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Genetic Evaluation of Some Biochemical Characters of Barley Varieties Grown under Salinity

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Abstract. The main objective of this study was to investigate the genetic system controlling the nucleic acids and the total protein content in barley grown under different concentrations of salinity including the control treatment.

The additive genetic variance was more important than dominance genetic variance in the inheritance of DNA content under S1 treatment. While additive and dominance types of genetic effects showed an equal importance in the inheritance of RNA content under S0 treatment and total protein content under S1 treatment.

The average degree of dominance was found to be over dominance for DNA content, RNA content and total protein content. The negative and positive alleles were somewhat equally distributed among the parental populaitons in most cases. The dominant genes are in excess in the parents in case of RNA content under S0 treatment and DNA content under S1 treatment.

The low values of narrow-sense heritability in all cases indicated that the traits were greatly influenced by the environmental factors.

The variety C.C.89 seems to possess most of the dominant genes for DNA content under S0 treatment. California Mariout possess an excess of recessive over dominant genes under S2 treatment for total protein content. While dominance excess recessive under S0 treatment for DNA content.

Introduction

Chloride salinity suppressed cell enlargement and cell division proportionally in leaves and that DNA and RNA levels decreased per leaf, [1]. It was suggested that the sites most inhibited under chloride salinity would be protein and nucleic acid, [2]. Changes in nucleic acid content and total protein content often reflect important biological events. Therefore, a knowledge of the genetic basis of the nucleic acids and total protein content is important.

In view of the presence of the widespread genotype-environmental interactions, genetical analysis from single environment could hardly provide reliable and general

general picture regarding the genetic mechanism controlling the most important biological macromolecules, i.e. nucleic acids and total protein content. The experiment was designed to determine the nature and magnitude of gene effects controlling nucleic acids and total protein contents from a 6-parent diallel set of barley *(Hordeum vulgar* L.).

Materials and Methods

Six diverse parents, viz, (1) C.C. 89, (2) C.C. 163, (3) Borg El-Arab 6, (4) California Mariout, (5) Line 474.1 and (6) Line 272.3.4 and their all possible crosses, including reciprocals, were grown under salt treatments of 5000 ppm (S1) and 10,000 ppm (S2) along with their control (S0). A sand culture technique developed by Heakal *et al.*, [3] was used. The Hoagland No. 1 nutrient solution was used as the base nutrient media. Also calcium was incorporated in the solutions using CaCl2 and adjusted at 25% of the equivalents of Na+ present.

Sampling was carried out at the tillering stage using fresh leaves. Nucleic acids and protein were extracted by applying the methods reported by Cherry [4]. Total protein was estimated photometrically according to the technique adapted by Lowery *et al.*, [5], using Folinc-phenol reagent (1N).

Diallel analysis was done according to the methods poroposed by Hayman [6 and 7] and Jones [8] was employed to study the genetics of various attributes reported in this investigation. Narrow-sense heritability was calculated according to Mather and Jinks [9].

Results and Discussion

The parents showed genetic diversity for DNA content in case of S0 and S1 treatments and for RNA content just in case of the control treatment. Significant variances due to the F1's revealed genetic variability in the F1 hybrids (Table 1). The diallel analysis as outlines by Jinks [10] and Hayman [6 and 7] is an attempt to partition phenotypic variation into genotypic and environmental components and to further subdivide genotypic variation into its additive and dominance gene effects. Those values can be used to draw inferences about the genetic system controlling these characters. The analysis of variance of Wr-Vr (Table 2) showed that the differences between arrays were highly significant for DNA content under S0 treatment and RNA content under S1 treatment, indicating the presence of either non-independent gene distribution or epistatic effects.

The analysis of variance of diallel table as constructed by Hayman [6 and 7] and modified by Jones [8] was applied to test additive and dominance gene effects for all

Table 1. Analysis of variance for biochemical characters of six barley varieties grown under salinity stress

	D.F.	DNA content mg/g D.W.			RNA content mg/g D.W.			Protein content mg/g D.W.		
		S0	S1	S2	S0	S1	S2	S0	S1	S2
Total	83	1.56	0.38	0.19	5.92	1.27	0.55	375.30	235.94	149.96
Blocks	3	4.20	0.57	0.51	4.15	6.41	0.12	27.12	309.04	33.57
Genotypes	20	2.44*	0.78**	0.32**	17.70**	2.80**	0.85*	647.24*	607.15**	373.66**
Parents	5	2.29*	0.86**	0.18	12.09**	0.74	0.37	240.30	181.48	55.51
Crosses	14	2.59*	0.81**	0.35**	17.34**	3.43**	0.96*	567.70*	802.51**	304.43**
Par vs. Crosses	1	1.16	0.001	0.64**	50.77**	4.37**	1.72*	3795.63*	0.38	2933.66**
Error	60	1.14	0.23	0.13	2.08	0.50	0.47	302.07	108.55	81.22

*, ** are significant and highly significant at 5% and 1% levels of probability, respectively.

Table 2. Analysis of variance of Wr-Vr values in the six parents dialel cross in barley grown under salinity stress

	D.F.	DNA content mg/g D.W.	RNA content mg/g D.W.	Total protein content mg/g D.W.
S0 = control				
Blocks	3	0.07	19.43	30,780.86
Arrays	5	0.86*	5.94	14,029.94
Error	15	0.09	3.84	37,204.95
S1 = 5000 ppm				
Blocks	3	0.15	0.24	37,488.36
Arrays	5	0.05	2.04**	31,340.58
Error	15	0.02	0.20	12,341.91
S2 = 10,000 ppm				
Blocks	3	0.05	1.60	54,661.88
Arrays	5	0.03	0.16	13,766.24
Error	15	0.03	0.06	8,630.78

*, ** are significant at 5% and 1% levels of probability, respectively. 8 Significant at 5% level probability.

traits under different treatments (Table 3). Highly significant values for the additive component (a) were found for DNA content in S1, RNA content in S0 and total protein content in S1. This results revealed the existence of substantial additive gene effects under such conditions. The significant effect of (b) component indicated that dominance was present and played an important role in the inheritance of all traits under all treatments except DNA content under S2. The existence of significant (b1) value illustrated directional dominance effect in the inheritance of DNA content in S2, RNA content in S0 and total protein content under both S0 and S2 treatments. On the other hand, significant (b2) component suggested unequal distribution of the dominant alleles among the six parents for DNA content under S1, RNA content in case of S0 and total protein content under salinity treatments.

By means of second degree statistics from the diallel table, as proposed by Hayman [6] and Jinks [10], various genetic parameters were computed to provide further information about each trait. Estimations of such parameters are presented in Table 4. The D component due to the additive effects of the gene gave negative values and were not significantly different from zero in case of DNA content, RNA content under S2 treatment, and total protein content under both S0 and S2 treatments. These results indicated that the differences between the parents were proba-

Table 3. Analysis of variance of diallel cross for three biochemical characters of barley

	D.F.	Treatment	DNA content mg/g D.W.	Total protein RNA content mg/g D.W.	content mg/g D.W.
a	5	S0		7.39**	56.08
		S1	0.22**		281.94**
		S2	0.03	0.06	38.94
b	15	S0		3.43**	197.05*
		S1	0.19**		108.68**
		S2	0.10	0.26*	111.58**
b1	1	S0		12.71**	948.79**
		S1	0.00		0.09
		S2	0.16*	0.43	733.49
b2	5	S0		4.66**	146.49
		S1	0.31**		195.75**
		S2	0.04	0.09	71.75
b3	9	S0		1.72**	141.62
		S1	0.14*		72.37*
		S2	0.12**	0.34**	64.60**

(a) additive effects of genes, (b) dominance effects of genes, (b1) mean dominance deviaiton, (b2) dominance deviation due to the rth parent and (b3) a part of dominance deviation that is unique to each F1.
* and ** significant at the 0.05 and 0.01 levels of probability, respectively.

bly due to environmental variation [11]. For RNA content under S0 treatment and total protein content under S1 treatment, the D and H1 components were found to be statistically significant, revealing that both additive and non additive types of gene action were involved. For RNA content at S0 and total protein content at S1, the H2 component was highly significant and smaller than H1, indicating unequal allels frequency. The overall dominance effects of heterozygous loci h2 were highly significant just for RNA content under S0 treatment, which indicated that the effect of dominance is due to heterozygosity.

Table 4. Estimates of genetic parameters and ratios for the three studied attributes of barley varieties grown under salinity stress

	DNA content mg/g D.W.			RNA content mg/g D.W.			Total protein content mg/g D.W.		
	S0	**S1**	**S2**	**S0**	**S1**	**S2**	**S0**	**S1**	**S2**
D		0.16	–0.04	3.01*		–0.33	–182.25	21.36*	– 65.85
F		0.19	–0.04	2.83		–0.35	–284.79**	– 53.76**	– 63.74
H1		0.91	0.53	15.90**		1.53*	672.74**	528.38**	440.26
H2		0.71	0.53	11.40**		1.60*	528.13**	347.21**	362.65
h		0.04	0.06	11.78**		0.82	785.56**	14.52	436.72
E		0.23	0.13	2.08*		0.47	302.07**	108.55**	81.22
$(H1/D)^{1/2}$		2.83		2.03				4.97	
H2/4 H1		0.20		0.18				0.16	
$\frac{(4\,DH1)^{1/2}+F}{(4\,DH1)^{1/2}-F}$		1.66		1.51				0.60	
h/H2		0.06		1.03				– 0.04	
Heritability %		17.10		32.21				39.61	

The estimated degree of dominance was more than one for DNA content at S0 and total protein content at S1 treatments, suggesting overdominance. The estimate of the ratio (4 DH1)1/2 + F/(4 DH1)1/2 – F which gives the relative estimate of dominant and recessive allels gave values over 1 in case of DNA content at S1 and RNA content at S0, revealing that for every recessive gene there were about 2 dominant genes or gene groups. The value below unity, in case of total protein content at S1, indicated that the recessive genes among the parents were more important than the dominant genes. Low estimates of narrow-sense heritability were found indicating that the traits were greatly influenced by the environmental factors.

The genetic relationship among the selected parents and progenies was analyzed using the technique of Jinks [10] – Hayman's [7] diallel cross analysis and the graphical analysis which was based on the variances and the covariances of the arrays.

The significance of the regression coefficient plus the uniformity of Wr-Vr over arrays satisfy the assumptions underlying the theory of the diallel-cross analysis in case of DNA content under S1 treatment (Fig. 1). The distribution of parents on the

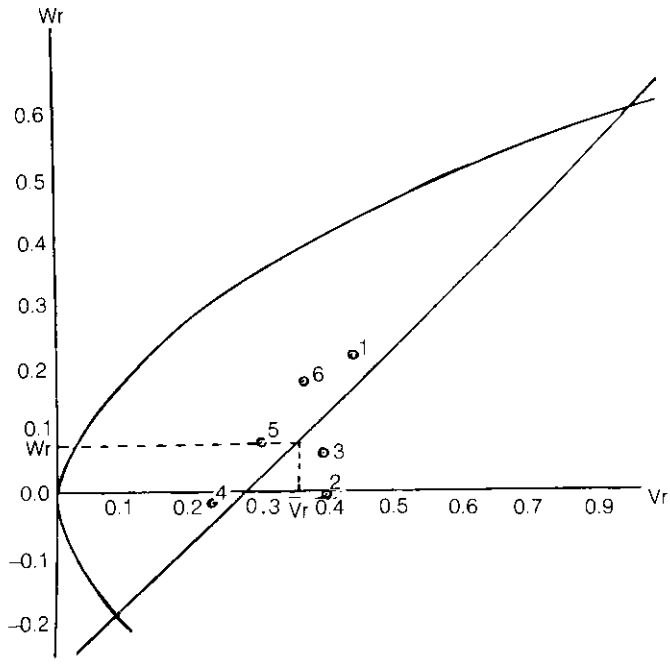

Fig. 1. Wr,Vr graph analysis for the DNA content under S_1 treatment.

diallel graph places "C.C. 89" at the recessive side and "California Mariout" at the dominant side. Parents 2, 3, 5 and 6 have positions nearly at the middle regression line, indicating that these parents possess different proportions of genes exhibiting dominance. The regression line, intercepted the Wr axis below the origin suggesting overdominance which is in accordance with the result detected from the parameter (H1/D)1/2. For RNA content the regression coefficient was not significantly different from unity, but significantly different from zero (b= 0.841 + 0.24). The regression line intercepts Wr axis below the origin (Fig. 2), indicating overdominance in the F1. As indicated by the distribution of the points representing the different arrays along the regression line, "C.C. 89" possess an excess of dominant over recessive genes for RNA content under S0 treatment. "C.C. 163" possess an excess of recessive genes. The regression coefficient for the F1 was not significantly different from zero (b = 0.22 + 0.38), indicating the presence of a non-allelic interaciton between

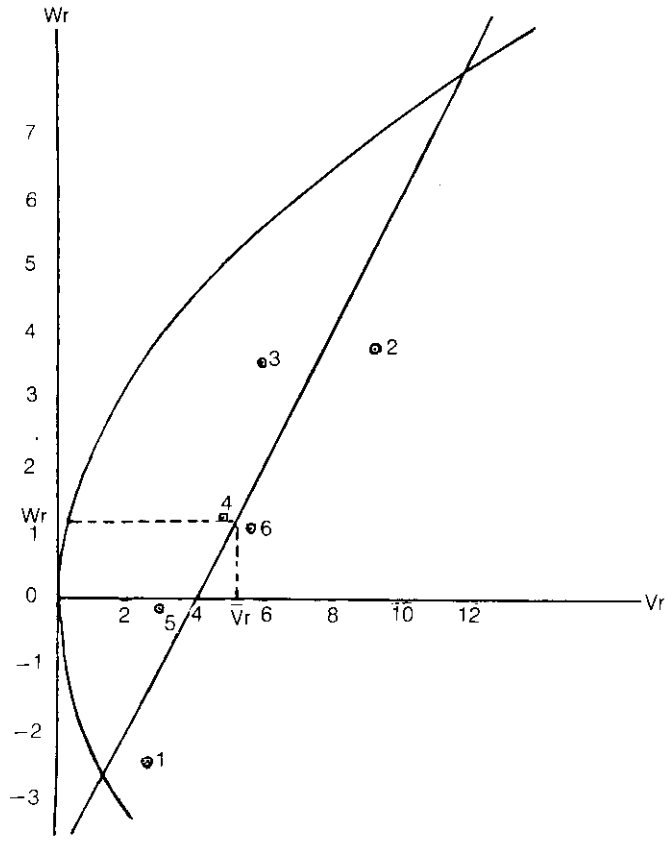

Fig. 2. Wr,Vr graph analysis for the RNA content under S_0 treatment.

the factors determining the expression of the total protein content under S1 treatment. The regression line intercepts the Wr axis in a negative position, revealing overdominance (Fig. 3). California Mariout and line 474.1 occupy position near the end of the regression line in the recessive side. Since both parents had a higher total protein content value, it can be stated that the two parents are carrying most the recessive alleles.

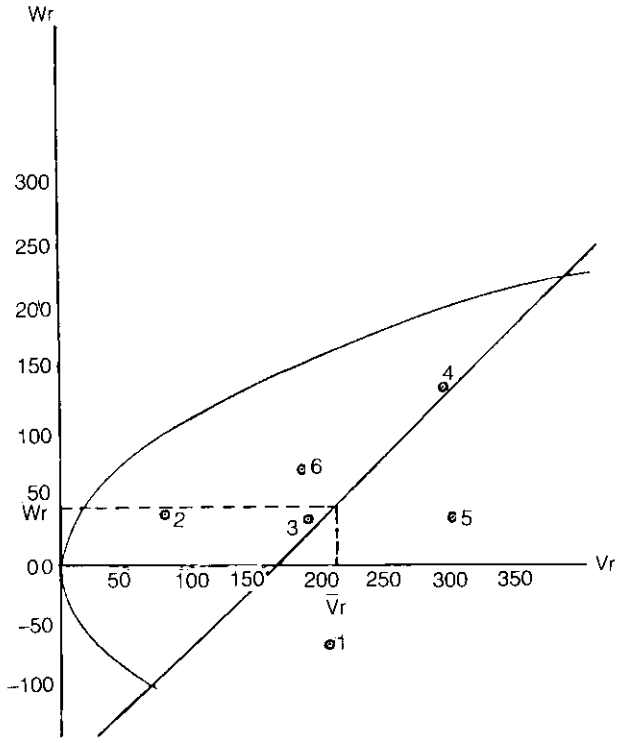

Fig. 3. Wr,Vr analysis for the total protein content under S_1 treatment.

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التقويم الوراثي لبعض الصفات الكيميائية الحيوية في الشعير النامي تحت تأثير الملوحة

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ملخص البحث. يهدف هذا البحث إلى دراسة النظام الوراثي الذي يتحكم في وراثة الحموض النووية والبروتين تحت تركيزات مختلفة من الملوحة.

أظهرت هذه الدراسة أن التأثير المضيف للجينات كان أكثر أهمية من التأثير الراجع إلى السيادة، وذلك فيما يتعلق بوراثة الحمض النووي الدايزوكسي ريبوز DNA تحت التركيز الأول بينما تساوي كل من التأثير المضيف والسيادة في وراثة الحمض النووي الريبوزي RNA في معاملة المقارنة وكذلك المحتوى البروتيني تحت التركيز الأول.

قدرت درجة السيادة ووجدت أنها فائقة للحمض النووي الدايزوكسي ريبوز DNA والحمض النووي الريبوزي RNA والمحتوي البروتيني ـ تتوزع الآليات الموجبة والسالبة بنظام متساو في الأباء. كما كانت الكفاءة الوراثية منخفضة مما يوضح أن هذه الصفات تتأثر بالعوامل البيئية.

أوضحت الدراسة أن الأب C.C.89 يحتوي على معظم الجينات السائدة لمحتوى الحمض النووي الريبوزي RNA والصنف كاليفورنيا ماريوت يحتوي على الجينات ـ المتنحية تحت التركيز الثاني من الملوحة وذلك لصفة المحتوى البروتيني.