Genetic studies on drought resistance in wheat

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Twenty five genotypes of wheat (T. aestivum) were screened underpots and field experiment at Sids Agriculture Research Station.Beni Sweif Governorate for some agronomic and morphologicalcharacters that are considered to be criteria for selectingdrought tolerance genotypes. The selected six wheat genotypesfrom the screening experiments were used to study the geneticsystem controlling the investigated characters and its relationsunder different soil moisture levels. The selected genotypes forthis study were mainly based on the data of grain yield anddrought susceptibility index (5). This index was calculated fromthe obtained data using the formula presnted by John et al.(1984).These six selected lines (parents) from screening experimentwere three tolerent which produce high grain yield per plant undermoisture stress levels (01 = 225 mm) and (D2 = 175 mm) as comparedwith the control treatment (DO = 500 mm). The value of droughtsusceptibile index (5) was low than one. indicating that parentswere drought tolerent. These parents are NS 732- PIMA, Veery ”s”and sakha 69. One moderate tolerent parent was selected. The parentPVN ”s” - MN70121 and two otheres i.e. (STP-YRx WALO (3)- ERA andKavco. were highly susceptible to water stress.The aims of the second experiment were to study the geneticIvariance components. phenotypic correlations and genotypiccorrelations between different characters under water stressconditions.The studied characters included, plant height. grain yieldper plant. number of kernels per spike. 1000 kernel weight,number of stomata on adaxial surface of flag leaf, rootlength. root dry weight. harvest index, total DNA contentand total RNA content. Most of the studied characters wereaffected by moisture stress treatments (D1) and (02) exceptnumber of stomata on upper flag leaf surface. The greatest decreased in the average of plant height, grain yield. number of kernels per spike. 1000 kernel weight. total DNA content andtotal RNA content were observed under (D2) treatment as comparedwith the control for al~ Fl hybrids and the parents. The line . :Veery ”s” was the most tolerent parent producing high grain yield,number of kernel per spike, root dry weight and longest root lengthunder water stress treatments (01=225 mm) and (D2=175 mm). The mostaffected parents were STP-YR x WALD(3)-ERA and Kavco which gave ~ >’, ;the lowest grain yield. number of kernels per spike and 1000 kernel (,0 0’weight. Both parents were considered susceptible ones.Additive gene effects were more important in the inheritanceof 1000 kernel weight and of stomata on upper flag leaf surface.Both additive and non-additive gene effects showed an equal Iimportance in the inheritance of plant height, grain yield per ’;.:plant, number of kernel/spike, root length, root dry weight,harvest index. DNA and RNA content under (01) and (D2) treatments.The averag degree of dominance was found to be overdominancefor all characters under different water lev~ls except, (106)for number of stomata on upper flag leaf surface which showedpartial dominance. The negative and positive alleles were notequally distributed among the parental population for most studiedatttibutes under all treatments.The dominant genes are in excess in the parents in case of grainyield per plant, number of kernels/spike, root length and harvestindex under (DO and 01) treatments. Low estimates of narrow senseheritability for the~e characters could indicate that the traitswere greatly influenced by the environmental factors.Parent (Veery ”5”) seems to possess most of the dominant genes forgrain yield per plant. number of kernels per spike, root length.root dry weight. harvest index and total DNA content.KavcO ”s” posses an excess of recessive genes for grain yieldper plant, number of kernels per spike. lOOOkernel weight,root length and total DNA content.Highly significant positive phenotypic correlation was foundbetween plant height and each of grain yield per plant, number

ofwhereas, a highly significant negative correlation was obtainedkernels per spike ,root length, root dry weight and RNA content ,"between plant height and harvest index. Highly significantpositive phenatypic correlation was estimated between grain yieldper plant and each of number of kernels per spike. 1000 kernelweight. root length, root dry weight,harvest index. root lengthroot dry weight. harvest index, total DNA content and total RNAcontent . Highly positive phenotypic correlation was found betweennumber of kernels/spike and each of root length, root dryweight, harvest index and total RNA content. The same trend was found between 1000 kernel weight and rootlength under all treatments, root dry weight and harvest index.A highly significant positive phenotypic correlation wasobserved between number of stomata and each of root dry weightand total RNA content under all treatments. Highly positive phenotypic correlation was found between rootlength and each of root dry weight under all treatments, DNADNA content, and RNA.The same trend was observed between root dry weight and eachof total DNA content and total RNA content.Highly positive phenotypic correlation was obtained betweentotal DNA and total RNA contents.A negative genotypic correlation was estimated between plantplant height and each of grain yield/plant, number of kernelsper spike and total RNA content. Grain yield/plant showed positive'genotypic correlation with each of root length, root dry weight.number of kernel per spike, 1000 kernel weight, total DNA contentand total RNA content under all treatments. A negative genotypiccorrelation was found between number of kernels and 1000 kernelweight.Positive genotypic correlation was detected between total DNAcontent and total RNA content under all treatments.It seems to be that any morphological or physiologicalimprovement that reduces transpiration or increase absorption ofsoil water could postpone water deficit and reduce the harmfuleffect of water stress.In wheat, rabid growth, extensive root system, low number ofstomata ,1000 kernel weight and number of kernels per spike may beconsidered good selection criteria for drought tolerance genotypes.Further research is required to study the effect of water stresson chloroplasts (cp DNA) and mitacondria (mt DNA) and RNA as well.