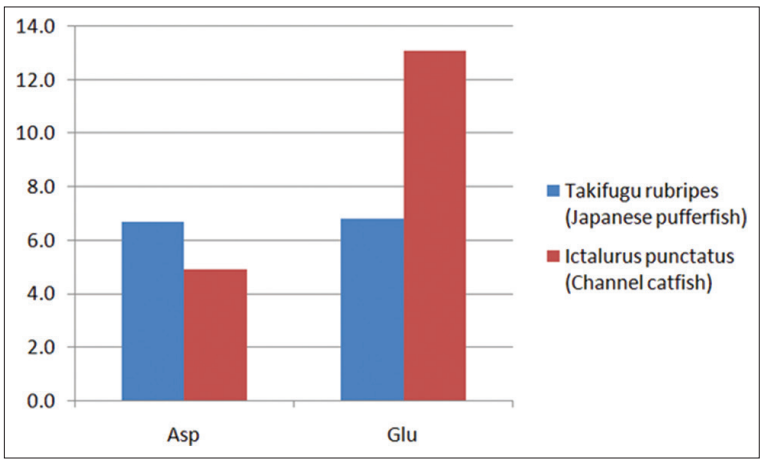

Fig. 3: Negatively charged amino acid (%) of repressor element 1-silencing transcription factor of teleost fishes

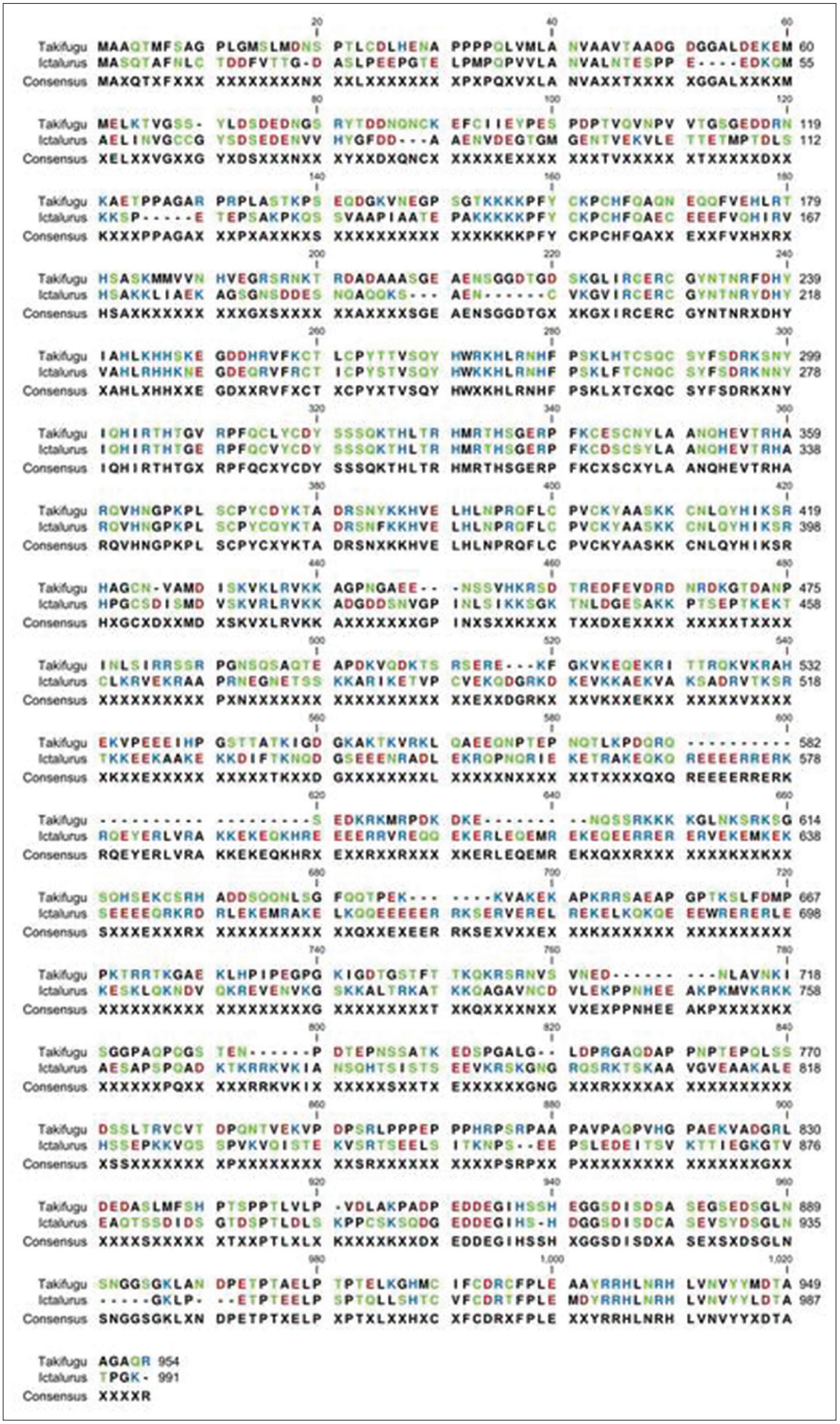

Fig. 4: Multiple sequence analysis of repressor element 1-silencing transcription factor of teleost fishes

The total number of amino acids that were identified was 991. Positively charged amino acid (%) and negatively charged amino acid (%) of REST of teleost fishes were depicted in Figs. 2 and 3.

In the present research work, protein multiple sequence alignment represented in polarity coloring scheme demonstrates variable sites as well as conserved sites of proteins (Fig. 4) in Japanese pufferfish and channel catfish.

CONCLUSION

Proteins are critical structural building blocks of living organisms. Elucidating the causes of deviation in protein evolutionary rates is fundamental for many disciplines including molecular evolution and structural biology. The current research analysis clearly manifests that protein evolution occurred within the REST of Japanese pufferfish (*T. rubripes*) and channel catfish (*I. punctatus*).

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