

FIELD EVALUATION AND SELECTION OF RESISTANCE TO RUST DISEASES (*Puccinia Spp.*) IN WHEAT SOMACLONAL VARIANT LINES

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Received on: 1/4/2008

Accepted: 10/4/2008

ABSTRACT

Forty somaclonal variant lines, produced from Sakha-69 wheat cultivar, using stepwise *in vitro* selection method, using *p*-fluorophenylalanine (PFP) as *in vitro* mutagenic agent for developing mutant lines resistant to rust diseases, were field evaluated, as well as their parent, at Sakha area, for grain yield and leaf rust (LR) severity as average coefficient of infection (ACI). The experiment was set up in a randomized complete block design, with two replicates due to small amount of seeds. There were highly significant differences among genotypes for grain yield, but there were no significant differences for ACI. Seventeen somaclones were selected for their low LR infection and high grain yield.

Two field experiments were conducted, at Sakha and Nubaria locations, to evaluate the seventeen selected somaclones, as well as their parent. They were laid out in a randomized complete block design, with two replications. Some morphological characters were recorded at the two locations (plant height, 1000-grain weight, number of grains per spike and number of spikes and grain yield per square meter). Two other characters were recorded only at Nubaria area (harvest index and date of maturity). Either highly significant or significant differences were reported for plant height, number of spikes / m² and 1000-grain weight among somaclones, as well as their parent at the two areas, and grain yield / m² at Sakha area and date of maturity at Nubaria location. Meanwhile, differences were not significant for other morphological characters.

Disease severity analysis revealed significant effects of genotypes on the severity of LR(leaf rust) and SR(stem rust) at Nubaria and YR(yellow rust) at Sakha as ACI.

Cluster analysis of morphological characters and rusts severity (as ACI) was conducted to determine the relation between the parent and its somaclones.

The results obtained from the analysis of variance and cluster analysis indicated that there were clear differences among somaclones, as well as their parent.

In conclusion, the present study revealed that, *in vitro* selection method, was effective for producing valuable variations as somaclonal variant lines. Several of these somaclones were superior to the parent in grain yield and resistance to rust diseases, so that they might be selected and subjected to further evaluation for the production of new lines.

INTRODUCTION

Wheat (*Triticum aestivum* L.) is grown over a wide area in the world than any other major crop. It is the principal food for nearly one-third of the world population (Wiese, 1987). As an important staple food, wheat occupies an important place in crop breeding program in Egypt. Although wheat production in Egypt has been improved during recent years, continuous improvement in wheat productivity is highly desirable because of the increasing demand by the still-growing human population. However, during the last few years, grain yield improvement in wheat cultivars has not been substantial due to rust diseases, which include leaf rust (*Puccinia recondita*), stem rust (*Puccinia graminis tritici*) and stripe rust (*Puccinia striiformis*), which are, from the economic point of view, the most important group of diseases on a world scale at the present time. In Egypt, however, leaf rust of wheat, caused by *P. recondita*, is still the main wheat disease due to the favorable climatic conditions, the susceptibility of the old wheat cultivars (Nazim *et al.*, 1976 and 1983) and the dynamic state of the fungal virulence (Sherief *et al.*, 1992). During the last three decades, yellow rust disease, caused by the fungal pathogen, *Puccinia striiformis*, was very destructive in different seasons and hit most of the Egyptian wheat cultivars in 1967,

1995 and 1997 and was almost epidemic in 1985 and 1998 (EL-Daoudi, 1998, El-Daoudi *et al.*, 1996).

One of the main objectives of wheat improvement program is to generate genetically diverse germplasm that has a high grain yield potential, wide adaptation and durable resistance to important diseases, such as the rusts. Conventional breeding methods would probably be more efficient, if aided by modern tools, such as somaclonal variation and molecular markers. Somaclonal variants, heritable changes, that result from *in vitro* procedures, has forced for plant breeders to reconsider importance roles of these methods. The ability to select somaclone variation can yield a pool of individuals, upon which selection procedure may be applied for isolation of unique forms of standard cultivars. Oberthur *et al.* (1993) obtained two wheat somaclones, showing increased field resistance to leaf rust (*Puccinia recondita f.sp.tritici*).

In the present study, field evaluation for rust diseases for somaclonal variant lines was made to determine the relationship between the somaclones and their parent and select the most resistant and productive ones from them.

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MATERIALS AND METHODS

Plant materials:

The wheat cultivar, Sakha-69, was used to produce somaclonal variant lines, using stepwise *in vitro* selection method. P-fluorophenylalanine (PFP) has been used as *in vitro* mutagenic agent for developing mutant lines resistant to rust diseases (Barakat and Milad, 2006). The calli, derived from mature embryos, were transferred to the medium, containing 100 μM /L PFP. They were monthly subcultured on a fresh medium, with a gradually increasing concentration of PFP by 100 μM until it reached 500 μM . The calli were, then, transferred to the regeneration medium free of PFP. Forty somaclonal variant lines were obtained and grown during 2004/2005 winter season to obtain R_1 seeds.

Field evaluation :

Sakha-69 cultivar (S-69) and the R_1 seeds of its somaclonal variant lines (S_1 to S_{40}) were grown during the season of 2005/2006 at the Farm of Sakha Agricultural Research Station, Agricultural Research Center (ARC), Egypt. The experiment was set up in a randomized complete block design, with two replicates due to small amount of seeds. The experimental plot consisted of one row, 3 m long and 20 cm apart. Grain yield / m^2 and the severity of leaf rust (LR) was recorded for each genotype, but there was no infection with yellow rust (YR) in this season at Sakha area. Seventeen somaclonal variant lines were selected for their low LR infection and high grain yield.

Two field experiments were conducted during the season of 2006/2007 at two location, the first one was the Farm of Sakha Agricultural Research Station, Agricultural Research Center, the second was the Farm of Nubaria Research Station, to evaluate the seventeen selected somaclonal variant lines, as well as their parent. The two experiments were laid out in a randomized complete block design, with two replications. The experimental plot consisted of two rows, 3m long with a spacing of 20 cm among rows.

At harvesting time, in the two locations, ten plants were randomly chosen to measure plant height, 1000-grain weight and the number of grains per spike. Also, number of spikes and grain yield per square meter were recorded. Harvest index and date of maturity were recorded only at Nubaria.

Disease evaluation:

To initiate rusts infection, spreader and rows of susceptible varieties were planted among plots and around the experiments.

In each plot, six plants were randomly selected to collect the data of rust diseases as follows.

- (1) The severity was recorded by using the percent leaf area affected (Stubbs *et al.*, 1986) for leaf (LR) and yellow rusts (YR), and stem area affected by stem rust (SR). The severity of YR was recorded at Sakha station area, but the

severity of LR and SR were recorded alone at Nubaria area.

- (2) The reaction was estimated for each genotype as: (R= resistant; small uredia often surrounded by a necrosis, MR= moderately resistant; small to medium uredia often surrounded by chlorosis or necrosis, X= intermediate; random distribution of variable-sized uredia, MS= moderately susceptible; medium-sized uredia might be associated with chlorosis or rarely necrosis, and S= susceptible; large uredia without chlorosis or necrosis). The scale of reaction had a constant value; i.e., R=0.2, MR=0.4, X=0.6, MS=0.8 and S = 1.0. The constant value was multiplied with severity score of each genotype to obtain average coefficient of infection (ACI) (Stubbs *et al.*, 1986 and Woldeab *et al.*, 2007). ACI was calculated. For example: $20\text{MR}=20 \times 0.4=8$.

Data analysis:

Analysis of the morphological data and diseases severity, as ACI, was conducted, using two methods, as follows:

- 1) Analysis of variance (ANOVA) was applied as a randomized complete block design (RCBD), with two replicates, and each area was separately analyzed. To know the homogeneity of error variances for the studied traits. Hartley test (Winer, 1971) was used. Comparisons among means were made via the least significant difference multiple range test. The data were analyzed using SAS (2007) program.
- 2) Cluster analysis was conducted, using NTSYS-pc (Numerical taxonomy and multivariate analysis system (Version 2.101) (Rohlf, 2000). The standardized traits mean values (mean of each trait was subtracted from the data values and the results were divided by the standard deviation) were used to regenerate similarity coefficients, according to Jaccards (1908), a dendrogram was generated from the similarity matrix by the unweighted pair group method with arithmetic averages (UPGMA) (Sokal and Michener, 1958).

RESULTS AND DISCUSSION

The first season :

The results, presented in Table (1), indicated that there were highly significant differences among the forty somaclonal variant lines, as well as their parent (S-69), for grain yield / m^2 , but there were no significant differences for ACI of LR disease.

The somaclone, S_{13} , had the highest average of grain yield (0.878 kg/m^2), and there was no significant difference between it and the S-69 parent (0.820 kg/m^2) as well as some other somaclones (S_3 , S_5 , S_{15} and S_{22}). The lowest significant averages were recorded with somaclones, S_{24} and S_{10} (0.268 and 0.413 kg/m^2 , respectively) (Table 2).

Seventeen somaclones were selected, according to the average of grain yield and the degree of LR severity as ACI.

The second season

Grain yield and its components:

Using Hartley test (Winer, 1971), it was found that there was no homogeneity of error variances. Hence, each location was separately demonstrated.

Analysis of variance in Table (3) showed either highly significant or significant differences for plant height, number of spikes / m² and 1000- grain weight (g) among somaclones selected for rusts resistance, as well as the parent (S-69), at the two location, and grain yield / m² (Kg) at Sakha area, and date of maturity at Nubaria area. Differences were not significant for number of grains / spike at the two areas and grain yield / m² and harvest index at Nubaria area.

The somaclone, S₂₅, had the significantly highest plant height at the two areas Nubaria and Sakha (123.9 and 127.5 cm, respectively), but, there were no significant differences between it and S₂₉ and S₂₄ (122.5 and 123.9 cm, respectively) at Nubaria area. Whereas, the significantly shortest plants were recorded in S₂ (92.9 and 100 cm at the two areas, respectively), but it was not significantly different from S₁₃, S₂₈, S₈ and S₁₇ (102.4, 101.6, 100.8 and 99.3 cm, respectively) at Nubaria area.

The highest significant mean number of spikes / m² was that of S₃₉ (824.9 spikes/ m²) at Nubaria area and there were no significant differences between it and S₂₅, S₂₈ and S₂₉ (769.0, 789.6, and 780.1 spikes/m², respectively). The lowest one was the average of S₁₅ (629.5 spikes / m²) and it had no significant differences with some other averages (Table 4), such as S₁₁, S₃ and S₁₃. At Sakha, S₁₅ had the highest one (1268.0 spikes / m²), but it did not significantly differ from some other means, such as S₁₁, S₁₄ and S₃₆. The lowest one was that of the parent, S-69, (643.1 spikes/m²) and was not significantly different from other five means (Table 4).

Moreover, the highest 1000-grain weight (g) was recorded at Nubaria area for S₂ and S₁₇ (50.1 g for both somaclones) and there were no significant differences between them and several other genotypes, such as S₁₅, S₂₄ and S₂₈. Two genotypes; S₈ and S₂₉, gave the lowest 1000-grain weight (35.0 and 30.5 g, respectively). At Sakha area, S₂ and S₃ gave the heaviest grains, their averages of 1000-grain weight were 57.5 and 53.0 g, respectively. Also S₂₅, S₂₉ and S₃₃ had the lowest grain weight (38.0, 40.5 and 43.0 g, respectively) (Table 4).

Table (4), also, reveals that the parent, S-69, and the twelve somaclones had the same mean of maturity date (154 days) and there were significant differences among them and the other five genotypes. The somaclone, S₂, was the earliest one (141.5 days). This trait was recorded only at Nubaria area.

Grain yield/ m² was recorded and it was significantly affected by genotypes only at Sakha area. The somaclone, S₃₉, had the highest productivity (1.290 kg/m²). Also, there were no significant differences between it and other seven somaclones (S₂, S₃, S₁₁, S₁₄, S₁₅, S₁₇, and S₂₄). S₂₅, S₂₉ and S₃₃ somaclones had the significantly lowest average grain yields (0.345, 0.425 and 0.530 kg/m², respectively).

The results of this field evaluation revealed the same results achieved by Barakat *et al* (2005). They performed field evaluations for selected resistant somaclones obtained from virulence survey of leaf and stripe rusts under green- house conditions, as well as their parents, and reported that significant somaclonal variation could be generated for a number of agronomic traits. The occurrence of genetic changes in plants, derived from cell cultures (somaclonal variations) had been previously documented (Larkin and Scowcroft, 1981). They, also, reported extensive heritable somaclonal variations in bread wheat. Variations for morphological and biochemical traits were observed among 142 regenerants of a Mexico breeding line "Yaqui 50 E" and their progeny. The variant characters, which included the highest values of awns, tiller number, grain colour, heading date, gliadin protein and α - amylase regulation, were heritable through two seed generations. Based on these studies, Larkin and Scowcroft (1981) suggested that somaclonal variation might encompass two mechanisms, one operating to generate a mutant gene and the other, in some cases, operating to make the homozygous mutant. Chromosome loss or addition was not evident as the primary case of the variation in wheat. That rapid and easily accessible source of variation could be used in breeding programs (Karp, 1995).

Disease severity analysis:

Analysis of variance in Table (5) revealed significant effects of genotypes on the severity of LR and SR at Nubaria area and YR at Sakha area as ACI (Average coefficient of infection).

1. Leaf rust (LR):

Data in Table (6) indicated that S₂ and S₂₄ were the highest susceptible genotypes (100 and 80 ACI) and S₃₉ was more resistant than the other genotypes (1 ACI) and there were no significant differences between it and ten other genotypes.

2. Stem rust (SR):

The parent, S-69, and its S₄, S₈, S₉, S₁₃, S₁₄, S₂₈ and S₃₉ somaclones were the most resistant genotypes for stem rust at Nubaria area and they had the same ACI (0.2). In addition, there were no significant differences among them and S₂₄, S₂₅, S₃₆, S₃₃ and S₂₉. On the other hand, S₁₁ was the highest susceptible somaclone (75 ACI) (Table 6).

3. Yellow rust (YR):

Data in Table (6) revealed that the genotypes that had the highest resistance to YR were S₂, S₂₈, and

S₁₃. They recorded the lowest ACI (0.5,10, and 12, respectively). Also, S₃₆ was not significantly different from S₂₈ and S₁₃ and had an ACI of 20. The somaclones, S₂₉, S₃₃ and S₂₅, recorded the highest severity as ACI (100,100, and 95).

The previous data revealed that there were some somaclones, which were resistant to one rust (S₂ resistant to YR, S₈ resistant to SR and S₃ and S₁₁ resistant to LR). While, others were resistant to two rusts together, but, they were susceptible to the third one (S₉, and S₁₄ were resistant to LR and SR). The third group was resistant to two rusts, but, moderately resistant to the other one (S₄, S₂₈, S₃₆ and S₃₉), but, there was only one somaclone (S₁₃) that had a low ACI value for the three rust diseases.

Barakat and Milad (2006) reported that some somaclones, derived from the PFP treatment were found to have a mutated resistance to yellow rust disease of wheat. Previously, similar results, with the some results of the present investigation, had been reported (Chauhan and Singh, 1995). They observed somaclonal variation of some morphological traits, as well as leaf rust reaction, among wheat variants.

In most disease resistance mechanism, associated host molecules are products of secondary metabolism. Widholm (1987) proposed the selection of variants disturbed, with respect to the appropriate biosynthetic pathway as a novel means of isolating disease-resistant variants. Many classes of resistance compounds were phenolic in nature, synthesized via the shikimic acid pathway. A pivotal step in phenolic biosynthesis was the conversion, catalysed by phenylalanine ammonia-lyase, of phenylalanine into p-fluorophenylalanine acid. *In vitro* selection for resistance to the phenylalanine analogue p-fluorophenylalanine isolated cell lines, which over-accumulated phenolics (Palmer and Widholm, 1975; Berlin *et al*, 1982), due to possible overproduction of phenylalanine ammonia-lyase. Selection for elicitor-induced phenylalanine analogue p-fluorophenylalanine – resistance may result in localized overproduction of phenolics in response to pathogen challenge. Berlin *et al* (1982) reported that the resistance mechanisms included: (a) overproduction of phenylalanine and (b) increased activity of phenylalanine ammonia-lyase, which could detoxify p-fluorophenylalanine by converting it to a secondary metabolite p-fluorocinnamic acid.

In vitro selection of somatic wheat calli, resistant to toxic fusarium metabolites, using double-layer and culture filtrate techniques, were reported by several investigators (Yang *et al.*, 1998; Abdallah *et al*, 2002). Inheritance of improved leaf rust resistance in somaclones of wheat had been reported (Oberthur *et al.*, 1993).

When the agronomic traits, coupled with rust resistance are considered, some unique genotypes may be selected; namely: 1- The somaclone, S₂, was the shortest and earliest genotype and it had a high grain yield, grain weight and resistance to YR, but, low severity as ACI for SR; 2- The somaclones, S₁₃, S₁₄,

S₂₈, S₃₆ and S₃₉, had either high or moderate grain yield and high resistance to either two or the three rusts.

Somaclonal variation of some morphological traits and leaf rust reaction among regenerants derived from callus of bread wheat cultures, were reported by Chauhan and Singh (1995).

Cluster analysis:

One of the aims of this study was to determine the relation between the parent, S-69, and its somaclones.

Cluster analysis is a collection of statistical methods, which identifies groups of samples that behave similarly or show similar characteristics.

The standardized mean values of morphological traits and rust severity, as ACI, were used to construct a similarity matrix (Table 7). The similarity coefficients ranged from 0.05 to 0.86, suggesting a broad genetic base for wheat genotypes. Table (7) presents the morphological similarity estimates of the 162 pairwise comparisons among the somaclones and their parent, S-69.

Figure (1) illustrates the clustering of the somaclones and their parent (S-69). Five clusters were obtained at 0.5 similarity level, the first cluster included the parent (S-69) and the somaclone, S₄. Within the second cluster, two clearly separated clusters could be discerned at 0.6 similarity level, one included the somaclones, S₉, S₁₁ and S₁₅, and the other included S₁₃, S₃₆, S₁₄, S₃₉, S₁₇, S₂₄ and S₂₈. It is clear that this group included more of the unique genotypes and they differed from the parent, S-69. The third cluster included the somaclones, S₈ and S₃₃, and they had the highest similarity level (0.86). The fourth and fifth clusters, each included two somaclones (S₂₅ and S₂₉) and (S₂ and S₃), respectively.

The results obtained from the analysis of variance and cluster analysis indicated that there were clear differences among somaclones, as well as their parent. Jayasankar and Dennis (2003) suggested that the *in vitro* selection had a significant potential to produce genetically improved plants, compared to their parents.

From the results of the present study, it was concluded that: 1- *In vitro* selection method was effective for producing valuable variations in the form of somaclonal variant lines, 2- Several of these somaclones were superior to the parent in grain yield and resistance to rust diseases, so that they might be selected and subjected to further evaluation for the production of new lines.

ACKNOWLEDGEMENTS

The author would like to express her appreciation to Professor Dr. M.I. Shaalan, Professor Dr. M.M.EL Rouby, Professor Dr. M.N. Barakat and Professor Dr. A.E. Nawar (Crop Science Dept., Faculty of Agriculture, El-Shatby, Alexandria University, Egypt) for their advice, help in statistical analysis and writing this paper.

Table1: Analysis of variance for grain yield and ACI for LR for the selected somaclones for rusts resistance, as well as their wheat cultivar parent (Sakha-69) during 2005/2006 season.

SOV	DF	Grain yield/m ²	ACI
Replicates	1	0.0001	352.44
Genotypes	40	0.0267**	197.80
Error	40	0.0070	297.44

** : Significant at 0.01 probability levels.

Table 2: Means of grain yield /m² for the selected somaclones for rusts resistance, as well as their wheat cultivar parent (Sakha-69) during 2005/2006 season.

Genotype	Grain yield/ (kg/m ²)	Genotype	Grain yield/ (kg/ m ²)	Genotype	Grain yield/ (kg/ m ²)
S-69	0.820	S14	0.605	S28	0.608
S ₁	0.602	S15	0.808	S29	0.760
S ₂	0.538	S16	0.678	S30	0.543
S ₃	0.800	S17	0.753	S31	0.518
S ₄	0.635	S18	0.613	S32	0.648
S ₅	0.800	S19	0.688	S33	0.658
S ₆	0.630	S20	0.645	S34	0.268
S ₇	0.625	S21	0.678	S35	0.630
S ₈	0.685	S22	0.813	S36	0.570
S ₉	0.743	S23	0.538	S37	0.668
S ₁₀	0.413	S24	0.745	S38	0.683
S ₁₁	0.775	S25	0.638	S39	0.605
S ₁₂	0.748	S26	0.750	S40	0.710
S ₁₃	0.878	S27	0.608		

L.S.D. at 0.05 level= 0.169 kg.

Table 3: Analysis of variance for grain yield and its components for the selected somaclones for rusts resistance, as well as their wheat cultivar parent (Sakha-69) during 2006/2007 season.

SOV	DF	Plant height (cm)	No. spikes/ m ²	No. grains/ spikes	1000-grain weight(g)	Grain yield / m ² (kg)	Harvest index %	Date of maturity (days)
Nubaria								
Replicates	1	28.62	2336	0.16	6.33	0.04	1.69	1.36
Genotypes	17	127.45**	7223 **	0.46	52.99*	0.12	59.43	32.60**
Error	17	21.57	1624	0.41	18.34	0.10	39.6	0.83
Sakha								
Replicates	1	140.03	2889	0.01	1.00	0.04		
Genotypes	17	58.36**	64973**	0.36	42.29**	0.13**		
Error	17	6.79	20443	0.35	6.35	0.02		

*, **: Significant at 0.05 and 0.01 probability levels, respectively.

Table 4: Means of grain yield and its components in the selected somaclones for rusts resistance, as well as the wheat cultivar parent (Sakha-69) at Nubaria and Sakha areas.

Genotype	Plant height (cm)		Number of spikes / m ²		1000- grain weight (g)		Grain yield/ (kg/ m ²)	Date of maturity (days)
	Nubaria	Sakha	Nubaria	Sakha	Nubaria	Sakha	Sakha	Nubaria
S-69	109.8	113.0	675.0	643.1	46.0	50.0	0.905	154.0
S ₂	92.9	100.0	704.9	854.4	50.1	57.5	1.105	141.5
S ₃	106.5	117.5	639.6	651.7	48.0	53.0	1.130	146.0
S ₄	106.0	112.5	675.0	842.7	47.0	48.0	0.970	151.5
S ₈	100.8	117.5	664.6	1073.2	35.0	43.5	0.830	154.0
S ₉	105.2	117.5	645.2	1062.7	44.1	45.0	0.920	154.0
S ₁₁	114.1	115.0	630.0	1247.5	47.4	47.0	1.070	146.5
S ₁₃	102.4	117.5	640.1	1058.2	43.5	49.5	1.000	154.0
S ₁₄	111.9	115.0	730.1	1107.5	44.5	51.0	1.060	154.0
S ₁₅	113.8	115.0	629.5	1268.0	49.3	49.0	1.080	154.0
S ₁₇	99.3	115.0	649.2	1068.6	50.1	47.5	1.135	154.0
S ₂₄	116.4	120.0	675.0	964.7	49.2	49.0	1.090	154.0
S ₂₅	123.9	127.5	769.0	892.2	43.8	38.0	0.345	154.0
S ₂₈	101.6	120.0	789.6	971.0	48.9	46.0	0.985	154.0
S ₂₉	122.5	120.0	780.1	1101.6	30.5	40.5	0.425	145.0
S ₃₃	107.1	120.0	680.2	909.7	42.6	43.0	0.530	154.0
S ₃₆	108.8	120.0	97.0	1102.9	46.3	49.0	0.900	154.0
S ₃₉	113.0	117.5	824.9	978.4	47.4	51.5	1.290	154.0
LSD _(0.05)	9.8	9.8	85.0	301.7	9.0	5.3	0.260	1.9

Table 5: Analysis of variance for average coefficient of infection (ACI) for leaf, yellow and stem rusts (LR, YR and SR) for the selected somaclones for rusts resistance, as well as their wheat cultivar parent (Sakha-69).

SOV	D.f.	Nubaria		Sakha
		LR	SR	YR
Replicates	1	544.4	527.5	756.3
Genotypes	17	1370.4**	676.3**	1833.6**
Error	17	344.2	48.9	77.8

** : Significant at 0.01 probability levels.

Table 6: Means of average coefficient of infection (ACI) for leaf, yellow and stem rusts, (LR, YR and SR) for the selected somaclones for rusts resistance, as well as their wheat cultivar parent (Sakha-69).

Genotype	Nubaria		Sakha
	LR	SR	YR
S-69	33	0.2	65
S ₂	100	20	0.5
S ₃	25	30	50
S ₄	14	0.2	50
S ₈	48	0.2	50
S ₉	12	0.2	70
S ₁₁	25	75	55
S ₁₃	10	0.2	12
S ₁₄	10	0.2	80
S ₁₅	28	15	50
S ₁₇	35	20	30
S ₂₄	80	3	70
S ₂₅	50	3	95
S ₂₈	50	0.2	10
S ₂₉	55	12.5	100
S ₃₃	50	12.5	100
S ₃₆	12	4.1	20
S ₃₉	1	0.2	50
LSD_(0.05)	39.15	14.75	18.61

Table 7: Morphological similarity matrix, based on Jaccard's coefficient for Sakha-69 wheat cultivar and its somaclones determined from analysis, using the mean values of grain yield , grain yield components and average coefficient of infection (ACI).

	S-69	S ₂	S ₃	S ₄	S ₈	S ₉	S ₁₁	S ₁₃	S ₁₄	S ₁₅	S ₁₇	S ₂₄	S ₂₅	S ₂₈	S ₂₉	S ₃₃	S ₃₆	S ₃₉
S-69	1.00																	
S ₂	0.27	1.00																
S ₃	0.33	0.70	1.00															
S ₄	0.57	0.46	0.54	1.00														
S ₈	0.29	0.15	0.23	0.20	1.00													
S ₉	0.38	0.27	0.33	0.38	0.64	1.00												
S ₁₁	0.29	0.36	0.43	0.38	0.38	0.57	1.00											
S ₁₃	0.35	0.43	0.50	0.44	0.58	0.53	0.53	1.00										
S ₁₄	0.53	0.37	0.42	0.53	0.39	0.61	0.61	0.58	1.00									
S ₁₅	0.47	0.38	0.44	0.47	0.50	0.67	0.79	0.73	0.78	1.00								
S ₁₇	0.39	0.47	0.44	0.56	0.40	0.56	0.47	0.63	0.68	0.56	1.00							
S ₂₄	0.47	0.47	0.53	0.65	0.41	0.56	0.47	0.71	0.75	0.63	0.72	1.00						
S ₂₅	0.50	0.05	0.15	0.33	0.33	0.50	0.32	0.32	0.63	0.40	0.42	0.48	1.00					
S ₂₈	0.39	0.38	0.44	0.56	0.50	0.67	0.47	0.63	0.60	0.56	0.75	0.82	0.50	1.00				
S ₂₉	0.18	0.06	0.12	0.25	0.33	0.33	0.31	0.31	0.42	0.26	0.35	0.42	0.60	0.44	1.00			
S ₃₃	0.21	0.08	0.15	0.13	0.86	0.55	0.31	0.50	0.33	0.43	0.33	0.35	0.36	0.43	0.36	1.00		
S ₃₆	0.50	0.31	0.38	0.41	0.54	0.50	0.50	0.79	0.63	0.69	0.59	0.67	0.44	0.59	0.38	0.46	1.00	
S ₃₉	0.50	0.29	0.33	0.43	0.37	0.43	0.50	0.63	0.76	0.65	0.57	0.71	0.57	0.57	0.45	0.32	0.68	1.00

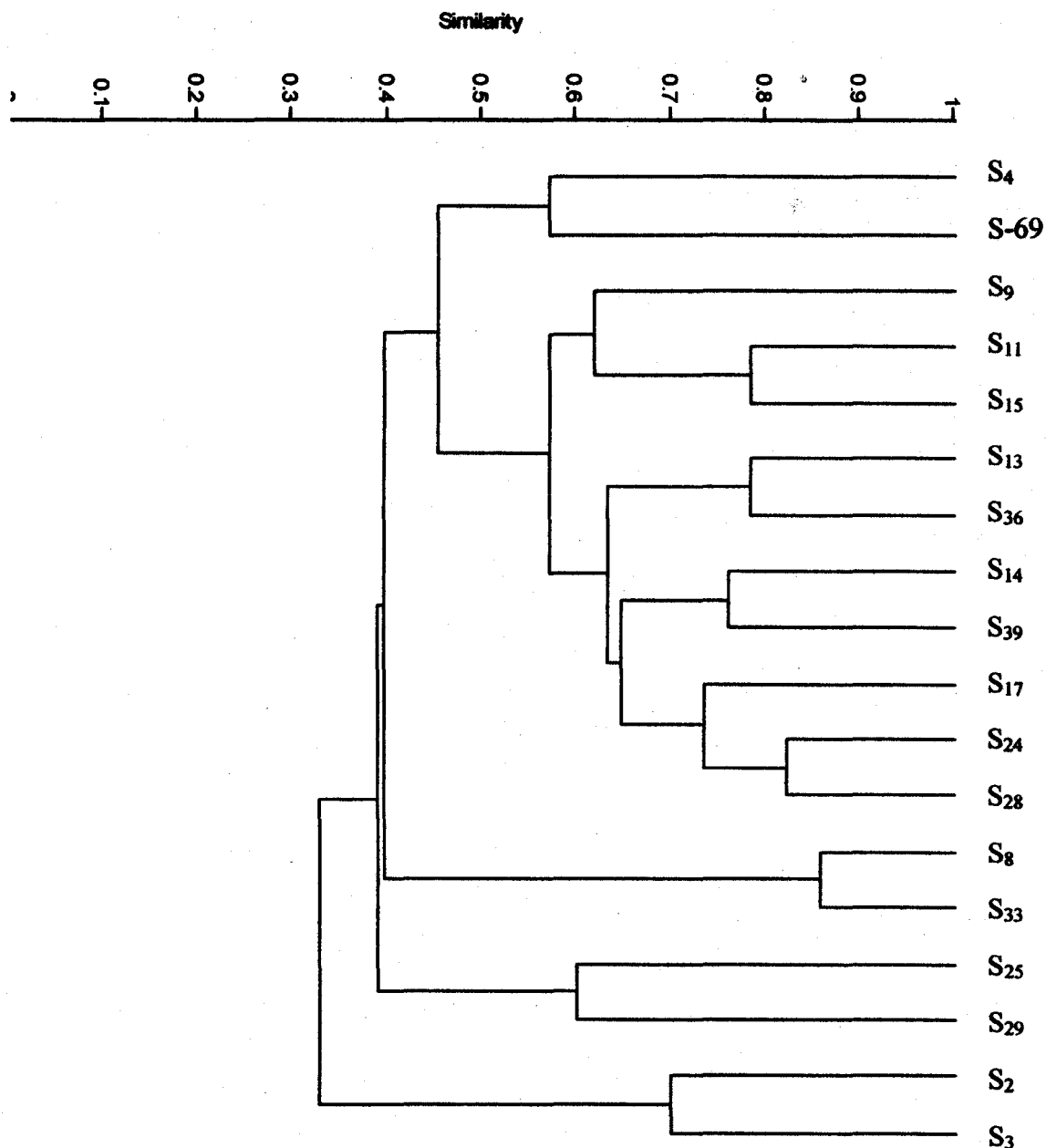


Fig. 1: Dendrogram for Sakha-69 wheat cultivar and its somaclones, based on a cluster analysis (UPGMA) of phenotypic similarities (Jaccard's coefficient) for grain yield, grain yield components and average coefficient of infection (ACI).

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الملخص العربي

تقويم حقلّي وانتخاب للمقاومة للأصداء (*Puccinia spp.*) في Somaclonal Variant Lines في القمح

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تم إنتاج أربعين somaclones من صنف القمح "سحا - ٦٩" باستخدام الانتخاب المعملي بطريقة Stepwise بواسطة مركب p-fluorophenylalanine (PFP) كمادة للانتخاب المعملي لإنتاج خلايا طافرة مقاومة لمرض الصدا الأصفر. تم تقويم هذه المنتخبات بالإضافة إلى الأب (صنف القمح سحا-٦٩) حقلًا في منطقة سحا وذلك لمحصول الحبوب ومتوسط معامل العدوي لمرض صدا الأوراق (ACI). تم إجراء التجربة في صورة تصميم قطاعات كاملة العشوائية (في مكررتين) وقد أثبتت النتائج أن هناك فروق معنوية جداً بين التركيب الوراثية في صفة محصول الحبوب، بينما لم توجد فروق معنوية بينها في درجة الإصابة (ACI). تم إنتخاب سبعة عشر somaclones تبعاً لصفة محصول الحبوب ودرجة الإصابة. وتم تقويم هذه المنتخبات بالإضافة إلى الأب في تجربتين، إحداهما في منطقة سحا والأخرى في منطقة النوبارية. أجريت كل من التجريبتين في صورة تصميم قطاعات كاملة العشوائية (في مكررتين). تم قياس بعض الصفات المورفولوجية في المنطقتين (ارتفاع النبات ووزن ألف حبة و عدد الحبوب بالسنبلة ومحصول الحبوب بالمتر المربع)، و صفات أخرى تم تقديرها في منطقة النوبارية (معامل الحصاد وتاريخ النضج). وجدت فروق معنوية أو معنوية جداً في صفات ارتفاع النبات وعدد السنابل بالمتر المربع ووزن الألف حبة وذلك في المنطقتين، ومحصول الحبوب بالمتر المربع في منطقة سحا وتاريخ النضج في النوبارية. بينما لم تظهر باقي الصفات فروقا معنوية بين التركيب الوراثية. وتحليل شدة الإصابة بالأمراض، وجدت فروق معنوية جداً بين التركيب الوراثية في الإصابة بالصدأين (SR و LR) في النوبارية والصدأ (YR) في سحا وذلك عند تقدير الإصابة في صورة ACI. استخدم تحليل Cluster للصفات المورفولوجية و صفات الإصابة بالأصداء لتحديد العلاقة بين الأب والمنتخبات. ولوضحت للنتائج المتحصل عليها من تحليل التباين وتحليل Cluster أن هناك فروقا واضحة بين التركيب الوراثية. يستنتج من هذه الدراسة أن الانتخاب المعملي فعال لإنتاج اختلافات، وكثير من هذه الاختلافات كانت متفوقة على الأب في محصول الحبوب ومقاومة لأمراض الأصداء تحت الدراسة ولذلك يمكن انتخابها وإجراء المزيد من التقويم لإنتاج سلالات جديدة. and was not