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Ecological Risk Assessment of Genetically-Modified Ornamental Plants

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A B S T R A C T

Classic plant breeding has increased the beauty and utility of ornamental plants, but through the application of biotechnology completely new traits could be developed in plants. Creation of blue color petal in carnation and rose are examples demonstrating the optional of biotechnology in creating novel traits out of the scope of the conventional hybridization. Application of genetic engineering in ornamental plants is not limited to changes in color. Resistance to pests and diseases, enhancement of flowering, extended cut flowers life and modification of flower structure are examples of other important traits that could be modified using modern biotechnology. It is predicted that genetic engineering will revolutionize ornamental plants industry in the future. With the introduction of any new technologies, concerns are raised about their safe use and deployment. Concerns have also been raised about the possible negative impacts of commercialization of genetically modified (GM) ornamental plants on the ecosystem. The concerns have several different origins and providing responses to these concerns and not addressing them is the main objective of this paper. This article considers GM ornamental plants in the context of current ecological risk assessment principles, research results achieved, and current regulatory frameworks.This article can be very useful for biotechnologists, biosafety specialists, and authorities concerned.

Key Words

Risk assessment, Transgenic ornamental plants, Biosafety.

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Nucleotide sequence and molecular characterization of β-1,4-endoglucanase gene from *Bacillus subtilis* strain B5d

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A B S T R A C T

The present investigation was conducted to characterize enzymatic and molecular aspects of a beta 1 and 4 endoglucanase gene in *Bacillus subtilis strain* B5d.The gene was amplified with specific primers and its sequence was deposited in the NCBI (accession number ofKF670724). Sequence and phylogenetic analyses were performed using the Vector NTI and Mega 4 software. The PCR product comprised of 794 bp, encoding a peptid of 264 amino acids in length. Amino acid sequence analysis showed that the gene encoding beta 1 and 4 endoglucanase in *B. subtilis* B5d had multiple domains including cellulose binding domain belongs to family 3 and catalytic domain belong to glycoside hydrolase family 5.The enzyme activity was assessed in temperature range of 30-70 °C and pH 4.6. The results showed that the maximum catalytic activity of the enzyme occurred at 55 °C and was estimated at 461.83 U/L. The stability of the enzyme was measured at different pH and temperatures values and the results showed that the enzyme was stable at pH 5-10 and temperature values up 60 °C.

Key Words

Beta 1 and 4 endoglucanase, *Bacillus subtilis*, Phylogenetic analysis, Enzyme stability.

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PCR detection of transgenic maize in Iran on the basis of P35S

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A B S T R A C T

In the past two decades, biotechnology in genetic engineering has led the production of genetically modified organisms (GMOs) all around the world. The statistics of GMO cultivation has lightened the significant importance of GMOs worldwide, and shows that they are widely consumed by public. Maize is one of the most important transgenic crops which has widely cultivated and consumed in many countries. The aim of this study is the detection of genetically modified maize in Iran markets. First, three samples of transgenic maize were prepared from Shiraz's Custom and their DNA was extracted using Cetyl Tri-methyl Ammonium Bromide (CTAB) method. The control PCR test of native maize was performed on Invertase (IVR) gene which is present in all corn types. For detection of genetically modified maize, the PCR test based on P35S promoter which present in most transformation vectors was optimized using specific primers (P35S1 and P35S2). Then, DNA of 37 maize samples collected from seven major cities of Iran and six maize samples from Jihad Agriculture Organization were extracted. PCR tests for the IVR gene and P35S were performed. Respectively, the 226 bp and the 195 bp amplicons were amplified. PCR products were cloned by T/A cloning in JM107 using *pTZ57R* plasmid for sequencing and preparing the positive controls. 46 samples collected from the market, Customs and Jihad Agriculture Organization were shown to be 100% positive for the native IVR gene and 56.5% (26 samples) positive for the exogenous P35S. This study showed that a high percentage of transgenic maize is present in Iran's consumption market. However, no action has been taken toward labeling and the consumer awareness of these food products.

Key Words

Transgenic maize, PCR, P35S Promoter.

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Determination of Diazinon residue levels in Cherry, *Cerasus avium* supplied to Tehran central fruit and vegetable market

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A B S T R A C T

Some of the top decision makers in the ministry of Jihad-e-Agriculture, ministry of Health and the Department of the environment emphasize on a ban on genetically modified products and are in favor of continuous use of synthetic pesticides while over 170 million hectare of the transgenic products are cultivated all around the world. To determine the diazinon residue level in sweet cherry, 40 samples were collected from Tehran Central Market. These products were produced in five main cherry producing cities such as Lavasan, Shahriar, Qazvin, Mashhad and Urumia. Samples were prepared and extracted by the standard method of QuEChERS. The GC/ MS analysis was used to determine the levels of Diazinon residue in the samples. The amount of pesticides measured was compared with the national and Codex MRLs. 10% of the samples contained Diazinon residue levels higher than the MRL value (0.05 mg/ kg) including 4 samples from Mashhad (0.3 mg/kg) and Lavasan (0.29 mg/kg). The remaining samples (90%) had no detectable residue levels of this insecticide. The results obtained in this study can be used for the future planning of pesticides application in the high risk areas of the country. Therefore, the continuous blockade of taking advantage of alternative products and methodologies which could reduce the pesticide usage like production of transgenic plants may result in the production of toxic food baskets for the consumers which may result in the spread of incurable diseases in the society.

Key Words

QuEChERS, Diazinon residue, Cherries, GC/MS.

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Identification of *PEPCK-C* polymorphism using PCR- RFLP method and its association with economic traits in native fowl of Khorasan Razavi province

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ABSTRACT

This study aimed to determine the PEPCK-C gene polymorphism in a population of native fowl in Khorasan Razavi. This gene encodes an enzyme with the same name in most organisms. This enzyme plays a key role in the gluconeogenesis. There are two types of this gene namely, cytosolic (PEPCK-C) and mitochondrial (PEPCK-M) types. In this study, blood samples were randomly collected from 100 native fowl of Khorasan Razavi. DNA was extracted using modified salting out method and then a fragment with the length of 1000 bp using a pair of primers was amplified. This fragment covers the promoter and exon 3 of PEPCK-C gene. For genotyping, the PCR-RFLP method using the *BstE*II digesting enzyme was performed. The GLM procedure of SAS 9.1 was used to study the association of the PEPCK-C gene polymorphism with economic traits. Three genotype patterns including AA, AB and BB were observed with frequencies of 0.46, 0.35 and 0.19, respectively. The effects of genotypes were significant for birth weight ($P<0.01$), weight at 12 weeks of age ($P<0.0001$) and average egg weight between 28 to 32 weeks of age ($P<0.002$). Other studied traits were not significantly influenced by genotypes of this gene. Based on the results of this study the BB genotype had the greatest impact on birth weight, weight at 12 weeks of age and average egg weight. Therefore, the selection based on the polymorphism of this gene could be useful for improving body weight and egg weight of Khorasan Razavi native fowl.

Key Words

PEPCK-C gene, Economic Traits, Polymorphism, Khorasan Razavi, Native fowl.

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The antioxidative effect of some shoot and root inducers in *Pistacia vera* (Qazvini and UCB-1 rootstocks) under *in vitro* conditions

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ABSTRACT

Pistacia vera cv. Qazvini and UCB-1 rootstocks are two worldwide well-known pistachio rootstocks. They are valuable because of their tolerance to salinity and drought (Qazvini), and the resistance to cold and to Verticillium diseases (UCB-1). To improve vegetative and growth quality of pistachio and also to enhance the rooting efficiency, the effect of Scopoletin, iron source (Fe-EDDHA and Fe-EDTA) on growth characteristics as well as peroxidase activity was studied. In addition, the effect of the different concentrations of Ca^{2+} and Mg^{2+} cations, the temperatures and EDTA concentrations were investigated at various levels. The results indicated that Scopoletin increased the shooting percentage and enhanced the growth quality. It also affected the peroxidase activity (α=0.05) significantly in comparison with the control. Results also revealed that applying Fe-EDDHA instead of Fe-EDTA in the culture media increased the rooting efficiency up to two fold in comparison with the control. There was also a direct relationship between the rooting rate and the enzyme activity, suggesting peroxidase as a predictive marker in the rooting phase of *Pistacia vera*. The kinetic properties of enzyme revealed the positive role of cations, 30°C (as an optimum temperature) and a negative role of EDTA on the enzyme activity.

Key Words

Fe-EDDHA, Peroxidase, *Pistacia vera*, Rooting, Scopoletin, Shooting.

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Evaluation of enzyme and relative gene expression of Ascorbate Peroxidase *(Cm APX)* under salt stress in sistan melon Landrace *(Cucumis malo L.)*

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A B S T R A C T

Salinity is one of the undesirable environmental factors which affects both growth and crop production. The stresses cause a wide range of reactions in plants including the change in gene expression and cellular metabolism and the change in growth rate and production. To study the activity of the antioxidant enzyme Ascorbate Peroxidase (APX) and the expression level of its encoding gene in three Sistan melon Landraces *(Cucumis malo* L.*)*, a factorial experiment was conducted in completely randomized design with three replications under control and salinity conditions (250mM and 350mM of NaCl). The relative expression of APX was compared by Real time PCR and enzyme activity was assayed in three melon landraces of Ghandak, Sefidak and Sefidak khatdar. According to the results, at 250 mM salinity level, the CmAPX gene expression showed an increase in comparison to control in all the three landraces and this increase in expression was significant at 5% in Ghandak and Sefidak landraces. At 350 mM salinity level, CmAPX gene expression was decreased in all the three studied landraces. At this level of salinity, the expression of CmAPX gene in the Khatdar Sefidak landrace significantly decreased (at 5% level) in comparison to control. More increase in antioxidant activity of APX with stable expression of CmAPX gene in Ghandak landrace was detected that shows this landrace could tolerate against salt stress better than the others. Decreased expression of this gene in Sefidak khatdar landrace with reduced enzymatic activity showed sensitivity of this landrace to salinity. We suggest that other genes related to antioxidant enzymes as well as their relationship with each others be examined in Sistan melon landraces.

Key Words

CmAPX, Gene Expression, Salt Stress, Melon, Real Time PCR.