1. A dual-function probe based on naphthalene for fluorescent turn-on recognition of Cu2+ and colorimetric detection of Fe3+ in neat H2O

Accession number: 20184706116870

Authors: Li, Na-Na (1); Ma, Yu-Qing (1); Sun, Xue-Jiao (1); Li, Ming-Qiang (1); Zeng, Shuang (1); Xing, Zhi-Yong (1); Li, Jin-Long (2)

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Corresponding author: Xing, Zhi-Yong(zxying@neau.edu.cn)

Source title: Spectrochimica Acta - Part A: Molecular and Biomolecular Spectroscopy


Volume: 210

Issue date: 5 March 2019

Publication year: 2019

Pages: 266-274

Language: English

ISSN: 13861425

CODEN: SAMCAS

Document type: Journal article (JA)

Publisher: Elsevier B.V.

Abstract: A simple naphthalene derivative, 6-hydroxy-2-naphthohydrazide (NAH), was designed and synthesized through two facile steps reactions with the 6-hydroxy-2-naphthoic acid (NCA) as the starting material. In neat H2O (10% 0.01 M HEPES buffer, v/v, pH = 7.4), probe NAH showed a highly selective and sensitive response towards Fe3+ via perceptible color change and displayed "turn-on" dual-emission fluorescence response for Cu2+. The binding stoichiometry ratio of NAH/Cu2+ and NAH/Fe3+ were all confirmed as 1:1 by the method of fluorescence job's plot and UV–Vis job's plot, respectively. Probe NAH can be used over a wide pH range for the determination of Fe3+ (2.0–10.0) and Cu2+ (6.0–10.0) without interference from other co-existing metal ions. A possible detection mechanism was the hydrolysis of NAH upon the addition of Fe3+ or Cu2+, thereby leading to the formation of 6-hydroxy-naphthalene-2-carboxylic acid (NCA) which was further confirmed by the various spectroscopic techniques including FT-IR, 1H NMR titration and HRMS. Moreover, NAH was successfully applied to the detection of Cu2+ and Fe3+ in tap water, ultrapure water and BSA. © 2018 Elsevier B.V.

Number of references: 45

Main heading: Naphthalene

Controlled terms: Colorimetry - Fluorescence - Metal ions - Metals - Probes

Uncontrolled terms: 6-Hydroxy-2-naphthohydrazide - Colorimetric detection - Detection mechanism - Dual emissions - Dual function - Naphthalene derivatives - Spectroscopic technique - Stoichiometry ratio

Classification code: 531.1 Metallurgy - 741.1 Light/Optics - 804.1 Organic Compounds - 941.4 Optical Variables

Measurements

DOI: 10.1016/j.saa.2018.11.031

Funding Details: Sponsor: Natural Science Foundation of Heilongjiang Province

Compendex references: YES

Database: Compendex

Compilation and indexing terms, Copyright 2018 Elsevier Inc.

Data Provider: Engineering Village

2. Loci and candidate genes in soybean that confer resistance to Fusarium graminearum

Accession number: 20184706130333

Authors: Zhang, Chanjuan (1); Zhao, Xue (1); Qu, Yingfan (1); Teng, Weili (1); Qiu, Lijuan (2); Zheng, Hongkun (3); Wang, Zhenhua (1); Han, Yingpeng (1); Li, Wenbin (1)

Author affiliation: (1) Key Laboratory of Soybean Biology in Chinese Ministry of Education (Key Laboratory of Soybean Biology and Breeding/Genetics of Chinese Agriculture Ministry), Northeast Agricultural University, Harbin; 150030, China; (2) Institute of Crop Science, National Key Facility for Crop Gene Resources and Genetic Improvement (NFCRI), Chinese Academy of Agricultural Sciences, Beijing; 100081, China; (3) Bioinformatics Division, Biomarker Technologies Corporation, Beijing; 101300, China

Corresponding author: Wang, Zhenhua(zhenhuawang_2006@163.com)

Source title: Theoretical and Applied Genetics


Issue date: 2018

Publication year: 2018

Language: English
Abstract: Key message: Association analysis techniques were used to identify and verify twelve single nucleotide polymorphisms (SNPs) associated with Fusarium graminearum resistance. Two novel candidate genes were obtained.

Abstract: Fusarium graminearum causes seed and root rot and seedling damping-off of soybean, leading to severe yield loss. Presently, the genetic basis of resistance to F. graminearum is elucidated in only four soybean accessions, which is not sufficient for resistance improvement. The objective of the present study was to identify the genome-wide genetic architecture of resistance to F. graminearum in landraces and cultivated soybeans based on a growth room evaluation. The resistance levels of 314 diverse accessions were tested, and 22,888 single nucleotide polymorphisms (SNPs) with a minor allele frequency of > 0.05 were developed using the specific-locus amplified fragment sequencing (SLAF-seq) approach. Twelve SNPs were identified as associated with F. graminearum resistance, and these SNPs were located at 12 genomic regions on eight chromosomes (Chr.) and could explain 5.53–14.71% of the observed phenotypic variation. One SNP, rs9479021, located on Chr.6, overlapped with qRfg_Gm06, the known QTL for resistance to F. graminearum. The other SNPs were novel and associated with resistance to F. graminearum. Nine novel candidate genes were predicted to contribute to resistance to F. graminearum according to the haplotype and transcript abundance analysis of the candidate genes. The identified markers and resistant cultivars are valuable for the improvement of resistance to F. graminearum. © 2018, Springer-Verlag GmbH Germany, part of Springer Nature.

Number of references: 36

Main heading: Genes

Controlled terms: Cultivation - Fungi - Nucleotides

Uncontrolled terms: Abundance analysis - Amplified fragments - Association analysis - Fusarium graminearum - Genetic architecture - Phenotypic variations - Resistant cultivars - Single nucleotide polymorphisms

Classification code: 461.2 Biological Materials and Tissue Engineering - 461.9 Biology - 821.3 Agricultural Methods

DOI: 10.1007/s00122-018-3230-3

Compendex references: YES
Database: Compendex
Compilation and indexing terms, Copyright 2018 Elsevier Inc.

Data Provider: Engineering Village

3. Thioredoxin silencing-induced cardiac supercontraction occurs through endoplasmic reticulum stress and calcium overload in chicken

Accession number: 20184706113144

Authors: Yang, Jie (1); Gong, Yafan (1); Liu, Qi (1); Cai, Jingzeng (1); Zhang, Bo (2); Zhang, Ziwei (1, 3, 4)

Author affiliation: (1) College of Veterinary Medicine, Northeast Agricultural University, Harbin; 150030, China; (2) Center for Animal Epidemic Disease Prevention and Control, Fushun; Liaoning; 113006, China; (3) Key Laboratory of the Provincial Education Department of Heilongjiang for Common Animal Disease Prevention and Treatment, College of Veterinary Medicine, Northeast Agricultural University, Harbin; 150030, China; (4) Key Laboratory of Animal Cellular and Genetic Engineering of Heilongjiang Province, Harbin; 150030, China

Corresponding author: Zhang, Ziwei(zhangziwei@neau.edu.cn)

Source title: Metallomics

Abbreviated source title: Metallomics

Volume: 10
Issue: 11
Issue date: November 2018
Publication year: 2018
Pages: 1667-1677
Language: English
ISSN: 17565901
E-ISSN: 1756591X

Document type: Journal article (JA)

Publisher: Royal Society of Chemistry

Abstract: The thioredoxin (Txn) system is the most crucial antioxidant defense mechanism in the myocardium, and hampering the Txn system may compromise cell survival. Calcium (Ca) imbalance is associated with a variety of cardiomyopathies, and dysregulation of Ca2+ homeostasis is often considered a critical starting point for heart disease. However, the roles of Txn and the Txn system in maintaining Ca2+ homeostasis in cardiomyocytes have been infrequently reported. Here, we examined the expression of genes associated with Ca2+ channels using a model of Txn suppression in cardiomyocyte cultures (siRNA and Txn inhibitor) and report that Txn knockdown can
cause Ca2+ overload in the myocardial cytoplasm and release of endoplasmic reticulum (ER) Ca2+, which induces ER stress. Our results showed that Txn knockdown could lead to cytosolic Ca2+ overload through upregulated gene expression of Ca2+ channel-related genes in the cytoplasmic and ER membranes. Furthermore, we find that excessive Ca2+ concentrations in the cytoplasm may increase myocardial contraction, and heat shock proteins may play a protective role throughout the process. Our present study reveals a novel model of regulation for low Txn expression in myocardial injury. © The Royal Society of Chemistry.

Number of references: 50
Main heading: Gene expression
Controlled terms: Calcium - Cell membranes - Cytology - Physiology - Proteins
Classification code: 461.2 Biological Materials and Tissue Engineering - 461.9 Biology - 549.2 Alkaline Earth Metals - 804.1 Organic Compounds
DOI: 10.1039/c8mt00206a
Funding Details: Number; Acronym; Sponsor: 31872531; NSFC; National Natural Science Foundation of China
Compendex references: YES
Database: Compendex
Compilation and indexing terms, Copyright 2018 Elsevier Inc.
Data Provider: Engineering Village

4. Properties and Structure of Bacterial Cellulose-Tea Polyphenol Composite Film

Accession number: 20184706122168
Authors: Wang, Bo (1); Gong, Han (1); Chang, Peng (1); Shi, Shuo (1); Xia, Xiufang (1); Zhang, Dongjie (2)
Author affiliation: (1) College of Food Science, Northeast Agricultural University, Harbin; 150030, China; (2) College of Food Science, Heilongjiang Bayi Agricultural University, Daqing; 163319, China
Corresponding author: Xia, Xiufang(Xxfang524@163.com)
Source title: Shipin Kexue/Food Science
Abbreviated source title: Shipin Kexue/Food Sc.
Volume: 39
Issue: 17
Issue date: September 15, 2018
Publication year: 2018
Pages: 229-235
Language: Chinese
ISSN: 10026630
Document type: Journal article (JA)
Publisher: Chinese Chamber of Commerce
Abstract: Bacterial cellulose-tea polyphenol composite films were prepared by soaking bacterial cellulose hydrogel in tea polyphenol solution and then thermally drying it. The optimization of tea polyphenol concentration and soaking time was done based on the antimicrobial activity, mechanical properties, light transmittance, water absorption, water vapor permeability and structure of bacterial cellulose-tea polyphenol composite films. Our aim was to obtain composite films with strong antibacterial activity and good flexibility. The results showed that the concentration of tea polyphenols was positively correlated with the antibacterial ability of the composite films. When tea polyphenol concentration was greater than 0.2%, the inhibition zone diameter was significantly changed (P 0.05) when soaking time exceeded 4 h. Four hours was therefore selected as the optimal soaking time. The cellulose-tea polyphenol composite film had a characteristic absorption peak of bacterial cellulose. Compared with the pure film, the composite film was more compact, closely linking tea polyphenols to bacterial cellulose molecules. © 2018, China Food Publishing Company. All right reserved.
Number of references: 28
Main heading: Composite films
Controlled terms: Cellulose - Cellulose films - Mechanical permeability - Mechanical properties - Microorganisms - Tensile strength - Water absorption - Water vapor
Uncontrolled terms: Anti-bacterial activity - Bacterial cellulose - Characteristic absorption - Film properties - Film structure - Tea polyphenols - Water vapor permeability - Water vapor transmission rate
Classification code: 461.9 Biology - 802.3 Chemical Operations - 811.3 Cellulose, Lignin and Derivatives - 951 Materials Science
Numerical data indexing: Percentage 2.00e-01%, Time 1.44e+04s
DOI: 10.7506/spkx1002-6630-201817037
Compendex references: YES
Database: Compendex
5. Lycopene Triggers Nrf2-AMPK Cross Talk to Alleviate Atrazine-Induced Nephrotoxicity in Mice

Accession number: 20184706105964
Authors: Lin, Jia (1); Xia, Jun (1); Zhao, Hua-Shan (1); Hou, Rui (1); Talukder, Milton (1, 4); Yu, Lei (1); Guo, Jian-Ying (1); Li, Jin-Long (1, 2, 3)
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Corresponding author: Li, Jin-Long(JinLongli@neau.edu.cn)
Source title: Journal of Agricultural and Food Chemistry
Volume: 66
Issue: 46
Issue date: November 21, 2018
Publication year: 2018
Language: English
ISSN: 00218561
E-ISSN: 15205118
CODEN: JAFCAU
Document type: Journal article (JA)
Publisher: American Chemical Society
Abstract: Atrazine (ATR), an environmental persistent and bioaccumulative herbicide, has been associated with environmental nephrosis. Lycopene (LYC) exhibits important properties of nephroprotection, but there are limited data on the specific underlying mechanism. The primary objective of this study was to explore the therapeutic effect of LYC on ATR-induced nephrotoxicity in mice. The mice were divided randomly into 6 groups and treated as follows: control (C), 5 mg/kg LYC group (L), 50 mg/kg ATR group (A1), 200 mg/kg ATR group (A2), 50 mg/kg ATR plus 5 mg/kg LYC group (A1+L), and 200 mg/kg ATR plus 5 mg/kg LYC group (A2+L) by oral gavage administration for 21 days. We found that pretreatment with LYC significantly suppressed the ATR-induced renal tubular epithelial cell swelling. Furthermore, LYC mitigated ATR-induced dysregulation of oxidative stress markers by reducing MDA, H2O2 levels, and increasing SOD, GPx, CAT concentration, and Nrf2 activation. Moreover, LYC activated the autophagic flux by a detectable change in autophagy-related genes (Beclin-1 and ATGs) and proteins (p62/SQSTM) and by the formation of autophagic vacuole (AV) and LC3 aggregation, in parallel with AMPK activation (pAMPK/AMPK). Herein, ATR-up-regulated nuclear factor erythroid 2-related factor 2 (Nrf2) expression and Nrf2-regulated redox genes, including quinoneoxidoreductase-1 (NQO1) and heme oxidase-1 (HO1), whereas LYC down-regulated those of the above genes. In addition, LYC suppressed ATR-induced activation of autophagy (increased LC3II/LC3I, ATGs, Beclin1, and p62, in parallel with increased AMPK activation). Collectively, our findings identified a cross talk between AMPK-activated autophagy and the Nrf2 signaling pathway in LYC-mediated nephroprotection against ATR-induced toxicity in mice kidney. © 2018 American Chemical Society.
Number of references: 82
Main heading: Crosstalk
Controlled terms: Chemical activation - Gene expression - Herbicides - Mammals
Uncontrolled terms: Lycopenes - nephroprotection - Nephrotoxicity - Nuclear factor erythroid 2-related factor 2 - Oxidative stress markers - Primary objective - Signaling pathways - Therapeutic effects
Classification code: 461.9 Biology - 804 Chemical Products Generally - 804.1 Organic Compounds
Numerical data indexing: Age 5.75e-02yr
DOI: 10.1021/acs.jafc.8b04341
Compendex references: YES
Database: Compendex
Compilation and indexing terms, Copyright 2018 Elsevier Inc.
Data Provider: Engineering Village

6. Recent Advances in Understanding the Radioprotective Effect of Natural Products

Accession number: 20184706122174
Authors: Liu, Liyuan (1); Chen, Min (1); Zhao, Haitian (1); Yao, Lei (2, 3)
Author affiliation: (1) Department of Food Science and Engineering, School of Chemistry and Chemical Engineering, Harbin Institute of Technology, Harbin; 150000, China; (2) National Soybean Engineering Technology Research Center, Northeast Agricultural University, Harbin; 150000, China; (3) Heilongjiang Green Food Science Research Institute, Harbin; 150027, China
Corresponding author: Zhao, Haitian(zhaoht9999@163.com)
Source title: Shipin Kexue/Food Science
Abbreviated source title: Shipin Kexue/Food Sc.
Volume: 39
Issue: 17
Publication year: 2018
Pages: 269-274
Language: Chinese
ISSN: 10026630
Document type: Journal article (JA)
Publisher: Chinese Chamber of Commerce
Abstract: With the development of nuclear industry, radiation technology has been increasingly widely used in medical diagnosis and treatment, and radiation has become increasingly close to people's lives. However, radiation is greatly harmful to the hematopoietic, immune, and nervous systems. As non-toxic and harmless radiation protection agents, natural products have great application prospects. In this paper, we review the recent progress made in understanding the radioprotective effect of natural products such as polyphenols, polysaccharides, alkaloids and saponins, which will provide valuable information for studying the radiation protection of natural products. © 2018, China Food Publishing Company. All right reserved.
Number of references: 58
Main heading: Radiation protection
Controlled terms: Alkaloids - Diagnosis - Metabolites - Nuclear industry - Polysaccharides
Uncontrolled terms: Application prospect - Natural products - Non-toxic - Polyphenols - Radiation technologies - Radioprotective - Recent progress - Saponins
Classification code: 461.6 Medicine and Pharmacology - 804 Chemical Products Generally - 804.1 Organic Compounds - 914.1 Accidents and Accident Prevention
DOI: 10.7506/spkx1002-6630-201817043
Compendex references: YES
Database: Compendex
Compilation and indexing terms, Copyright 2018 Elsevier Inc.
Data Provider: Engineering Village

7. Can deep learning identify tomato leaf disease?
Accession number: 20184706087009
Authors: Zhang, Keke (1); Wu, Qiufeng (2); Liu, Anwang (1); Meng, Xiangyan (2)
Author affiliation: (1) College of Engineering, Northeast Agricultural University, Harbin; 150030, China; (2) College of Science, Northeast Agricultural University, Harbin; 150030, China
Corresponding author: Wu, Qiufeng(qiufeng@neau.edu.cn)
Source title: Advances in Multimedia
Abbreviated source title: Adv. Multimedia
Volume: 2018
Issue date: 2018
Article number: 6710865
Language: English
ISSN: 16875680
E-ISSN: 16875699
Document type: Journal article (JA)
Publisher: Hindawi Limited, 410 Park Avenue, 15th Floor, 287 pmb, New York, NY 10022, United States
Abstract: This paper applies deep convolutional neural network (CNN) to identify tomato leaf disease by transfer learning. AlexNet, GoogLeNet, and ResNet were used as backbone of the CNN. The best combined model was utilized to change the structure, aiming at exploring the performance of full training and fine-tuning of CNN. The highest accuracy of 97.28% for identifying tomato leaf disease is achieved by the optimal model ResNet with stochastic gradient descent (SGD), the number of batch size of 16, the number of iterations of 4992, and the training layers from the 37 layer to the fully connected layer (denote as "fc"). The experimental results show that the proposed technique
is effective in identifying tomato leaf disease and could be generalized to identify other plant diseases. © 2018 Keke Zhang et al.

Number of references: 48

Main heading: Fruits

Controlled terms: Deep neural networks - Neural networks - Stochastic models - Stochastic systems

Uncontrolled terms: Combined model - Deep convolutional neural networks - Fully-connected layers - Number of iterations - Optimal model - Plant disease - Stochastic gradient descent - Transfer learning

Classification code: 821.4 Agricultural Products - 922.1 Probability Theory - 961 Systems Science

Numerical data indexing: Percentage 9.73e+01%

DOI: 10.1155/2018/6710865

Compendex references: YES

Database: Compendex

Compilation and indexing terms, Copyright 2018 Elsevier Inc.

Data Provider: Engineering Village

8. Design and test of wireless power transmission system in solar greenhouse based on microwave transmission technology

Accession number: 20184706107256

Authors: Wang, Lishu (1); Liu, Lei (1); Wang, Jinfeng (1); Wen, Jingchen (1); Qiao, Shuaixiang (1); Wang, Shuyu (1)

Author affiliation: (1) Institute of Electrical and Information, Northeast Agricultural University, Harbin; 150030, China

Source title: Nongye Gongcheng Xuebao/Transactions of the Chinese Society of Agricultural Engineering

Abbreviated source title: Nongye Gongcheng Xuebao

Volume: 34

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Issue date: August 15, 2018

Publication year: 2018

Pages: 214-224

Language: Chinese

ISSN: 10026819

CODEN: NGOXEO

Document type: Journal article (JA)

Publisher: Chinese Society of Agricultural Engineering

Abstract: The power supply of the sensors driving circuit inside the solar greenhouse was restricted by the wired power supply, it is necessary to modularize and simplify the installation of the sensor and the design of the power supply. The wireless transmission and microwave transmission technologies were used as the power supply for the sensor drive circuit in the greenhouse in this paper. Based on the built-in photovoltaic microwave wireless power transmission system, the influence of various environmental factors on the transmission efficiency during the transmission process from the transmitting end to the receiving end was explored. The electromagnetic radiation of the transmitting antenna was simulated by using Ansoft HFSS software, and the radiation range of the transmitting antenna was obtained. On basis of energy conservation law and microwave theory, the relationship between received power and radiation efficiency, receiving distance and antenna size under the conditions of ideal environment and illumination intensity was analyzed by using MATLAB software. Taking the electromagnetic wave environment in the greenhouse at different distances and different time periods in one day of December in Harbin's winter as the test object, the influence of the electromagnetic wave environment on the receiving power of photovoltaic microwave wireless power transmission system was tested and analyzed. The method of improving the transmission efficiency of solar greenhouse wireless transmission system was further explored. The structure of microstrip antenna array was given and the design concept of RC varactor diode automatic phase modulation circuit was proposed, and the reason why the RC varactor automatic phase modulator was used to make the phase of each array element in phase was deduced theoretically. Based on this theory and research, the microstrip antenna array was simulated and analyzed subsequently. Aiming at the design problem of microwave emission source, a design scheme of microwave power source with low power loss was proposed. The theoretical circuit diagram was given and simulated. The effect that microstrip antenna array can improve and enhance wireless transmission efficiency in solar greenhouse had been verified by further experiments. The test results showed that the system can effectively supply power for the sensor equipment within 8 m when the transmitting power was 500 W by microwave wireless transmission method and it can get 19.28 dB antenna gain of the maximum radiation direction of the microstrip antenna with 6×7 structure. Compared with the horn antenna, the gain of the microstrip antenna array is improved, that is, the orientation of the microstrip antenna array is better. The transmission efficiency can be improved by using the microstrip antenna array method, and the average receiving power can be increased by 1.58 W in the range of 0 ~8 m. © 2018, Editorial Department of the Transactions of the Chinese Society of Agricultural Engineering. All right reserved.

Accession number: 20184706122175
Authors: Wu, Yutong (1); Cui, Menghan (1); Wang, Yuqi (1); Kong, Baohua (1); Chen, Qian (1)
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Corresponding author: Chen, Qian(chenqianego7@126.com)
Source title: Shipin Kexue/Food Science
Abbreviated source title: Shipin Kexue/Food Sc.
Volume: 39
Issue: 17
Issue date: September 15, 2018
Publication year: 2018
Pages: 275-280
Language: Chinese
ISSN: 10026630
Document type: Journal article (JA)
Publisher: Chinese Chamber of Commerce

Abstract: Freezing is an important food preservation technique in the food industry; however, it has negative effects on food quality. Ultrasonic-assisted freezing is a novel food freezing technique that can accelerate freezing rate, refine ice crystal size, and improve the quality of frozen foods. This review elucidates the mechanism of ultrasound-assisted freezing and the effect of ultrasound on ice crystal formation. Meanwhile, it summarizes the effects of ultrasound-assisted freezing on the quality of frozen foods and the commonly used technical parameters of ultrasound-assisted freezing. Moreover, future development directions are discussed. Hopefully, this review can provide theoretical support for the application of ultrasound-assisted freezing in the food industry. © 2018, China Food Publishing Company. All right reserved.

Number of references: 55
Main heading: Thermal processing (foods)
10. Cloning and Analysis of AmCesA1 Gene in Acacia mangium

**Accession number:** 20184706117204  
**Authors:** Ren, Jian (1); Yin, Yuqing (1); Zhang, Huihui (1); Chen, Dian (1); Wang, Kexin (1); Wang, Yong (1)  
**Author affiliation:** (1) Key Laboratory of Biology and Genetic Improvement of Horticultural Crops in Northeast Region, Ministry of Agriculture College of Horticulture and Landscape Architecture, Northeast Agricultural University, Harbin; 150030, China  
**Corresponding author:** Wang, Yong  
**Source title:** Linye Kexue/Scientia Silvae Sinicae  
**Abbreviated source title:** Linye Kexue/Sci. Silvae Sinicae  
**Volume:** 54  
**Issue:** 8  
**Issue date:** August 1, 2018  
**Publication year:** 2018  
**Pages:** 79-87  
**Language:** Chinese  
**ISSN:** 10017488  
**Document type:** Journal article (JA)  
**Publisher:** Chinese Society of Forestry  

**Abstract:** Objective Acacia mangium is widely cultivated in southern China for paper production. Cellulose synthase (CesA) plays a vital role in the synthesis of cellulose, which is an important factor in controlling the quality and yield of wood fiber. In this study, we cloned a cellulose synthase gene of A. mangium, and studied its response to hormones to help the understanding of the synthesis of cellulose and the high fiber yield of A. mangium. Method A CesA was obtained from A. mangium seedlings by RT-PCR and RACE, named AmCesA1 (AY643519). The gene was analyzed by bioinformatics software. The copy form of the gene was determined through using Southern analysis. The expression level of the gene in different tissues and the expression of gibberellin, 6-BA and methyl jasmonate were determined by real-time fluorescence quantitative PCR. Result The molecular size of AmCesA1 is 3,793 bp, and its ORF is 3,249 bp, suggesting that this gene encodes 1,082 amino acids. Protein molecular formula is C5495H8491N1457O1579S50. The number of positive charge amino acid residues (Arg + Lys) is 121, and the number of negative charge amino acid residues (Asp + Glu) is 125. The isoelectric point is 6.51, which means that it is acidic protein. Its instability coefficient is 40.82, belonging to the unstable protein. The amino acid primary structure analysis of AmCesA1 showed that it had the conserved D, D, D and QxxRW functional domains of cellulose synthase, and had a unique P-CR region and the HVR region and N-terminal zinc finger structure. There were six transmembrane regions at the C-terminus, but the two transmembrane regions at the N-terminus were not significant. Secondary structure analysis showed that it had more α-helix, random coil, but fewer β-turn, while β-sheet number varies greatly due to the different algorithms. Cluster analysis showed that AmCesA1 had similarity with Glycine max GmCesA1 and Arachis duranensis AdCesA1. But it did not appear to be close to the results of woody plants. Further comparison with Arabidopsis thaliana cellulose gene family amino acid sequence indicated a fact that AmCesA1 was similar to AtCesA1 and AtCesA10 in A. thaliana, and its similarity was 86% and 80%, suggesting that it had the same function as A. thaliana AtCesA1 and AtCesA10. Southern analysis showed that AmCesA1 was present in multiple copies of the Acacia tree genome. Real-time quantitative PCR showed that AmCesA1 was widely expressed in roots, stems and leaves, and the differences among them were not significant. AmCesA1 had a response to GA3, 6-BA and MeJA treatments, in which the response to GA3 was relatively strong. Conclusion AmCesA1 cloned in this study is a member of the plant CesA family, presumably involved in the formation of primary cell walls. The gene was responsive to gibberellin, 6-BA and methyl jasmonate, and the expression level of the gene was up-regulated in different hormone treatments, which indicates that the gene was involved in the positive regulation of the hormone response. © 2018, Editorial Department of Scientia Silvae Sinicae. All right reserved.

**Number of references:** 32  
**Main heading:** Quality control  
**Controlled terms:** Amino acids - Cellulose - Cloning - Cluster analysis - Gene expression - Gene expression regulation - Plants (botany) - Polymerase chain reaction - Proteins - Wood  
**Uncontrolled terms:** Acacia mangium - AmCesA1 - Bioinformatics software - Gene cloning - Hormone response - Primary structure analysis - Real-time quantitative PCR - Zinc finger structure  
**Classification code:** 461.8.1 Genetic Engineering - 461.9 Biology - 723 Computer Software, Data Handling and Applications - 801.2 Biochemistry - 804.1 Organic Compounds - 811.2 Wood and Wood Products - 811.3 Cellulose, Lignin and Derivatives - 913.3 Quality Assurance and Control  
**Numerical data indexing:** Percentage 8.00e+01%, Percentage 8.60e+01%  
**DOI:** 10.11707/j.1001-7488.20180809  
**Compendex references:** YES  
**Database:** Compendex
11. Transcriptome profiling analysis characterized the gene expression patterns responded to combined drought and heat stresses in soybean

Accession number: 20184706131126
Authors: Wang, Libin (1); Liu, Lijun (1); Ma, Yuling (1); Li, Shuang (1); Dong, Shoukun (1); Zu, Wei (1)
Author affiliation: (1) College of Agriculture, Northeast Agricultural University, Harbin; 150030, China
Corresponding author: Zu, Wei(neau_soybean@163.com)
Source title: Computational Biology and Chemistry
Volume: 77
Issue date: December 2018
Publication year: 2018
Pages: 413-429
Language: English
ISSN: 14769271
Document type: Journal article (JA)
Publisher: Elsevier Ltd
Abstract: Heat and drought are the two major abiotic stress limiting soybean growth and output worldwide. Knowledge of the molecular mechanisms underlying the responses to heat, drought, and combined stress is essential for soybean molecular breeding. In this study, RNA-sequencing was used to determine the transcriptional responses of soybean to heat, drought and combined stress. RNA-sequencing analysis demonstrated that many genes involved in the defense response, photosynthesis, metabolic process, etc. are differentially expressed in response to drought and heat. However, 1468 and 1220 up-regulated and 1146 and 686 down-regulated genes were confirmed as overlapping differentially expressed genes at 8 h and 24 h after treatment, and these genes are mainly involved in transport, binding and defense response. Furthermore, we compared the heat, drought and the combined stress-responsive genes and identified potential new targets for enhancing stress tolerance of soybean. Comparison of single and combined stress suggests the combined stress did not result in a simple additive response, and that there may be a synergistic response to the combination of drought and heat in soybean. © 2018 Elsevier Ltd
Number of references: 83
Main heading: Drought
Controlled terms: Heating - Network security - RNA - Transcription - Transcription factors
Uncontrolled terms: Differentially expressed gene - Gene expression patterns - Metabolic process - Molecular breeding - Molecular mechanism - Soybean - Stress tolerance - Transcriptional response
Classification code: 444 Water Resources - 461.2 Biological Materials and Tissue Engineering - 461.9 Biology - 723 Computer Software, Data Handling and Applications
Numerical data indexing: Time 2.88e+04s, Time 8.64e+04s
DOI: 10.1016/j.compbiolchem.2018.09.012
Compendex references: YES
Database: Compendex
Compilation and indexing terms, Copyright 2018 Elsevier Inc.
Data Provider: Engineering Village

12. Covalent conjugates of anthocyanins to soy protein: Unravelling their structure features and in vitro gastrointestinal digestion fate

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Abstract: Seeking for healthier dietary foods without compromising their quality has become the first choice for consumers. Various components in foods are able to interact with each other and form conjugates to improve their functionality and nutritional value. The present study investigated on the formation and structural properties of covalently linked conjugates using soy protein isolate (SPI) and black rice anthocyanins at different ratios. The in vitro digestion fate of the conjugates under simulated gastrointestinal conditions was also evaluated. Fourier transform infrared spectroscopy analysis indicated that the secondary structures of SPI was changed upon conjugation with anthocyanins as there was a decrease in $\alpha$-helix and $\beta$-sheet content. Three-dimensional fluorescence also revealed that the tertiary structure of SPI was less compact after conjugation with anthocyanins as a result of the unfolding of polypeptide chains. The conjugates were shown to have higher degree of hydrolysis than SPI. However, transepithelial transport of peptides across Caco-2 cell monolayer was decreased in SPI after conjugation with anthocyanins. The results of this study suggest that incorporation of anthocyanins in SPI is a way to reconcile consumer demand for healthier foods with better quality and functionality. © 2018

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Main heading: Anthocyanins

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