

## IMPACT OF MATING SYSTEM ON GENETIC VARIABILITY AND CORRELATION COEFFICIENTS IN COTTON (*G. BARBADENSE* L.)

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**ABSTRACT:** Biparental mating ( BIP ) attempted in the  $F_2$  of a cotton cross Giza 75 X Karshencky<sub>2</sub> to know the relative efficiency of biparental mating over  $F_3$  selfed in terms of release of genetic variability and to know the shift in the association pattern of components of various characters in cotton. Sixty biparental progenies and sixteen  $F_3$  selfed progenies were then evaluated for six productive characters and five fiber quality properties. Analysis of variance revealed highly significant differences among intermated progenies. Biparental, intermated progenies, proved its superiority over selfing by registering high mean values in desirable direction for all characters. The range in intermated population was wider as compared with  $F_3$  selfed population. The lower limit of range was high in BIP, in the same time the upper limit was higher for most the characters suggesting that intermating helped in releasing more variability. High genetic variability combined with high heritability in broad sense was noticed in biparental progenies for all characters under study. The magnitude of non-additive were largely in biparental for all characters as compared with  $F_3$  selfed. However, the magnitude of additive component was larger in  $F_3$  selfed population for most characters. This could be emphasized by high narrow sense heritability. Correlation studies indicated that, several new associations in terms of direction and magnitude was observed. The undesirable strong negative association that existed among the characters related with yield and quality in  $F_3$  population were broken or converted into non-significant and positive upon intermating. This was attributed to breakage of undesirable linkage by forced recombinations induced by biparental mating, thereby offering a great scope of selecting new recombinants combining both yield and quality characters in intermated progenies and could be used in cotton breeding program

**Key words:** Cotton – biparental – intermating population genetic - variability – genetic correlation

### INTRODUCTION

The genetic improvement of any crop relies mainly on the presence of substantial magnitude of variability in the populations. In cotton, since selection with local material has been going on for a long time, the genetic variability for yield and its components have been exhausted. Further, breakthrough in productivity will have to come from controlled crosses designed to create new and wide variability (Ashri, 1998).

The conventional breeding methods like pedigree, bulk and backcrossing methods with some modification are the most common in the improvement of cotton. However, these methods have certain

limitations. The rate of homozygous is very high which reduces chances of recombination. This also retains tight and accumulation of undesirable linkage blocks due to continuous selfing in the segregating generations as well as utilizes only fixable effects (Raju *et al.*, 2010). Further negative association among yield components and high genotype by environmental interaction prevent full exploitation of genetic variability for such characters. Therefore, breaking up of linkages to release the concealed variability becomes necessary for isolation of desirable superior lines. This could be achieved by subjecting the  $F_2$  generation to biparental mating.

Biparental mating, on the other hand, is expected to break larger linkage blocks and

provide more chances for recombinations to occur mop up desirable genes and a results release concealed variability. It's a useful system of mating for generation of increased variability and may be applied where desired variation for traits of interest is lacking (Pradeep and Sumalini, 2003; Rudra et al., 2009 and Guddadamath et al., 2011). The review for its use in cotton is very scanty Tyagi, 1986 indicated that the biparental intermated was more amenable to improve through selection than F<sub>3</sub> selfed. However, Soliman, 2003 and Abd El-Salam, 2005 cleared that biparental mating system was more effective in breaking undesirable linkage. Thus, the present study was therefore under taken 1) to evaluate the efficiency of intermating in F<sub>2</sub> generation in a cross for creating variability, 2) to compare the performance of intermitted progenies with the F<sub>3</sub> selfed generation and 3) to study the effect of intermating on the association among yield and quality characters.

## MATERIALS AND METHODS

Ten randomly selected male plants were mated to each of six randomly selected female plants using North Carolina Design II (NCII) in the F<sub>2</sub> population of cotton cross Giza75 (G. 75 X Karshenky<sub>2</sub> (Kar<sub>2</sub>) to generate 60 biparental progenies (BIP) or intermated progenies. The F<sub>2</sub> plants used in the intermating also were selfed to produce 16 F<sub>3</sub> selfed progenies. Thus, the 60 BIPs from the NCII and 16 F<sub>3</sub> progenies with original parents were raised in a randomized block design with three replications at Sakha Agric. Res. Stat. during 2012 growing season. Each biparental or/and F<sub>3</sub> progenies was represented by three rows of 4.0 m length, 70 cm row weadth and 30 cm plant spacings. All recommended agronomic practices were applied during the growing seasons. The data were recorded on five guarded plants in both BIP and F<sub>3</sub> selfed progenies on eleven quantitative characters viz, boll weigth (BW), seed cotton yield (SCY), lint yield (LY), lint percentage (LP), seed index (SI), lint indx (LI), fiber fineness as micronaire reading (F.F.), fiber strength as pressly index (FS), fiber length as 2.5% span length (FL), uniformity ratio (UR) and degree of yellowness(+B)

## Statistical analysis;

The data were subjected to statistical analysis of variance outlined by Comstock and Robinson, 1952 and developed by Kearsy and Pooni, 1996 and Singh and Pawar, 2002. The mean and range in respected to each characters were calculated in the biparental as well as F<sub>3</sub> progenies. The phenotypic and genotypic coefficients of variation were also calculated. Their heritability in broad and narrow senses were obtained in each population according to Kearsy and Pooni, 1996 as formula :

$$\text{Heritability in broad sense ( } h^2_b \text{ )} = \frac{\sigma^2_g}{\sigma^2_p} \times 100$$

$$\text{Heritability in narrow sense ( } h^2_n \text{ )} = \frac{\sigma^2_A}{\sigma^2_P} \times 100$$

$$h^2_n ( F_3 ) = \frac{3/4 \sigma^2_A}{3/4 \sigma^2_A + 3/16 D + E} \times 100$$

Where  $\sigma^2_g$ ,  $\sigma^2_A$ ,  $\sigma^2_D$ ,  $\sigma^2_E$ , and  $\sigma^2_P$  refer to genotypic, additive, dominance, environmental and phenotype variances respectively.

Genotypic correlation coefficients were calculated using the analysis of variance and covariance procedures proposed by Falconer and Muckay, 1996 as follows :

$$\text{Genotypic correlation ( } rg \text{ )} = \frac{\sigma_{gij}}{\sqrt{\sigma^2_{gi} \times \sigma^2_{gj}}}$$

Where:  $\sigma_{gij}$  is the genotypic covariance of character i and j  
 $\sigma^2(g_i \text{ and } g_j)$  are the genotypic variance of characters I and j

## RESULTS AND DISCUSSION

Breeder very often use segregating populations as source population to exercise selection for identifying homozygous recombinant lines with better performance to develop new varieties. Most often, the source F<sub>2</sub> population of single cross hybrids and/or double cross hybrids would offer limited opportunities for achieving high success because of narrow genetic base and impose restrictions on the chance of better recombination and also associated with the weakness of causing rapid homozygous as well as low genetic variability. On the other side, biparental mating is expected to break larger linkage blocks and provide more changes for recombinations to occure (Abo Arab, 1999).

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Analysis of variance for mating design in biparental intermated progenies (Table 1) revealed highly significant mean squares due to male, females and their interaction for all studied characters. Significant male or/and female indicating that there was enough additive genetic variability for further exploitation. However male X female interactions were also highly significant demonstrating the presence of non-additive genetic variance. Genetic variation composed of additive and/or non-additive would be necessary to make further improvement in such characters. Similar results were obtained by *Tyagi, (1987); El-Harony, (1999) and Hassan, (2012)*.

The comparison of mean and range of expression of different characters (Table 2) between BIP and F<sub>3</sub> selfed indicated that mean values of BIPs were higher than mean values of F<sub>3</sub> for most characters (Shift in the mean values in desirable direction). The superior mean performance of biparental progenies could be attributed to accumulation of favourable genes in positive direction. Desirable mean values of the BIP could also be due to creation of more variability of breakage of undesirable linkage which otherwise concealed the genetic variability in F<sub>3</sub> population, similar results were obtained by *Sharma and Kalia, (2003) and El-Shazly, (2013)*.

As compared to the F<sub>3</sub> population, BIP populations have shown considerable higher mean values for all the characters indicating the dominance deviation and epistatic interaction in BIP populations. The mean performance appear to be improved with respect to all yield and fiber characters in the biparental population, which can be attributed to exploitation of additive genetic effects on account of mop up of alleles influencing the characters (*Rudra et al., 2009*)

The estimates of genetic variation make the task of breeder easy, so as to make effective selection. The release of hidden genetic variability by breaking undesirable linkage might be another reason for increasing mean performance and higher variability of biparental population (*Raju et al., 2010*). The range of expression of

characters in intermated population was wider as compared with F<sub>3</sub> selfed population. It is note worthy that the lower limit of range was higher in BIP for most characters. At the same time, the upper limit was higher compared to F<sub>3</sub> progenies for most characters, suggesting that intermating has helped in releasing more variability than selfing. The higher variability in the biparental populations could have resulted from the additional opportunity for genetic recombinations. However, reduced variability in BIP particularly for lint percentage could be due to presence of genes controlling this character in coupling phase. (*Vinayan and Govindrasu, 2010*).

The BIP had greater GCV and PCV with respect of all characters than F<sub>3</sub> selfed generation. This could be attributed to the fact that biparental mating in F<sub>2</sub> generation caused forced recombinations, thereby undesirable linkage, especially in repulsion phase were broken down, which resulted in the release of hidden genetic variability.

Lint percentage as well as most fiber quality characters showed lower values of GCV and PCV. However most yield characters and fiber fineness showed high GCV and PCV values. This may be attributed to the predominance of repulsion phase linkage. *Kampli et al., 2002*, reported high GCV and PCV for some yield characters. While *Araujo et al., 2012*, reported that the lowest GCV and PCV values were associated with fiber quality characters is due to the smaller number of genes influencing their responses.

The estimates of genetic variability (Table 3) revealed that the magnitude of non-additive were largely in biparental for all characters as compared with F<sub>3</sub> selfed. These could be emphasized by dominance ratio, which more than unity. This trend was reversed in F<sub>3</sub> selfed, since the additive component played a major role in the inheritance of most studied characters, except for seed index and fiber strength which under control both additive and non additive gene effects. Similar results were previously obtained by *Iqbal et al., (2005); Lukange et al., 2007 and Khan et al., (2009)*.

Table 1

**Impact of mating system on genetic variability and correlation .....**

Table 2

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**Table (3): Assessment of additive ( A ), dominance ( D ) genetic component of variation, environmental ( E ) variance, degree of dominance  $\sqrt{\frac{D}{A}}$  and heritability in broad and narrow senses for the studied characters in different populations in cotton.**

Characters	POP.	$\sigma^2A$	$\sigma^2D$	$\sigma^2E$	VD/VA	H <sup>2</sup> <sub>n</sub>	H <sup>2</sup> <sub>b</sub>
B.W	BIP	0.057	0.382	0.044	2.595	11.78	90.85
	F <sub>3</sub>	0.077	0.050	0.020	0.81	66.79	77.55
SCY	BIP	64.070	207.453	31.610	1.79	21.16	89.66
	F <sub>3</sub>	118.732	34.201	18.472	0.60	78.159	83.79
L.Y	BIP	11.190	34.1	4.838	1.75	22.32	90.35
	F <sub>3</sub>	20.248	1.210	2.211	0.24	86.17	87.46
L.P	BIP	2.034	3.479	0.975	1.31	31.36	84.97
	F <sub>3</sub>	5.219	-	0.548	-	87.72	87.72
SI	BIP	0.301	2.168	0.149	2.68	11.51	94.32
	F <sub>3</sub>	0.452	0.719	0.138	1.26	55.39	77.43
LI	BIP	0.348	1.067	0.124	1.76	22.48	91.99
	F <sub>3</sub>	0.715	-	0.032	-	94.47	94.47
F.F	BIP	0.088	0.371	0.037	2.05	17.78	92.57
	F <sub>3</sub>	0.362	-	0.022	-	92.44	92.44
F.S	BIP	0.354	0.858	0.115	1.56	26.66	91.37
	F <sub>3</sub>	0.182	0.434	0.052	1.54	61.68	66.90
F.L	BIP	0.396	3.409	0.445	2.93	9.32	89.52
	F <sub>3</sub>	1.258	0.252	0.114	0.45	85.40	89.68
UR	BIP	1.771	11.377	2.163	2.53	11.56	85.87
	F <sub>3</sub>	9.553	-	1.041	-	87.31	87.31
+B	BIP	0.211	1.178	0.115	2.36	14.05	92.36
	F <sub>3</sub>	4.147	-	0.178	-	94.58	94.58

Estimates of additive genetic component from advanced generations would be more reliable than those of the corresponding F<sub>2</sub> generation. Since, estimates from F<sub>2</sub> might be biased in presence of repulsion phase linkages, which over – estimate of non additive variance and may therefore, conceal additive variation. These effects

could dissipate in intermating. If this proposition holds, true, superior recombinants should be expected in the progenies of biparental matings compared with selfed progenies as suggested by *Ontagodi, (2009)*. So the intermating system is very much helpful in breaking the

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repulsion phase linkage and estimates of genetic variance are reliable.

Comparison of heritability in broad and narrow senses between BIP and  $F_3$  selfed (Table 3) revealed that change of heritability in broad ( $H^2_b$ ) towards higher side in biparental progenies over selfing. This occurred probably due to increased of genetic variance to total phenotypic variance, due to cryptic genetic change that have been brought about one cycle of intermating. On the other side, narrow sense heritability was higher in  $F_3$  selfed than intermated populations for all studies characters. This was due to a great role of additive genetic variance.

By considering together all variability parameters along with the mean performance. It may be concluded that intermating in  $F_2$  segregating population is the best for throwing high variability. This variability is also associated with high heritability. Cotton is an often-self pollinated crop, where lack of variability has been implicated as one of the important causes for lack of desired progress in breeding programs. Hence, the present report on the use of biparental mating in early segregation generation like  $F_2$ , could be much use in widening variability and consequently in making considerable gain in improving productivity.

**Character association:** Genotypic association in biparental intermated progenies and  $F_3$  selfed progenies (Table 4) revealed significant genotypic correlation coefficients among boll weight with other yield characters and fiber fineness in BIP only. Boll weight is a very important character for the breeder for developing high yielding genotypes, due to its positive linkage with all yield characters. *Makhdoom et al., 2010* reported that boll weight is the key independent yield component and play prime role in managing seed cotton yield. Boll weight has a direct influence on the yield and positively correlated with seed cotton yield (*Iqbal et al., 2006* and *Farooq et al., 2013*). Most yield components were positively correlated with each other and with seed cotton yield. In the same time,

most yield characters were positively correlated with fiber fineness in both populations. In contrast, fiber fineness showed negatively associated with the other fiber characters.

It is interest to note that, cotton production systems are commonly oriented towards yield, while is recognized as a major components of profitability, lint quality is also a very important crop characteristics as has been increasingly important issue since advancement of improved textile factories.

The study of correlation showed negative association between most yield characters with most fiber quality characters, especially in  $F_3$  selfed population. Such a negative association brought up the question of the relative importance of both parameters or the level of expected yield reduction. The value of the end product is determined by quality characteristics, and a high yield genotype will be low economic value if its fiber properties are not acceptable. Similar conclusion was reported by *Desalegen et al., (2009)* and *Karademit and Gencer, (2010)*.

A comparison of direction and magnitude of association among characters between biparental intermated progenies and  $F_3$  selfed progenies (Table 4) indicated that, several new associations in terms of direction and magnitude of associations was observed. Lint percentage had a significant negative association with fiber strength, fiber length and uniformity ratio in  $F_3$  progenies. But in intermated progenies these associations were broken and changed to positive and non significant with each of fiber strength and fiber length and significant with uniforming ratio. Similary lint index with fiber strength, fiber length, uniformity ratio and lint yellowness. It was non-significant and negative in  $F_3$  selfed population, but it changed to non significant positive association upon intermating. The association of seed cotton yield/plant where broken and changed to positive and significant with each of lint percentage, lint index and fiber fineness in biparental, while it was positive but non-significant with fiber strength, length and uniformity ratio.

Table 4



The desirable shifts in association between various characters may be attributed to breakage of undesirable linkages among the genes, which controlled such characters, and resulted in newer recombinants, which presumably, were due to changes from a coupling to repulsion phase linkage. Similar type of shift in the association has been reported by Tyagi (1987) observed shift in association between lint yield and halo length, lint percentage with lint index and fiber fineness. While, Abd El-Salam *et al.*, (2013) reported that the correlation coefficient between seed index with lint percentage was negative and significant with respect to pedigree population, but, it was changed to non-significant in recurrent selection.

Keeping in mind the change in association in yield and fiber characters upon intermating, it could be concluded that a few more cycles of planned intermating could dissipate the negative association among fiber and yield characters and that a simultaneous improvement in yield and quality would be possible.

Character association in such populations may be explained on the basis of linkage and/or pleiotropy. In the case where the favourable and unfavourable genes are linked together, it is expected that with the breakage of linkage by intermating in the  $F_2$  or further segregating generations, the negative associations are likely to be minimized. Thus, in the present study, the reduction or complete disappearance of negative associations in intermated progenies as compared to  $F_3$  selfed progenies may be due to breakage of linkage upon intermating in BIP.

## **Conclusion**

From the results of the present study, it could be inferred that biparental population developed by intermating in  $F_2$  plants produced higher desirable mean values for yield and fiber characters along with high genetic variability coupled with heritability in broad sense for such characters, than the  $F_3$  selfed populations. Further, undesirable character associations between yield and its components with fiber quality character were

broken or reduced by intermating in  $F_2$ . Changes in correlation coefficients, particularly from unfavorable to favorable ones, would provide greater scope for increasing the frequency of rare recombinants under the biparental mating approach. Thereby biparental mating offer a good scope for selecting new recombinants combining both quality and yield potential by exercising simultaneously for yield and fiber characters. These recombinations could be used in cotton breeding program.

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## **تأثير نظام التزاوج داخل العشيرة على التباين الوراثى ومعامل الارتباط فى اقطان الباريادنس**

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### **الملخص العربى**

أجريت هذه الدراسة بهدف معرفة الكفاءة النسبية لنظام التزاوج داخل العشيرة مقارنة بعائلات الجيل الثالث الذاتى وذلك فى إطلاق أو ظهور الإختلافات الوراثية الكامنة وكذلك لمعرفة التغير فى نمط الإرتباط لمختلف الصفات فى أقطان الباريادنس .

تم تقييم ستون هجينا ناتجة من نسل التزاوج داخل عشيرة الجيل الثانى للهجين جيزه ٧٥ × كارشنى مع ستة عشر عائلة من الجيل الثالث الذاتى ، " آباء الهجن " لصفات المحصول وجودة التيلة وقد استخدم تصميم قطاعات كاملة العشوائية فى تنفيذ التجربة وأظهرت النتائج ما يلى :

- أظهر تحليل التباين إختلافات عالية المعنوية بين النسل الناتج من التزاوج داخل العشيرة.
- تفوق النسل الناتج من التزاوج داخل العشيرة الجيل الثانى على نسل الجيل الثالث الذاتى وظهر ذلك فى تسجيل أعلى قيم للمتوسطات فى الإتجاه المرغوب لكل الصفات .
- أظهر المدى إختلافات واسعة فى نسل الهجن الرجعية بالمقارنة بعشيرة الجيل الثالث حيث وجد أن الحد الأدنى للمدى كان اعلى وكذلك الحد الأعلى لمعظم الصفات فى عشيرة الهجن الرجعية مما يدل على أن التزاوج داخل العشيرة يُساعد فى ظهور الإختلافات الوراثية.
- تم ملاحظة قدر كبير من الإختلافات الوراثية مرتبطة مع درجة التوريث العالية بالمعنى الواسع فى نسل الهجن الرجعية مقارنة بعشيرة الجيل الثالث الذاتى .
- كانت مساهمة التباين الوراثى الغير مضيف الأكبر بالنسبة للتباين الكلى فى نسل الهجن الرجعية لكل الصفات مقارنة بنسل الجيل الثالث وذلك بسبب ظهور الإختلافات الوراثية الخفية والتي ظهرت من خلال دورة واحدة من التزاوج داخل العشيرة .
- بينما كان التباين الوراثى المضيف الأكثر أهمية فى التباين الكلى فى نسل عشيرة الجيل الثالث الذاتى لمعظم الصفات وتم تأكيد ذلك بارتفاع درجة التوريث بالمعنى الضيق لهذه الصفات .
- أظهرت دراسة الإرتباط الوراثى ظهور إرتباطات جديدة سواء كانت فى الإتجاه أو الأهمية فمثلا الإرتباط السالب الغير مرغوب بين صفات المحصول وصفات جودة التيلة الموجود فى عشيرة الجيل الثالث تم كسره أو تحوله الى إرتباط موجب وغير معنوى فى النسل الناتج من التزاوج داخل العشيرة نتيجة ظهور إتحدات وراثية جديدة فى النسل الناتج من التزاوج داخل العشيرة تجمع فى صفاتها بين المحصول العالى وصفات الجودة الجيدة .ويمكن استغلال هذه التراكيب الوراثية الجديده فى برامج تربية القطن لتحسين المحصول و صفات الجوده .

**Table (1): Analysis of variance for the studied characters in biparental progenies in cotton cross G. 75 x kar<sub>2</sub>**

S.OV	DF	B.W	SCY	LY	LP%	SI	LI	Mic	Pres.	Length	UR	+B
Rep.	2	0.0242	13.43	9.500	2.2546	0.3946	0.4638	0.0021	0.1029	0.4774	1.496	0.0576
Male	9	0.6349*	456.86*	78.108*	20.2584*	4.0551*	3.6270*	0.7739*	2.5085*	4.6579*	27.041*	2.4373*
Female	5	0.6778*	698.12*	118.771*	6.3095*	2.4941*	1.6603*	0.8757*	3.1446*	6.1780*	10.015*	1.7705*
M X F	45	0.3308*	186.90*	30.413*	3.5840*	1.7749*	0.9313*	0.3155*	0.7582*	3.0018*	10.696*	0.9985*
Error	118	0.0442	31.31	4.838	0.9751	0.1486	0.1240	0.0369	0.1145	0.4453	2.163	0.1149

\* Significant at 5% probability level.

**Table (2): Means, SE, range, GCV % and PCV % for the studied characters in different populations in cotton**

Characters	Biparental			F3 selfed			GCV %		PCV %			
	Mean	±	SE	Range	Mean	±	SE	Range	BIP	F <sub>3</sub>	BIP	F <sub>3</sub>
BW	3.10	±	0.030	2.2-4.3	2.86	±	0.029	2.3-3.7	21.37	9.05	22.41	10.31
SCY	53.85	±	0.738	27.7-74.0	43.38	±	1.07	25.3-71.6	30.59	22.52	32.33	24.61
LY	19.98	±	0.298	9.42-28.64	16.07	±	0.422	9.93-25.49	33.59	24.44	35.14	26.13
LP%	37.36	±	0.124	33.0-40.6	36.90	±	0.191	32.8-41.2	6.28	5.36	6.82	5.72
SI	11.08	±	0.068	8.8-12.9	10.26	±	0.079	8.4-12.2	14.18	6.70	14.6	7.67
LI	6.63	±	0.055	4.92-8.20	6.02	±	0.070	4.35-7.64	17.99	12.16	18.77	12.51
FF	4.18	±	0.031	3.4-5.2	4.22	±	0.041	3.5-5.00	16.22	12.13	16.86	12.63
F.S	10.06	±	0.052	8.4-11.7	9.95	±	0.074	8.8-11.00	10.94	4.69	11.44	5.22
FL	32.89	±	0.090	30.00-35.2	32.30	±	0.082	30.4-34.2	5.93	3.08	6.27	3.25
UR	84.89	±	0.179	77.2-90.5	84.46	±	0.355	78.4-88.	4.3	3.17	4.61	3.39
+B	8.75	±	0.053	7.1-11.4	9.37	±	0.101	7.5-11.6	13.47	18.64	14.0	19.0

**Table (4): Genotypic correlation coefficients among various characters in BIP and F<sub>3</sub> selfed families**

		BW	SCY	LY	LP	SI	FF	F.S	FL	UR	+B
SCY	BIP	0.266*									
	F <sub>3</sub>	0.579*									
LY	BIP	0.334*	0.985**								
	F <sub>3</sub>	0.648**	0.982**								
LP	BIP	0.466**	0.410**	0.557**							
	F <sub>3</sub>	0.611*	0.333	0.566*							
SI	BIP	0.805**	0.016	0.041	0.096						
	F <sub>3</sub>	0.909**	0.516*	0.546	0.400						
LI	BIP	0.876**	0.251*	0.357**	0.655**	0.815**					
	F <sub>3</sub>	0.886**	0.482	0.516**	0.876**	0.791**					
F.F	BIP	0.352*	0.365**	0.431**	0.505**	0.187	0.434**				
	F <sub>3</sub>	0.66	0.137	0.256	0.672**	0.190	0.554**				
F.S	BIP	0.114	0.154	0.229	0.120	0.321	0.047	0.400**			
	F <sub>3</sub>	0.257	0.334	0.329	0.497*	0.016	0.307	0.745**			
F.L	BIP	0.067	0.092	0.017	0.156	0.083	0.157	0.522**	0.848**		
	F <sub>3</sub>	0.177	0.532	0.511*	0.573*	0.200	0.260	0.307	0.921**		
UR	BIP	0.138	0.096	0.167	0.424**	0.071	0.185	0.025	0.403**	0.308*	
	F <sub>3</sub>	0.262	0.068	0.026	0.521*	0.095	0.278	0.563*	0.934**	0.965**	
+B	BIP	0.157	0.266*	0.267*	0.205	0.103	0.040	0.321*	0.171	0.205	0.022
	F <sub>3</sub>	0.027	0.529*	0.423	0.309	0.097	0.157	0.226	0.255	0.505*	0.024*

\*, \*\* significant at 0.05 and 0.01 probability levels, respectively.

r = 0.250 and 0.354 for 58 df ( BIP )

r = 0.497 and 0.623 for 14 df ( F<sub>3</sub> )

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UR	84.89	±	0.179	77.2-90.5	84.46	±	0.355	78.4-88.	4.3	3.17	4.61	3.39
+B	8.75	±	0.053	7.1-11.4	9.37	±	0.101	7.5-11.6	13.47	18.64	14.0	19.0

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