# Identification of S1 families as diploid pollinators for the development of salt tolerant hybrids in sugar beet

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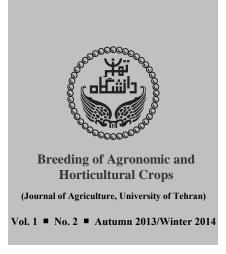
## Abstract

In order to identify and selection salt tolerant hybrids based on tolerance indices, 17 sugar beet three-way cross hybrids produced by crosses between 17 salinity improved S1 pollinators and a cytoplasmic male sterile (CMS) single cross as female, along with three control genotypes were grown in 2007 in Rudasht Station (Isfahan) under saline (12 dS/m and 8 dS/m for water and soil) and non-saline field conditions using a randomized complete block design with five replications. Five salt tolerance indices including stress susceptibility index (SSI), stress tolerance index (STI), mean productivity (MP), geometric mean productivity (GMP) and stress tolerance (TOL) were used to evaluate the white sugar yield in stress and non-stress conditions. Correlation analysis showed that MP, GMP and STI had significantly positive correlation coefficient with white sugar yield under both stress and non-stress conditions suggesting that these indices are more efficient for determining salt tolerant genotypes. Based on multivariate biplot, triple plot and cluster analysis, hybrids number 7233-29/19 * (7112*261), 7233-29/35 * (7112*261), 7233-29/34 * (7112*261), 7233-29/28 * (7112*261) and 7233-P.29 * MSC2 recognized as salt tolerant genotypes and hybrids number 7233-29/1 * (7112*261), 7233-29/5 * (7112*261) and 436 HYBRID were introduced as salt sensitive genotypes. Genotype number 7233-29/35 * (7112*261) with highest white sugar yield in stress condition was the best.

**Keywords:** hybrid, salt tolerance, sugar beet, tolerance index, white sugar yield.

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# Study the yield, quality, and infection index to powdery mildew disease in local populations of sainfoin in condition of Lorestan province

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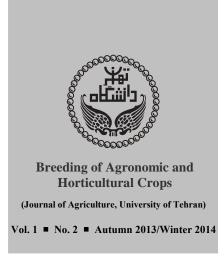3. Professor, Natural Resource Gene Bank Group, Research Institutes of Forest and Rangelands, Tehran, Iran

## Abstract

The *Onobrychis viciafolia* is one of the forage and rang land plants that is adapted and spread to different climates of Iran. One of the important disease of this plant is powder mildew in the Lorestan province which damages second and next cutting stages of this plant. To study the correlation between disease severity and forage quality, seeds of 34 populations were planted in field of Khorram Abad city with Ranomize block design by three replications on years of 2008-2011. Evaluation made against powdery mildew disease by four cuttings for three years but it was 2 years for forage quality. There was significant positive correlation between disease severity of infected plants with powdery mildew and percent of total protein (P<0.05). Population of Kermansah with maximum forage yield were higher than any other populations which was rather tolerance to powder mildew. Polycross and Oshnavieh populations with low disease severity index were tolerant. The disease was caused to decrease of forage yield and forage quality of the sainfion populations.

**Keywords:** *Onobrychis sativa*, quality and quantity of forage, real powdery mildew, relation, Sainfion.

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# Genetic study of some morphological characteristics in sugar beet using diallel cross analysis and GGE Biplot methodology

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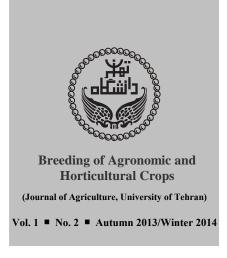
## Abstract

In order to study the mode of genetic control and heritability of morphological characteristics important for the improvement of root weight, sugar yield and white sugar yield in tropical beet, Griffing's diallel cross method along with the biplot display of diallel data were applied. Nine sugar beet lines including 7112-36, 7173, 474, 452, 261, 436-104, SB-FIROZ, RR607 and 436 were crossed in one-way diallel cross. Parental lines along with 36 consequent hybrids were implemented at Safiabad Agricultural Research Center, Dezful, Iran in 2009. The experimental design was a triple lattice with three replications. The traits root length, root diameter and crown height was measured. Analysis of variance showed significant differences among genotypes for root length and crown height at one percent and for root diameter at five percent probability levels. The highest broad-sense heritability was estimated for root length, a trait that was mainly controlled by non-additive gene effects. For root diameter and crown height, additive gene effects were found to be more important than non-additive effects. General combining ability (GCA) of genotypes was significant for all the three morphological characters at five percent probability level. The GGE bi-plot graphical analysis was used to evaluate the potential utility of the O-type lines. The parent 7173 had a positive, significant GCA for root diameter. The best hybrids for short root length, large root diameter and short crown height were 7173 × 436, 436-104 × 436 and 436 × 261, respectively.

**Keywords:** biplot, diallel cross, morphological characteristics, sugar beet.

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# Validation of common wheat genotypes for bread making quality using STS-PCR markers

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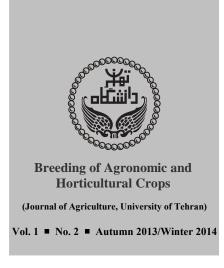4. Associate Professor, Institution of Agronomy and Plant Breeding, Karaj, Iran

## Abstract

Bread-making quality in hexaploeid wheat is a complex trait for breeding programs. High molecular weight glutenin subunits (HMW-GS) have an important effect on dough stability and elasticity. The *Glu-1* loci that are encoded these subunits are located on the long arms of group-1 homologues chromosomes of the A, B and D genomes. In this work we used PCR-based DNA markers to distinguish wheat bread-making quality. Good and poor wheat bread-making quality is associated with two allelic pairs at the *Glu-D1* complex locus, designated 1Dx5–1Dy10 and 1Dx2–1Dy12, respectively. Among the glutenin subunits encoded at *Glu-B1*, thec1Bx7 allele that is usually expressed with 1By8 or 1By9 subunits, contribute moderately well to good quality. The specific DNA markers as: 450, 576, 612, 527, 2373 and 669 bp respectively were characterized for 1Dx5, 1Dy10, 1Dy12, 1By8, 1Bx7 and 1Dy9 alleles. In this research, we report the development of an alternative screening method based on DNA markers at seedling stage for wheat bread making quality.

**Keywords:** bread-making quality, glutenin, molecular markers, PCR, wheat.

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# Discrimination and preliminary selection of self-compatible progenies resulted from controlled crosses in almond using specific primer SFF-SFR

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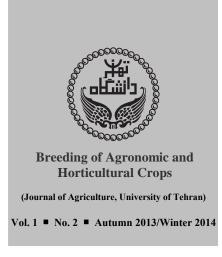
## Abstract

Self-incompatibility in almond and *Prunus* species is an important genetic trait that prevents self-fertilization. Self-incompatibility in almond is controlled gametophytically by the multiallelic S-locus. This study was done in order to identification and preliminary selection of self-compatible progenies resulted from controlled crosses in almond using specific primer SFF-SFR. Some important morphological traits of parental crosses were evaluated using almond descriptor. Also, offspring's ($F_1$) of five crosses including; A (Tuono × 101 Genotype), B (Supernova × 101 Genotype), C( Genco × Shahrood 21), D (Tuono × Shahrood 12) and E (Tuono × shahrood 17) were tested using PCR in order to DNA amplification and self-compatibility evaluation. Results of PCR method found that self-compatible progenies showed 449 bp band, while this band not observed in self-incompatible progenies. In addition, all self-incompatible progenies appeared no $S_1$ allele at any condition.

**Keywords:** almond, self-incompatibility, $S_f$-allele, S1-allele, SFF-SFR primer, PCR.

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# Evaluation of cytogenetical and morphological diversity of some Iranian *Trigonella foenum-graceum*

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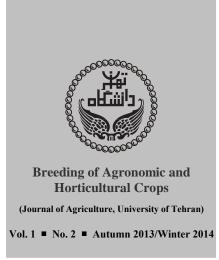
**Abstract**

Karyotypes of eleven Iranian populations of *Trigonella foenum-graceum* were investigated. Somatic chromosome numbers of examined populations were determined as 2n = 14. Chromosomal parameters were examined as follows: Long arm length (TL), Short arm, total chromosome length, arm ratio, r-value, form percentage of chromosome, total form percentage of karyotype. Chromosomes were mostly metacentric, but some submetacentric chromosomes were also observed. The genotypes number 3, 4, and 6 were classified into symmetric class of 2A and others stand to 1A. The Results of analysis of variance based on completely randomized design (CRD) showed a significant differences among the genotypes for all traits (P<0.01). Cutting dendrogram resulted from cluster analysis (UPGMA) based on 9 parameters.

**Keywords:** diversity, Karyotype, *Leguminosae*, morphological, *Trigonella foenum-graceum*.

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# Study of the inheritance of agronomic characters using line × tester crosses in sunflower (*Helianthus annuus* L.)

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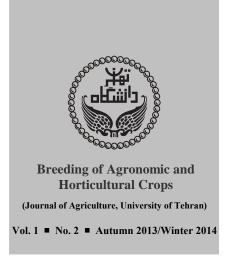4. Research scientist, Agricultural and Natural Resource, Research Center of West Azerbaijan, Iran

## Abstract

Determining general and specific combining ability of lines is necessary to use them as parents of hybrid varieties. In addition, estimates of the heritability of characters helps in selecting suitable breeding methods and predicting genetic gains of the traits. To determine general and specific combining abilities and gene effects of agronomic characters, five CMS lines and four restorer lines (tester) were crossed in a line × tester scheme. Hybrids were evaluated using a randomized complete block design with three replications. The results showed that CMS lines 52, 330, 344 and testers $R_{25}$ and $R_{50}$ had high general combiners for seed and oil yield. Hybrids $R_{25} \times 222$ and $R_{23} \times 52$ also showed high specific combining ability for seed and oil yield. For head dry weight, seed weight per head, seed yield with hull, seed yield, oil percentage and oil yield, non-additive genetic effects were important. Plant height and seed number per head were controlled by both additive and dominance effects.

**Keywords:** additive effect, dominance effect, general combining ability, heritability, specific combining ability.

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# Evaluation of morphological variations in different endemic *Thymus caramanicus* Jalas. species to Iran

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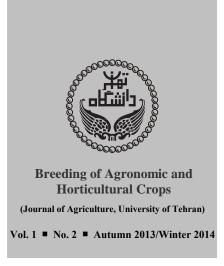
## Abstract

Evaluation of morphological variations in 70 genotypes of seven accessions of *Thymus caramanicus* Jalas. Growing in central Iran was carried out, for determining valuable characters for future breeding programs and medicinal purposes. In this study 30 quantitative and qualitative characters were evaluated. The results revealed great variabilities of important traits among populations. Results of simple correlation analysis showed the existence of significant, positive and negative correlations among some important characters. Factor analysis was also used for defining of the determinant factors and the characters constituted in each factor. Factor analysis showed that flowering stem length, second internode length, leaf length, leaf width, number of flowers per inflorescence, inflorescence length, number of bracts, calyx length and corolla length constituted the main factors. Principal component analysis explained over 84 percent of the variation related to main effective characters. Populations of *T. caramanicus* separated into two groups by cluster analysis using Ward method. Populations which were collected from Kerman and Esfahan provinces placed in a same group and populations from Semnan province were placed in an independent group. The most similar populations were Rabor and Kashan. The Rabor population characterized by having valuable traits such as largest flowering stem, longest second internode and largest leaf, can be introduced for breeding and medicinal purposes.

**Keywords:** cluster analysis**,** factor analysis, quantitative and qualitative characteristics, *Thymus caramanicus* Jalas.

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# Evaluation of salinity tolerance in wheat varieties and its relation with Molecular markers

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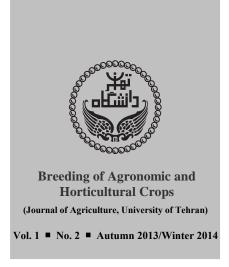4. Ph.D. Candidate, Plant Biotechnology, Department of Agronomy and Plant Breeding, Faculty of Agricultural Sciences, University of Mohaghegh Ardabili, Ardabil, Iran

## Abstract

Wheat (*Triticum aestivum* L.) is a major staple food crop for more than one third of the world population and is the main staple food of Asia. Over 800 million hectares of land throughout the world are salt affected. Salinity is a major obstacle to food production because it substantially reduces the average yield of major crops. This study was conducted to evaluate the response of 24 cultivars and genotypes of wheat (*Triticum aestivum* L.) to NaCl salinity at early seedling growth and correlation between affected morphophysiological traits and molecular markers. Genotypes grew in hydroponic nutrient solution, under control (tap water) and salt stress (45 and 90 mM NaCl) conditions. Results of ANOVA analysis showed that there are significant difference (in one percent P-value) between genotypes and all of measured traits in different levels of salinity. A total of 20 RAPD and 34 ISSR primers were tested to investigate genetic diversity in 24 wheat genotypes. Of these, only 15 ISSR and 6 RAPD primers produced polymorphic bands and were further used for genetic diversity and regression analysis. Cluster analysis was performed based on jaccard coefficient and all genotypes were divided into 4 groups. Average genetic distance between genotypes was 0.486, showed that there is considerable variation among these genotypes. Regression analysis, also, revealed that there are significant relations between measured traits and using markers were investigated.

**Keywords:** genetic variance, ISSR markers, RAPD markers, regression analysis, salinity stress.

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# Review Article
# Transgressive segregation phenomena in breeding of crop plants

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**Abstract**

Sometimes when hybridization in quantitative traits due to occurring of transgressive segregation phenomena in F2 and other generations, phenotypes are observed that are outside the scope of their parents. Transgressive segregates can be fixed via selfing and selection. Classical genetic and QTL studies know complementary action of genes as the main reason for the occurrence of the above phenomenon. The transgressive segregation phenomena through cross between parents with a positive and significant GCA values for all traits are somewhat predictable. It seems, to increase the likelihood of this phenomenon, bulk single seed and recurrent selection among breeding methods are the most effective methods. Transgressive segregation phenomena are widely used in the improved of various quantity characteristics such as tolerance to stresses such as cold, heat, drought and salinity.

**Keywords:** complementary action of genes, bulk single seed, hybridization, quantitative characteristics, recurrent selection.

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