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Variability, Correlation and Regression Analysis in Third Somaclonal Generation of Barley

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Abstract

Assessment of variability for qualitative and quantitative characters in twenty five SC_3 (somaclonal third generation) families of barley along with their mother cultivar Dissa was made. Two male sterile plants appearing like 'gigas' were obtained in one somaclonal family. Such plants had empty anther sac and spikelets remained open with wide angle for longer period. Segregation for two rowed and six rowed barley plants occurred in four somaclonal families where mother cultivar was six rowed. Considerable amount of variability existed among somaclonal families for plant height, tiller number, spike area, spikelet and grain number, 100 grain weight and grain yield per plant. Tiller number, grain number and 100 grain weight were the major characters for variation in grain yield in the population.

Key words: barley, SC_3 generation, qualitative and quantitative characters, somaclonal variation.

Introduction

Creation of genetic variability through tissue culture and its exploitation have become a major thrust for crop improvement programme. Somaclonal variation found among regenerated plants may not be stable because of physiological disturbances and epigenetic causes. In advance somaclonal generations, these nongenetic causes are eliminated and whatever variation is found is due to genetic changes. Somaclonal variation in advanced generations is sufficiently stable and can be potentially used in crop improvement programme. Variation in morphological characters and *Helminthosporium* resistance in SC_2 generation and biochemical and cytological characters in SC_3 seeds of barley have been reported (Kole and Chawla, 1992; 1993). The present investigation was undertaken to study variability for qualitative and quantitative characters and to determine inter-relationships among yield and yield contributing characters in third somaclonal (SC_3) generation of barley.

Materials and Methods

The experimental materials comprised second generation seed progenies (SC_3 generation) obtained from 25 initial somaclones, regenerated from *in vitro* selected resistant calli against *Helminthosporium sativum*, derived from immature embryo explant of cultivar Dissa. The detailed procedures of regeneration are described earlier (Chawla and Wenzel, 1987). The 25 SC_3 families along with parent cv. Dissa were grown at Pant Nagar(29^oN, $79^o3'E$, 243.83msl), Uttaranchal, India during winter season in randomized block design with 3 replications. Each plot consisted of 5 rows of 2m length with intra- and inter-row spacings of 7.5 and 25cm. Plants

were carefully observed for changes in qualitative characters. Data were recorded on ten randomly selected plants from each plot in each replication for nine quantitative characters viz., plant height, tiller number per plant, days to heading, exertion of peduncle from flag leaf, spike area, spikelet number and grain number per spike, 100 grain weight and grain yield per plant. Estimates of phenotypic and genotypic coefficients of variation (Burton, 1952), heritability in broad sense and genetic advance (Johnson *et al*., 1955), correlation coefficient (Robinson *et al*., 1951) and regression analysis (Draper and Smith, 1981) were done following standard statistical methods.

Results and Discussion

Two plants in the progenies of one somaclonal family were quite distinct from early growth phase which appeared like *gigas*. Chromosome counts from root tip of SC_3 seeds of this family indicated these plants to be normal diploid. These plants were male sterile with empty anther sac and florets remained opened for longer time with wide angle. Such male sterility is due to segregation of nuclear recessive gene(s), induced through the process of tissue culture.

Segregation for two rowed and six rowed barley plants occurred in the progenies of four somaclonal families where the parent variety Dissa was six rowed. Segregation of such somaclonal variants is due to genetic changes, induced through the process of tissue culture.

Among the quantitative characters studied mean squares due to somaclonal families were highly significant for all the characters studied, except days to heading and exertion of peduncle from flag leaf, indicating presence of somaclonal variation. Somaclonal variation for morphological traits has been reported by Dunwell *et al*. (1986) and Sozinov *et al*. (1988). The estimates of phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) were low for plant height and 100 grain weight; moderate for spike area and number of spikelets and grains per spike; and high for tiller number and grain yield per plant (Table 1). The estimates of heritability were low for plant height and spike area; moderate for tiller number and grains per spike and grain yield per plant; and high for spikelet number and 100 grain weight. Genetic advances were moderate for tiller number, spikelet number and grain yield per plant and low for rest of the characters. Moderate genetic advance coupled with moderately high to high heritability for spikelet number and grain yield indicates preponderance of additive gene action for these two characters. The results of heritability and genetic advance are in agreement Sinha and Saha (1999).

The results on genotypic and phenotypic correlations (Table 2) indicated that grain yield per plant had positive and significant correlations with tiller number, spikelet and grain number per spike and 100 grain weight at both genotypic and phenotypic levels. Similar results have been reported by Singh (1999). Among inter-character correlations, tiller number had positive and significant correlation with spikelet number, grain number and 100grain weight. Spikelet number also showed positive and significant correlation with 100 grain weight, although two rowed barley plants having less spikelet number had higher test weight. The overall results of correlation indicated the scope of selection of plants having higher tiller, spikelet and grain number with higher test weight which would be high yielding.

The stepwise multiple regression analysis following step up procedure indicated tiller number was the most important variable accounting 40.4% variability in grain yield. The other two variables that were sequentially included in the regression equations were grain number per spike and 100 grain weight with the corresponding R^2 values of 0.52 and 0.60. This indicates that tiller number, grain number and grain weight jointly decided 60 % variation in grain yield. Therefore, selection of plants should be based on the above three character for improvement in grain yield.

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Table 1. Mean, range, phenotypic and genotypic coefficients of variation, heritability and genetic advance for seven quantitative Characters

Characters	Mean	Range		Coefficients of variation (%)		Heritability in broad sense (%)	Genetic advance as % of mean
		Min.	Max.	Phenotypic	Genotypic		
Plant height (cm)	81.57	75.03	98.00	9.27	5.58	36.3	6.93
Tiller number / plant	21.73	9.33	30.33	28.29	21.76	59.1	34.47
Spike area (cm2)	25.77	20.78	34.76	19.81	12.33	38.75	15.79
Spikelet No.	64.50	51.99	87.27	20.08	18.13	81.44	33.67
Grain No.	50.75	35.4	64.3	16.03	12.64	62.23	20.53
100 grain weight (g)	3.7	2.79	4.26	9.30	8.23	78.40	15.14
Grain yield per plant (g)	24.04	11.5	34.7	27.61	22.98	69.00	39.39

Table 2. Genotypic (G) and phenotypic (P) correlation coefficients among seven quantitative characters in SC_3 generation of barley

		Tiller No.	Spike area	Spikelet No.	Grain No.	100 grain weight	Grain yield per plant
Plant Height	G	0.527**	0.086	0.625**	0.021	0.111	0.194
	P	0.123	0.123	0.340**	0.038	0.028	0.034
Tiller No.	G		0.393**	0.268*	0.436**	0.247*	0.673**
	P		0.100	0.236*	0.342**	0.214	0.628**
Spike area	G			0.521**	0.891**	0.089	0.374**
	P			0.431**	0.495**	-0.009	0.179
Spikelet No.	G				0.525**	0.391**	0.365**
	P				0.452**	0.295**	0.308**
Grain No.	G					0.012	0.697**
	P					-0.104	0.532**
100 grain weight	G						0.458**
	P						0.396**

*, ** : Significant at P=0.05 and 0.01, respectively.