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《林木蛋白质组学研究》适用于生物化学、分子生物学和遗传学专业及所有对蛋白质组学感兴趣的大学师生、科研人员和研究生参考。

内容简介

针对蛋白质组学研究热点、难点问题，《林木蛋白质组学研究》主要汇聚了《林木蛋白质组学研究》组近年来在林木蛋白组学方面的研究进展和部分成果。主要内容包括蛋白质组学在林木生长发育、非生物逆境胁迫（干旱、高温、低温）、适应性进化等方面的研究内容。

作者简介

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前言

媒体评论

在线试读部分章节

Chapter 1 Advances in Proteomics Research on Forest Tree

Abstract: Forest plays an important role in maintenance of ecosystem equilibrium and provides material energy. It has a set of mechanism of its own growth, development, and metabolism. Proteomics is a crucial means to reveal the material life phenomenon in biology nowadays. In this chapter, the trend of technical system of proteomics, such as extraction, separation, identification method of protein, was introduced and existing problem was indicated. In addition, different research direction of forest proteomics (i.e. tress response, wood formation, developmental regulation, pest control) were discussed respectively combined with overseas research. Finally, the prospect to its future development was given.

1.1 Introduction

With the advent of the post-genome era, proteomics have been a rapid development. Compared with genomics, proteomics can provide some unparalleled advantages. Firstly, it more accurately identifies the proteins and obtains related functions. Secondly, the “ one gene, one protein (or function) ” hypothesis is thus not applicable at present time, to a certain extent, proteomics can detect post translational modifications (PTMs) (Agrawal and Rakwal, 2006). Although proteomics research has been used on a large number of species, it mainly concentrated on model species and animals. About less than 5% of species was plant which focused on model plants such as Arabidopsis (*Arabidopsis thaliana*), wheat (*Triticum aestivum*), rice (*Oryza sativa*) and maize (*Zea mays*), poplar (*Populus trichocarpa*), etc. (Jorr í n-Novo et al., 2009; Oeljeklaus et al., 2009). The species involved in the forest were less, which is disaccord with forestry importance in the ecosystem. Due to global climate change, energy shortages, the contradictions between human and nature will stand out in the future. Forestry role in human life will strengthen increasingly. So, it is a very meaningful work to spread proteomics research on forest trees to solve production problems. In this section, the research progress of proteomic technology system and hot research topics are being reviewed. Finally, the prospect of proteomics research in the forestry is discussed.

1.2 Research progress on proteomic technology system

1.2.1 Protein extraction method Chapter 1 Advances in Proteomics Research on Forest Tree

Abstract: Forest plays an important role in maintenance of ecosystem equilibrium and provides material energy. It has a set of mechanism of its own growth, development, and metabolism. Proteomics is a crucial means to reveal the material life phenomenon in biology nowadays. In this chapter, the trend of technical system of proteomics, such as extraction, separation, identification method of protein, was introduced and existing problem was indicated. In addition, different research direction of forest proteomics (i.e. stress response, wood formation, developmental regulation, pest control) were discussed respectively combined with overseas research. Finally, the prospect to its future development was given.

1.1 Introduction

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1.2 Research progress on proteomic technology system

1.2.1 Protein extraction method

Extraction of high concentration and high purity protein is the most important in the process of the whole proteomics research. Because proteins include many complex biochemical properties, such as charge number, molecular weight, hydrophobicity, hydrophilicity, post-translational modification, and interaction with other molecules, and these properties are changed along with the species difference, such as developmental stages, cell and tissue types, and different growth conditions, many protein extraction methods were established. Harvesting the maximum amount of protein to match protein analysis (such as liquid chromatography and mass spectrometry) and protein identification is the most perfect method (Sheoran et al., 2009). It is a challenging to extract protein from plant tissues or cells, because of abundant metabolites and complex cell structure, for example the presence of plant cell walls. Usually, the protein content in plant cell is relatively low, and most of these proteins are proteases and oxidative enzymes (except dormant seeds and pollen) (Jamet et al., 2006), the metabolites of plant cells (such as pigments, phenolic mixture, lipids, polysaccharide) has a wide spectral range, these metabolites can cause pollution during protein extraction, which will impact protein separation and following analysis (Jamet et al., 2006). So far, a lot of protein extraction methods have been reported, phenol method and trichloroacetic acid- acetone precipitation method (TCA method) are commonly used in many plant tissues (Carpentier et al., 2005; Delaplace et al., 2006; Giavalisco et al., 2003). Extraction of membrane proteins, low abundance proteins and hydrophobic

proteins is the main bottleneck of conventional extraction methods (Lilley and Dupree, 2006). Thus, many researchers have improved on it, such as Bio-rad company developed ProteoMiner low-abundance protein enrichment kits (Walton and Jayaraman, 2009); a cysteine shotgun method was used to probe the protein structure (Johnson et al., 2007; Tsai et al., 2008); microfluidic devices were used to separate and concentrate proteins in the bacterial cells (Bao and Lu, 2008), which is based on the principles of physics rather than chemical and biological reactions. Electrophoresis and microfluidic technology is also been used for sample preparation (Walton and Jayaraman, 2009). The general principle is as follows: firstly, preconcentrate low-abundance proteins using polydimethylsiloxane equipment, then isoelectric focusing (IEF) electrophoresis separates proteins, finally SDS-PAGE separates proteins based primarily on molecular weight, which is the three-dimensional gel electrop

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