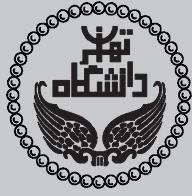


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Evaluation genetic control of yield, yield components, stem and flag leaf angle in bread wheat (*Triticum aestivum L.*) under drought stress condition

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Abstract

Combining ability, gene action, heritability and other genetic parameters in bread wheat under drought stress condition were evaluated using half diallel design. Nine wheat cultivars and 36 derived F1 assessed in a randomized complete block design with three replications in Shahid Bahonar University of Kerman research field in 2013. Evaluated genotypes showed high diversity for all traits. General combining ability (GCA) was highly significant for all traits and specific combining ability (SCA) was significant for all traits except stem angle. These results show the additive and non-additive effects on genetic control of these traits. Validity test of Hayman model showed the effect of epistasis on genetic control of all traits apart from stem angle. This dilemma makes breeding more obscure for these traits. Narrow heritability varied from 0.06 for flag leaf angle to 0.49 for stem angle. High Baker ratio, absent of epistasis and high narrow heritability show high response to selection in breeding programs for stem angle. Selection during segregation generation would be effective for this trait. Non-additive effects (dominant and epistasis) were highly important in genetic control of other traits. Bulk, single seed descent and double haploid methods are appropriate for these traits in breeding programs.

Keywords: combining ability, degree of dominance, epistasis, gene action, heritability.



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Genetic diversity of wheat genotypes by RAPD markers

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Abstract

The genetic diversity of 48 wheat genotypes was studied by RAPD markers at 2012 in laboratory of Department of Agronomy and Plant Breeding, University of Mohaghegh Ardebili. 10 primers from 70 used primers showed suitable banding patterns. These primers totally produced 73 polymorphic bands with mean 7.3 for each primer. The number of bands for 55 and 59 primers were 5 and 11, respectively. The total numbers of polymorphic bands within varieties verified between 7-57 bands that mean of bands number were 0.7 for 'Azadi' and 5.7 for 'Ghods'. There was remarkable diversity among varieties based on Nei's gene variation index. The primers 30 and 18 had the highest (0.408) and lowest (0.226) genetic diversity, respectively. The cluster analysis on based of Nei's distance and UPGMA method, distinguished four different groups. In this grouping, external varsities lied separately in second group. Thus, RAPD marker was successful in separating external from internal varsities. Based on principal coordinates analysis three coordinates accounted for only 61.7 percent of variation which indicated the proper distribution of markers across wheat genome under study because of relatively low percentage determined by the three first coordinates.

Keywords: cluster analysis, genetic diversity, polymorphism, principal coordinate analysis (PCoA), random primer.

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Evaluation of genetic diversity some of Iranian parsley native populations using morphological characteristics and physiological properties

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Abstract

In order to evaluate the genetic diversity some native populations of parsley Iran, 21 parsley populations collected from different regions of Iran and cultured as an augmented design in Shahid Chamran University of Ahvaz in 2011-12. Some of morphological characteristics including (Time of emergence, plant height, fresh and dry weight, Seed weight, Chlorophyll content) and antioxidant Properties (carotenoids, vitamin c, catalas and peroxidase) of these populations were evaluated. The analysis of variance showed that there were significant differences between genotypes in morphological characteristics and carotenoid. The principal component analysis declared four components which accounted 68.35 percent of total variation. Cluster analysis using the UPGMA classified populations to 3 main groups. The first group with shortest mean of emergence, highest mean fresh and dry weight per plant, and maximum amount of vitamin C and peroxidase activity and catalase compared to other groups as compatible the populations are introduced in the Ahwaz conditions. A total can be of the diversity among the native populations of parsley as a valuable genetic resource for the breeding works.

Keywords: catalase, cluster analysis, genetic diversity, parsley, peroxidase.

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Use multivariate analysis for the study of agronomic and morphological traits of sainfoin (*Onobrychis viciifolia* Scop) populations

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Abstract

This experiment was conducted to investigate the genetic diversity, relationship between morphological, agronomic and qualitative traits and to identify components of forage yield using some multivariate statistical methods in local sainfoin populations. The experiment was conducted as randomized complete block design with three replications in Agricultural and Natural Resources Research Center of West Azerbaijan, Iran. The results of ANOVA showed that there were significant differences among accessions for the studied traits. Results indicated that correlation coefficients of forage yield with number of branches per main stem, number of leave and number of stem were significantly positive but with harvest index leaf and degree day emergence was significantly negative. Forage yield had no correlation with plant height but plant height was correlated with number of leave. Principal component analysis revealed six components which justified more than 76 percent of the total variation, and classified as Yield, Dry weight, Plant size, Harvest index leaf, Morphological-phenological traits and Flowering rate, respectively. On the basis of stepwise regression analysis, number of stem, plant height and number of leave justified the majority of hay yield variation. Hence, these characters could be used for selecting high yield cultivars. Thus, direct effect of these three traits on forage yield were calculated 0/726, 0/226 and -0/984, respectively by Path analysis. Finally, on the basis of the current result in this research compared with previous findings, it can be concluded that multivariate statistical methods can be useful to find relationships between quantitative characters in sainfoin.

Keywords: correlation, path analysis, principal component, regression, sainfoin.

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Effect of water deficit stress on yield, water use efficiency and harvest index of sesame (*Sesamum indicum* L.) varieties

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Abstract

Drought stress is one of the important environmental factors reducing grain yield of plants in arid and semiarid regions. Study the effect of water deficit stress on yield, water use efficiency and harvest index of sesame varieties, this experiment was conducted as a split plot based on a randomized complete block design with three replications, at Agriculture and Natural Resources Research Center in Parsabad, Ardebil Province, in 2008-2009. In this experiment, irrigation was allocated to the main factor at three levels (50, 75 and 100 percent of plant water requirement) and ten sesame varieties. The CROPWAT-4 software was applied to calculate the amount and time of irrigation (water requirements of plants) in studied irrigation regimes. Results of the analysis of variance showed significant differences between cultivars and irrigation regimes for grain, biological yield, harvest index, water use efficiency for grain and biological yield traits. Interaction between irrigation regimes and cultivars were significant on grain water use efficiency and harvest index traits. Comparisons of means showed that under water stress condition, the grain and biological yield were decreased and the value of water use efficiency for grain, biological yield and harvest index were increased. In irrigation treatment with amount of 50 percent plant water requirement, the amounts of harvest index, grain water use efficiency for grain and biological yield were greater than other two treatments. 'Karaj 1', 'Ultan' and 'IS' varieties had the highest value and 'Indian 14' cultivar had the lowest value of biological yield, water use efficiency used for grain and biological yield. Therefore, 'Karaj 1', 'Ultan' and 'IS' varieties due to high yield, water use efficiency for grain and biological yield had ability to growing in water deficit regions.

Keywords: CROPWAT, drought, oil crops, sesame, water requirement.

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Evaluation of tolerance to water stress in some sesame genotypes

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Abstract

To study genetic diversity and drought tolerance in sesame genotypes, an experiment in a randomized complete block design with three replications in 2010-2011 was conducted at the Agricultural Research Field, University of Birjand under stress and non-stress conditions. The aim of this study was the testing of yield, tolerance index and bi-plot analysis. Materials included genotypes Birjand, Khusf, Torbate-jam, Safi-Abad, Darab 1, Darab 14, Bandar Abbas, Yellowite, Dashtestan 2, Dashtestan 5, Line 2 and Line TN234. The irrigation was carried in 100 and 200 mm evaporation of A class pan in normal and stress conditions respectively. The compound analysis of variance showed that the genotypes were different in the most traits except for capsule length, capsule width and the number of capsules. The drought stress was affected on the most traits except for capsule length, capsule width. Mean comparisons showed that the genotypes Bandar Abbas and Darab 1 have the highest and Safiabad and Darab 14 lines have the lowest YP. The genotypes Darab 1 and Line TN234 have highest and the genotypes Birjand and Darab 14 have the lowest YS. The maximum damage of drought stress was on the capsule number, economic yield, leaf number and harvest index and the minimum damage were on the auxiliary branch number, seed weight, capsule weight, plant height and biomass. Correlation analysis showed that STI, GMP, MP and Harm are appropriate and selection on their identified darab1 and TN234 line as desirable genotypes.

Keywords: cluster, components, correlation, index, plot.

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Genetic analysis of grain yield and its components in bread wheat genotype using diallel

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Abstract

To estimate the genetic components of yield and yield components in wheat genotypes crossed by diallel, in a randomized complete block design with three replications in Agricultural and Natural Resources Research Center of Tehran, were studied in the autumn of 2012. Seven parents of Gaspard, Chamran, WS-82-9, DN-11, M86-4, M86-6 and M86-12 with 21 hybrids were evaluated. Plant height, number of grain spike⁻¹, kernel weight, grain yield peduncle length⁻¹, the number of infertile florets and the number of days to flowering were evaluated. Analysis of variance showed significant differences between genotypes. Model Jinks-Hayman honest model for 1000-seed weight and grain yield showed Graphical analysis of traits with known that the peduncle length⁻¹, plant height, number of grain spike⁻¹ and kernel weight were affected by the partial genetic dominance effect and another traits were affected by over genetic dominance. The general combining analysis in WS82-9 line showed the highest GCA, effect for plant height, seed number, kernel weight, peduncle length and the grain number per spike⁻¹. Also, the DN-11 line and Charmin cultivar had a high GCA effect for kernel weight. So parents can be the breeding programs for the production of high yielding varieties of wheat used for bread. Hybrid of 2×1 and 3×5 showed high levels (s_{ij}) for the number of grains per spike and grain weight.

Keywords: combination, genetic effect, heritability, wheat.

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Compatibility among some almond cultivars and genotypes crosses using of fluorescence microscopy

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Abstract

Based on the self-incompatible and some cross-incompatible almond cultivars and genotypes; compatibility and pollen tube penetration to ovary were investigated in three crosses group among two cultivars and three genotypes in Shahed university in 2013. The first group included the genotype 'A_{9.7}' as female parent and 'Tuono' with genotypes 'A₂₃₀', 'A_{10.11}', 'A_{8.39}' as male parents, the second group contained 'Tuono' as the female parents, the 'Sahand' cultivar with genotypes 'A₂₃₀', 'A_{1.16}' and 'A_{9.7}' as male parents and third group included 'Shokofeh' cultivar as the female parent with genotypes 'Sahand', 'Tuono' and 'A₂₃₀', 'A_{1.16}' as male parent were. 120 hours after controlled crosses, pistils fertilized with different pollens, isolated and the frequency of pollen tube growth was evaluated by Fluorescence microscope in different parts of pistils. Results showed that crosses ♂'A_{9.7}' × ♀ 'Tuono' (mean 3.33 pollen tube penetrates in the ovary) ♂'A_{8.39}' × ♀ 'A_{9.7}' (average 4.33, pollen tube penetrates in the ovary) and ♀'A_{1.16}' × ♀ 'Shokofeh' (average of 4.33 pollen tube penetrates in the ovary) highest number of pollen tubes penetrated to ovary and so they are very compatible for orchard establishment and crossing programs. With respect to compatibility and percentage of fruit set in Crosses, to achieve optimum performance can of pollinizer 'A_{9.7}', 'A_{1.16}' and 'Sahand' In order to female parent 'Tuono', 'A_{9.7}' and Shokofeh were used.

Keywords: crosses, cross-compatible, ovary, pollen tube growth, self incompatibility.

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Synthetic amphiploid production from the crosses between some bread wheat cultivars and *Aegilops triuncialis* L.

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Abstract

Aegilops triuncialis L. ($2n=4x=28$; $C^tC^tU^tU^t$) is one of the tetraploid *Aegilops* species harboring valuable genes for resistance to many biotic and abiotic stresses. In the present study the bread wheat cultivars 'MV17', 'Navid', 'Omid', 'Pishgam', 'Zarin' were crossed with an accession of *Ae. triuncialis* and the resulted F_1 and F_2 (obtained by the selfing of F_1 plants) hybrids studied using the conventional cytogenetic methods. The cross ability (seed set per pollinated floret) of wheat cultivars was significantly different with an average of 46.24 percent. Chromosome counting confirmed the presence of 35 ($n=5x=35$; $ABDU^tC^t$) chromosomes in a sample of F_1 seeds. The mean frequency of F_2 seeds (per floret) was 3.54 percent. The F_2 seeds fell in two distinct classes of shrank and smooth seeds. Chromosome counting in root tip cells revealed 40-70 chromosomes in a sample of F_2 seeds, indicating the occurrence spontaneous amphiploid ($2n=10x=70$; $AABBDDU^tU^tC^tC^t$) formation in F_2 generation. Induced polyploidy using colchicine was also successful in one of the treated F_1 seeds, producing 70 chromosome seeds. Study of the metaphase I of the meiosis in F_1 hybrids on average revealed 7 rod bivalents and 21 univalents in each Pollen Mother Cell (PMC). F_1 seeds generally matured 30 days later than that of their wheat parents. The frequency of BC_1F_1 seeds resulting from crossing of F_1 with the wheat parent was about 1.27 percent which was lower than F_2 seed frequency.

Keywords: amphiploid, evolution, interspecific hybridization, polyploid.

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Diversity in some grape (*Vitis Vinifera L.*) cultivars and elite genotypes using morphological traits

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Abstract

In this study, the phenotypic diversity of grape varieties and genotypes of the Hamedan province was studied for preliminary selection of superior cultivars according to the morphological and pomological properties in order to use in breeding programs. For this subject, comparison and grouping of 32 grape cultivars and genotypes by using 61 traits including; 5 phenological and vegetative characters, 41 traits related to fruit and amount of resveratrol in 15 parts of plant was done according to grape descriptor and related methods. According to the results some traits such as spikelet weight, berry color, length of peduncle, length of berry tail, weight and length of seed and amount of cis & trans-resveratrol in seeds of ripe and unripe fruit had high coefficient of variation. Simple correlation coefficients between traits indicated the existence of significant, positive as well as negative correlations among some important vegetative, bunch, berry and seed measured traits. Factor analysis reduced the assessed traits to 10 main factors justifying 74.22 percent of total variation. Cluster analysis at Euclidean distance of 5 divided all cultivars and genotypes into seven main subclusters and traits such as growth vigor, bunch size, berry density in bunch, anthocyanin coloration of berry, TSS, thickness of berry skin, ratio of bunch weight to spikelet weight, bunch length and ratio of bunch length to bunch width were important factor in separation of main clusters. Based on the results, cultivars and genotypes including 'Kyoho', 'Ahmad Mowla'ii', 'Aangoshte Aros', 'Keshmeshi sefid', 'Keshmeshi ghermez', 'Asgari'Tehran' and 'Genotype1-row1' in some of the important traits such as late flowering habit, TSS and storage, table grape and amount of protein and resveratrol were better than the other cultivars and genotypes.

Keywords: cluster analysis, correlation coefficient, grape, morphological traits, resveratrol.

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