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Novel Markers of the Antioxidant Response in Ornamental Species: Isolation and Molecular Characterization of the Tdp1 (Tyrosyl-DNA Phosphodiesterase) Genes

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The Tdp1 gene encoding Tyrosyl-DNA phosphodiesterase has been extensively investigated in mammalian and yeast cells, due to the role of this DNA repair enzyme in the protection against oxidative DNA damage (Hassine and Arcangioli, 2009 EMBO J 28: 632-640), while limited information on its function are currently available in plants. Due to their sessile lifestyle, plants are continuously exposed to harmful genotoxic environmental conditions which cause overproduction of Reactive Oxygen Species (ROS), affecting crop quality and productivity (Bray and West, 2005 New Phytol 168: 511-528). Within this context, the search for and the characterization of novel functions involved in the plant antioxidant response, particularly in the nuclear compartment, are required. In *Medicago truncatula* (barrel medic), the Tdp1 alpha and beta genes, encoding the two isoforms are up-regulated in the aerial parts and roots of plantlets exposed to heavy metals and water stress, respectively, suggesting for their role in the response to oxidative stress (Macovei *et al.*, 2009 53rd SIGA Annual Congress, 16-19 September, Torino, Italy). Ornamental crops, such as those included in the genera *Petunia* and *Pelargonium*, are routinely used in breeding programs aimed at obtaining new and desired gene combinations which control leaf type, flower colour, plant shape and architecture. The search for novel genotypes characterized by resistance to abiotic stresses is another relevant goal for ornamental breeders. The availability of marker genes, used as indicators of the plant antioxidant response, might help assessing the experimental conditions for the selection of new valuable genotypes. The isolation of Tdp1 genes from ornamental crops (kindly supplied from Albani and Ruggieri s.s.a., Italy) of the genus *Petunia* is currently in progress by Reverse Transcriptase-Polymerase Chain Reaction. Quantitative Real Time Polymerase Chain Reaction will be used to evaluate the expression profiles of the *Petunia* Tdp1 genes under oxidative stress conditions.

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Effect of STS, Akacid and 8-Hydroxy-Quinoline Sulfate on Vase Life and Colony Count of Preservative Solution in *Lilium candidum*

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Two levels of Silver Thio-Sulfate dip treatment (98.7 mg·l⁻¹, Distilled water; each for 6 hours) and 9 levels of preservative mixtures (Silver Thio Sulfate with concentrations of 25, 50 and 70 mg·l⁻¹; 8-HQS with concentrations of 150, 300, 450 mg·l⁻¹; Akacid with concentrations of 100, 300 & 500 mg·l⁻¹) on vase life of *Lilium Candidum* was investigated. The experiment conducted in a randomized design factorial arrangement (3 × 3 × 4), with three replications. One control was added to experiment to enable evaluation of the results in ANOVA design as well and mean comparison was done. The recorded traits included opening time for first, second and third florets, overall vase life, colony count of preservative mixtures at the end of period. Results show that STS dip treatment had no significant effect on research variables. STS in preservative mixtures in applied concentrations yielded the lowest vase life and colony count at all. Akacid while proved efficient in reducing the bacterial colony count just caused in more vase life in 500 mg·l⁻¹ without STS pretreatment. 300 mg·l⁻¹ 8-HQS caused highest vase life. There was a positive and highly significant correlation between vase life and colony count which raises the possibility that not all bacteria are detrimental to cut flowers vase life.

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Using SNPs Markers for Resistance Breeding in *Lilium*

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A molecular framework was developed to study two of the most serious diseases in *Lilium* (Fusarium and Lily Mottle Virus LMoV). Genetic maps were constructed using three different molecular marker systems (AFLP, NBS and DArT). QTLs for Fusarium resistance and the locus for LMoV resistance were mapped on these genetic maps. Even though, some DArT markers were successful converted into a user friendly PCR markers, the converting process was not easy, and the resolution of these maps should be further increased. Therefore, SNP (single nucleotide polymorphism) markers were developed in lily using 454 sequencing technology. The 454 sequencing technology enables the high throughput development of EST-SNPs markers. The co-dominant SNPs markers will be added to the currently available maps and thus high resolution integrated genetic maps can be expected. SNPs markers were developed through sequencing the cDNA isolated from lily leaf of 4 different genotypes and the detected SNPs were genotyped in two populations. The first is a F1 population of 98 genotypes (LA population: *L. longiflorum* 'White Fox' x Asiatic 'Connecticut King'), and the second is a backcross of 97 genotypes of 'Connecticut King' x 'Orlito' (= 'Connecticut King' x 'Pirate'). Next, Fusarium and the LMoV disease resistances will be mapped on these updated maps. All the linked DArT and SNPs markers to these two diseases will be identified. While, there is no need to convert SNPs markers which are ready to be used, the DArT markers will be converted into PCR markers. All the identified markers will be tested in a wide set of germplasm to be validated. The markers that show, after validation in germplasm, high significant correlations with Fusarium and LMoV will be nominated to be used for MAS in lily.

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Four Wild Species of *Magnoliaceae* Appear Different Resistances to Cold Stress

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There are many wild ornamental species of *Magnoliaceae* distributed in natural forest of Guizhou (China). They are still not popular in our life because of their weak cold hardiness. In order to acclimatize and utilize wild *Magnoliaceae*, the resistances to cold stress of four woody species such as *Michelia chapensis* Dandy, *Michelia crassipes* Law, *Parakmeria lotungensis* Law and *Tsoongiodron odorum* Chun were studied with two-year-old plants as experimental material. The results showed that there were significant differences in temperature of LD50, malonaldehyde content and SOD activity among the four species. *Parakmeria lotungensis* Law had the lowest temperature of LD50 at -17.07 °C while *Tsoongiodron odorum* Chun had the highest at -6.38 °C. Although the temperatures, at which plants achieved their highest malonaldehyde content *in vivo*, were always above their temperature of LD50 in the four species, *Parakmeria lotungensis* Law had the least distinction and *Tsoongiodron odorum* Chun the largest. SOD activity in *Tsoongiodron odorum* Chun increased obviously when the temperature dropped from 5 °C to -4 °C, but declined slowly while the temperature fall below -4 °C. However, the other species appeared little response in SOD activity to the temperature change.

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Pronamide-Induced Polyploidy in *Rhynchosytilis gigantea*

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The effect of pronamide on *in vitro* germinated seeds of *Rhynchosytilis gigantea*