Scholar Publishing Group
Academic Journal of Agricultural Sciences
https://doi.org/10.38007/AJAS.2022.030407
ISSN 2789-8415 Vol. 3, Issue 4: 89-103

The Physiological Mechanism of Plant Stress Based on Different Protein Composition

Xiang Zeng*

Nanjing University of Vocational Industry Technology, Nanjing, China

**corresponding author*

Keywords: Differential Proteomics, Plant Stress Growth Mechanism, Active Natural Products, Defense Mechanism

Abstract: Different Proterozoic have different applications in physiological mechanisms of plant stress. Plant proteins have strong responses to abiotic stresses such as drought, salt stress, low temperature, and anaerobic stress, as well as biological stresses such as pests, bacteria, and fungal infections. Mechanism, with different effects in different physiological mechanisms. The purpose of this article is to better understand the damage mechanism of plants after being stressed. By studying the adaptation and defense mechanisms of plants to the environment, this article uses genetic algorithms to conduct proteomics research on differential proteomics, analyze their differences, and Experimental analysis of the growth mechanism of plants in adversity. Use mathematical analysis and mathematical statistics to statistically classify the data. Use big data to fit the data. Then, through different protein composition, the physiological mechanism of plant stress Research experiments analyze the different effects. The experimental data show that in the more adverse environment, the stronger the plant's self-protection, the more proteins transcribed to adapt to the adverse environment. The experimental results show that different protein compositions play a pivotal role in the physiological mechanism of plant stress. The use of proteins has a protective effect on the plant's adversity. The research results have been applied to the growth of plants, which has increased the growth rate of plant colors by about 15%. It laid a solid foundation for future research on physiological mechanisms of adversity.

1. Introduction

Different proteomics have different applications in the physiological mechanism of plant adversity. Different organisms have different self-protection and responses in different adversity environments. Therefore, studying the situation of plants in different adversity environments is

currently the hot topic Different from the genome, the proteome as a whole, the types of proteins expressed by different cells in different physiological or pathological states are different. Proteins are the implementers of gene functions, and therefore they have an important role in protein structure, location and protein-protein interaction The research will provide a direct basis for clarifying the nature of life phenomena. Differential proteomics is an important part of proteomics research, including the expression patterns and functional patterns of specific proteins, and is an important tool for studying plant physiology, development, and genetics. Differential proteomics focuses on the screening and identification of differences and changes in proteomes between samples in different species or states, which is a very important research direction.

At present, research on plant protein expression profiles under different conditions in China is increasing, and many genes related to gene mutation, development,Adversity, new proteins (or genes) that interact with plants and microorganisms, but there are few reports that further prove the function of these new proteins (or new genes). The idea of proteomics research should be shifted from protein expression to protein function research [1-2]. Therefore, using functional genomics and biochemical methods to further confirm new protein functions will be the direction of future plant proteomics research. At present, the main research method of differential proteomics is still the combined application of 2D-E separation and MS identification. The 2D-E-based method makes up for the weakness of 2D-E and is more suitable for differential proteomics research. In addition to 2D-E technology, several other technical means, such as multi-dimensional liquid chromatography separation technology, ICAT technology, protein chip technology and other differential proteomics research technologies can be used as a complement to 2D-E technology [3].

Anderegg L D L found that range change is one of the most common ecological responses to anthropogenic climate change, with major consequences for the ecosystem. Unfortunately, the ecophysiological forces that limit the boundaries of a range are difficult to understand, so it is difficult to predict range changes mechanically. In order to explore the physiological mechanisms of drought stress to control the drought range boundaries of trees, Anderegg LDL and other scholars quantified the altitude variation of drought resistance and drought-related functional traits of a widely-existing gymnosperm, Ponderosa pine and angiosperms (trembling poplar- Populus tomentosa) a tree species of the southwestern United States. Specifically, they quantified growth, water stress (xylem tension before dawn and noon), drought resistance (branch conductivity, leaf / conifer size, tree height, leaf area, and leaf area and Changes in sapwood area ratio) and drought resistance (xylem plug resistance, hydraulically safe edges, wood density). Although the water stress of the two tree species increases and grows at the lower edge of the range, the yellow pine and poplar show different patterns of clinical trait variation. Anderegg L D L found that trembling aspens increased the drought resistance of their hay edges by growing stronger but higher carbon density branches and leaf tissues, which meant increasing growth costs within their growing range [4]. Wang X found that plant drought tolerance is a complex trait and requires a global perspective to understand its underlying mechanisms. The proteomics aspects of plant drought response have been extensively studied in model plants, crops, and wood plants. Wang X discovered proteomics studies on leaf drought response in recent years. Wang X revealed the drought response mechanisms of different plants. Although drought-responsive proteins show different types, proteomic analysis shows that in terms of perception and signal transduction, clearance of reactive oxygen species, osmoregulation, gene expression, protein synthesis / transformation, cell structure adjustment, and carbohydrate and energy metabolism Both have undergone significant changes. Wang X believes that combined with physiological and molecular results, leaf proteomics studies can help identify some potential drought-tolerant proteins and / or metabolic pathways. These findings provide new clues for understanding the molecular basis of plant drought tolerance [5].

The study of current plants based on the physiological mechanisms of plant stress in different

protein composition studies has a guiding role in the development of plants. The purpose of this article is to better understand the damage mechanism of plants after being stressed. By studying the adaptation and defense mechanisms of plants to the environment, this article uses genetic algorithms to conduct proteomics research on differential proteomics, analyze their differences, and Experimental analysis of the growth mechanism of plants in adversity. Use mathematical analysis and mathematical statistics to statistically classify the data. Use big data to fit the data. Then, through different protein composition, the physiological mechanism of plant stress Research experiments analyze the different effects. The experimental data show that in the more adverse environment, the stronger the plant's self-protection, the more proteins transcribed to adapt to the adverse environment.

2. Proposed Method

2.1. Plant Growth Characteristics in Different Environments

Environmental conditions and adverse factors often have significant adverse effects on plant growth and development, and even cause plant death. Abiotic stress (including causing certain physical or chemical conditions, such as salt plant stress, cold damage, drought, high impact temperatures, heavy metals And mechanical damage, etc.) and biological stress (by various biological factors such as fungi, bacteria, viruses, nematodes, dodder, etc.). In the prior art process devices, very complex changes in physiological and biochemical and molecular and cellular levels on the indicator body occur [6-8]. As a very complicated physiological change process, the molecular mechanism of plant stress response has not been fully elucidated after being stimulated. Plant stress is regulated by the outside world through a series of signaling molecules to regulate the expression of related genes and proteins, and its appearance And physiological changes in biochemical levels to adapt to adversity [9-11]. Mining, therefore, important artistic genes (proteins) to analyze the molecular mechanism of technology and further cultivate plant varieties have important significance [12-14]. Using proteomics techniques to quantitatively change the relationship between qualitative and protein, proteins, and stress responses, not only can identify the protein factors related to the existing technology, but also reveal the relationships between them to help people understand plant stress and physiological responses more comprehensively. The host defense relationship, biochemical and molecular biology stress response signal response mechanism, is a response to the study of plant stress [15-17]. Plants proteomics have been commonly used methods in recent years, including Arabidopsis, rice, corn, barley One of the important content of wheat and soybean, various major plants respond to biological stresses such as fungi, bacteria, viruses and proteomics of nematodes and the latest research on the molecular mechanism of PR to further understand plant resistance would also be beneficial The selection and breeding of varieties resistant to plant biological stress, the growth conditions are shown in Figure 1:

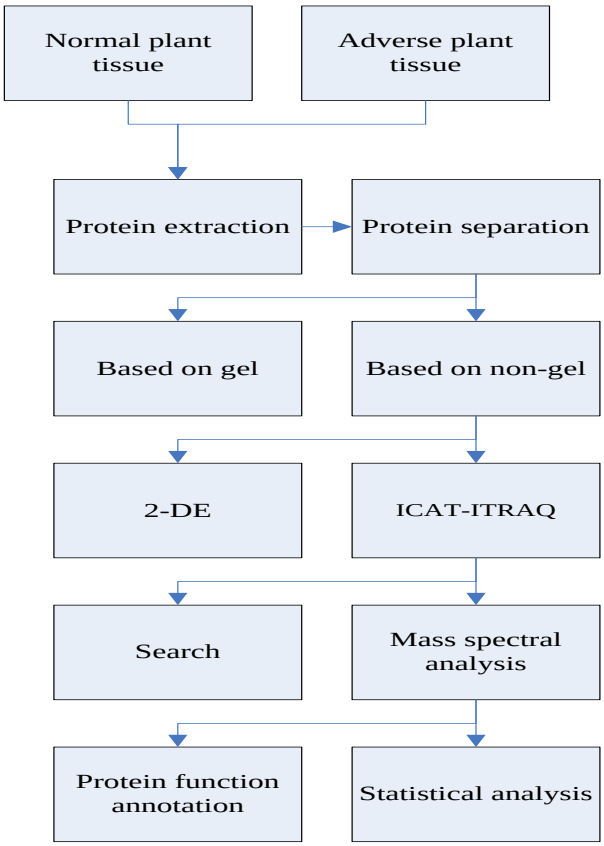

Figure 1. Experiment flow

2.2. Proteomics Research Methods in Plant Biology

Generally speaking, in the early stage of research on plant differential proteomics, various appropriate methods need to be adopted to extract proteins from normal plants and control plants separately, and then isolate and identify the proteins. At present, the commonly used research methods can be mainly divided into two proteomics research lines based on gel and non-gel respectively [18-20].

2.3. Study on the Use of Plant Proteins in Adverse Environments

Calculation of filtration thickness in the filter layer:

$$L = \frac{\lg（N_2 / N_1)}{K} \tag{1}$$

Filter diameter: D

$$D = \sqrt{\frac{4V}{0.1\prod}} \tag{2}$$

Basic filtering equation:

$$\frac{\mathrm{dq}}{\mathrm{d}\tau} = \frac{1}{\mathrm{u}} \frac{\Delta \mathrm{p}}{\mathrm{rl} + R} \tag{3}$$

Required Box Size:

$$V_{\mathrm{p}} = N \times A \times B \times H \tag{4}$$

Number of plant cell extractors required :

$$\mathrm{n} = \frac{V_F \times E}{K \times V_P} \tag{5}$$

Competition inhibition among plant cells :

$$\frac{\mathrm{k}}{\mathrm{m}}(1+\frac{\mathrm{I}}{\mathrm{K_i}}) \tag{6}$$

Non-competitive inhibition between plant cells :

$$\frac{1}{\mathrm{v}}(1+\frac{I}{\mathrm{k_i}}) \tag{7}$$

No competitive inhibition :

$$-\frac{1}{\mathrm{K}}(1+\frac{I}{K_{\mathrm{i}}}) \tag{8}$$

No competitive inhibition :

$$V_X = (0.77+31.244) \times \frac{T_2}{T_1} \times \frac{P_1}{P_2} \tag{9}$$

Value-added coefficient of plant cells :

$$Q = V_G \times P \times C \times \Delta T \tag{10}$$

Selected from the expressed protein at all time points of relative quantification using the traq technique. at different time points, proteome changes in three cultivars reflected different physiological responses to drought stress. The results showed that pre-stress treatment, proteome, proteome RAC875 experienced no significant changes in the sword.

2.4. Features and Research Methods of Proteomics

(1) Proteomics takes proteomics as the research object.It analyzes the composition, expression level and modification status of proteins, understands the interactions and connections between proteins, and studies the rules of protein regulation of life activities at the overall level. From the functional level, it explores the laws of life activities and explains unknown life phenomena. It has made outstanding contributions to exploring the expression patterns of known genes and proving the stress resistance of plants [21-23].

(2) Proteomics research methods Previously, research methods for proteomics mainly used different antibodies to find proteins in a mixture. This method was not only costly but also time-consuming, which greatly restricted the development of proteomics. Protein two-dimensional electroplate protein two-dimensional electroplate technology is based on the isoelectric point of the protein in the first isoelectric focusing electrophoresis; then it is transferred to SODS-poly

acrylamide gel and separated according to the relative molecular weight. Proteins have different isoelectric points, so by setting different pH gradients, proteins can be aggregated at different pHs according to different isoelectric points to complete the first-direction separation.In addition, SDS can make proteins with different amounts based on different molecular weights. Charge so that proteins can be separated based on molecular weight. Through the combination of these two electrophoresis technologies, proteins form thousands of points on a two-dimensional map, and proteins can be separated for identification in a large throughput [24].

(3) Protein mass spectroscopy With the development of mass spectrometry technology, scientists have begun to apply mass spectrometry technology to protein analysis. The principle is to use different mass-to-charge ratios of each protein or peptide in the mass spectrometer to have different movement times, so that these proteins Or peptides for data collection analysis. Protein mass spectrometry methods can be divided into two categories. The first is quantitative proteomics labeled with stable isotopes, such as iTRAQ and TMT; the second is unlabeled quantitative technology, such as label-free. In general, the iTRAQ method is more accurate, but has strong restrictions on samples and is suitable for small samples; although the label-free technology can detect more samples at one time, the reproducibility of this technology will be lower [25].

2.5. Comparative Proteomics Characteristics of Abiotic Stress

(1) Differences in protein expression of plants under salt stress In recent years, the area of secondary saline-alkali land has expanded, and the demand for saline-tolerant plants has been increasing. In the process of adapting to salt stress, plants gradually evolved regulation methods and metabolic mechanisms such as Na + compartmentalization and accumulation of osmotic protective substances. The use of proteomics to study the differences in protein expression types and contents between wild-type and salt-tolerant types has significant ecological and economic effects on studying the salt tolerance of cultivated plants and screening salt-tolerant plants. Plants' perception of salt stress mainly depends on the transfer of protein kinases.For example, under high salt conditions, the plant's root cell wall and the protoplasmic are rigidly separated.This mechanical movement separation will be recognized by mechanical sensors and converted into chemical signals. Through the MAP cascade pathway, P44MMK4 kinase is activated and then passed down, causing changes in ion levels, and receptor protein kinases have similar effects. Proteomic analysis of salinity tolerance in plants of the red sea limpet and jujube tree found that the expression of proteins involved in isoprene synthesis was up-regulated and that of basic metabolism-related proteins was down-regulated. Too much salt ions will cause plant body ions to be imbalanced, but some plants can restrict the excessive salt ions to the vacuole or excrete them by up-regulating the expression of membrane transporters such as vacuole H + -ATPase or Na + / H + transporter. cell. The results of two-dimensional electrophoresis analysis of corn leaves showed that the expression levels of stress response protein and thyroidal cavity 19KDa protein were significantly down-regulated. Similar conclusions were also expounded in the fruit tree salt stress experiments, and the increase in Cl-plasma levels led to toxic effects on plants. Therefore, under salt stress, the normal life activities of plants will be severely disturbed. The impact on plants is mainly to reduce the level of photosynthesis, the toxic effects of some ions, and the ability to regulate the growth of plants, which will lead to metabolic disorders in plants. .

(2) Differences in protein expression in plants under drought stress

In recent years, as desertification has become more serious year by year, the demand for drought-resistant plants has increased. The direct effect of drought on plants is that the lack of water causes stoma ta to close, reducing transpiration, hindering the upward transport of water and inorganic salts in the roots; the strong light accompanied by drought often has a certain degree of

damage to chlorophyll; the water balance is damaged, Leaf greening; cell growth slowed; reduced metabolism promoted protein synthesis; decreased expression of Tabasco peroxidase and catalase led to hydrogen peroxide accumulation. Studies on white mustard showed that, under severe drought, the decline in the levels of chlorophyll a-b binding proteins and other light-complementing proteins severely impaired chloroplast light capture and photo system function, accompanied by a decrease in water content, leading to a decline in photosynthesis rates. The plant's drought resistance is mainly manifested by the accumulation of breathalyse in cells, changing the conformation of some enzymes involved in photosynthesis, up-regulating the expression of proteins with thermal stability or protection, changing the expression of stress and signaling genes, and strengthening the cell wall Inhibit the metabolism of organic matter and protect the body protein from damage. Different from salt stress, plants have a complete set of protection mechanisms for photosynthetic enzymes and heat-natural proteins in the face of mild drought stress.The main manifestations are: the expression of PSI and PSII peripheral proteins is up-regulated to maintain light Systemic activity; under regulation, the expression of Rubicon enzyme decreases first and then increases, and the expression of Rubisco activating enzyme in potato leaves is increased, which has the role of carbonation to protect the active site of Rubisco enzyme to protect; protein kinases, enzymes, and molecular partners participate The plant's drought resistance process and the protection and expression of key proteins have been maintained, and the survival status and time of plants under drought conditions have been maintained and extended. A relatively complete regulatory system has been formed. With the development of mass spectrometry technology, scientists have begun to apply mass spectrometry to protein analysis. The principle is to use different mass-to-charge ratios of each protein or peptide to have different movement times in the mass spectrometer, so that these proteins or peptides can be analyzed. Data acquisition and analysis. Protein mass spectrometry methods can be divided into two categories. The first is quantitative proteomics labeled with stable isotopes, such as iTRAQ and TMT; the second is unlabeled quantitative technology, such as label-free. In general, iTRAQ's method is more accurate, but has strong restrictions on samples and is suitable for small samples; although label-free technology can detect more samples at one time, the reproducibility of this technology will be lower.

3. Experiments

3.1. Experimental Identification of Plant Proteins in Various Adverse Environments and Multiple Adverse Environments

The compositional charge structure was analyzed according to the difference of the mass charge ratio m/z of the sample ions. mass spectrometry was used to reveal the phosphorylation sites of many proteins in the photosynthetic system ii complex and to compare stress (e.g., heat excitation) with protein phosphorylation sites under normal conditions, providing scientific data for studies of chloroplast function under stress conditions. identification of differential proteins isolated by 22de gel electrophoresis using peptide quality fingerprinting and database retrieval methods has the advantages of low consumption and high efficiency, and is suitable for large-scale and high-throughput protein identification work. The peptide sequence can be read out directly by using tandem mass spectrometry. become the technical pillar of protein identification. Tandem mass spectrometry and isotopic labeling are used in differential proteomics studies to directly quantitatively analyze differences in protein expression levels by skipping the electrophoretic separation process. Although the technology is still in the exploratory stage, it has great potential for application. The development of other new mass spectrometry has also developed towards high sensitivity, high accuracy, high analytical speed and stronger multistage mass spectrometry.

3.2. Experimental Steps for Protein Separation

(1) Separate differential proteins by electrophoresis in two different directions according to the isoelectric point and molecular weight of the protein.

(2) The differential proteins are mainly characterized by changes in electrophoretic mobility, the emergence or disappearance of protein dots, and the enhancement or reduction of concentrations.

(3) The differential expression of proteins in two wheat varieties of slow stripe rust and high stripe rust was studied by two-way electrophoresis. the experimental steps are shown in figure 2.

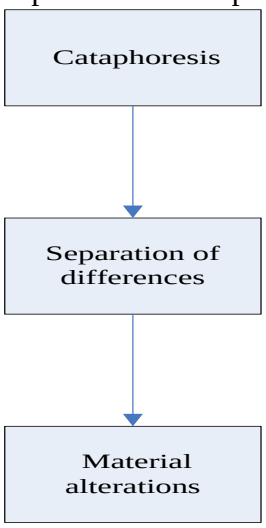

Figure 2. Experiment 2

3.3. Experimental Processes of Plant Proteins in Various Adverse Environments and Multiple Adverse Environments

(1) By placing isolated plant proteins in the adverse environment of abiotic water stress and observing the changes of plant proteins, it is found that the transcription of plant proteins becomes slower and the growth becomes slower.

(2) By placing isolated plant proteins in the adverse environment of the pathogen and observing the changes in the proteins, the proteins are self-protectively transcribed and the corresponding enzymes transcribed against the pathogen.

(3) The regulation mechanism of plant protein in adverse environment can be obtained by observing the change of protein in biological environment and high salt environment. The methods for protein identification include amino acid sequence analysis, composition analysis, peptide mass fingerprint and peptide sequence label analysis.

4. Discussion

4.1. Experimental results of different protein composition in water stress growth of plants

The effects of different concentrations of PEG treatment on the germination rate of wheat seeds are shown in Table 1. The germination rate of wheat seedlings significantly decreased under PEG stress, and with the increase of PEG concentration, the germination rate of wheat seedlings decreased. This shows that the germination speed of wheat seeds was seriously affected under different concentrations of PEG treatment, and the results are shown in Figure 3:

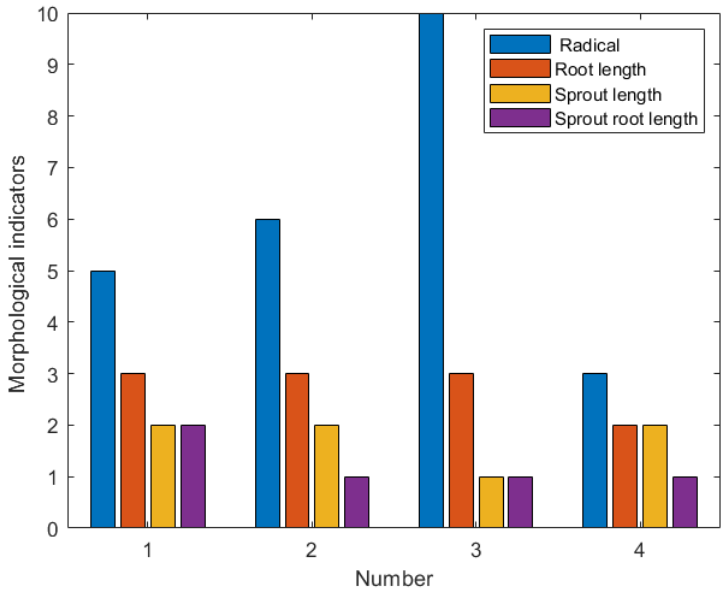

Figure 3. Effect of different concentrations of PEG on morphological indexes of wheat

Table 1. Morphological indicators

Morphological indicators	10 Potency	20 Potency
Radical	3	2
Root length	3	2
Sprout length	3	1
Sprout root length	12	2

4.2. Comparison of Results of Different Protein Composition under Plant Stress Growth Stress

According to the above experiments, it is known that as desertification becomes more serious year by year, the demand for anti-drought plants is increasing. The direct effect of drought on plants is that the lack of water causes stoma ta to close, reducing transpiration, hindering the upward transport of water and inorganic salts in the roots; the strong light accompanied by drought often has a certain degree of damage to chlorophyll; the water balance is damaged, Leaf greening; cell growth slowed; reduced metabolism promoted protein synthesis; decreased expression of Tabasco peroxidase and catalase led to hydrogen peroxide accumulation. Studies on white mustard showed that, under severe drought, the decline in the levels of chlorophyll a-b binding proteins and other light-complementing proteins severely impaired chloroplast light capture and photo system function, accompanied by a decrease in water content, leading to a decline in photosynthesis rates. The plant's drought resistance is mainly manifested by the accumulation of breathalyse in cells, changing the conformation of some enzymes involved in photosynthesis, up-regulating the expression of proteins with thermal stability or protection, changing the expression of stress and signaling genes, and strengthening the cell wall Inhibit the metabolism of organic matter and protect the body protein from damage. Different from salt stress, plants have a complete set of protection mechanisms for photosynthetic enzymes and heat-natural proteins in the face of mild drought stress.The main

manifestations are: the expression of PSI and PSII peripheral proteins is up-regulated to maintain light Systemic activity; under regulation, the expression of Rubisco enzyme decreases first and then increases, and the expression of Rubisco activating enzyme in potato leaves is increased, which has the role of carbonation to protect the active site of Rubisco enzyme to protect; protein kinases, enzymes, and molecular partners participate The plant's drought resistance process and the protection and expression of key proteins have been maintained, and the survival status and time of plants under drought conditions have been maintained and extended. A relatively complete regulatory system has been formed. The experimental data is shown in Figure 4:

Table 2. Disease specific protein

Morphological indicators	Cell index	20 Potency	40 Potency
Radical	3	2	1
Root length	3	2	2
Sprout length	3	1	3
Sprout root length	12	2	5

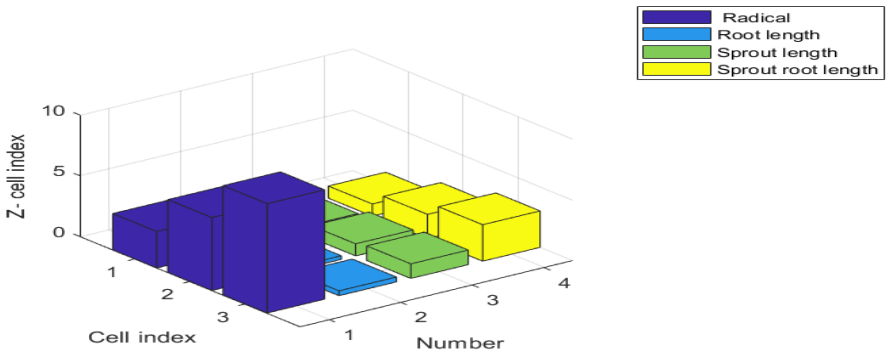

Figure 4. Disease specific protein

4.3. Comparison of Experimental Results of Different Protein Composition in Plant Stress Growth

With the development of mass spectrometry technology, scientists have begun to apply mass spectrometry to protein analysis. The principle is to use different mass-to-charge ratios of each protein or peptide to have different movement times in the mass spectrometer, so that these proteins or peptides can be analyzed. Data acquisition and analysis. Protein mass spectrometry methods can be divided into two categories. The first is quantitative proteomics labeled with stable isotopes, such as iTRAQ and TMT; the second is unlabeled quantitative technology, such as label-free. In general, iTRAQ's method is more accurate, but has strong restrictions on samples and is suitable for small samples. Although label-free technology can detect more samples at one time, the reproducibility of this technology will be lower. The resulting data is shown in Figure 5:

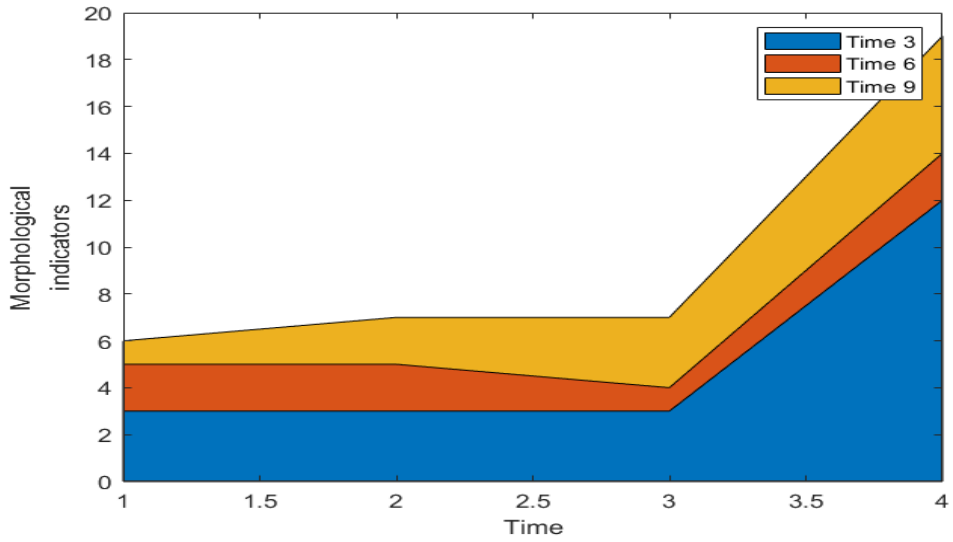

Figure 5. Combination of gene and protein

Table 3. Morphological indicators

Morphological indicators	Time 3	Time 6	Time 9
No.1	3	2	1
No.2	3	2	2
No.3	3	1	3
No.4	12	2	5

4.4. Responses of Different Protein Compositions in the Environment of Plant Stress

Under the same conditions, two-dimensional electrophoresis was performed on the protein of the leaves of Avicenna marina in high-salt and non-salt cultures. 167 protein spots appeared after two-dimensional electrophoresis of the protein in the leaves of Avicenna marina under salt conditions, and 165 protein spots appeared after two-dimensional electrophoresis of the proteins in the leaves of Avicenna marina under salt conditions. The molecular weight of the protein ranges from 20 to 100kD, and the isoelectric point range is shown in Table 4. In high-salt culture and non-salt culture, most of the proteins in the leaves of Avicenna are the same, and only four proteins are different. There were 3 protein spots under high-salt culture, which did not appear under salt-free culture, and were named SR1, SR2, and SR3. One protein spot appeared in leaves of Avicenna marina soil under salt-free culture, but not in high-salt culture Name it SR4. It is preliminarily believed that these four proteins are related to the salt resistance of the bony soil. The conclusion is shown in Figure 6:

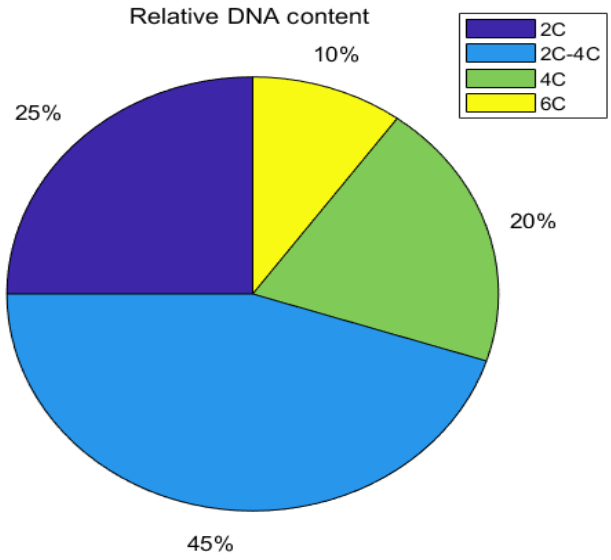

Figure 6. Relative DNA content

Table 4. Relative DNA content

Relative DNA	2C	2C-4C	4C
Content	12	2	5
Percentage	50%	45%	70%

5. Conclusion

Based on the above experiments on water stress using proteomics, some key factors of water stress response have been identified, and multiple metabolic pathways involved in plant response to water stress have been revealed. The protein abundance of wheat cultivars under drought stress was studied by shotgun proteome strategy. The drought-tolerant, drought-tolerant and drought-tolerant seeds were subjected to periodic drought treatment in a greenhouse. After the treatment, proteins were extracted from leaves, and 1299 proteins were analyzed. It was experimentally verified that at different time points, the proteome changes of the three cultivars reflected their different physiological responses to drought stress. The results showed that in the early stage of stress treatment, there was no significant proteome change in Excalibur, while the proteome of RAC875 changed significantly. The experiment proved that the strong drought tolerance of Kennan GA42 was related to the obvious up-regulation of the above 6 deferentially expressed protein spots. After SD-PAGE and CBB staining, about 803 reproducible protein spots were obtained on each gel. Through the above experiments, different results can be obtained for growth in different environments.

Research on physiological mechanisms of plant stress based on different protein composition. For the separation of proteins, although two-dimensional electrophoresis has irreplaceable advantages, its scale needs to be further strengthened. 2D gel electrophoresis staining and transfer are difficult and time-consuming. In addition, there are inherent limitations in the separation capacity during operation, coupled with extremely acidic, extremely alkaline, low abundance, and water-insoluble proteins are difficult to present.Based on different protein composition studies in

the physiological mechanism of plant stress in samples, high salt ion concentrations, Protein quantification, etc. and high-quality protein preparation. The study of different protein composition in the study of physiological mechanisms of plant stress has guiding significance for plant growth in different environments.

The above experimental results show that different proteomics have different applications in physiological mechanisms of plant stress. Plant proteins are very strong against abiotic stresses such as drought, salt stress, low temperature, and anaerobic stress, as well as biological stresses such as pests, bacteria, and fungal infections. The response mechanism has different effects in different physiological mechanisms. The purpose of this article is to better understand the damage mechanism of plants after being stressed. By studying the adaptation and defense mechanisms of plants to the environment, this article uses genetic algorithms to conduct proteomics research on differential proteomics, analyze their differences, and Experimental analysis of the growth mechanism of plants in adversity. Use mathematical analysis and mathematical statistics to statistically classify the data. Use big data to fit the data. Then, through different protein composition, the physiological mechanism of plant stress Research experiments analyze the different effects. The experimental data show that in the more adverse environment, the stronger the plant's self-protection, the more proteins transcribed to adapt to the adverse environment. The experimental results show that different protein compositions play a pivotal role in the physiological mechanism of plant stress. The use of proteins has a protective effect on the plant's adversity. The research results have been applied to the growth of plants, which has increased the growth rate of plant colors by about 15%. It laid a solid foundation for future research on physiological mechanisms of adversity.

Funding

This article is not supported by any foundation.

Data Availability

Data sharing is not applicable to this article as no new data were created or analysed in this study.

Conflict of Interest

The author states that this article has no conflict of interest.

References

[1] Intharawijitr K, Iida K, Koga H. Simulation study of low latency network architecture using mobile edge computing. IEICE TRANSACTIONS on Information and Systems, 2017, 100(5): 963-972.

[2] Al-Shqeerat H A K, Al-Shrouf M A F, Hassan M R, . Cloud computing security challenges in higher educational institutions-A survey. International Journal of Computer Applications, 2017, 161(6): 22-29.

[3] Khan S, Parkinson S, Qin Y. Fog computing security: a review of current applications and security solutions. Journal of Cloud Computing, 2017, 6(1): 19.

[4] Sarkar M, Banerjee S, Badr Y. Configuring a trusted cloud service model for smart city exploration using hybrid intelligence. International Journal of Ambient Computing and Intelligence (IJACI), 2017, 8(3): 1-21.

[5] Hu P, Ning H, Qiu T, . Fog computing based face identification and resolution scheme in internet of things. IEEE transactions on industrial informatics, 2016, 13(4): 1910-1920.

[6] Menon V G, Prathap P M J. Moving from vehicular cloud computing to vehicular fog computing: Issues and challenges. International Journal on Computer Science and Engineering, 2017, 9(2): 14-18.

[7] Moreno-Vozmediano R, Montero R S, Huedo E, . Cross-site virtual network in cloud and fog computing. IEEE Cloud Computing, 2017, 4(2): 46-53.

[8] Yu Feng, Mao Zhizhong, Jia Mingxing. Recursive identification for Hammerstein-Wiener systems with dead-zone input nonlinearity. Journal of Process Control,2018,23(8):1108-1115.

[9] Wang Xuehai, Ding Feng. Modelling and multi-innovation parameter identification for Hammerstein nonlinear state space systems using the filtering technique. Mathematical & Computer Modelling of Dynamical Systems,2016,22(2):113-140.

[10] Gao Xuehui, Ren Xuemei, Zhu Changsheng .Identification and control for Hammerstein systems with hysteresis non-linearity. IET Control Theory & Applications,2017,9(13):1935-1947.

[11] Bhandari N, Rollins D. Continuous-time Hammerstein nonlinear modeling applied to distillation. AIChE Journal,2018,50(2):530-533.

[12] Wang Qingchao, Zhang Jianzhong. Nonlinear predictive control for continuous stirred-tank reactor using Hammerstein model. Journal of Nanjing University of Science and Technology,2016,34(5):618-623.

[13] Ma Xinying, Shi Huafeng, Su Chengli. Predictive control algorithm based on fuzzy Hammerstein model and its application to pH process. Computers & Applied Chemistry,2018,30(10):1122-1126.

[14] Veen G, Wingerden J W, Verhaegen M. Global identification of wind turbines using a Hammerstein identification method. IEEE Transactions on Control Systems Technology,2016,21(4):1471-1478.

[15] Huo Haibo, Zhu Xinjian, Hu Wanqi. Nonlinear model predictive control of SOFC based on a Hammerstein model. Journal of Power Sources,2018,185(1):338-344.

[16] Filipovic V Z. Consistency of the robust recursive Hammerstein model identification algorithm. Journal of the Franklin Institute,2017,352(5):1932-1945.

[17] Wang Jiandong, Zhang Qinghua, Ljung L. Revisiting Hammerstein system identification through the two-stage algorithm for bilinear parameter estimation.Automatica,2019,45(11):2627-2633.

[18] Ding Feng, Shi Yang, Chen Tongwen. Gradient-based identification methods for Hammerstein nonlinear ARMAX models. Nonlinear Dynamics,2017,45(1-2):31-43.

[19] Ma Liang, Liu Xinggao. Recursive maximum likelihood method for the identification of Hammerstein ARMAX system. Applied Mathematical Modelling,2016,40(13-14):6523-6535.

[20] Ding Feng, Deng Kepo, Liu Ximei. Decomposition based Newton iterative identification method for a Hammerstein nonlinear FIR system with ARMA noise. Circuits Systems & Signal Processing,2018,33(9):2881-2893.

[21] Wang Cheng, Tang Tao. Several gradient-based iterative estimation algorithms for a class of nonlinear systems using the filtering technique. Nonlinear Dynamics,2018,77(3):769-780.

[22] Li Meihang, Liu Ximei, Ding Feng. The maximum likelihood least squares based iterative estimation algorithm for bilinear systems with autoregressive moving average noise. Journal of the Franklin Institute,2017,354(12):4861-4881.

[23] Bai Erwei, Li Kang. Convergence of the iterative algorithm for a general Hammerstein system identifi-cation.Automatica,2018,46(11):1891-1896.

[24] Bai Erwei, Fu Minyue. A blind approach to Hammerstein model identification. IEEE Transactions on Signal Processing,2019,50(7):1610-1619.

[25] Wang Jiandong, Sano A, Chen Tongwen. Identification of Hammerstein systems without explicit parameterisation of non-linearity. International Journal of Control,2019,82(5):937-952.