HETEROSIS AND COMBINING ABILITY FOR PROTEIN CONTENT% IN RICE (*Oryza sativa L*).

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ABSTRACT

Heterosis and combining ability of protein content in rice were studied by using 5x5 half diallel cross. Five local and exotic rice varieties with different protein content % were used. Parental and their hybrid varieties were arranged in a randomized complete block design with three replication .Protein content % was estimated. Analysis of variance showed highly significant differences among genotypes, highly significant and positive estimates of heterosis were recorded for protein content % when it measured as a deviation from mid-parent in three crosses, on the other hand and highly significant and positive estimated of heterosis was recorded (Giza 179x IR 64) rice cross when it was measured highly significant a deviation from the better parent. Further the general to specific combining ability ratio was (1.16) suggested the influence of both additive and non additive genetic variances in the inheritance of such character.

Only BG304 variety rice shows highly significant and positive estimate of general combining ability (GCA) effects with value 0.821, proving that this parent appeared to be good combiner in rice crosses for improving this trait. The best crosses were Hexi 12x IR 64, Giza 179x IR 64 and Milyang 97x IR 64. These crosses gave 0.562, 0.630 and 0.492, specific combining ability (SCA) estimates, respectively .The crosses which gave highly significant and positive estimates could be used as a donor for increase this trait.

Broad narrow sense values were high for this character; the additive gene action plays an important role in the inheritance of this character,although genetic variation appeared to be influenced predominantly by genes with additive and dominance effect.

INTRODUCTION

Rice (*Oryza sativa* L.) is the world's most important food crop providing more than 20% caloric intake for over 3.5 billion people (Anonymous, 2013). It is a nutritious cereal crop, provides 15 per cent of protein consumed by world's population besides being the chief source of carbohydrate and protein, it also provides minerals and fiber (Veeresha *et al.*, 2015). Grains quality has now become important in order to improve the nutritional status of the improved varieties. This has to be combined with good morphological as well as yield characters (Thattil and Perera, 1991). Protein content can define most of the physicochemical properties of cooked rice (Juliano, 1993). The primary chemical components of the grain are starch , protein and lipids .These components causes to used rice whole grain, flour or starch .The most abundant are protein and lipids (Ring,1995). And (Juliano 1985) stated that rice is unique among cereals because it has a storage protein named "Oryzenin" which has more balanced amino-acid profile compared to the prolamin-rich storage proteins. Indica rices have a protein content that varies

from, 9 to19.3% and japonica rices may content 5. 9 to 16. 5%. Japonica rice had 20% prolamin and indica rice had 30% prolamin as reported by (Hibino *et al.* 1989). Protein content of rice has been studied by some researchers and they indicated that this trait is quantitative trait (Shenoy *et al.* 1991). Protein content was controlled by genetic effects of triploid endosperm, cytoplasm and diploid maternal plant (Shi *et al.,* 1996). Won *et al.* (2002)   reported that the effects of dominance were highly significant for protein content, indicating the importance of the dominance gene action on protein content

Reorientation of breeding methodologies is therefore a perquisite where genetic analysis of morpho-agronomic and other quantitative traits on systematic lines can be devised. Choice of suitable parents is of paramount importance since performance of parents is not always a true indicator of its combining ability in hybrid combination (Sharma and Mani, 2008). The knowledge of combining ability is useful to assess nicking ability among genotypes and at the same time elucidate the nature and magnitude of gene actions involved. The combining ability analysis gives an indication of the variance due to general combining ability (GCA) and specific combing ability (SCA) which represents a relative measure of additive and non-additive gene actions respectively .Breeders use these variance components to measure the gene action and to assess the genetic potentialities of parent in hybrid combinations. Diallel matting designs provide reliable information about GCA and SCA of parents and their cross combinations and are helpful in estimating various types of gene actions within affordable resources. (Dar *et al.*,2014)

Heterosis in rice was first reported by Jones (1926) both positive and negative heterosis is useful in crop improvement, depending on the breeding objectives. Heterosis is expressed in three ways, depending on the criteria used to compare the performance of a hybrid (Gupta, 2000). These three ways are mid-parents heterosis (the performance of a hybrid compared with the average performance of its parents), better parent heterosis or heterobeltiosis (the performance of a hybrid compared with that of the best parent in the cross) and standard heterosis (the performance of a hybrid compared with high yielding variety in the region). From a practical point of view, standard heterosis is the more important of the two levels of heterosis because it is aimed at developing desirable hybrids superior to commercial varieties.

Heterosis breeding is an important genetic tool that help enrich many other desirable quantitative and qualitative traits in crops (Srivastava, 2000). Therefore, the present investigation aims to study the mean heterosis of protein content as deviation from mid –parent and better parent as well as the combining ability of protein content in 5x5 diallel cross and genetic variance component

MATERIALS AND METHODS

Five local and exotic rice varieties with different protein content represented in Table 1 were provided from the genetic stock of the Rice

Research and Training Center. These cultivars were planted during 2013 growing season in three planting dates with 15 days interval to overcome the differences in their heading time. At heading crosses in all possible combination excluding reciprocals of 5x5 diallel cross and a sum of 10 direct crosses were resulted. The five parents along with 10 crosses were grown in complete randomized block design experiment with three replications during the 2014 season. Each replication consisted of three row for each parent and cross. In both seasons, plants were individually transplanted in the spacing of 20x20 cm apart between seedlings and rows. All the recommended cultural practices and fertilizer were followed. At harvest, five random plants from each cross were harvested individually for determination of total nitrogen according to A.O.A.C (1990) methods and protein content was calculated by multiplying the value of total nitrogen by 5.95.

Table 1: Protein content of the selected rice varieties.

Varieties	Protein %
Hexi 12	12.09
Giza 179	6.66
Milyang 97	9.26
BG 304	10.45
IR 64	7.85

Parents under study were selected upon the significant status of the protein content and using the analysis of variance with three sources of variance, replicates, genotype and error. Statistical analysis was conducted following Singh and Chaudhary (1985).Analysis of variance was subjected to Randomized Complete Block Design (RCBD) according to Snedecor and Corchran (1989).

Heterosis effects were estimated as deviation of mid-parent (M.P) and better parent (B.P) according to Mather and Jinks (1971) as follow:

$$\text{Heterosis over the mid} - \text{parent} = \frac{\bar{F}1 - \bar{MP}}{\bar{MP}} x100$$

S.E(F1- $\bar{MP}$)=(3Me/2r)1/²

$$\text{Heterosis over the better- parent} = \frac{\bar{F}1 - \bar{B}.\bar{P}}{\bar{B}.\bar{P}} \times 100$$

S.E(F1- $\bar{BP}$)=(2Me/r)1/²

Where, Me=error mean squares for parents and F1 an individual environment ;$\bar{MP}$= mean mid –parent value=(P1+P2)/2;P1=performance of parent one;P2= mean performance of parent two; $\bar{BP}$= mean of better-parent value; r-number of replication.

The combining ability analysis was statistically mad according to Griffing's (1956) method 2 Model 1

Heritability estimated were computed in both broad (h²b %) and narrow senses (h²n %) for F2 generation according to Mather (1949) and Allard (1960) as follow;

σ² general combining ability $=\frac{1}{p+2}(M.s\ GCA - M.s\ SCA)$

σ² specific combining ability $=M.s\ SCA - M.s\ E$

σ² additive $=2\ \sigma^2\ GCA$

σ² Dominance $=\sigma^2\ SCA$

Heritability brood sense $=\dfrac{\sigma^2\ A+\sigma^2\ D}{\sigma^2\ A+\sigma^2\ D+\sigma^2\ E}$

Heritability brood sense $=\dfrac{\sigma^2\ A}{\sigma^2\ A+\sigma^2\ D+\sigma^2\ E}$

RESULTS AND DISCUSSION

Data in Table 2 represents the mean square (MS) of the three sources of variance for protein content %.The mean square estimates showed high significant differences among the five genotypes for this trait .These results clearly sowed the amount of variability that does exist between the tested genotypes as well as their segregations

Table 2: Pooled ANOVA for protein content trait in the selected rice genotypes.

S.O.V	D.F	M.S
Replications	2	0.06
Genotypes	4	15.14**
Error	8	0.049
C.V%		2.45%

*, **Significant at 0.05 and 0.01 levels of probability, respectively

Heterosis

Data presented in Table 3 indicated that highly significant positive values of heterosis were recorded for protein content as a deviation from mid-parent in three cross. These values of heterosis were ranged between 3.24% for the cross BG 304 x IR 64 and 11. 21% for Giza 179x IR 64. Also data in Table 3 revealed that the heterosis values for protein content of one cross(Giza 179x IR 64) was positive highly significant as deviation from the better parent (9.83) , while the remaining crosses recorded negative significant mean heterotic for this trait. These results in turn suggested that heterotic effects play a fairly important role in inheritance of protein content. The significant of interaction among parent and their crosses mean square indicated that average heterosis could be highly significant in all crosses for protein content%, (Table,4). The obtained results are in agreement with those reported by Chao (1972) and El-Kady and El-Hissewy(1999).

Table 3: Heterosis of protein content as deviation from mid-parent and better patent for all the studies crosses.

Crosses	Performance			Heterosis	
	P1	P2	F1	MP	BP
Hexi 12x Giza 179		6.68	7.12	-22.79**	-39.47**
Hexi 12x Milyang 97		9.26	8.28	-21.23**	-29.61**
Hexi 12x BG 304	11.76	10.45	8.00	-9.51**	-14.57**
Hexi 12x IR 64		6.85	9.60	-4.23**	-17.54**
Giza179x Milyang 97		9.26	6.55	-17.23**	-28.76**
Giza 179x BG 304	6.68	10.45	8.36	-2.39**	-20.90**
Giza 179x IR 64		6.85	7.52	11.21**	9.83**
Milyang 97x BG 304	9.26	10.45	9.27	-5.97**	-11.32**
Milyang 97x IR 64		6.85	8.57	6.35**	-7.49**
BG 304 x IR 64	10.45	6.85	8.93	3.24**	-14.55**
L S D at 5%				0.2895	0.3342
L S D at 1%				0.3907	0.4512

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

Combining ability:

Data in Table 4 showed that the analysis of variance for protein content %.The results showed that the genotypes mean square were highly significant for this trait .These findings indicated the presence of large variation among genotypes under study. Similarly, the results in Table 4 indicated that mean square of parents and crosses were highly significant for this character. These findings indicated overall wide difference among these populations.

Table 4: Analysis of variance for mean performance of genotype, 5 parents, their crosses, their interaction and combining ability for protein content.

S.O.V	D.F	S.S	M.S
Replications	2	0.13	0.06
Genotypes	14	96.98	6.92**
Parents crosses	4	59.43	14.85**
PxF1	9	35.10	3.90**
Error	1	2.44	2.44*
GCA	28	3.40	0.12
SCA	4	23.58	5.89**
Error	10	8.73	0.87**
	28	1.13	0.040
GCA/ SCA			1.16

*, **Significant at 0.05 and 0.01 levels of probability, respectively

Also data in Table 4 showed that the mean square of general and specific combining ability values of protein content were highly significant which appeared considerable genetic variability among the cultivars used in the present study. Further the general to specific combining ability ratio (1.16) showed the influence of both additive and non additive genetic variances in

the inheritance of such characters. These findings were inclose agreement with those recorded by Sood (1978) and El-kady and El-Hissewy (1999)

Additionally, the results in Table 5 showed that the estimates of general combining ability effects (GCA) revealed wide differences among the parents. Negative and significant (GCA) effect was estimated for Hexi 12, Giza 179 and IR 64. However, positive values were recorded for the other two rice cultivars, but Millyang97 had non –significant effects is indicating that this cultivar is natural for the inheritance of protein content character. Meantime, BG304 is the only parent that shows highly significant and positive estimate of (GCA) effects with value 0.821, proving that this parent appeared to be good parental combiner in rice crosses for improving this trait.

Tabel 5: Values of general and specific combining ability effects for protein content in rice parents and crosses.

	Hexi 12	Giza 179	Milyang 97	BG 304	IR 64	G.C.A
Hexi 12		-1.237**	-1.259**	-0.385**	0.562**	-0.988**
Giza 179			-0.697**	0.169	0.630**	-1.257**
Milyang 97				-0.105	0.492**	0.075
BG 304					-0.041	0.821**
IR 64						-0.476**
L S D at 5% SCA	0.253					
L S D at 1%SCA	0.342					
L S D at 5% GCA	0.124					
L S D at 1% GCA	0.167					

*,**Significant at 0.05 and 0.01 levels of probability, respectively.
S.E.g   = 0.0607
S.E (Sij) =0.1567

The data in Table 5 show that three crosses showed highly significant positive estimates of specific combining ability (SCA) .The best crosses were Hexi 12x IR 64, Giza 179x IR 64and Milyang 97x IR 64. These crosses gave 0.562, 0.630 and 0.492, (SCA) estimates, respectively .The crosses which gave highly significant and positive estimates could be used as a donor for increase this trait. However, highly significant and negative estimates of (SCA) were recorded for four crosses and ranged between –o.389 for the cross Hexi12 x BG304 to -1.259 the cross Hexi 12 x Milyang97.These negative values of (SCA) revealed that non additive effects or undesirable types, could be present in these combinations of rice crosses for protein content character. On the other hand these findings lead to the conclusion that high estimates of (SCA) effects, in any cross combination, might not necessarily be dependent upon the general combining ability effects in the involved parents. The other rice crosses showed insignificant, either positive or negative estimates of (SCA) effects for this character.

An autogenous crop like rice, exploitation of non additive genetic variance as such would be impractical. However, using bi-parental or recurrent selection in segregation material, followed by conventional selection, is likely to lead to substantial trait improvement .Further, advantage of segregation material through bulk, pedigree, single seed descent or single

pod descent methods, as suggested by Gupta and Dahiya (1986),would be rewarding.

Genetic components and heritability:

This part of investigation aimed to study the magnitude of genetic variance component. The results in Table 6 indicated that the additive genetic variance (σ^2A) for protein content (%) was higher than non additive (σ^2D).These results indicated that this trait is largely governed by additive gene action. This result is in close agreement with Sood (1978) , El-kady and El-hissewy(1999)and Shorifi and Naghi (2011).

Table 6: Estimated of additive genetic variance (σ^2A), dominance genetic variance (σ^2D), and heritability in broad narrow senses for the protein content %trait.

Trait	σ^2A	σ^2D	σ^2E	hbs	hns
Protein content%	1.51	0.74	0.040	98.54	72.99

Concerning the heritability estimates in broad sense, the results in Table 6 indicated that heritability value is high for this character .On the other hand, heritability estimate in the narrow sense is high also. These results also indicated that the additive gene action plays an important role in the inheritance of this character.

The inheritance pattern of variation for protein content in the five rice genotypes was revealed by diallel data, although genetic variation appeared to be influenced predominantly by genes with additive and dominance effect, the presence of a significant additive component is expected genetic gain because of selection, a potentially useful advance in high protein content, (Shorifi and Naghi, 2011).

In order to increase rice protein content, breeders must under- stand the mechanism of inheritance of this trait and genetic worth of the parents or hybrid vigor of crosses .The efficiency of rice breeding programs based on protein content con be increased with knowledge of the genetic mechanism. Protein content was controlled by additive and non additive gene effects and exhibited moderate narrow –sense heritability. These results is similar to these reported earlier by El-kady and El-Hissewy (1999) and Won *et al.*(2002). Finally, it seems that improvement of protein content would be possible through selection for this trait by utilizing the genetic material under study.

CONCLUSION

Heterosis effects play a fairly important role in inheritance of protein content with their parents in this experiment, and this study showed that positive and high heterosis for protein content as well as significant SCA effects were most promising combinations for best F1 in rice which need to be tested on protein content. The additive gene action plays an important role in the inheritance of this character, although genetic variation appeared to be influenced predominantly by genes with additive and dominance effect,

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قوه الهجين والقدره علي التالف لمحتوي البروتين في الأرز

نسرين نظمي بسيوني و مريم طلعت ويصا
قسم بحوث سخا- كفر الشيخ معهد المحاصيل الحقليه -مركز البحوث الزراعية

أقيمت هذه التجربه لدراسه قوه الهجين في مجتوي البروتين عند قياسه كإنحراف عن متوسط الابوين أومتوسط الأب الأعلي وكذلك دراسه القدره علي التالف لمحتوي البروتين في الأرز بإستخدام نظام الهجن المتعدده.تم إستخدام خمسه أصناف أرز محليه وخارجيه تختلف في محتوي البروتين بالإضافه إلي الهجن الناتجه من هذه الأصناف حيث تم زراعتها في مزرعه مركز بحوث والتدريب الأرزبإستخدام تصميم القطاعات الكامله العشوائيه. وتم تقدير البروتين في كل من الأصناف والهجن

أشارت النتائج إلي ما يلي:

وجد إختلافات عاليه المعنويه بين الأصناف والهجن الناتجه في محتوي البروتين ،ولقد أوضحت النتائج قوه هجين معنويه موجبه بالقياس لمتوسط الأبوين في ثلاث هجن فقط في محتوي البروتين ،بينما كانت واضحه في هجين واحد (جيز١٩٧ xاي ار)٦٤ فقط بالنسبه وذلك عند قياسها كإنحراف عن متوسط الأب الأعلي

كما كانت النسبه بين القدره العامه علي التالف إلي القدره الخاصه علي التالف١,١٦ كما أظهرت النتائج علي مدي تأثر التباين الوربثي المضيف والغير الضيف في وراثه محتوي البروتين،وكان الصنف بيجي٣٠٤هو أفضل الاصناف في القدره العامه علي الخلط ،كما سجل ٣ هجن تنائج معنويه وموجبه في القدره الخاصه علي التالف وكانت هذه الهجن (هكسي١٢ xاي ار٦٤)و(جيز١٩٧ xاي ار٦٤)و(ميلينج٩٧ xاي ار٦٤)وكان كلا من درجه التوريث علي المدي الواسع و درجه التوريث علي المدي الضيق عاليه القيمه ممـا يوضح تأثر هذه الصفه بالجينات المضيفه والسائده.