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Part-A- (Pure and Applied Sciences)

Combining ability analysis and gene action for some characters of pea (*Pisum sativum*L.) genotypes

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| Article info | Abstract |
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| Original: 22/11/2017 Revised: 30/12/2017 Accepted: 06/02/2018 Published online: | Seven pea varieties <i>Pisumsativum</i> were sown in half diallel cross excluding reciprocals at winter season of 2013-2014 at Qliasan research station. During the winter season of 2014-2015, 28 genotypes (21 crosses + 7 parents) were sown in completely Randomized block design (CRBD), with three replications at Qliasan research station. The analysis of variance confirmed that the mean squares due to genotypes were highly significant for the characters secondary branches, fresh stem weight, dry stem weight and dry root weight, but it is significant for primary branches, fresh leaf weight and fresh root weight. The mean squares due to GCA and SCA were highly significant for most characters. The cross 4×5 showed maximum value for most characters. The crosses 3×4, 3×6 and 4×5 showed maximum heterosis values for the studied characters. Maximum positive GCA effect values produced by the parents 4, 5 and 6 for most characters, while maximum SCA effect values produced by the cross 4×5 for most characters. The ratio of $\sigma^2_{gca}/\sigma^2_{sca}$ was less than unity for all characters. Average degrees of dominance due to all characters were more than unity, revealing the importance of non-additive gene effect in controlling the inheritance of these characters. |
| Key Words: Pea, Diallel genetic analysis, Combining ability, Gene action. | |

Introduction

Pea is a major winter annual crop of temperate regions of the world and was originally cultivated in the Mediterranean basin [1]. Its adaptation to relatively cool conditions has enabled its cultivation to spread beyond the area of initial domestication into Europe, Africa, and Asia. In tropical areas, it is cultivated during the cold months [2]. The papilionoid/fabaceae field pea annual crop plant *pisumsativum* ($2n=14; \geq 5000$ Mbp nuclear genome), which is a useful model for genetical investigations on leaf, inflorescence and flower morphogenesis, is a stipulate plant. The genetic material presently available in this system allows dissection of functions performed by stipules [3]. In the plants of vegetative phase, stem, stipules, petioles, rachis, leaflets and tendrils have chlorophyllous green color. At the stage of flowering- cum- fruiting, the chlorophyllous green color is shared by some additional plant structures/ organs, including inflorescence pedicel, floral calyx and carpels, pods and developing embryos. Surface- area- wise, stipules are the major chlorophyllous organs, next to leaves. Being chlorophyllous, it is believed that stipules are photosynthetic. However, the relative contribution of stipules versus leaves to photosynthesis at nodes is not yet quantitatively characterized. The regularity in the inheritance established by Mendel is the fundament on which are build the selection process and improve the methods for selection – genetic assessment of genotypes and the methods of selection [4]. The knowledge of gene action is very useful to a plant breeder in the selection of parents for hybridization, the estimation of some other genetic parameters and choice of breeding procedures for the genetic improvement of various quantitative characters. In an autogamous crop exploitation of non- additive genetic variance as such would be impractical [5]. Diallel crosses have been

widely used in genetic research to investigate the inheritance of important traits among a set of genotypes. These were devised, specifically 78/9*-y, to investigate the combining ability of the parental lines for the purpose of identification of superior parents for use in hybrid development programs [6].

The aim of this investigation was to estimate general and specific combining ability values for some vegetative characters among seven pea varieties and their hybrids to identify appropriate parents and crosses for the traits evaluated to assess their potential use in pea breeding programs.

Materials and methods

This study was conducted at Qliasan Agricultural research station, college of agricultural sciences/ University of Sulaimani, 2Km north west of the city of Sulaimani (35° 34' 307" N latitudes; 45° 21' 992" E with an altitude 765masl). Seven varieties of field pea were crossed in all possible combinations without reciprocals namely: Avolla(1), America(2), Jeza(3), Joneor(4), Pack Land(5), Wild Local arvena(6), Samara(7).

Seeds of 21 F1 hybrids and their parents were sown in a complete randomized block design. With three replications on 15th November 2015. Each plot consisted of 21 F1 or parent plants on a single 3m row which were 50cm apart, plant spacing was 10 cm apart. All recommended cultural practices were performed for the experiment.

A. Studied characters:

Data of vegetative growth were recorded from five plants of each genotype from each replication: Number of primary branches/plant MS, Number of secondary branches/plant, Stem fresh weight(g), Stem dry weight(g), Leaf fresh weight(g), Leaf dry weight(g), Root fresh weight(g) and Root dry weight(g).

B. Statistical Analysis and the Estimation of Genetic parameters:

Data recorded on parents and the F1 hybrids were analyzed together as suggested by Singh and Chaudhary, (1979) [7]. Statistical analysis was performed for each character. A complete randomized block design, with three replications was implemented [8].

C. The Combining Ability Analysis:

According to the results the significant differences were found between hybrids in CRBD analysis. All data were taken from 7 parents and 21 hybrids, and combining ability analysis was performed according to the procedure of Griffing, (1956)[9] using method II model I as elaborated by Singh and Chaudhury, (1985)[10]. The GCA and SCA were estimated using the general liner model.

D. The Estimation of Heterosis:

It is the heterosis where F1 is superior to mid-parental value. In other words superior to average of two parents [11].

$$\text{Heterosis (H)\%} = \frac{\text{F1} - \text{M.P}}{\text{M.P}} \times 100$$

t-test is used to know the significance of heterosis:

$$t = H / \sqrt{V(H)}$$

V(H)= The variance of heterosis

$$VH = 2 \sigma^2 e$$

$$\sigma^2 e = \text{mse}/r$$

E. Heritability:

Heritabilities in broad and narrow sense were estimated depending on the variance of general and specific combining abilities, and on the variance of experimental error according to Singh and Chaudhury, (1985)[10]. Heritability (n.s) is considered to be high when more than 50%, medium when the result is in the

range of 20-50% and it is low when the result is less than 20% [12], the Average Degree of Dominance (\bar{a}):

The degree of dominance mean for all traits was estimated as follows:

$$\bar{a} = \sqrt{\frac{2\sigma^2 D}{\sigma^2 A}} = \sqrt{\frac{2\sigma^2 sca}{2\sigma^2 gca}} = \sqrt{\frac{\sigma^2 sca}{\sigma^2 gca}}$$

- If: \bar{a} = zero Indicates non dominance.
- \bar{a} =1 Indicated complete dominance.
- \bar{a} <1 Indicated partial dominance.
- \bar{a} >1 Indicated over dominance.

Results and Discussion:

Data in Table 1 illustrate the mean squares due to variance sources of the studied characters. The mean squares due to genotypes were highly significant for the characters secondary branches, fresh stem weight, dry stem weight, and dry root weight, but the mean squares due to genotypes for the characters primary branches, fresh leaf weight and fresh root weight were significant. The mean squares due to GCA were highly significant for all characters except fresh leaf weight which was significant. The mean squares due to SCA were highly significant for all characters except primary branches which was insignificant, fresh root weight was not significant [13; 14; 15 ; 16]. Found significant differences between varieties for growth characters. Similar results exhibited by other researchers [17; 18;19].

Table -1: The mean squares of variance analysis for genotypes, general and specific combing ability for parents, F1 and crosses.

| S.O.V. | d.f | Number of primary branches/plant MS | Number of secondary branches/plant | Stem fresh weight(g) | Stem dry weight(g) | Leaf fresh weight(g) | Leaf dry weight(g) | Root fresh weight(g) | Root dry weight(g) |
|------------------|-----|-------------------------------------|------------------------------------|----------------------|--------------------|----------------------|--------------------|----------------------|--------------------|
| Blocks | 2 | 3.655 | 85.750 | 398.715 | 57.677 | 35525.082 | 2756.315 | 0.520 | 2.422 |
| Genotypes | 27 | 1.691* | 66.308** | 1849.951** | 56.896** | 5575.778* | 180.154** | 3.730* | 0.139** |
| GCA | 6 | 0.925** | 55.933** | 877.780** | 34.368** | 2292.624* | 106.501** | 2.252** | 0.087** |
| SCA | 21 | 0.460* | 12.437** | 542.042** | 14.564** | 1734.584** | 46.780** | 0.955 | 0.035** |
| Error | 54 | 0.963 | 16.676 | 649.249 | 18.876 | 2665.917 | 51.216 | 2.090 | 0.038 |
| Total | 83 | | | | | | | | |
| Mse' | | 0.321 | 5.559 | 216.416 | 6.292 | 888.639 | 17.072 | 0.697 | 0.013 |

Data in Table 2 explain the average of studied characters for F1 generation and their parents. Maximum value due to root fresh weight produced by the cross 1×6 , which was 5.617 g and for number of primary branches /plant and root dry weight they were 5.00 and 1.213g respectively produced by the cross 3×6. While for the characters stem fresh weight, stem dry weight, leaf fresh weight and leaf dry weight were 125.323, 19.777, 242.147 and 41.740g respectively produced by the cross 4×5. Maximum number of secondary branches/ plant produced by the cross 5×6 with 20.000 branches. The lowest value for number of primary branches was 2.000 branches exhibited by the cross 2×3, while the cross 2×7 showed the lowest value for the characters number of secondary branches, stem fresh weight and stem dry weight with 1.667,

15.330 and 1.527g respectively. The cross 5×7 give the lowest value for the characters root fresh weight and root dry weight with 2.040 and 0.467g respectively. While the lowest value for the characters leaf fresh weight and leaf dry weight produced by the cross 6×7 with 56.733 and 6.993g respectively.

Parent 1 give maximum value for the characters stem dry weight and root dry weight with 6.293 and 0.867g respectively and parent 4 showed maximum value for the characters stem fresh weight and root fresh weight with 28.687 and 3.627g respectively while for the characters leaf fresh weight and leaf dry weight produced by parent 5 with 137.503 and 26.087 g respectively, parent 6 produced the highest value for primary and secondary branches/ plant with 4.000 and 9.000 respectively.

Parent 7 showed the lowest value for the characters primary branch number, stem fresh weight, leaf fresh weight root fresh weight and root dry weight with 2.000 , 12.513, 45.803, 1.457 and 0.427g respectively. Previous workers reported that number of branches per plant lies between 1-4 branches among the parents and 1-5 branches among the hybrids [20].

Table- 2: Average of crosses and parents for studied characters.

| <i>Crosses and parents</i> | <i>Number of primary branches/ plant</i> | <i>Number of secondary branches/ plant</i> | <i>Stem fresh weight(g)</i> | <i>Stem dry weight(g)</i> | <i>Leaf fresh weight(g)</i> | <i>Leaf dry weight(g)</i> | <i>Root fresh weight(g)</i> | <i>Root dry weight(g)</i> |
|----------------------------|--|--|-----------------------------|---------------------------|-----------------------------|---------------------------|-----------------------------|---------------------------|
| 1 x 2 | 3.000 | 3.000 | 31.493 | 3.247 | 127.783 | 23.193 | 4.027 | 1.033 |
| 1 x 3 | 4.000 | 4.333 | 37.427 | 5.853 | 130.277 | 23.703 | 4.127 | 0.937 |
| 1 x 4 | 2.667 | 5.333 | 65.447 | 12.703 | 137.660 | 28.630 | 4.280 | 0.947 |
| 1 x 5 | 3.667 | 2.333 | 27.807 | 5.017 | 102.700 | 18.260 | 2.123 | 0.713 |
| 1 x 6 | 4.333 | 13.667 | 59.393 | 9.927 | 103.010 | 21.050 | 5.617 | 1.087 |
| 1 x 7 | 3.333 | 7.000 | 29.750 | 5.230 | 119.623 | 23.090 | 3.810 | 0.850 |
| 2 x 3 | 2.000 | 3.000 | 20.747 | 1.767 | 128.603 | 19.097 | 2.843 | 0.593 |
| 2 x 4 | 2.667 | 3.000 | 35.140 | 10.043 | 95.907 | 21.167 | 2.917 | 0.760 |
| 2 x 5 | 2.667 | 3.333 | 37.250 | 6.970 | 147.190 | 23.070 | 3.917 | 1.100 |
| 2 x 6 | 2.333 | 4.333 | 38.957 | 5.290 | 138.277 | 18.057 | 3.750 | 0.850 |
| 2 x 7 | 3.000 | 1.667 | 15.330 | 1.527 | 79.090 | 11.200 | 3.127 | 0.537 |
| 3 x 4 | 3.333 | 4.333 | 60.460 | 10.797 | 152.847 | 26.303 | 3.730 | 0.737 |
| 3 x 5 | 3.000 | 2.000 | 25.333 | 4.207 | 93.097 | 16.303 | 2.200 | 0.557 |
| 3 x 6 | 5.000 | 5.333 | 60.977 | 9.113 | 144.307 | 20.953 | 5.493 | 1.213 |
| 3 x 7 | 3.000 | 3.333 | 32.723 | 3.007 | 115.473 | 19.487 | 2.587 | 0.723 |
| 4 x 5 | 4.333 | 10.667 | 125.323 | 19.777 | 242.147 | 41.740 | 5.447 | 1.130 |
| 4 x 6 | 2.333 | 16.333 | 47.523 | 7.423 | 100.303 | 18.660 | 4.747 | 0.897 |
| 4 x 7 | 3.000 | 4.333 | 61.170 | 11.997 | 61.573 | 21.933 | 3.163 | 0.603 |
| 5 x 6 | 4.000 | 20.000 | 79.203 | 13.777 | 146.170 | 28.273 | 4.547 | 1.047 |
| 5 x 7 | 3.333 | 4.333 | 17.573 | 3.347 | 102.663 | 18.730 | 2.040 | 0.467 |
| 6 x 7 | 3.667 | 11.333 | 29.137 | 3.880 | 56.733 | 6.993 | 3.227 | 0.653 |
| 1 | 2.667 | 1.667 | 21.250 | 6.293 | 81.650 | 23.063 | 2.997 | 0.867 |
| 2 | 2.333 | 1.667 | 13.803 | 3.440 | 56.457 | 9.070 | 2.943 | 0.683 |
| 3 | 2.667 | 3.333 | 15.420 | 1.377 | 53.803 | 6.320 | 2.420 | 0.543 |
| 4 | 3.333 | 8.333 | 28.687 | 4.587 | 57.080 | 10.827 | 3.627 | 0.750 |
| 5 | 2.667 | 1.667 | 15.463 | 4.677 | 137.503 | 26.087 | 1.653 | 0.587 |
| 6 | 4.000 | 9.000 | 27.137 | 4.127 | 54.887 | 9.843 | 3.060 | 0.727 |
| 7 | 2.000 | 4.333 | 12.513 | 2.313 | 45.803 | 9.380 | 1.457 | 0.427 |
| LSD .05 | 1.607 | 6.685 | 41.711 | 7.112 | 84.521 | 11.715 | 2.366 | 0.320 |

Data in Table 3 explain the heterosis values produced as the percentage of F1s deviation from mid parental values. The differences between parents and their hybrids caused significant positive and negative heterosis values. Maximum positive heterosis value for primary branch number was 50% produced by the crosses 1×3

and 3×6 while for leaf fresh weight and leaf dry weight were 175.689 and 206.804% respectively produced by the cross 3×4, while for root dry weight it was 91.076% produced by the cross 3×6 and for stem fresh weight, stem dry weight 967.716 and 326.988% respectively produced by the cross 4×5 and the cross 5×6 showed maximum positive heterosis value for secondary branch number with 275.000%. The positive values of heterosis reveal the effect of over dominance genes effect for the parent of higher value, while the negative heterosis values reflect the partial dominance genes effect for the parent with lower value. Similar results reported by Sheikh Abdulla, (2010)[20] and Ali, (2015)[21].

Table- 3: Estimation of heterosis values for the crosses

| <i>Crosses and parents</i> | <i>Number of primary branches/plant</i> | <i>Number of secondary branches/plant</i> | <i>Stem fresh weight(g)</i> | <i>Stem dry weight(g)</i> | <i>Leaf fresh weight(g)</i> | <i>Leaf dry weight(g)</i> | <i>Root fresh weight(g)</i> | <i>Root dry weight(g)</i> |
|----------------------------|---|---|-----------------------------|---------------------------|-----------------------------|---------------------------|-----------------------------|---------------------------|
| 1 x 2 | 20.000 | 80.000 | 79.688 | -33.288 | 85.050 | 44.357 | 35.578 | 33.333 |
| 1 x 3 | 50.000 | 73.333 | 104.127 | 52.629 | 92.357 | 61.339 | 52.369 | 32.861 |
| 1 x 4 | -11.111 | 6.667 | 162.119 | 133.517 | 98.457 | 68.958 | 29.240 | 17.113 |
| 1 x 5 | 37.500 | 40.000 | 51.480 | -8.538 | -6.276 | -25.697 | -8.674 | -1.835 |
| 1 x 7 | 30.000 | 156.250 | 145.495 | 90.531 | 50.890 | 27.938 | 85.471 | 36.402 |
| 1 x 7 | 42.857 | 133.333 | 76.227 | 21.534 | 87.713 | 42.340 | 71.108 | 31.443 |
| 2 x 3 | -20.000 | 20.000 | 41.987 | -26.644 | 133.273 | 148.170 | 6.029 | -3.261 |
| 2 x 4 | -5.882 | -40.000 | 65.404 | 150.249 | 68.944 | 112.766 | -11.213 | 6.047 |
| 2 x 5 | 6.667 | 100.000 | 154.556 | 71.745 | 51.774 | 31.241 | 70.413 | 73.228 |
| 2 x 6 | -26.316 | -18.750 | 90.311 | 39.824 | 148.379 | 90.941 | 24.931 | 20.567 |
| 2 x 7 | 38.462 | -44.444 | 16.504 | -46.929 | 54.684 | 21.409 | 42.121 | -3.303 |
| 3 x 4 | 11.111 | -25.714 | 174.154 | 262.102 | 175.689 | 206.804 | 23.374 | 13.918 |
| 3 x 5 | 12.500 | -20.000 | 64.058 | 38.987 | -2.673 | 0.617 | 8.020 | -1.475 |
| 3 x 6 | 50.000 | -13.514 | 186.567 | 231.193 | 165.538 | 159.270 | 100.487 | 91.076 |
| 3 x 7 | 28.571 | -13.043 | 134.296 | 62.963 | 131.859 | 148.238 | 33.448 | 49.141 |
| 4 x 5 | 44.444 | 113.333 | 467.716 | 326.988 | 148.887 | 126.151 | 106.313 | 69.077 |
| 4 x 6 | -36.364 | 88.462 | 70.263 | 70.390 | 79.166 | 80.552 | 41.974 | 21.445 |
| 4 x 7 | 12.500 | -31.579 | 196.942 | 247.729 | 19.695 | 117.090 | 24.459 | 2.550 |
| 5 x 6 | 20.000 | 275.000 | 271.847 | 212.988 | 51.952 | 57.380 | 92.928 | 59.391 |
| 5 x 7 | 42.857 | 44.444 | 25.628 | -4.244 | 12.013 | 5.620 | 31.190 | -7.895 |
| 6 x 7 | 22.222 | 70.000 | 46.969 | 20.497 | 12.689 | -27.241 | 42.878 | 13.295 |
| <i>S.E</i> | 5.580 | 17.491 | 22.335 | 23.647 | 12.174 | 13.929 | 7.396 | 6.169 |

Data in Table 4 explain the GCA effect values for the parents. Parent 1 showed maximum positive GCA effect value for root dry weight with 0.112, while parent 4 give maximum positive value for stem fresh weight and stem dry weight with 16.225 and 3.333 respectively while for the characters leaf fresh weight and leaf dry weight they were 27.581 and 4.776 respectively produced by parent 5 and for the characters primary branch number , secondary branch number and root fresh weight were 0.492, 4.714 and 0.679 respectively produced by parent 6. maximum negative GCA effect values for the characters primary and secondary branch number, and stem fresh weight were -0.545, -2.767 and -11.099 respectively produced by parent 2. Parent 7 exhibited maximum negative GCA effect values for the characters stem dry weight, leaf fresh weight, leaf dry weight, root fresh weight and root dry weight with -2.034, -25.998, -3.930, -0.725 and -0.176 respectively. The positive GCA effect values indicate clearly a high contribution of these parents to increase the value of these characters in their crosses, while the negative values indicate to the contribution of these parents in reducing the values of these characters in their crosses. The negative GCA value indicate to the ability of these parents to reduce the value of this character, while the positive value of GCA indicates to the tendency of these parents to increase the value of this character.

Table -4: Estimation of GCA effects for the parents

| parents | Number of primary branches/plant | Number of secondary branches/plant | Stem fresh weight(g) | Stem dry weight(g) | Leaf fresh weight(g) | Leaf dry weight(g) | Root fresh weight(g) | Root dry weight(g) |
|------------|----------------------------------|------------------------------------|----------------------|--------------------|----------------------|--------------------|----------------------|--------------------|
| 1 | 0.122 | -0.841 | -1.399 | 0.294 | 2.623 | 3.165 | 0.287 | 0.112 |
| 2 | -0.545 | -2.767 | -11.099 | -1.799 | -3.443 | -2.405 | -0.103 | -0.006 |
| 3 | 0.048 | -1.952 | -4.212 | -1.602 | 1.274 | -1.898 | -0.175 | -0.049 |
| 4 | -0.026 | 1.566 | 16.225 | 3.333 | 4.872 | 2.724 | 0.460 | 0.031 |
| 5 | 0.122 | -0.063 | 4.112 | 1.170 | 27.581 | 4.776 | -0.424 | -0.012 |
| 6 | 0.492 | 4.714 | 7.006 | 0.638 | -6.908 | -2.433 | 0.679 | 0.101 |
| 7 | -0.212 | -0.656 | -10.633 | -2.034 | -25.998 | -3.930 | -0.725 | -0.178 |
| S.E | 0.267 | 1.111 | 6.935 | 1.182 | 14.053 | 1.948 | 0.393 | 0.053 |

Data in Table 5 illustrate the estimation of SCA effect for F1 hybrids indicating that the cross 4x5 give the highest positive SCA effect values for stem fresh weight, stem dry weight, leaf fresh weight, leaf dry weight and root fresh weight with 66.685, 8.784, 102.100, 14.794 and 1.986 respectively. While for the characters primary branch number and root dry weight they were 1.306 and 0.375 respectively produced by the cross 3x6. Maximum negative values for the characters stem dry weight, leaf dry weight and root fresh weight were -2.937, -9.127 and -1.164 respectively produced by the cross 1x5, but for the crosses leaf fresh weight and root dry weight were -43.351 and -0.169 g respectively produced by the cross 3x5 and the cross 4x6 produced maximum negative SCA value for primary branch number and stem fresh weight with -1.287 and -14.009 respectively. The cross with positive SCA effect value confirm the high value for this cross compare to its parents, while the negative value of SCA effect value indicate to the low value of this parents compare to its parental values. The positive value of SCA effect indicating that the contributions of these parents are important in increasing the values of these characters in their hybrids.

Table- 5: Estimation of SCA effects for the F1 Hybrids

| Crosses | Number of primary branches/plant | Number of secondary branches/plant | Stem fresh weight(g) | Stem dry weight(g) | Leaf fresh weight(g) | Leaf dry weight(g) | Root fresh weight(g) | Root dry weight(g) |
|------------|----------------------------------|------------------------------------|----------------------|--------------------|----------------------|--------------------|----------------------|--------------------|
| 1 x 2 | 0.269 | 0.787 | 5.690 | -1.738 | 21.010 | 2.987 | 0.418 | 0.140 |
| 1 x 3 | 0.676 | 1.306 | 4.736 | 0.672 | 18.787 | 2.990 | 0.590 | 0.087 |
| 1 x 4 | -0.583 | -1.213 | 12.320 | 2.587 | 22.572 | 3.295 | 0.108 | 0.017 |
| 1 x 5 | 0.269 | -2.583 | -13.207 | -2.937 | -35.097 | -9.127 | -1.164 | -0.174 |
| 1 x 6 | 0.565 | 3.972 | 15.485 | 2.505 | -0.298 | 0.872 | 1.227 | 0.087 |
| 1 x 7 | 0.269 | 2.676 | 3.481 | 0.480 | 35.405 | 4.409 | 0.824 | 0.130 |
| 2 x 3 | -0.657 | 1.898 | -2.245 | -1.321 | 23.179 | 3.953 | -0.303 | -0.138 |
| 2 x 4 | 0.083 | -1.620 | -8.288 | 2.020 | -13.116 | 1.401 | -0.865 | -0.052 |
| 2 x 5 | -0.065 | 0.343 | 5.935 | 1.110 | 15.459 | 1.253 | 1.019 | 0.331 |
| 2 x 6 | -0.769 | -3.435 | 4.748 | -0.039 | 41.034 | 3.448 | -0.250 | -0.032 |
| 2 x 7 | 0.602 | -0.731 | -1.239 | -1.130 | 0.937 | -1.911 | 0.531 | -0.066 |
| 3 x 4 | 0.157 | -1.102 | 10.145 | 2.576 | 39.108 | 6.031 | 0.020 | -0.032 |
| 3 x 5 | -0.324 | -1.806 | -12.868 | -1.851 | -43.351 | -6.021 | -0.626 | -0.169 |
| 3 x 6 | 1.306 | -3.250 | 19.881 | 3.588 | 42.348 | 5.838 | 1.565 | 0.375 |
| 3 x 7 | 0.009 | 0.120 | 9.267 | 0.153 | 32.605 | 5.869 | 0.062 | 0.165 |
| 4 x 5 | 1.083 | 3.343 | 66.685 | 8.784 | 102.100 | 14.794 | 1.986 | 0.324 |
| 4 x 6 | -1.287 | 4.231 | -14.009 | -3.038 | -5.254 | -1.078 | 0.184 | -0.022 |
| 4 x 7 | 0.083 | -2.398 | 17.277 | 4.208 | -24.894 | 3.693 | 0.004 | -0.036 |
| 5 x 6 | 0.231 | 9.528 | 29.784 | 5.479 | 17.904 | 6.484 | 0.868 | 0.171 |
| 5 x 7 | 0.269 | -0.769 | -14.206 | -2.279 | -6.512 | -1.561 | -0.235 | -0.130 |
| 6 x 7 | 0.231 | 1.454 | -5.537 | -1.214 | -17.954 | -6.090 | -0.151 | -0.056 |
| S.E | 0.756 | 3.144 | 19.615 | 3.345 | 39.747 | 5.509 | 1.113 | 0.150 |

The estimation of $\sigma^2_{\hat{g}ii}$ present in table 6 confirms that parent 2 showed maximum positive the $\sigma^2_{\hat{g}ii}$ for the character number of primary branches per plant with 0.083. While maximum value for number of secondary branches per plant due to this variance produced by parent 6 with 18.519. Maximum positive value due to $\sigma^2_{\hat{g}ii}$ for the characters stem fresh weight and stem dry weight produced by parent 4 with 118.977 and 6.914 respectively. Parent 5 exhibited maximum positive $\sigma^2_{\hat{g}ii}$ due to the characters leaf fresh weight and leaf dry weight with 168.265 and 11.428 respectively. Maximum positive $\sigma^2_{\hat{g}ii}$ for root dry weight was 0.023 produced by parent 6. Parents with high positive value for the variance of gca indicate to their contribution in increasing the value of the characters in their hybrids. The highest value for $\sigma^2_{\hat{g}ii}$ indicated that this parent can able to increase the value of this character in its hybrids.

Table- 6: Estimation of $\sigma^2_{\hat{g}ii}$ for the parents

| parents | Number of primary branches/ plant | Number of secondary branches/ plant | Stem fresh weight(g) | Stem dry weight(g) | Leaf fresh weight(g) | Leaf dry weight(g) | Root fresh weight(g) | Root dry weight(g) |
|---------|-----------------------------------|-------------------------------------|----------------------|--------------------|----------------------|--------------------|----------------------|--------------------|
| 1 | -0.199 | -2.998 | -142.320 | -4.108 | -585.547 | -1.363 | -0.382 | 0.004 |
| 2 | 0.083 | 3.952 | -21.099 | -0.957 | -580.574 | -5.598 | -0.454 | 0.008 |
| 3 | -0.212 | 0.106 | -126.541 | -1.627 | -590.804 | -7.780 | -0.434 | 0.006 |
| 4 | -0.213 | -1.253 | 118.977 | 6.914 | -568.689 | -3.959 | -0.252 | 0.008 |
| 5 | -0.199 | -3.702 | -127.371 | -2.826 | 168.265 | 11.428 | -0.285 | 0.008 |
| 6 | 0.028 | 18.519 | -95.195 | -3.787 | -544.702 | -5.464 | -0.004 | 0.002 |
| 7 | -0.169 | -3.275 | -31.209 | -0.059 | 83.483 | 4.066 | -0.061 | 0.023 |

The estimation of the variance due to sca effect for the parents present in Table 7. Parent 6 recorded maximum value due to this variance for the characters number of primary branches per plant and secondary branches per plant with 3.816 and 139.211 respectively. Maximum values for this variance due to the characters stem fresh weight, stem dry weight, leaf fresh weight, leaf dry weight, root fresh weight and root dry weight recorded by parent 5 with 5532.351, 114.642, 12582.433, 354.582, 6.318 and 0.297 respectively. Parents with the high value for this variance indicate to their contribution in transferring these characters to a few number of their hybrids, while the low value of σ^2_{sca} recorded by parents indicate to their contribution in transferring these characters to most of their hybrids. The high value of σ^2_{sij} indicated to the contribution of this parent in transferring this character to one or a few number of its hybrids, while the low value of σ^2_{sij} indicated to the ability of this parent in transferring this character to most of its hybrids.

Table- 7: Estimation of $\sigma^2_{\hat{s}ij}$ for the parents

| parents | Number of primary branches/ plant | Number of secondary branches/ plant | Stem fresh weight(g) | Stem dry weight(g) | Leaf fresh weight(g) | Leaf dry weight(g) | Root fresh weight(g) | Root dry weight(g) |
|---------|-----------------------------------|-------------------------------------|----------------------|--------------------|----------------------|--------------------|----------------------|--------------------|
| 1 | 0.770 | 23.680 | 254.197 | 14.280 | 2234.126 | 102.345 | 2.855 | 0.060 |
| 2 | 0.906 | 9.573 | -213.317 | 0.345 | 1519.240 | 13.751 | 1.179 | 0.134 |
| 3 | 2.161 | 10.631 | 398.386 | 14.143 | 5600.194 | 135.839 | 2.067 | 0.202 |
| 4 | 2.647 | 30.413 | 4886.300 | 110.494 | 11727.608 | 252.971 | 3.518 | 0.088 |
| 5 | 0.919 | 102.865 | 5532.351 | 114.642 | 12582.433 | 354.582 | 6.318 | 0.297 |
| 6 | 3.816 | 139.211 | 1392.889 | 48.851 | 2592.611 | 97.143 | 3.608 | 0.160 |
| 7 | 0.567 | 16.165 | 630.506 | 25.906 | 3301.924 | 110.700 | 1.042 | 0.070 |

Data in Table 8 illustrate the estimation of some genetic parameters for all studied characters. The ratio of $\sigma^2_{gca}/ \sigma^2_{sca}$ was found to be less than unity for all studied characters, and restricted between 0.148 and 0.814 for the characters leaf fresh weight and number of secondary branches per plant respectively. The estimation of the parameter average degree of the dominance for all characters were more than unity for all

characters and restricted between 1.109 to 2.329 for the characters number of secondary branches per plant and leaf fresh weight respectively. Heritability in broad science was found to be low to moderate and restricted between 0.221 for number of primary branches per plant to 0.520 for number of secondary branches per plant, while heritability in narrow science for all characters was found to be low, and restricted between 0.082 for leaf fresh weight to 0.322 for number of secondary branches per plant. Using hybridization was found to be the best method to improve these characters in which they recorded the low value due to the parameters heritability in narrow science. These results confirm the suitability of hybridization method to improve these characters. High heritability 0.73 was found previously for plant high by Sultana et al., (2002)[18] but Sood and Kalia, (2006) [22] calculated heritability in broad and narrow sense to be 0.94 and 0.49 respectively. High heritability 0.84 was found previously for this character number of branches/ plant [18], while moderate heritability 0.44 was calculated for basal branches/ plant by Sardana et al., (2007)[2] and Vangeand Egbe, (2009)[23] showed high heritability value 0.84 for this character.

Table- 8: Estimation of some genetic parameters

| Parameters | Number of primary branches/ plant | Number of secondary branches/ plant | Stem fresh weight(g) | Stem dry weight(g) | Leaf fresh weight(g) | Leaf dry weight(g) | Root fresh weight(g) | Root dry weight(g) |
|---------------------------------|-----------------------------------|-------------------------------------|----------------------|--------------------|----------------------|--------------------|----------------------|--------------------|
| <i>Mse'</i> | 0.321 | 5.559 | 216.416 | 6.292 | 888.639 | 17.072 | 0.697 | 0.013 |
| σ^2_{gca} | 0.022 | 1.866 | 24.495 | 1.040 | 51.999 | 3.312 | 0.058 | 0.003 |
| $\sigma^2_{sca} = \sigma^2_D$ | 0.046 | 2.293 | 108.542 | 2.757 | 281.982 | 9.903 | 0.086 | 0.007 |
| $\sigma^2_{gca}/\sigma^2_{sca}$ | 0.481 | 0.814 | 0.226 | 0.377 | 0.184 | 0.334 | 0.668 | 0.374 |
| σ^2_A | 0.045 | 3.731 | 48.990 | 2.080 | 103.999 | 6.624 | 0.115 | 0.006 |
| \bar{A} | 1.441 | 1.109 | 2.105 | 1.628 | 2.329 | 1.729 | 1.223 | 1.634 |
| $b.s^2h$ | 0.221 | 0.520 | 0.421 | 0.435 | 0.303 | 0.492 | 0.224 | 0.503 |
| $n.s^2h$ | 0.108 | 0.322 | 0.131 | 0.187 | 0.082 | 0.197 | 0.128 | 0.215 |

Conclusion

Significant mean squares for genotypes due to all characters confirm the necessity of genetic analysis. Specific combining ability in all of the characters was larger than those of general combining ability, confirming the importance of non-additive gene effect in controlling the inheritance of these characters. Parents Joneor and Pack land contributed the best combinations and superiority in most characters, and cross Joneor \times Pack land produced the best values and heterosis in most characters.

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