

## Genetic Analysis for Seed Quality Traits in a Diallel Cross of Spring Barley

Sana Medimagh<sup>1\*</sup>, Sonia Mansouri<sup>1</sup>

<sup>1</sup>(Field Crop Laboratory, National Agronomic Research Institute of Tunisia / University of Carthage, Tunisia)

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### **Abstract:**

**Background:** Combining ability effects are very effective genetic parameters in deciding the next phase of breeding programs. This work was undertaken to examine the quality of seeds in six genetically diverse barley parents, and evaluate their general combining ability (GCA) and specific combining ability (SCA) effects toward determining the seed quality.

**Materials and Methods:** In the present study, plant material consisted of a set of six diverse genotypes of spring barley (*Hordeumvulgare* L.), namely Martin, Taj, Ardhaoui, Sahli, Rihane and Salmas crossed in a complete diallel design and their thirty F1 crosses. All these 30 F1 hybrids along with their six parental cultivars were planted in complete randomized block design (CRBD) with three replications under rainfed conditions at the National Agricultural Research Institute of Tunisia (INRAT) research at sub-humid Beja location.

**Results:** The analysis of variance revealed highly significant differences among the parents and their F1 hybrids for all the traits. Highly significant genotypic variation for all traits studied was partitioned into variation due to GCA, SCA and REC effects. High Protein content seems to be linked to the Grain number per spike and to ear type. Rihane is a good combiner to improve spike length and consequently, the number of grain per spike.

**Conclusion:** The analysis of variance of combining abilities showed significant differences for GCA and SCA in F1 hybrids. The genetic gain through the maternal inheritance received from female relatives, explained that suitability of general and specific skills of parents are of importance to teach their offsprings adaptation to environments.

**Key Word:** Barley (*Hordeumvulgare* L.); Diallel; GCA and SCA effects; Seed quality.

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### I. Introduction

Spring barley (*Hordeumvulgare* L.) is the second major cereal crop in Tunisia after wheat. It is widely used for stock feed, human food as well as for malting and brewing. The national program is based on the exploitation of the local and old cultivar populations, and on the introduction of foreign germplasm<sup>7</sup>. Until now, more barley research efforts in Tunisia have been invested in improving yield production than in improving quality product. Local landraces are preferred for food preparations rather than the improved cultivars<sup>14,8</sup>. According to Gallais<sup>10</sup>, the genetic improvement of barley aims to bring together the maximum of favorable genes in the same genotype and the variety. The prediction of the performances of the hybrids could be analyzed from the first generation F1. Diallel analysis can provide the necessary genetic information for breeding programs<sup>15</sup>. It is a mating design to predict combining ability of the parents involved the inheritance of traits. The concept of combining ability was enunciated by Sprague and Tatum<sup>25</sup>. The combining ability analysis is an efficient method for screening germplasm and to determine the ability of the genotypes to be included or not in a breeding program on the basis of their general combining ability (GCA), specific combining ability (SCA) and reciprocal effects. Therefore, this method is very contributive in choosing potential parents with desired genetic variance, vigor and in some cases through maternal effects<sup>13</sup>. Indeed, the GCA is considered as a useful indirect criterion for the choice of the parents<sup>28</sup>. The parents having high GCA values could be used in the creation of the improved lines<sup>21</sup>. The SCA makes it possible to select the best favorable alleles<sup>20</sup> when a hybrid combines well only in certain crosses, which means that it has a good SCA<sup>24</sup>. The objective of this study was to select barley genotypes as the best combiners for spike and seed traits, and estimate the best combinations based on the evaluation of their general and specific combining abilities effects in hybrids for some quality seed traits in spring barley.

## II. Material and Methods

### Experimental protocol

The studied plant material consists of thirty F<sub>1</sub> hybrids resulting from a complete diallel cross between six varieties of six-row barley (Martin, Ardhaoui, Sahli and Rihane) and of two-row barley (Taj and Salmas). Parents were chosen on the basis of the following criteria: variety with a long history of cultivation; a newly improved successfully grown variety and local landrace. The main characteristics of the six parental lines are given in Table no 1.

**Table no 1:** Origin, spike type and nature of parents of barley genotypes

Parents	Origin	Spike type	General information
Martin	Forein local improved cultivar	6	Introduced from Algeria on 1931; Mainly grazed by sheep.
Taj	Improved cultivar Introduced from ICARDA Registered in Tunisia INRAT -1985	2	Origin: W12198 - Australia. High protein, smaller kernels, adapted to low rainfall areas.
Ardhaoui	Local Tunisianbarleylandrace	6	Grown in the south of Tunisia.
Sahli	Local Tunisian barley landrace	6	Grown in the center of Tunisia.
Rihane	Improved cultivar Registered in Tunisia INRAT - 1987	6	The widely grown variety in Tunisia.
Salmas	Improved cultivar Introduced from ICARDA	2	Plumbed grain and low protein content. Mainly used as a check in international ICARDA barley nurseries.

**Study Design:** All these 30 F<sub>1</sub> hybrids along with their six parental cultivars were planted in a randomized complete block design (RCBD) with three replications.

The treatments were seeded in rows of 1.5 m length spaced 25 cm.

**Study Location:** The experiment was conducted under rainfed conditions at the National Agricultural Research Institute of Tunisia (INRAT) research location in Béja.

**Sample size:** 36genotypes.

### Measured parameters

Data were collected on three randomly selected plants for spike length (cm), grain number per spike, thousand kernel weight (g), beta glucan content and protein content.

Thousand barley grains were measured by a seed counter Numigral X5. Thousand kernel weights were done in gram.

Grain beta-glucan content (in %) andprotein content (in %) are determined by near infrared spectrometry NIR Systems Model 5000 scanning monochromator instrument.

### Statistical analysis

Data was analyzed using GenStat 7.1 computer software<sup>11</sup> for analysis of variance. The level  $P < 0.05$  was considered as the cutoff value or significance.

The data were further subjected to combining ability analysis as outlined by Griffing's<sup>12</sup> Model-I, Method-I using AGROBASE software<sup>2</sup>.

The results from the field experiments are represented on the basis of significance at 5 and 1% levels. Significant differences were further subjected to least significance difference test (LSD).

## III. Resultand Discussion

The analysis of variance,showed in Table no 2, revealed highly significant differences among the parents and their F<sub>1</sub> hybrids for all the traits. The genotype effect proves highly significant for all traits studied. This result is a consequence of the existence of genetic differences between parent<sup>3</sup>.

**Table no 2:**Analysis of variance for different seed traits in spring barley

Traits		Spike length	Grain number per spike	Thousand kernel weight	Beta glucan content	Protein content
Source of variation <sup>1)</sup>	df	Mean squares				
Genotype	35	6.586**	1313.07**	175.894**	0.175**	6.739**
REP	2	1.967ns	243.58**	0.348**	0.037**	0.044**
Error	70	1.571	45.59	0.003	0.000	0.000
Total	37					

ns, \* and \*\*: not significant, significant at the 5% and 1% levels of probability, respectively.

<sup>1)</sup>df: degree of freedom; REP: Replication.

**Combined analysis of different seed traits:**

The combined analysis of different traits of barley based on Griffing’s method 1(Model A) in a 6\*6 diallel crosses are presented in Table no 3. The effects of general (GCA) and specific combining abilities (SCA) are determined in the case where the genotype effect is significant. Highly significant genotypic variation for all traits studied was partitioned into variation due to GCA, SCA and REC effects (Table no3).

**Table no 3:** Combined analysis of different seed traits of spring barley based on Griffing’s method 1(Model A)

Traits		Spike length	Grain number per spike	Thousand kernel weight	Beta glucan content	Protein content
Source of variation <sup>1)</sup>	df	Mean squares				
GCA	5	2.512**	2240.578**	141.401**	0.209**	6.502**
SCA	15	2.179**	214.756**	69.386**	0.046**	1.916**
REC	15	2.107**	59.659**	20.287**	0.020**	1.158**
Error	70	0.524	15.198	0.001	0.000	0.000
Total	105					

ns, \* and \*\*: not significant, significant at the 5% and 1% levels of probability, respectively. <sup>1)</sup>df: degree of freedom; GCA: General Combining Ability; SCA: Specific Combining Ability; REC: Reciprocal effects.

**Estimates of specific combining ability (SCA) effects:**

The estimates of SCA effects and reciprocal effects of the crosses for seed traits in spring barley are presented in Table no 4.

**Table no4:** Estimation of specific combining ability and reciprocal effects of the crosses in spring barley

Cross	Traits				
	Spike length	Grain number per spike	Thousand kernel weight	Beta glucan content	Protein content
Martinx Taj	0.877	-7.22	9.638	0.265	0.241
MartinxArdhaoui	0.974	9.50	0.674	-0.024	-0.540
MartinxSahli	0.385	10.67	1.969	0.108	-0.717
MartinxRihane	-0.976	-0.89	-6.946	-0.005	-0.240
MartinxSalmas	0.182	-11.17	7.478	-0.110	0.033
Tajx Martin	-0.367	0.00	-0.010	-0.090	-0.220
TajxArdhaoui	-0.656	-11.00	-1.596	-0.038	1.628
TajxSahli	0.738	-6.50	-2.386	-0.175	0.516
TajxRihane	1.460	-9.56	2.924	-0.034	0.799
TajxSalmas	-1.281	16.83	-2.747	-0.064	-1.684
Ardhaouix Martin	-0.400	1.83	-0.760	0.080	-0.420
Ardhaouix Taj	1.083	4.00	-2.400	0.005	0.760
ArdhaouixSahli	-0.715	1.72	-5.925	-0.165	-0.586
ArdhaouixRihane	-0.326	8.83	2.980	0.177	0.002
ArdhaouixSalmas	0.566	-13.61	3.704	0.152	0.400
Sahlx Martin	1.333	8.17	1.685	0.000	-1.265
Sahlx Taj	-0.833	-3.00	-0.940	-0.015	0.660
SahlxArdhaoui	1.750	4.33	10.685	0.235	-1.250
SahlxRihane	0.019	2.33	1.644	0.069	0.105
SahlxSalmas	1.094	-10.78	3.939	-0.131	1.813
Rihanex Martin	-0.050	0.50	0.795	0.105	-0.975
Rihanex Taj	0.433	0.17	-0.455	-0.015	0.065
RihanexArdhaoui	0.783	0.00	1.485	-0.215	-0.880
RihanexSahli	1.550	6.67	2.830	0.045	0.935
RihanexSalmas	1.166	3.50	2.399	0.006	-0.035
Salmasx Martin	0.883	1.17	1.990	-0.005	-0.740
Salmasx Taj	0.433	-0.50	1.485	0.040	0.805
SalmasxArdhaoui	-1.883	-4.50	-1.420	0.035	0.560
SalmasxSahli	1.033	0.50	-2.625	0.050	0.325
SalmasxRihane	0.083	-16.33	-1.340	-0.135	-0.250

**Estimates of general combining ability (GCA) effects:**

The estimates of GCA effects of all genotypes for each trait are presented in Table no 5. The GCA effects were found significantly different for all traits.

**Table no 5:** Estimation of general combining ability effects for seed traits in spring barley

Traits	Parents					
	Martin	Taj	Ardhaoui	Sahli	Rihane	Salmas
Spike length	-0.279	0.434	0.470	-0.574	-0.363	0.312
Grain number per spike	9,111	-19,222	6,889	8,055	10,944	-15,778
Thousand kernel weight	-0.576	3.564	-1.623	-4.352	-1.657	4.644
Beta glucan content	0.017	-0.023	0.035	0.143	0.071	-0.243
Protein content	-0.578	1.384	-0.134	0.217	-0.430	-0.458

**Spike length (SL):**

Results showed lowly significant and positive SCA effects to the spike length for the following crosses (RihanexTaj), (RihanexArdhaoui), (RihanexSahli) and (RihanexSalmas) essentially with Rihane as female parent according to SCA values (Table no4). The significance of this component determines if the deviation of F1 from the average parents changes from one parent to other parent<sup>1</sup>. An increase in spike length both in wheat and multi- and two-rowed barley is among the most promising approaches to breeding for increased yield<sup>19</sup>.

For the spike length trait, a positive and significant GCA effects were recorded by Taj, Ardhaoui and Salmas (Table no 5). The genotypes Martin, Sahli and Rihane showed negative GCA effects (Table no 5). This parameter is important to select grain yielder varieties and not forage barleys. Parental forms studied in terms of spike length have submitted a higher proportion of dominant alleles and an almost symmetrical distribution of positive and negative alleles (Table no 5).

The selection of the spike lengths would be difficult to achieve in the first generations of selection<sup>26</sup>. Rihane is formally a good combiner to improve this character and consequently, the number of grain per spike. These genotypes selected for grain production were used essentially for feed and food<sup>8</sup>.

**Grain number per spike (GNS)**

Highly significant and positive SCA effects were obtained from crosses MartinxArdhaoui, MartinxSahli, TajxSalmas, ArdhaouixMartin, ArdhaouixTaj, ArdhaouixSahli, ArdhaouixRihane, SahlixMartin, SahlixArdhaoui, SahlixRihane, RihanexMartin, RihanexArdhaoui, RihanexSahli, RihanexSalmas, SalmasxMartinand SalmasxSahli (Table no4). These results indicate that these crosses could be considered promising in this respect. SCA values indicate highly positive gene effects for grain number per spike trait improvement essentially for the following crosses MartinxArdhaoui, MartinxSahli, TajxSalmas, ArdhaouixRihane, SahlixMartin and RihanexSahli (Table no4). Two-rowed parents showed pleiotropic gene effects due to the grain number per spike unlike six-row barleys. This shows that the row type plays a key role in the trait expression through dominance and epistatic effects. Crosses done between 2-rowed barley (Taj x Salmas) gave the highest SCA values. The reciprocal cross (Salmas x Taj) gave low and negative SCA value (Table no4). The GCA effects related to the spike and grain yield components of two and six rows barley varieties were the highest for the grain number per spike compared to GCA calculated for the other traits (Table no 5). Results showed that Rihane is the best general combiner. This explains partly, the applied classical pedigree breeding method to stabilize grain yield potential. This ability to break this high character at its offsprings gives it a top priority in our breeding programs as an important parent, when we want to improve the productivity in terms of grain yield. Highly significant negative GCA effects were detected for two-rowed genotypes Taj and for Salmas and highly significant positive GCA effects for six-rowed genotypes Martin, Ardhaoui, Sahli and Rihane (Table no 5). Moreover, the two-rowed varieties Taj and Salmas cannot compete with polystichum forms in terms of grains number per spike. The negative value for grain number per spike was in early generations, suggested a higher effect of recessive genes<sup>19</sup>.

**Thousand kernel weight**

Significant positive SCA effects were observed for the crosses MartinxTaj, MartinxSalmas and SahlixArdhaoui, (Table no 4). The two-rowed barley varieties Taj and Salmas have the highest and positive GCA values for thousand kernel weight but the six-rowed ones showed low and negative GCA values (Table no 5). Thousand kernel weight is a physical indicator of grain commonly used in breeding for characterization of grain weight and seems to be correlated with the head-row type<sup>4</sup>. Mean squares due to SCA where greater than GCA mean squares which indicated that dominance gene effects controlled the expression of thousand kernel weight. Variance components depicted higher SCA variance than GCA variance and higher dominance variance than additive variance indicating the importance of dominance gene effects for thousand kernel weight.

### Beta glucan content and Protein content

Concerning Beta glucan content, the two-rowed barley varieties Taj and Salmas showed significant negative GCA effects, while, GCA showed significant positive effects for the six-rowed ones (Martin, Rihane, Ardhaoui and Sahli, (Table no5). Significant positive SCA effects were estimated for the crosses MartinTaj and SahlixArdhaoui. These crosses were superior to the others (Table no4). We should indicate that the SCA values are very low compared to the other characters (Thousand kernel weight and Grain number per spike).

The GCA effects related to the spike and grain yield components of two and six rows barley varieties were highest for PC for Taj and Sahli. Moreover, the other varieties Martin, Salmas, Rihane and Ardhaoui showed negative GCA effects (Table no5). It was shown in later work that Martin, a selection in local mountain-barley populations, is very good from the point of view of quality storage proteins in the kernels, despite its low heritability<sup>5</sup>. High Protein content seems to be linked to the Grain number per spike and to ear type. In fact regarding Protein content, high significant positive SCA effects were estimated for the crosses SahlixSalmas, RihanexSahli, where female parent is a six-row type, followed by tow by six materials crosses, TajxArhdhaoui and her reciprocal ArdhaouixTaj (Table no4). These results highlight and confirm without doubt, the importance of the used selection methods to select barley varieties Martin and Rihane, genetically stabilized for grain yield and protein content.

Barley protein and beta-glucan content are polygenic traits<sup>18, 22</sup>. Due to the presence of more than one type of dominant gene action and double dominant epistatic effects present in the expression of this character, the selection of these characters in the first generation will be difficult. Selection based on progeny performance operator only additive component of genetic variance of this trait through a diallel cross led to all possible combinations among segregating selected strains could recover homozygous lines the most efficient. The BGC is controlled by a simple additive genetic system for barley and oats<sup>16</sup>.

For most parameters observed in the present study, we note the importance of additive effects and dominance in the control of the variance and the expression of these characters. These results are consistent with those of Yilmaz and Konak<sup>27</sup>. This suggests that the spatial variability in the test was not due to natural variability of soil, but rather basic plot variability across the experimental device<sup>17</sup>.

### IV. Conclusion

In conclusion, this study exhibited that all genotypes studied had genetic characteristics that distinguish them from each other. It had been showed that is very difficult to transgress characters such as quality from improved genotypes to local landraces. Characters controlled additively provide a mechanism for reliable selection in the early generations of selection. The genetic gain through the maternal inheritance received from female relatives, explained that suitability of general and specific skills of parents are of importance to teach their offsprings adaptation to extreme environments. The BGC as a high quality value added trait will be considered more in the future to identify barley lines adapted to new socio-economically demanding environments. Breeders would need to develop plant breeding based on a database of good phenotypic information. Parents having high GCA values may be used to produce improved lines in hybridization programs.

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