Short Communication



Genetics of index of drought resistance and seedling survival after desiccation associated with drought tolerance in bread wheat (*Triticum aestivum* L.)

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Wheat (Triticum aestivum L.), a major cereal crop is constrained by drought in many regions of the world. Because of severe limitations imposed by drought, development of cultivars with improved productivity under water stress is important for affected regions. But, the development of drought tolerant cultivars is hindered by lack of understanding of the mechanisms of drought tolerance and reliable selection techniques [1]. Although drought is a complex phenomenon, the different parameters influencing it were found to be under genetic control. It is, therefore essential to understand the genetic mechanism of the parameters associated with drought tolerance for its incorporation in a variety to obtain increased yield under moisture stress conditions. Two parameters viz., index of drought resistance (IDR) and seedling survival after desiccation (SSAD) used by Rand and Sharma [2] and Tomar and Kumar [3], respectively in their study for drought tolerance in wheat were also investigated here for their genetic control.

The experimental materials comprised of four spring wheat crosses *viz.*, S4/HPW89, Hindi 62/HS240, VL421/HS240 and VL421/PBW175 generated from three drought tolerant (S4, Hindi62 and VL421) and three drought susceptible (HPW89, HS240 and PBW175) parental genotypes, their F₁s, F₂s, back crosses (BC₁ and BC₂), second back cross generations (B₁₁, B₁₂, B₂₁ and B₂₂) and back cross selfed generations (B₁s and B₂s). All these populations were raised under glass house conditions for studying IDR and SSAD separately as described below:

1. Index of drought resistance (IDR): Ten seeds from each of the generation were grown in 20 \times 35 cm plastic tubes in soil and sand mixture in the ratio of 3:1. Three plastic tubes for P₁, P₂ and F₁; six for second back cross generations; twelve for BC₁ and BC₂; nine for B₁s and B₂s and twenty four in case of F₂ generation were kept. Five seedlings were retained per tube after germination and grown upto 2 leaf stage. The data were recorded for the length of the main seminal root (a), total length of first and second leaves (b) and width of the first leaf (c) using 12-14 days old seedlings. IDR was calculated over the standard variety VL421 by the method as suggested by Latyuk [4]:

2. Seedling survival after desiccation (%): Ten seeds in case of parents and F_1 's, twenty seeds in case of BC₁, BC₂, B₁s and B₂s, ten seeds in B₁₁, B₁₂, B₂₁ and B₂₂ and forty seeds of F₂ population were grown in a clay loam soil sand mixture of (3:1) in iron trays of size (50 × 38 × 10) cm. The seedling were well watered until 2-3 leaf stage. Water supply was then withheld until most of the seedling appeared to be wilting or dead. The trays were then re-watered, and the survival was counted after re-growth on 10th day.

The data of each population for both the characters were analyzed separately by joint scaling test of Cavalli [5] to determine the nature of gene action.

The results of joint scaling tests (3 and 6 parameter model) showed that additive-dominance model and digenic epistatic model were in adequate for both the characters (Table 1 and 2). This indicated that higher order interactions and/or linkage might be governing these characters. However, the various gene effects were estimated on the basis of 6 parameter model.

Presence of additive gene effects for IDR and complementary epistasis (h and I having same sign) for SSAD in the cross Hindi62/HS240 indicate the effectiveness of early selection for IDR and scope of obtaining transgressive segregants in later generations for SSAD.

Duplicate epistasis was present in the cross S4/HPW89 and VL421/PBW175 along with additive component and I type of interaction in the first cross for IDR, while for SSAD only cross V1421/PBW175

Table 1. Estimates of genetic parameters for index of drought resistance (IDR) in bread wheat

Crosses	χ2	m	d	h	i	j	I	Epis-	χ2
	(9 d.f.)							tasis	(6 d.f.)
$S_4 \times HPW89$	93.50*	164.91*±14.47	10.34*±3.03-	-237.81*±35.19	-101.85*±14.27	-16.91±11.89	141.65*±22.29	D	41.60*
Hindi62 imes HS240	20.68*	69.73*±17.91	12.25*±6.24	30.87±43.01	-1.99±18.71	-5.47±16.93	-1.92±30.95		20.54*
$VL421 \times HS240$	177.67*	117.78*±12.08	-39.74*±4.10-	-122.33*±31.62	-67.42*±11.82	98.87*±13.90) 59.20*±23.99	D	97.07*
VL421 × PBW175	34.41*	81.40*±13.71	14.98 <u>*±6.05</u>	-78.85*±35.41	7.32±15.67	-26.22±16.53	-63.77*±23.81	D	14.16*
*P ≤ 0.05									

Table 2. Estimates of genetic parameters for seedling survival after desiccation (SSAD) in bread wheat

Crosses	χ2	m	d	h	i	j		Epis-	χ2
	(9 d.f.)							tasis	(6 d.f.)
$S4 \times HPW89$	380.41*	100.34*±5.40	0.87±2.15	39.34*±15.83	-48.69*±5.60	-31.57*±6.81	-10.32±12.37		114.89*
$Hindi62 \times HS240$	84.97*	106.55*±7.97	-0.29±1.28	124.58*±22.15	-40.64*±7.99	-0.93±8.10	94.68*±14.75	С	42.11*
VL421 × HS240	132.66*	49.30*±5.61	27.77*±1.09	50.32*±15.63	20.24*±5.73	3.54±6.26	-24.22*±10.61	D	132.66*
VL421 × PBW175	317.86*	70-61*±5.21	8.92*±1.69	-18.75±14.48	-14.06*±5.28	-31.29*±6.00	36.18*±10.10		283.71*
*P ≤ 0.05									

showed additive gene effects along with I type of interaction. Duplicate epistasis was also observed in the cross VL421/HS240 for both IDR and SSAD along with j and I type of interaction for IDR and additive, dominance gene effects and i type of interaction for SSAD. So in these crosses for the improvement of both the characters, the approach of biparental mating/intermating among the selects in early generations could be advantageous.

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