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Molecular analysis of physiological stage of leaf senescence

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A B S T R A C T

Senescence is a final developmental stage of leaf, which is very important as genetic and physiological aspects. Many genes are activated at this stage and most of them show remarkable transcript. The function of senescence is to control regulatory physiological changes. This include cessation of photosynthesis, chloroplast degradation, chlorophyll loss and protein breakdown. Senescence can be initiated by a wide variety of different internal and external factors, as well as being an essential part of plant development; senescence in leaves is also induced prematurely by a number of different environmental stresses. Since plants cannot escape from adverse environmental conditions senescence is one mechanism that plants have evolved to cope with such problems. Interestingly, senescence could be induced in plants even after harvest. This phenomenon is observed in such vegetables like broccoli, lettuce and cabbage. Many different senescence–enhanced genes have been isolated, characterized and cloned. Expression analysis of these genes showed a broad range of expression some time before phenotypic changes to last stage of senescence. So it seems that many signaling pathways should be involved in this process.

Key Words

Gene Expression, Leaf Senescence, Post Harvest Senescence, Programmed Cell Death (PCD)

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Study of overexprexpression of the *BnFUL* gene in transgenic oilseed rape

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A B S T R A C T

Oilseed rape is one of the important oil plants that its cultivation has been expanded in Iran in recent years. Seed shattering before and during harvesting is a problem of cultivation of this plant can causes up to 50% yield decrease depending on the environmental conditions. Production of seed shatter tolerant plants can increase the yield. Different genetic and environmental factors can affect this trait. The *FUL* gene is one of the genetic factors in that its over expression could prevent silique opening and seed shattering. Rapeseed transgenic plants of three cultivars containing the *BnFUL* gene were produced and molecular studies were carried out on T_2 generations transgenic plants using PCR, Southern blotting and real time PCR. PCR showed that the *BnFUL* transgene has been inserted in the transgenic plants in addition to the internal gene. The copy number of transgene in transgenic and control plants were analyzed by Southern blotting which confirmed presence of at least one intact copy of the transgene in transgenic plants. Real time PCR showed that *BnFUL* gene expression in transgenic plants in comparison with control plants has been increased. Differences between the expression of transgenic plants in different lines could be because of position effect and copy number.

Key Words

Oilseed Rape, Transgenic Plant, *BnFUL* Expression, Copy Number

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Direct organogenesis and transformation of sour orange (*Citrus aurantium*) using citrus tristeza virus (CTV) coat protein coding gene

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A B S T R A C T

In this study transgenic plants of sour orange (*C. aurantium)* that is an important citrus rootstock were produced by *Agrobacterium*-mediated transformation. Epicotyl and hypocotyl segments-derived explants were co-cultured with *Agrobacterium* strain EHA105 carrying pFGC5941 plasmid containsing CTV coat protein (p25) gene. One of the main objects of present research was to improve the direct *in vitro* organogenesis efficiency in *C. aurantium*. Therefore different combination of BAP (0, 1, 2 mg/L) and NAA (0, 0.25, 0.5 mg/L) were used in selective medium to culture transformed explants. The highest regeneration (57%) was obtained from explant treated with 2 mg/L BAP and 0.25 mg/L NAA. Effects of wounding and vacuum infiltration on transformation efficiency were evaluated either. The best transformation efficiency (11.25%) was obtained from explants that were vacuum infiltrated during transformation and subsequently were cultured in medium containing 2 mg/L BAP and 0.25 mg/L NAA. PCR analysis using two different genes were performed to confirm transformation. Micro grafting of transformed shoots were carried out on non-transgenic, in-vitro grown seedlings.

Key Words

Agrobacterium tumefaciens, Direct Organogenesis, Epicotyl, Growth Regulators, Wounding

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Transfer of human interferon γ-oleosin genes to safflower (*Carthamus tinctorius* L.)

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A B S T R A C T

The use of plants as a source of medicine is traced back to long time ago. Modern biotechnology proviedes the possibility of production of valuable protein such as pharmaceutical protein in plant. In this study human Interferon gamma-oleosine genes under the control of Napin promoter were transferred to *Carthamus tinctorius* L. (safflower) by *Agrobacterium tumefaciens* strain LBA4404. Cotyledonal explants from safflower plant (*Carthamus tinctorius* L.) Padideh cultivar were used for transformation. The transformed plants were screened on MS medium containing 0.09 mg L^{-1} NAA, and 1 mg L^{-1} TDZ containing 40 mg L^{-1} kanamycin. Presence of transgenes was confirmed using polymerase chain reaction (PCR). Characterization of the transgenic plants is going on.

Key Words

Agrobacterium, *Carthamus tinctorius* L., Human Interferon Gamma-Oleosin Genes, Molecular Farming, Transformation

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Monitoring the Occurrence of Genetically Modified Maize at a Grain Receiving Port in Iran

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A B S T R A C T

This study was carried out to detect the presence of genetically modified maize in imported into Iran using molecular approaches. Five samples of imported maize from Argentina in the second half of 2010 were obtained from Bandar Imam Khomeini custom. Using specific primers for *CaMV 35S* promoter and *nos* terminator, PCR was performed. In this study *Invertase* gene of maize was used as internal control. The results showed that maize samples imported from Argentina were genetically modified and they have regulatory regions of *CaMV 35S* and *nos* in their genome. The shipment was not labled and there was no indication in the accompanying documents that the shipment “may contain living modified organisms”.

Key Words

Biosafety, Cartagena Biosafety Protocol, Maize, Transgenic Plants, Imports

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Pesticides residues (Endosulfan and Diazinon) in cucumber and tomato fields of Kohgiloyeh and Boyerahmad Province

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A B S T R A C T

Insistence on opposing transgenic plants and genetic engenearing by some individuals and/or organizations, hasresulted high levels of application of dangerous chemical pesticides in Iran. Samples of cucumber and tomato fruits were collected from various fields of Kohgiloyeh and Boyerahmad province and the residue of Endosulfan and Diazinon were determined in them. The highest amount of residue was of Diazinon in cucumber. The average residues of Diazinon in cucumber were 0.462, 0.669, and 0.205 mg/kg in Gachsaran, Boyerahmad and Kohgiloyeh respectively. However the internationally accepted maximum residue level of Diazinon in cucumber is 0.1 mg/kg. The residues of Diazinon in tomato were 0.504 and 0.534 mg/kg in Gachsaran and Dena respectively which are higher than the international levels. According to this research, the average residue of Diazinon in cucumber in the whole province was 0.355 to 3.5 times more than the maximum residue level. The residue of Endosulfan in tomato fields of Boyerahmad regions like Tangari, Keveshk, Tang Tamoradi and Sepidar. It was also higher than the international limits in Khairabad region at Gachsaran country. The residue of Endosulfan on cucumber was higher than the international levels in Tangari and Dornkore regions of Boyerahmad country and also Dehre, Dehkhalife and Shain brakan regions of Gachsaran, Delirech region of Dena country and in Zarghamabad of Kohgiloye country. The results showed not only the presence of high levels of Diazinon and Endosulfan residues in tomato and cucumber, but also showed that the period between pesticide use and marketing was also very short. It also shows that number of spraying, recommended dose and the interval between the spraying, were not taken into consideration. Continued restrictions on the application of transgenic plants is therefore considered as acceptance of the continued application of Endosulfan and Diazinon and their presence in food basket in Iran.

Key Words

Cucumber, Diazinon, Endosulfan, Pesticide Residue, Tomato, Transgenic

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Investigation of bovine lymphocyte antigen (BoLA-DRB3) by PCR-based RFLP in buffalo population of Khuzestan province

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A B S T R A C T

MHC locus codes antigens and leukocyte surface proteins which have roles on immune reactions and identification of foreign proteins. In cattle this locus is known as Bulla and is composed of three classes of genes: CLASS I, CLASS II and CLASS III and is located on short arm chromosome 23. Each of these classes of genes has complex and various genes and each gene may have dozens of alleles. The objective of this study was to study the variation of exon 2 of locus BoLA-DRB3 in buffalo population in Khuzestan province. In this study, the Heminested-PCR method was used to amplifing this exon. In order to determain the level of polymorphism, blood sample were collected from 80 buffalos in Shadegan, Ahwaz, Dashte azadegan, Dezfoul and Shoshtar cities. DNA extraction and exon 2 of the MHC gene was amplified by specific set of primers for this gene to produce a 284 bp fragment. The amplified fragments were digested with *Hae*III and *Rsa*I restriction endonuclease. Digested products were separated and were stained by vertical electrophoresis on 8% Polyacrylamide gel. After digestion with *Hae*III and *Rsa*I nine and ten alleles (restriction digestion pattern) were obtained at this locus respectively. Alleles a and b with 34.37 and 23.75 percent were the most frequent alleles when digested with *Hae*III and alleles a and b with 20 and 30 percent frequency were the frequent alleles when digested with *Rsa*I. We identified 17 genotypes using each of the restriction enzymes in this population.

Key Words

Polymorphism, MHC, Buffalo, PBR