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Bioinformatics Study on Sequence Characteristics of β-D-xylosidase in *Glycyrrhiza uralensis* Fisch

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ABSTRACT

Glycyrrhiza uralensis Fisch is a kind of commonly used herb in traditional Chinese medicine. Effective ingredients in *Glycyrrhiza uralensis* Fisch has anti-inflammatory and anti-virus effect. In this paper, the main physical characteristics of β-D-xylosidase from *Glycyrrhiza uralensis* Fisch are studied from the perspective of bioinformatics. The composition isoelectric point and hydrophobicity etc, of the polypeptide are studied by bioinformatics tools. The results show that the molecular weight of β-D-xylosidase in *Glycyrrhiza uralensis* Fisch is 31136.85, the theoretical isoelectric point is 9.56, the instability index is 29.87, the polypeptide does not exist in the transmembrane region, and there are three helical structures in the secondary structure. Finally, this paper summarizes the status and function of *Glycyrrhiza uralensis* Fisch in the development of traditional Chinese medicine.

Keywords: traditional Chinese medicine; β-D-xylosidase; *Glycyrrhiza uralensis* Fisch, Bioinformatics analysis

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INTRODUCTION

Glycyrrhiza uralensis Fisch belongs to euphorbia plants, its leaves alternate with 7 to 17 leaflets. It is a good medicine for the human body especially in Chinese traditional medicine, the medicinal parts are the root and rhizome, and herbs traits are cylindrical with 25 to 100 cm long, 0.6 to 3.5 cm in diameter. Its main functions are detoxification, expectorant cough, abdominal and so on [1, 2]. Recent studies show that the *Glycyrrhiza uralensis* Fisch could improve the phagocytic function of phagocytic cells, regulate the number and function of lymphocytes, inhibit IgE antibody formation, et al. *Glycyrrhiza uralensis* is mainly used to moderate the characteristics of toxic herbs in Traditional Chinese Medicine, which could be partly interpreted as detoxification [3]. The authors also identified experimentally that extracts from Glycyrrhiza uralensis could induce the expression of Nrf2 nuclear protein and its downstream genes. Peter Amwoga Ayeka, et al. thought that *Glycyrrhiza uralensis* is associated with immune-modulating and anti-tumor potential for unknown reason. But they experimentally investigated that the extraction from *Glycyrrhiza uralensis* plays a positive role in preventing the immunomodulation and antitumor [4]. Meanwhile, K. J. Kim, et al. found that the Licoricidin extracted from Glycyrrhiza uralensis Fisher could prevent UVA-induced photoaging of human dermal fibroblasts via its reactive oxygen species (ROS) scavenging [5]. When the bioinformatics is concerned, Keiichi Mochida studied that the genome assembly of *Glycyrrhiza uralensis*. The results of the study showed that the genome sequencing may provide an essential resource for *Glycyrrhiza uralensis* improvement through molecular breeding. The discovery of the study by Keiichi Mochida also indicated that useful genes for engineering bioactive components could be synthesized via biology approaches [6]. Study results by H. Akiyama et al. suggest that extracts from hydroponic and hybrid-cultivated *Glycyrrhiza uralensis* roots are equivalent in safety and efficacy. They also suggest that further studies should be emphasized on the studies on the extracts from wild plant resources [7]. Many functions of Glycyrrhiza uralensis are all explored by lots of scholars [8-10]. In this paper, main physical characteristics of extract (β-D-xylosidase) of *Glycyrrhiza uralensis* Fisch is studied from the bioinformatics view, and the status and function of *Glycyrrhiza uralensis* Fisch in the development of traditional Chinese medicine is also summarized.

MATERIALS AND METHOD

In order to study the application value of *Glycyrrhiza uralensis* Fisch, the related literatures published in PubMed, SinoMed, Embase and so on are summarized and analyzed. In addition, β-

D-xylosidase, the component of the Glycyrrhiza uralensis Fisch is analyzed, the peptide protein sequences data is from NCBI, and the accession number is BAJ51947.1.

Composition, molecular weight, theoretical isoelectric point and other parameters of β-D-xylosidase are investigated via the net [11]: http://web.expasy.org/protparam/. The hydrophobicity of β-D-xylosidase is analyzed by the website at [11] http://web.expasy.org/protscale/. The transmembrane region of β-D-xylosidase is analyzed by using the site [12]: http://www.cbs.dtu.dk/services/TMHMM/. Signal peptide analysis was performed using [13] http://www.cbs.dtu.dk/services/SignalP/. The website [14] http://bioinf.cs.ucl.ac.uk/psipred/ online analysis is used to study on β-D-xylosidase secondary structure information, the peptide curl, folding characteristics and so on. The homology modeling study utilizes the online tools provided at [15] https://swissmodel.expasy.org, and the site can give three-dimensional structural predictions [16]. Through the comprehensive analysis of the literature and the research results of this paper, the specific direction and future prospect of *Glycyrrhiza uralensis* Fisch in traditional Chinese medicine are put forward.

RESULTS AND DISCUSSION

Proteins as macromolecular compounds, are composed of amino acids, some of their physical and chemical properties are similar to amino acids, such as amphoteric ionization, isoelectric point, etc., but there are some difference between the proteins (peptides) and amino acids, such as high molecular weight, complex spatial structure and so on. Protparam system is a famous tool for studying the protein physical and chemical properties, the physical and chemical properties and composition of peptide β-D-xylosidase are respectively shown in Table 1 and Figure 1.

Table 1 Physical and chemical property analysis of β-D-xylosidase

Parameter	Perdition results
Number of amino acids	285
Molecular weight	31136.85
Theoretical pI	9.56
Formula	$C_{1399}H_{2195}N_{389}O_{395}S_{11}$
Total number of atoms	4389
Instability index	29.87

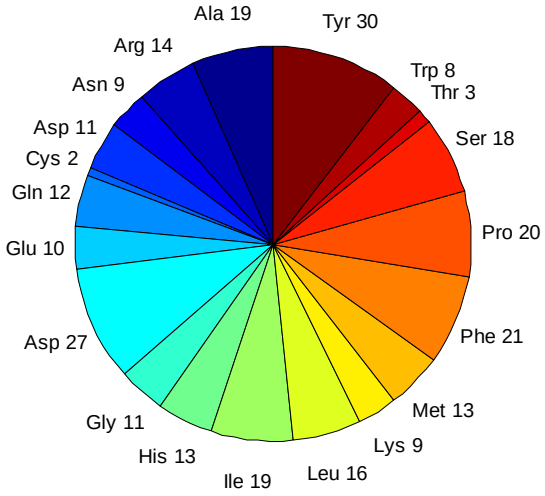

Figure 1: Amino acid composition of β-D-xylosidase

Hydrophobic and hydrophilic balance plays an important role in all aspects of protein structure and function. Hydrophobicity is an inherent characteristic of 20 kinds of amino acids, and it is one of the important factors in determining the final three-dimensional conformation of proteins. The composition of the hydrophobic amino acids in the protein affects the degree of protein folding, and the folding of the protein can be reflected by the hydrophilic sequences distribution. The hydrophobicity map of β-D-xylosidase was calculated using the Hphoh. / Kyte & Doolittle scale in ExPASy's ProtScale program (see Figure 2). Vertical value above 0 denotes the hydrophobic area; below value 0 denotes the hydrophilic area. Coordinate value represents the hydrophobicity score, the higher the score, the stronger the hydrophobicity, and the abscissa value represents the position of the amino acid sequences. As can be seen from Figure 2, the number of hydrophobic and hydrophilic amino acid residues of the peptide chain of β-D-xylosidase is approximately equal, and the peptide is biased towards neutral.

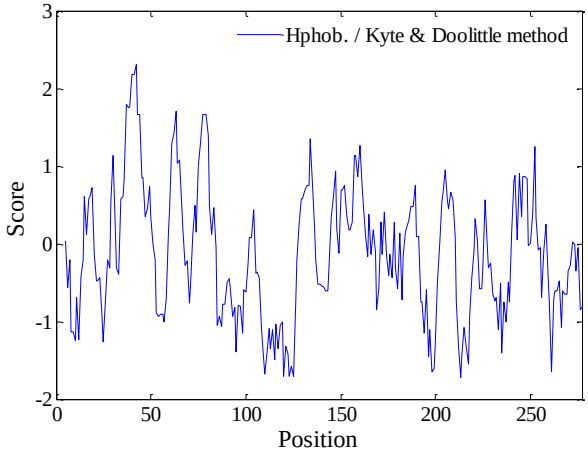

Figure 2: Hydrophobic characteristics of β-D-xylosidase

The transmembrane region of a protein refers to a portion of a protein that binds to the membrane lipid in the membrane, and most of the amino acids that make up the protein in the transmembrane region are hydrophobic amino acids. TMHMM is a kind of transmembrane helix prediction algorithm based on hidden Markov model. The transmembrane region of β-D-xylosidase predicted via TMHMM is as shown in Figure 3. The results show that transmembrane region does not exist in β-D-xylosidase, and the polypeptide is in an off-membrane position.

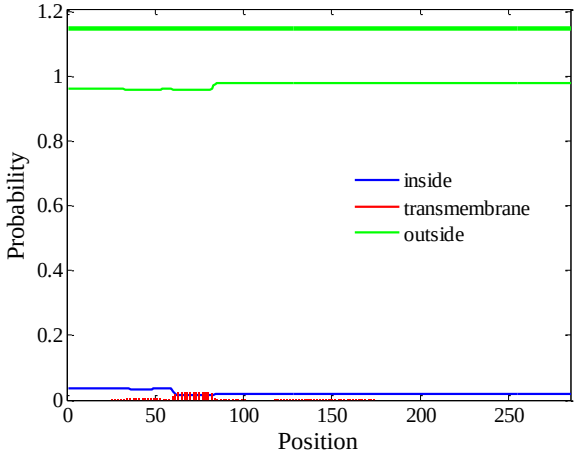

Figure 3: Transmembrane region prediction of β-D-xylosidase

The signal peptide is a short peptide that secures extracellularly proteins from cells to extracellular. Its typically length is 5-30 amino acids. SignalP is a useful tool for predicting the potential signal peptide cleavage sites in a given amino acid sequence based on the neural network algorithm. Signal peptide position of β-D-xylosidase calculated via SignalP is shown in Fig.4. C-score is the signal peptide cleavage site value, the C-score of shear position is generally the highest; S-score is the signal peptide value, the S-score of signal peptide region is generally highest; Y-score is the integrated score of shear point. Predictive results show that S-score of β-D-xylosidase is much smaller than the secretory protein standard value 0.5, which denotes that there is no signal peptide in β-D-xylosidase.

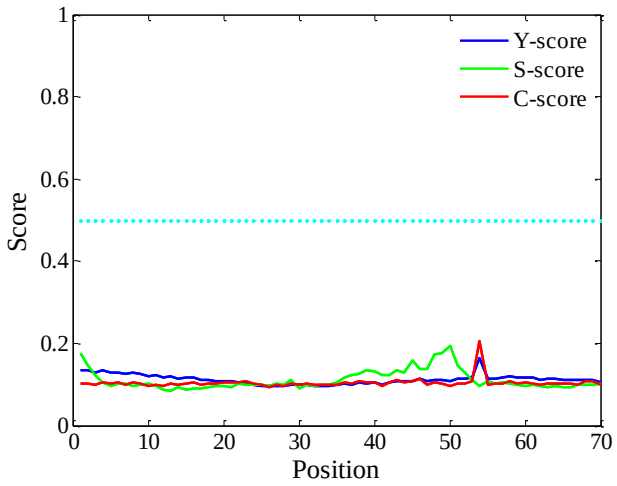

Figure 4: Signal peptide analysis of β-D-xylosidase

The Psipred prediction system is used for predicting the Secondary structure prediction for theβ-D-xylosidase. The Psipred prediction system uses blast homoperation, so the Psipred method is more reliable. Partial (1-120 amino acid residues) secondary structure predicted results of (via Psipred prediction system) β-D-xylosidase are shown in Figure 5.

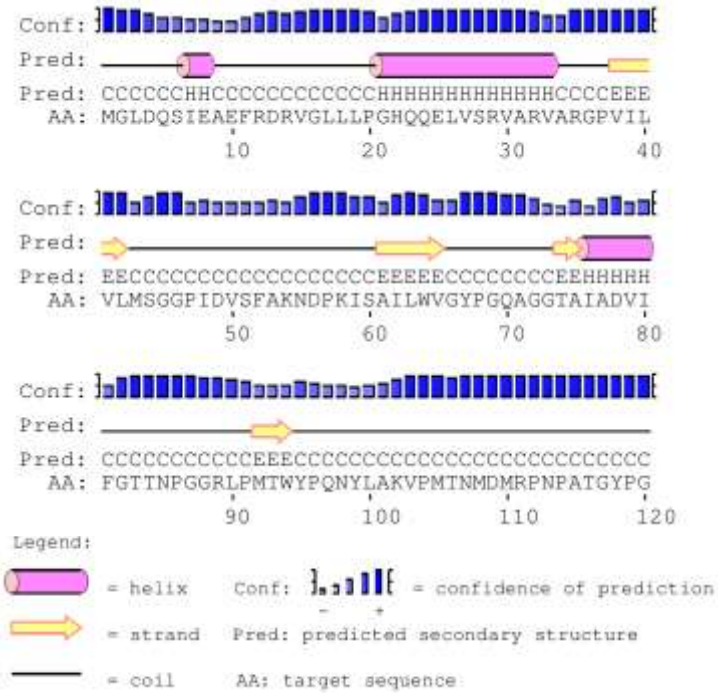

Figure 5: Secondary structure prediction (1-120 sequences) of β-D-xylosidase

Swiss-Model is the most widely used online modeling site, structures can be predicted by the site for its homology modeling system. At the same time, the Swiss-Model system also provides an algorithm to predict the three-dimensional structure of the polypeptide. The algorithm is used to predict the three-dimensional structure of β-D-xylosidase (see figure 6). As can be seen from Fig.

6, β-D-xylosidase is mainly composed of β-sheet, and there are still some small helical structures. In the figure, it also can be seen that there is no signal peptide in the structure.

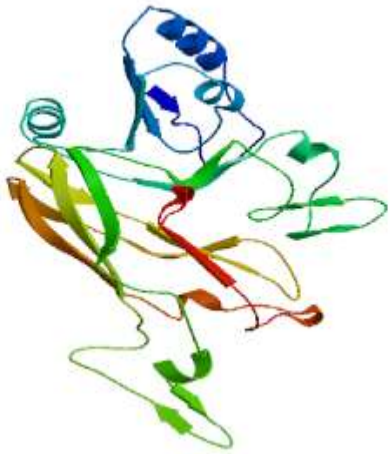

Figure 6: Tertiary structure of β-D-xylosidase

With the rapid development of genomics, and by experimentation or bioinformatics tools, the protein coding can be annotated and predicted, so a large amount of data for protein function has been accumulated. Although protein and related techniques can be used to obtain large amounts of protein expression data in the body and analyze its function, we currently know a large number of protein products (by gene), but studies on the function of them are relatively backward. For *Glycyrrhiza uralensis*, its application in traditional medicine in China has been a few thousand years of history. Although many scientists study its function from different aspect [17-21], in fact, for the specific mechanism of medicinal ingredients of *Glycyrrhiza uralensis*, it still need further study.

CONCLUSION

Since it is relatively cumbersome to determine the location of proteins in cells by experimentation, it is valuable to determine or predict the cellular localization of protein molecules by bioinformatics. The presence of a signal peptide or other target peptide fragment can help us to understand the possible localization of the protein in the cell, the other characteristics of the protein sequence can also be studied to reveal their localization in the cell because a large number of protein sequences do not include a typical target peptide fragment. In this study, the biological information contained in β-D-xylosidase systematically studied from the sequence of β-D-xylosidase, the basic physical and chemical properties of it is predicted, which provided a reference for understanding *Glycyrrhiza uralensis*. The three-dimensional

structure of the β-D-xylosidase is predicted too in order to understand the structural characteristics of β-D-xylosidase and reveal for further use of *Glycyrrhiza uralensis* in medicine.

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