

Estimation of genetic parameters and chromosomal localization of QTLs controlling agro-physiological indicators of drought tolerance in agropyron using wheat-agropyron disomic addition lines

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Abstract

In order to locate QTLs controlling agro-physiological indicators of drought tolerance and estimation of genetic parameters, disomic chromosome addition lines of *Agropyron elongatum* (donor) into the genetic background of Chinese Spring (recipient) were tested in the field under rainfed condition. Analysis of variance exhibited significant differences for seed per plant (SPP), seed per spike (SPS), seed weight (SW), earliness (ERL), grain filling period (GFP), relative water content (RWC) and leaf water potential (LWP) indicating the presence of genetic variability and possible chromosomal localization of QTLs monitoring agro-physiological criteria of drought tolerance in *Agropyron*. Comparison of means showed that the disomic addition lines 3E, 5E, 6E, 7E and 3E had the highest grain yield (GY), SPP, SPS, SW, HI, RWC and LWP respectively, while chromosomes 3E, 4E and 2E revealed the lowest amount of ERL, GFP and RWL, therefore QTLs controlling agro-physiological indicators of drought tolerance in *Agropyron* are distributed on chromosomes 2E, 3E, 4E, 5E, 6E and 7E among which chromosomes 3E, 5E and 7E are outstanding. High broad sense heritability was observed for all characters except SPP and LWP expressing low genetic potentials, high effect of environment and absence of additive gene action in the inheritance of SPP and LWP. High co-heritability was observed between SPS and RWC (2.953), GFP and RWL (1.925), SPS and GFP (1.813) and SPS, harvest index (HI), ERL and RWC with GY exhibiting that selection of either of the characters would simultaneously affect the others positively.

Key words: Agropyron; genetic parameters; disomic addition lines; gene location, drought stress.

Abbreviations: CS_ Chinese Spring, DW_dried weight, EAC_efficiency of added chromosome, ECV_environmental coefficient of variation, ERL_earliness, FW_fresh weight, GC_genotypic coefficient of variation, GCOV_genotypic covariation, GG_genetic gain, GY_grain yield, HI_harvest index, LWP_leaf water potential, MSE_error mean square, PCO_phenotypic covariation, PCV_phenotypic coefficient of variation, RWC_relative water content, RWL_relative water loss, SI_selection index, SPP_number of seed per plant, SPS_number of seed per spike, SW_seed weight, TW_turgor weight, Ve_environmental variation, Vg_genotypic variation, Vp_phenotypic variation.

Introduction

Drought is a major constraint in wheat production and the most important contributor to yield reduction in semiarid regions (Ehdaie and Waines, 1993; Kristin et al., 1997; Andrew et al., 2000). Breeding drought-resistant cultivars is, therefore, a major objective in plant breeding programmes for rainfed agriculture in these regions (Ehdaie et al., 1991; Ehdaie and Waines, 1993). The evaluation of grain yield performance in areas exposed to frequent stress remains the most widely applied criterion for characterizing cultivar adaptation to stressful conditions. Breeding for drought tolerance by selecting solely for grain yield is difficult because the heritability of yield under drought conditions is low, due to small genotypic variance or to the large genotype – environment interaction variances (Blum, 1988; Ludlow and Muchow, 1990; Kószegi et al., 1996). Therefore evaluation of some of the physiological traits involved in stress tolerance was proposed (Blum, 1988). The incorporation of such attributes into a potentially high-yielding genotype may improve its adaptability and thus its response to environmental variability (Jaradat, 1991; Steven

et al., 1990). Species related to wheat, including both distantly related and progenitor species, represent a large reservoir of useful variability that can be exploited in wheat improvement (Jiang et al., 1994; Friebe et al., 1996). They contain indispensable genes required for wheat improvement especially under an unfavourable environment. They generally have tolerance to biotic and abiotic stresses and survive under low input conditions. Most of the wide hybridization studies reported have been performed to transfer major genes for resistance to biotic stresses like disease (Sharma and Gill, 1984; Gale and Miller, 1987; Knott, 1987; Islam and Shepherd, 1991; Jiang et al., 1994). Not much work has been done on the transfer of quantitative traits such as drought, cold and salinity tolerance. This is mainly because of the fact that these traits are mainly governed by minor genes with small effects (QTLs). Because of the complex nature of drought tolerance, little information is available on the chromosomal location of the genes conditioning drought tolerance and related physiological traits affecting drought tolerance (Farshadfar, 1995). Disomic

alien addition lines (DAALs), in which single pairs of homologous chromosomes from a related species are added to the wheat complement, are worthwhile material to identify alien chromosomes carrying useful genes and form the starting point for the cytogenetic transfer of alien genetic material to wheat (Gale and Miller, 1987). Genetic materials such as alien additions are valuable genetic resources for both plant breeding and basic research (Szakács and Molnár-Láng, 2010). Alien chromosome addition lines have been developed for a variety of plant species and have been used for many purposes such as introducing valuable traits to the recipient species, mapping genes and markers on introgressed alien chromosomes, examining alien gene regulation, understanding meiotic pairing behavior and chromosome structure and isolating individual chromosomes and genes of interest (Islam and Shepherd, 1990; Ananiev et al., 1997; Bass et al., 2000; Muehlbauer et al., 2000; Jin et al., 2004; Szakács and Molnár-Láng, 2010). By growing the disomic addition lines under stress and non-stress growing conditions it is possible to find genes useful for making wheat adaptable to unpredictable conditions (Reddy et al., 2004; Zhao et al., 2008). As grain yield and various morphological and physiological characters contributing to grain yield under drought are greatly influenced by various environmental conditions, therefore it is necessary to separate the total variation into heritable and non-heritable components with the help of genetic parameters such as: genotypic and phenotypic coefficients of variation, heritability, coheritability and genetic gain (Ali et al., 2009; Kahrizi et al., 2010). The present investigation was carried out (i) to locate QTLs controlling agro-physiological predictors of drought tolerance (ii) to estimate genetic parameters and genetic diversity of the characters studied and (iii) to study association between the traits and yield under raised conditions.

Results and discussion

Descriptive statistics and variability

Analysis of variance exhibited significant differences for SPP, SPS, SW, ERL, GFP, RWC and LWP (Table 1) indicating the presence of genetic variability and possible chromosomal localization of QTLs monitoring agro-physiological criteria of drought tolerance in *Agropyron*. No significant difference was found between the addition lines for GY, HI and RWC, but as F-test in the analysis of variance can only detect large differences between the genotypes, therefore non-significance in the table of analysis of variance does not mean no significant difference between addition lines for the characters GY, HI and RWC, that is why mean comparisons classified these traits in different groups (Bassiri, 1990). Several researchers reported phenotypic divergence and extensive variation for RWC in wheat (del Moral et al., 2003; Kashif and Khaliq, 2004), in barley (Martin et al., 1989) and in wild relatives of wheat (Farooq et al., 2002). Comparison of means (Table 2) showed that the disomic addition lines 3E, 5E, 6E, 7E and 3E had the highest GY, SPP, SPS, SW, HI, RWC and LWP respectively, while chromosomes 3E, 4E and 2E revealed the lowest amount of ERL, GFP and RWL, therefore QTLs controlling agro-physiological indicators of drought tolerance in *Agropyron* are distributed on chromosomes 2E, 3E, 4E, 5E, 6E and 7E among which chromosomes 3E, 5E and 7E are outstanding. Farshadfar et al. (2002) showed that most of the QTLs controlling drought tolerance criteria in *Agropyron* are located on chromosomes 3E, 5E and 7E, which collectively

constitute 84.3% of the additive genetic variance. Farshadfar (2011) also reported that QTLs monitoring genotype \times environment interactions in *Agropyron* are located on chromosome 7E. The importance of chromosomes 3E (Dvorak, 1993) and 5E (Mahmood and Quarrie, 1993) were also investigated for salt tolerance.

Efficiency of added chromosomes (EAC)

Efficiency of added chromosomes (Table 3) showed that maximum EAC for the characters GY, SW, HI, ERL, GFP, RWC, RWL and LWP belonged to chromosomes 3E, 6E, 7E, 4E, 3E, 7E, (1E and 7E) and 3E. The efficiency of added chromosomes in wheat-barley disomic addition lines under drought condition was attributed to chromosomes 4H and 5H (Vaisi and Farshadfar, 2011) and in wheat-rye disomic addition lines was related to chromosomes 3R and 7R (Farshadfar et al., 2003) with positive effect and enhancement of drought tolerance

Genetic variability

Genetic parameters are presented in Table 4. PCV and GCV were low for Earliness, GFP and RWC. On the other hand, GG had the highest amount for SPS. High broad sense heritability estimate was observed for all characters except SPP and LWP indicating low genetic potentials, high effect of environment and absence of additive gene action in the inheritance of SPP and LWP. High broad sense heritability ($h^2_{bs} > 0.5$) (Stanfield, 2005) in the genetic of other criteria is a suitable basis for reliable selection of the characters investigated (Kandasamy et al., 1989; Thiyagarajan, 1990). Heritability estimates along with genetic gain are very useful in predicting expected gain under selection instead of heritability alone. High heritability estimates with high GG in SPS, SW, RWC, Earl and GFP indicates that due to additive gene effects direct selection may be effective in the inheritance of these traits (Manju and Sreelathakumary, 2002; Soomro et al., 2010). HI and RWL showed very low level of GG exhibiting high influence of environmental conditions for their expression under irrigated condition. Comstock and Moll (1963) reported that more diverse the environmental population the smaller the estimates of genetic variance which supports the present results of low estimates of GG for HI and RWL. Low heritability estimates also explained the presence of non-allelic interaction in the inheritance of SPP and LWP. Considering the broadsense heritability estimates, all the traits except SPP and LWP were ranked as high heritable suggesting that the parents used to develop addition lines in early generations were desirable. The high heritability estimates also revealed that the additive and additive \times additive effects were more effective than dominance and dominance \times dominance effects in the genetic of all characters except SPP and LWP. High heritable characters were least affected by environmental fluctuations, hence simple selection method would be effective for improvement of these traits under water shortage condition. GY, HI and RWL showed high heritability estimates with low GG, while LWP exhibited low heritability but higher GG. Higher broad-sense heritability estimates do not necessarily provide high values of genetic gain, therefore heritability alone provides no indication of genetic progress for the trait under selection (Ansari et al., 2002; Hussain et al., 1999; Larik et al., 1997). High heritability associated with low GG for GY, HI and RWL was probably due to non-additive gene action (dominance and epistasis) (Sharma and Tyagi, 1990, 1991) and the presence of genotype \times environment

Table 1. Analysis of variance for agro- physiological characteristics of disomic addition lines.

SOV	df	Mean Squares									
		GY	SPP	SPS	SW	HI	ERL	GFP	RWC	RWL	LWP
Rep.	2	0.887	8.375	43.565	8.417	0.002	10.500	10.500	1.396	0.002	9.042**
Gen.	7	1.948 ^{ns}	9.714**	355.790**	102.082**	0.011 ^{ns}	22.613**	29.899**	58.607**	0.016 ^{ns}	51.137**
Error	14	0.200	2.946	38.825	10.356	0.001	2.310	2.310	4.633	0.001	17.280
CV%		22.63	22.89	22.93	20.66	23.36	2.65	2.50	3.05	20.10	13.95

**Significant at 1% level of probability, *Significant at 5% level of probability,

(GY: grain yield; SPP: spike per plot; SPS: seed per spike; SW: 1000 seed weight; HI: harvest index; ERL: earliness

GFP: grain filling period; RWC: relative water content; RWL: relative water leaf; LWP: leaf water potential

Table 2. Mean comparisons of agro-physiological characteristics of dsomic addition lines.

Gen	GY	SPP	SPS	SW	HI	ERL	GFP	RWC	RWL	LWP
1	1.67bc	5.67b	23.63c	13.17bc	0.14cd	58.00bc	60.00bc	69.23cd	0.19bc	34.67a
2	2.02abc	5.67b	24.73c	15.07bc	0.15bcd	58.00bc	60.00bc	66.93cd	0.12d	32.00ab
3	2.84a	9.00a	29.77bc	16.04b	0.20ab	53.00d	66.00a	65.57d	0.17cd	35.00a
4	1.26cd	9.00a	26.50c	9.53c	0.10de	61.00a	57.00d	69.80c	0.16cd	29.00abc
5	2.19ab	9.33a	38.43ab	9.60c	0.15bcd	56.67c	61.33b	69.05cd	0.24b	26.33bc
6	0.50d	5.67b	5.72d	25.17a	0.05e	60.00ab	58.00cd	70.90bc	0.15cd	31.00abc
7	2.73a	6.33ab	26.67c	23.30a	0.25a	54.00d	65.00a	79.53a	0.34a	23.33c
8	2.60a	9.33a	41.92a	12.73bc	0.18bc	58.33abc	59.67bcd	74.23b	0.15cd	27.00abc
LSD 5%	0.783	3.006	10.91	5.636	0.055	2.662	2.662	3.769	0.055	7.280
Min	0.50	5.67	5.72	9.53	0.05	53.00	57.00	65.57	0.12	23.33
Max	2.84	9.33	41.92	25.17	0.25	61.00	66.00	79.53	0.34	35.00

GY: grain yield; SPP: spike per plant; SPS: seed per spike; SW: seed weight; HI: harvest index; ERL: earliness; GFP: grain filling period; RWC: relative water content; RWL: relative water loss; LWP: leaf water potential.

Table 3. Efficiency of added chromosomes for the characters investigated.

Genotypes	EAC _{gy}	EAC _{SPP}	EAC _{SPS}	EAC _{SW}	EAC _{HI}	EAC _{ERL}	EAC _{GFP}	EAC _{RWC}	EAC _{RWL}	EAC _{LWP}
1E	-0.3576	-0.3922	-0.4363	0.0345	-0.2222	-0.0056	0.0055	-0.0673	0.2666	0.2212
2E	-0.2230	-0.3922	-0.4100	0.1838	-0.1666	-0.0056	0.0055	-0.0983	-0.2	0.1851
3E	0.0923	-0.0353	-0.2898	0.2600	0.1111	-0.0913	0.1060	-0.1166	0.1333	0.2962
4E	-0.5153	-0.0353	-0.3678	-0.2513	-0.4444	0.0457	-0.0447	-0.0596	0.0666	0.0740
5E	-0.1576	0	-0.0832	-0.2458	-0.1666	-0.0284	0.0278	-0.0697	0.6	-0.0248
6E	-0.8076	-0.3922	-0.8635	0.9772	-0.7222	0.0286	-0.0279	-0.0448	0	0.1481
7E	0.05	-0.3215	-0.3637	0.8303	0.3888	-0.0742	0.0893	0.0713	0.2666	-0.1359

GY: grain yield; SPP: spike per plant; SPS: seed per spike; SW: seed weight; HI: harvest index; ERL: earliness; GFP: grain filling period; RWC: relative water content; RWL: relative water loss; LWP: leaf water potential.

interaction. In such cases simple selection may not be rewarding (Kumar et al., 2002) and breeders can select desirable transgressive segregants. A successful breeding method will be the one exploiting the non-additive gene effects. The methods which mop-up the non-additive effects are restricted recurrent selection by the way of intermating the most desirable segregants followed by selection (Joshi, 1979) and a diallel selective mating (Jensen, 1978). The knowledge of the genotypic and phenotypic variances for each parameter is necessary to construct a definite selection index (Sprague, 1966). Considering the value of SI (Table 4) maximum SI was attributed to SPS and SW and minimum to RWL and HI, respectively.

P and G - matrices

The most common way to represent the pattern and magnitude of the genetic basis of a series of traits is the genetic variance – covariance matrix, also known as the G-matrix. G-matrix is extremely useful for predicting the response to selection and improvement of the efficiency of selection over a short period. As G-matrix includes genetic covariance as well, it can also help to predict the indirect response to selection of one character from selection on another trait. If the genetic covariance between two traits is different from zero, selection on one trait will affect response to selection on the other (Guillaume and Whitlock, 2007; Kearsey and Pooni, 2004). Genetic covariances between

traits can occur because of linkage/linkage disequilibrium and pleiotropy (Kearsey and Pooni, 2004). According to the results (Table 5), the highest genetic covariance observed between SPS and SW, ERL, GFP, LWP and between SW and RWC and between RWC and LWP, respectively. Also these results showed that (Table 5), the highest phenotypic covariance observed between SPS, SPP and GY; between SW, SPP and SPS and between LWP, SPS and RWC respectively. High values of genetic and/or phenotypic covariance between two traits may represent a high level of variation (genetic, phenotypic or both) between two traits. Also the results suggested that selection for low quantity of ERL, SW and LWP and high value of SPS and GFP will increase GY indirectly (correlated response). Much of the covariation in small populations is due to correlated gene frequencies and loose linkages which are transient. They can normally be removed by random mating and keeping the population size large. Tight linkages and certain types of pleiotropy, on the other hand are difficult to manipulate (Kearsey and Pooni, 2004).

Co - heritability

Coheritability deals with simultaneous inheritance of two characters. It takes both genotypic as well as phenotypic covariances into account and helps in understanding changes taking place in pairs of polygenic characters. The high values of coheritability estimate suggest that increase in one

Table 4. Estimates of genetic parameters for the investigated traits.

Traits	Mean	σ_G^2	σ_P^2	$cov_{P(GY,i)}$	$cov_{G(GY,i)}$	h_{bs}^2	$c-h_{bs}^2$	PCV	GCV	GG	SI
GY	1.98	0.583	0.783	-----	-----	0.74	-----	44.79	38.65	1.36	1.60
SPP	7.50	2.2565	5.202	0.665	0.537	0.43	0.807	30.41	20.03	2.04	10.70
SPS	27.17	105.653	144.478	7.253	6.344	0.73	0.875	44.19	37.79	18.11	297.6
SW	15.58	30.574	40.931	-0.566	-0.981	0.75	1.733	41.01	35.45	9.84	84.30
HI	0.15	0.0033	0.0046	0.050	0.044	0.77	0.877	43.89	38.49	0.10	0.0094
Earli	57.38	6.768	9.077	-1.664	-1.857	0.75	1.116	5.25	4.53	4.63	18.70
GFP	60.88	9.196	11.506	1.896	2.090	0.80	1.103	5.75	4.98	5.58	23.70
RWC	70.66	17.979	22.624	0.875	0.569	0.80	0.651	6.73	6.00	7.79	46.60
RWL	0.19	0.0047	.0061	0.021	0.023	0.83	1.093	40.77	37.22	0.13	0.013
LWP	29.79	11.282	28.565	-0.800	-0.758	0.39	0.978	17.84	11.11	4.27	58.80

σ_G^2 : genotypic variance; σ_P^2 : phenotypic variance; $cov_{P(GY,i)}$: phenotypic covariance; $cov_{G(GY,i)}$: genotypic covariance; h_{bs}^2 : broadsense heritability; $c-h_{bs}^2$: broadsense co-heritability; PCV: phenotypic coefficient of variation; GCV: genotypic coefficient of variation; GG: genetic gain; SI: selection index.

Table 5. Phenotypic (Lower off-diagonal matrix) and Genotypic (Upper off-diagonal matrix) covariance matrix.

	GY	SPP	SPS	SW	HI	ERL	GFP	RWC	RWL	LWP
GY										
SPP	0.665									
SPS	7.253	19.710								
SW	-0.566	-9.078	-49.047							
HI	0.050	-0.008	0.343	0.089						
Earli	-1.664	-0.702	-8.227	-2.780	-0.131					
GFP	1.896	0.750	8.521	3.967	0.152	-10.185				
RWC	0.875	-2.153	2.449	14.053	0.142	-1.697	2.238			
RWL	0.021	-0.017	0.054	0.147	0.003	-0.114	0.133	0.234		
LWP	-0.800	1.327	-11.598	-8.569	-0.156	0.244	-0.423	-19.29	-0.217	

GY: grain yield; SPP: spike per plant; SPS: seed per spike; SW: seed weight; HI: harvest index; ERL: earliness; GFP: grain filling period; RWC: relative water content; RWL: relative water loss; LWP: leaf water potential.

polygenic trait will lead to simultaneous increase in another coheritable character. Thus coheritability may form a more meaningful index for achieving the breeding objectives (Singh and Narayanan, 1993). The lower diagonal of table 6 has the co-heritability values for pairs of characters. The range of co-heritability was from -4.125 (between SPP and 1000SW) to 2.953 (between SPS and RWC). The negative co-heritability between SPS and GY declared that selection based on lower value of SPS will increase grain yield indirectly. High co-heritability was observed between SPS and RWC (2.953), GFP and RWL (1.925), SPS and GFP (1.813) and SPS, HI, ERL and RWC with GY indicating that selection of either of the characters would simultaneously affect the others positively. Romena and Najaphy (2012) suggested that improving grain yield is related to the balance of SC and RWC in wheat under rain-fed condition. Many researchers reported that low Co2 uptake is consequence of decreasing in relative water content of leaves and stomatal conductance (Chaves et al., 2002; Cornic and Massacci, 1996; Fischer, 2007; Krause and Weis, 1991; Lawlor, 1995; Lawlor and Cornic, 2002).

Materials and methods

Plant genetic materials

To locate QTLs controlling agro-physiological predictors of drought tolerance and estimation of genetic parameters in *Agropyron*, a set of 8 disomic chromosome addition lines (1E to 7E) of *Agropyron elongatum* ($2n=2x=14$) (Donor) into the genetic background of Chinese Spring (CS) wheat ($2n=6x=42$) (Recipient) were tested in the field (Table 7). The genetic materials were evaluated under rainfed condition for one year at Research field of Campus of Agriculture and Natural Resources of Razi University, Kermanshah, Iran, during 2009-2010 growing season. The experimental design was a completely randomized block design with three replications. The plots consisted of 2m and at 15×25 cm

inter-plant and inter-row distances, respectively. Each plot consisted of 100 seeds (each row 50 seeds). At the time of harvesting 5 single plants were selected randomly and grain yield was determined. The following agro-physiological characters were also measured:

Agronomic characters

Grain yield per unit area (GY), biomass (total above-ground dry matter), harvest index (HI=GY/biomass), yield components (number of seed per spike = SPS, number of spike per plant = SPP and 1000- seed weight = SW), days from sowing to heading (earliness = ERL) and grain filling period (GFP = maturity date - heading date) for each treatment at each replicate were measured.

Water relations

Relative water content (RWC)

Five flag leaves (0.5 g) were taken and weighed for fresh weight (FW). Then, segments were placed in distilled water for 24 h and reweighed to obtain turgor weight (TW). Thereafter the leaf segments were oven dried for 48 h in 72°C and weighed (dried weight, DW). RWC was calculated using the following formula (Eric et al., 2005):

$$RWC(\%) = \left[\frac{FW - DW}{TW - DW} \right] \times 100$$

Relative water loss (RWL)

A sample of five flag leaves were taken from each genotype and fresh weight was measured (FW). The leaves were then wilted at 35°C for 5 h and reweighed (W5H). Then the samples were oven dried for 70°C and weighed again (DW).

Table 6. Co-heritability estimates between traits.

	GY	SPP	SPS	SW	HI	ERL	GFP	RWC	RWL
GY	0.807								
SPP	0.875	0.603							
SPS	1.733	0.580	0.827						
SW	0.877	-4.125	1.158	-0.191					
HI	1.116	0.669	1.219	1.429	1.143				
ERL	1.103	0.690	1.211	1.301	1.121	0.773			
GFP	0.651	0.164	1.813	0.695	0.662	0.615	0.704		
RWC	1.093	0.118	2.953	0.701	0.881	0.934	0.943	0.885	
RWL	0.948	-2.518	1.558	-0.116	0.326	2.570	1.925	0.639	0.822

Table 7. Disomic addition lines and Chinese Spring (CS).

Codes	Genome	Chromosomes
1	1E	44
2	2E	44
3	3E	44
4	4E	44
5	5E	44
6	6E	44
7	7E	44
8	CS	42

RWL was calculated by the following formula (Farshadfar et al., 2000):

$$RWL = \frac{FW - W5H}{FW - DW} \times 100$$

Leaf water potential (LWP)

LWP was measured on flag leaves of each replication using a pressure chamber (Model PMS Instrument Co.).

Biometrical genetic analysis

The recorded data were subjected to analysis of variance using SAS V9.1 software to ascertain existence of variability among the genotypes.

The phenotypic and genotypic coefficient of variation (PCV and GCV), broad sense heritability (h^2_{bs}), genetic gain and co-heritability were estimated according to (Farshadfar, 2010) from the components of variance and covariance as follows:

$$V_E = MSe$$

$$V_G = (MSg - MSe)/r$$

$$V_P = V_G + V_E$$

$$PCV = 100 \sqrt{\sigma_p^2 / \bar{x}}$$

$$GCV = 100 \sqrt{\sigma_g^2 / \bar{x}}$$

$$ECV = 100 \sqrt{\sigma_E^2 / \bar{x}}$$

$$h^2_{bs} = \sigma_g^2 / \sigma_p^2$$

$$GG = (i \cdot \sigma_g^2 / \sqrt{\sigma_p^2}) 100 / \bar{x}$$

$$E(MSP_v) = \sigma_{e_1}e_2 + r \sigma_{g_1}g_2$$

$$E(MSP_e) = \sigma_{e_1}e_2$$

$$\sigma_{g_1}g_2 = (MSP_v - MSP_e) / r$$

$$\sigma_{p_1}p_2 = \sigma_{g_1}g_2 + \sigma_{e_1}e_2$$

$$\text{Coheritability} = (\text{Gcov } X_1X_2 / \text{Pcov } X_1X_2) \times 100$$

$$SI = K \times (V_p)^{0.5}$$

Where, V_e = environmental variation, MSE = error mean square, V_g = genotypic variation, r = number of replication, V_p = phenotypic variation \bar{x} is the mean, σ_g^2 is genetic variance, σ_p^2 is phenotypic variance, PCV = phenotypic

coefficient of variation, GCV = genotypic coefficient of variation, ECV = environmental coefficient of variation, h^2_{bs} = broadsense heritability, GG = genetec gain, the standard selection differential (i) for 5% selection intensity was 2.06, $\sigma^2_{g(1,2)}$ = genetic covariance of characters 1 and 2, $\sigma^2_{p(1,2)}$ is phenotypic covariance for characters 1 and 2, $\sigma_{e_1}e_2$ = environment covariance of character 1 and 2, SI = value of selection index for each character and $K = 2.06$ at 5% selection intensity (Kang et al., 1983).

Efficiency of the added chromosome (EAC)

The EAC for each line was calculated (Farshadfar et al., 2003) as:

$$EAC = [(Character \text{ of addition line} - Character \text{ of CS}) / Character \text{ of CS}] \times 10$$

Conclusion

High genetic variability was found between Wheat-*Agropyron* disomic addition lines. Most of the QTLs controlling agro-physiological indicators of drought tolerance are located on chromosomes 3E, 5E and 7E, hence they can be used for improvement of drought tolerance in wheat through chromosome engineering. The maximum efficiency of added chromosomes for improvement of the characters GY, SW, HI, ERL, GFP, RWC, RWL and LWP belonged to chromosomes 3E, 6E, 7E, 4E, 3E, 7E, (1E and 7E) and 3E. High co-heritability estimate indicated that selection of SPS, HI, ERL and RWC will simultaneously increase grain yield under rainfed condition. Maximum SI was attributed to SPS and SW and minimum to RWL and HI, respectively. High heritability associated with low GG for GY, HI and RWL was due to non-additive gene action (dominance and epistasis) effects and presence of $G \times E$ interaction. Simple selection may not be rewarding and in such cases breeders can go for selecting desirable transgressive segregants. The methods which mop-up the non-additive effects are restricted recurrent selection by the way of intermating the most desirable segregants followed the selection and diallel selective mating.

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