

Bioinformatics study on translational initiation factor eIF-5a in *Panax ginseng*

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Abstract

Panax ginseng is a commonly used herb in traditional Chinese medicine with a wide range of valuable medicinal usages. Modern pharmacology studies reveal that the *Panax ginseng* has great immune enhancement function. Translation initiation factor eIF-5a is one of its active proteins which have important function. In this paper, several physical and chemical fundamental characteristics such as isoelectric point and the hydrophobicity, etc, of translation initiation factor eIF-5a are studied. The molecular weight of translational initiation factor eIF-5a in *Panax ginseng* is 17221.44, its theoretical isoelectric point is 5.46, the instability index of translational initiation factor eIF-5a is 29.93, it could be concluded that its structure is stable from the results. There is none transmembrane regions and signal peptide cleavage sites in amino acid sequences of the translation initiation factor eIF-5a. Then, the secondary structure, 3D structure and phosphorylation sites of translation initiation factor eIF-5a are predicted. The results show that the number of potential phosphorylation sites of translation initiation factor eIF-5a is 19 (potential value > 0.5). All these result benefit for further study on function and usage of translation initiation factor eIF-5a plant.

Introduction

In traditional Chinese medicine, *Panax ginseng* is a valuable herbal medicine, which has been applied to resist various diseases, contains saponins, sucrose, polysaccharides, amino acids, and so on. *Panax ginseng* has many good effects for health, such as anti-haemostatic [1], anti-tumor [2], antiaging [3], enhancing immunity [4] and antioxidative effect [5], etc; all of these effects can be used to treat disease. Many functions of *Panax ginseng* are explored by lots of scholars. Cesare Mancuso, *et al.* discussed the pharmacology and toxicology of *Panax ginseng*, they tent to think that *Panax ginseng* is benefit to central nervous system, metabolic, infectious and neoplastic diseases [6]. Chia-Rou Yeo, *et al.* studied the isolation and characterization methods of bioactive polyacetylenes *Panax ginseng* [7]. Byong-Kyu Shin, *et al.* explored the chemical diversity of saponins from *Panax ginseng*, they recapitulated the chemical structures and monoisotopic masses of saponins from *Panax ginseng* [8]. Ying Zhou, *et al.* studied the changes in element accumulation and antioxidative enzyme activities in *Panax ginseng*, the authors attend to think that the higher element accumulation activated multiple enzymes related to accumulation of phenolic compounds and their oxidation [9]. *Panax ginseng* in medicine has many effects on human health [10], and it is also used to treat many diseases [11], such as obesity and adipose inflammation [12], chronic obstructive pulmonary disease [13]. In bioinformatics, there are also lots of scientists studied these issues [14], Yun Sun Lee, *et al.* explored the transcriptomes and primary metabolite profiles of different *Panax ginseng* cultivars [15], Ming-Rui Li, *et al.* studied the genetic and epigenetic diversities of *Panax ginseng* [16]. But when the translation initiation factor eIF-5a is concerned, it plays a variety of functions in plant, may effect on cell senescence and death, so the translation initiation factor eIF-5a attracts many scholars [17]. In this paper, main physical characteristic of translation initiation factor eIF-5a in *Panax ginseng* is studied from the bioinformatics view.

Materials and methods

In order to, study the translation initiation factor eIF-5a in *Panax ginseng*, the peptide protein sequences data is download from NCBI (accession number: AIC33055.1). The fundamental characteristics of its sequence and the functional results are respectively studied in this paper.

Fundamental characteristics are studied via the protparam system and protscale system [18], TMHMM online system [19], *et al.* to explore its physical and chemical properties. Then the SignalP system [20], SOPMA online system [21], SWISS-MODEL system [22] and the online system NetPhos [23], *et al.* are used to study its Physiological functions. All prediction data are re-plotting for their aesthetic requirements.

Results and discussion

Physical and chemical properties of the translation initiation factor eIF-5a is studied by protparam system, protscale system, TMHMM online system, *et al.* partial fundamental properties is shown in Table 1. that is number of amino acids is 159, molecular weight is 17221.44, instability index is 29.93, the negatively residues and positively residues respectively are 25 and 19. TMHMM predicted system is used to predict the transmembrane region of translation initiation factor eIF-5a and the result show that there is no transmembrane region in translation initiation factor eIF-5a.

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Table 1. Fundamental properties of translation initiation factor eIF-5a.

Parameter	Perdition results
Number of amino acids	159
Molecular weight	17221.44
Theoretical pI	5.46
Formula	$C_{749}H_{1202}N_{206}O_{244}S_7$
Total number of atoms	2408
Instability index	29.93
Negatively residues (Asp + Glu)	25
Positively residues (Arg + Lys)	19

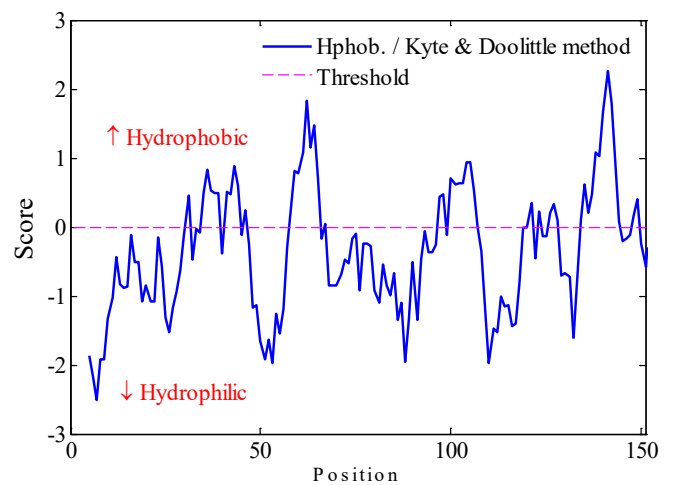
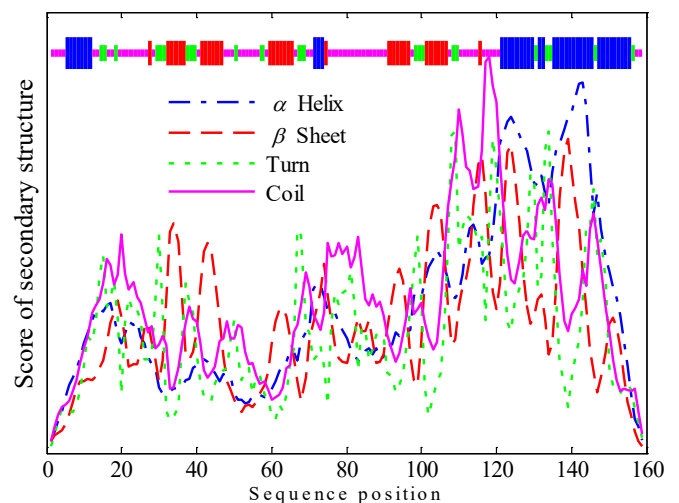
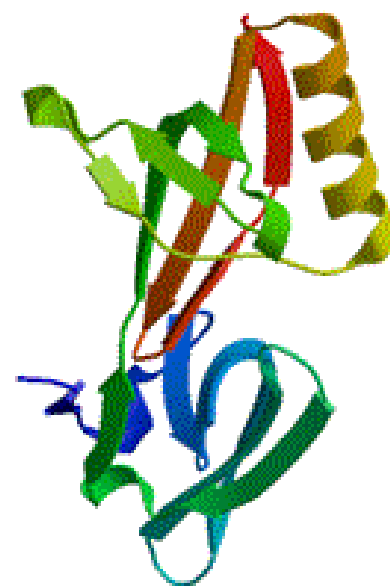
Hydrophobic and hydrophilic in translation initiation factor eIF-5a appears alternately. Hydrophobicity of translation initiation factor eIF-5a is predicted by the Hphob./Kyte & Doolittle scale in ExPASy's ProtScale program with window size = 9. The prediction result is shown in Figure 1, when the vertical value > 0 denotes the hydrophobic area, less than zero is the hydrophilic area. There is an opposite strong Hydrophobicity can be seen in translation initiation factor eIF-5a. It can be seen that there are more hydrophilic residues than the hydrophobic residues in general. Among the whole residues, only 2 absolutely value of residues area are more than 2.

When the function of the translation initiation factor eIF-5a is concerned, SignalP online prediction system is used to predict whether there is any signal peptide in its sequence. The prediction result shows that there is no signal peptide sequence in the translation initiation factor eIF-5a. Then the secondary structure of the translation initiation factor eIF-5a is predicted *via* the SOPMA online system with the parameters: Window width=17, Similarity threshold=8, and the Number of states=4(Helix: 0.5970, Sheet: 0.9710, Turn: 1.5730, and Coil: 0.7740). The result is shown in Figure 2. The result shows that in its secondary state, four rates for each state are: Alpha helix: 25.79%, Beta sheet: 20.75%, Turn: 14.47%, and Coil: 38.99%.

The famous Swiss-Model system is usually used to predict the 3D structure of a protein. The 3D structure of the translation initiation factor eIF-5a here is predicted by the online Swiss-Model system, and the result is shown in Figure 3. From Figures 2 & 3, it could be conclude that the translation initiation factor eIF-5a contains variety of secondary structural units with obvious folding levels, furthermore, the translation initiation factor eIF-5a presents a ellipsoidal entity shape.

Quantitative studies of protein phosphorylation are benefit to the study on their biological activities. The NetPhos protein phosphorylation site is used to predict the phosphorylation sites of the translation initiation factor eIF-5a. The result is shown in Figure 4. The value of serine phosphorylation sites is shown to be high, and there are two high potential Serine phosphorylation sites, three high potential Threonine phosphorylation sites and only one high potential Tyrosine phosphorylation site within the prediction results (potential value>0.8). All of the shown phosphorylation sites are potential value >0.5 and the other phosphorylation sites (potential value <0.5) are neglected.

Recent studies have found that translation initiation factor eIF-5a is closely related to the metabolism of polyamines and the occurrence of tumors, which is one of the hot research areas of concern in recent years. Application of *Panax ginseng* in traditional medicine for antitumor in China has been many years [24]. Lots of scientists have been studied its bio-functions by from different aspect, such as its antitumor and immunomodulatory activity [25], antioxidant activity [26], analgesic [27], anticomplement [28], and so on [29], but the specific mechanism of medicinal ingredients of *Panax ginseng* such as the translation initiation factor eIF-5a is still need further study especially from the perspective of bioinformatics [30].

**Figure 1.** Hydrophobic characteristics of translation initiation factor eIF-5a.**Figure 2.** Secondary structure of translation initiation factor eIF-5a.**Figure 3.** 3D structure of translation initiation factor eIF-5a.

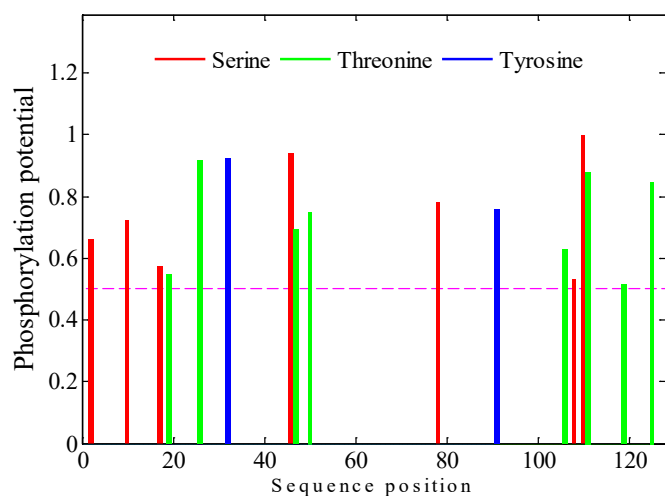


Figure 4. Phosphorylation site prediction results of the translation initiation factor eIF-5a.

Conclusion

Translation initiation factor eIF-5a is prevalent in eukaryotic and prokaryotic organisms. It is a highly conserved protein whose C-terminus is a nucleic acid binding domain, and N-terminus is highly conserved and contains a very unique amino acid. Translation initiation factor eIF-5a plays an important role in the protein translation extension phase by stimulating the activity of the protein involved in the ribosome. The molecular mechanism of the translation initiation factor eIF-5a has not yet been fully elucidated, and further research is needed to deepen the understanding of its function. In this study, the biological information especially the physical and chemical characters contained in translation initiation factor eIF-5a are systematically studied from its sequence, its other properties are predicted via several famous bioinformatics tools, which provided a reference for further research on *Panax ginseng*.

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