**_Original Research Article_**

# ASSESSMENT OF MAIZE (*Zea mays* L.) HYBRIDS ACROSS SPACINGS FOR VARIABILITY, TRAIT ASSOCIATION AND PATH ANALYSIS

## ABSTRACT

The present investigation was conducted with nine genotypes in randomized block design (RBD) during Rabi, 2019-20 across the spacings viz., 60 cm x 20 cm and 50 cm x 20 cm at the ICR farm, AAU, Jorhat. In pooled analysis of variance, the genotype mean square across spacing was significant to highly significant for all the traits except ears per plant. The mean square due to genotype x spacing was significant to highly significant for the traits days to 50% silk, ears per plant, leaf area index at 60 DAS (days after sowing), leaf area index at 90 DAS, harvest index and grain moisture. Each of the hybrids responded similarly from spacing to spacing for the traits viz., days to 50% pollen shed, days to 100% dry husk, anthesis-silking interval, plant height, ear length, ear diameter, kernel rows per ear, kernels per row, 100 kernel weight and grain yield per hectare. One or more hybrids responded differently in the two spacings for the traits viz., days to 50% silk, ear height, ears per plant, chlorophyll content, leaf area index 60 DAS, leaf area index 90 DAS, harvest index, grain moisture and grain yield per plant. High heritability coupled with high genetic advance was observed for plant height, ear height, kernels per row, chlorophyll content, leaf area index at 60 DAS, leaf area index at 90 DAS, harvest index, grain yield per plant and grain yield per hectare across spacing and it indicated the preponderant role of additive gene action for these traits. Significant genetic association of both grain yield per plant and grain yield per hectare with days to 50% pollen shed, days to 50% silk, day to 100% dry husk, kernels per row, leaf area index at 60 DAS and leaf area index at 90 DAS indicated that grain yield could be improved indirectly by selecting superior plants for easily heritable traits like days to 50% pollen shed, days to 50% silk and days to 100% dry husk across spacing. Genotypic path analysis revealed that the characters *viz*., days to 100% dry husk, days to 50% pollen shed,

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ear length and kernel rows per ear had the highest positive direct effects on grain yield per plant while days to 50% silk and kernels per row had the highest negative direct effect on grain yield per plant across spacing.

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## KEY WORDS

Genetic variability, heritability, correlation, path analysis, maize.

## ABBREVIATIONS

| | |
|---|---|
| **D50%PS** | days to 50% pollen shed |
| **D50%S** | days to 50% silk |
| **D100%DH** | days to 100% dry husk |
| **ASI** | anthesis-silking interval |
| **PH** | plant height |
| **EH** | ear height |
| **EL** | ear length |
| **ED** | ear diameter |
| **E/P** | ears per plant |
| **K/R** | kernels per row |
| **KR/E** | kernel rows per ear |
| **CHLC** | chlorophyll content |
| **LAI 60 DAS** | leaf area at 60 days after sowing |
| **LAI 90 DAS** | leaf area index at 90 days after sowing |
| **HI** | harvest index |

|  |  |
|---|---|
| **GM** | grain moisture |
| **100 KW** | 100 kernel weight |
| **G/P** | grain yield per plant |
| **GY/HA** | grain yield per hectare |

## INTRODUCTION

Maize occupies a distinguished position amongst the cereals. It is believed to have originated in Central America (Mexico). It is now grown in all the continents except Antarctica and under a more varied range of climates than any other cereal crop. Globally, maize ranks third in acreage, second in production and first in grain yield per unit area. In India, maize occupies an area of 9.4 m ha with a total production of 28.72 m ~~tones~~ tonnes and productivity of 3032 kg/ha (Directorate of Economics and Statistics, DAC & FW, 2017-18). In Assam, maize occupies an area of 28.42 thousand ha with a total production of 87.18 thousand ~~tones~~ tonnes and an average yield of 3067 kg/ha (Directorate of Economics and Statistics, Govt. of Assam, 2015-16). The main economic importance of maize stems from its diverse utilization as food, feed and raw material for industrial applications. Every part of the plant has economic value: grain, leaves, stalk, tassel and cob are all used to produce variegated food and non-food products. Maize grain contains about 70% of starch on an average, which makes it a highly suitable feedstock for bio-ethanol production. With the increase in human population as well as subsequent increase in the demand for food, changes in the climatic conditions and increasing concern for nutritional security, there is a need for dynamic plant breeding programme for evolving suitable maize varieties. Plant breeders attempt to concentrate in the same variety several genes responsible for higher productivity, adaptability, resistance and quality. A high yielding hybrid having predominant role in maize cultivation in a particular region is considered to ~~have possessed~~ possess maximum favourable genes available in the set of germplasm handled by the breeder for development of that hybrid. Such a hybrid is expected to give higher yield in its area of adaptation.

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Maize breeders across the globe have developed number of high yielding maize hybrids suitable for various agro-ecological situations as well as for varying agronomic practices. More grain yield can be obtained by choosing appropriate genotype, suitable seasons or locations, optimum fertilization and using other improved cultural practices. Varieties differ in their genetic potential to respond to various agronomic practices such as doses of fertilizers and spacing. Open-pollinated varieties of maize are usually poor yielder and require wider spacing or lesser plant population per unit area for better plant growth and production. The modern-day hybrids of maize have high grain yield potential with relatively erect leaves suitable for absorption of more solar radiation and better root system for nutrient and water use efficiency. Such maize hybrids are suitable to harvest higher grain yield per unit area through an enhanced plant density. Since the pioneering work of Shull in 1909, a number of maize hybrids ~~has~~ have been developed in the US and many other countries including India. Since the inception of hybrids in India in 1961, ~~the~~ researchers and farmers have witnessed a good number of public-bred and private-bred hybrids in maize. Some of the hybrids may perform well at high planting density. There is a need to screen different maize hybrids at varying planting densities to identify the promising ones with higher grain yield, deep root system, better ability to absorb ~~more~~ solar radiation, erect leaves and relevant attributes of grain yield. Maize hybrids respond differently depending upon the planting density with which they are grown. However, few hybrids may show neutrality or independence to varying planting density. Thus, the genetic variability, heritability and genetic advance for a trait. The correlation of various morphological and physiological traits may differ depending upon the response of the hybrids to varying plant populations. The direct and indirect effects of independent traits on a dependent trait such as grain yield may also be different in two or more planting densities.

## MATERIALS AND METHODS

### Materials and statistical analysis

The experiment was carried out in the instructional-cum-research (ICR) farm of Assam Agricultural University, Jorhat, during rabi season of 2019-20 for evaluation trial. The research field is located in the Upper Brahmaputra Valley Zone of Assam. The sowing of seeds was done on 20th of November 2019. The seeds of the eight maize hybrids namely, ADV 756, ADV 757, ADV 759, PAC 751, PAC 751 ELITE, CP 333 and CP 838 were obtained from Department of Plant Breeding and Genetics of the university while the seeds of the hybrid 91A21 was

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obtained from the local market. Eight test hybrids along with a recommended hybrid as check(C) (VMH 53) were used in the present study. A set of nine genotypes were evaluated for 19 different morpho-physiological traits viz., days to 50% pollen shed (D50%PS), days to 50% silk (D50%S), days to 100% dry husk(D100%DH), anthesis-silking interval (ASI), plant height (PH), ear height (EH), ear length (EL), ear diameter (ED), ears per plant (E/P), kernels per row (K/R), kernel rows per ear (KR/E), chlorophyll content (CHLR), leaf area at 60 days after sowing (LAI 60 DAS), leaf area index at 90 days after sowing (LAI 90 DAS), harvest index (HI), grain moisture (GM), 100 kernel weight (100KW), grain yield per plant (GY/P) and grain yield per hectare (GY/HA) at two different spacing levels such as normal spacing (60 cm x 20 cm) and narrow spacing (50 cm x 20 cm) with the plant populations 83,333 plants/ha and 1,00,000 plants/ha, respectively. The experimental design was a randomized block design with three replications. The plot means were subjected to the statistical and biometrical analysis namely, Statistical ranking, pooled analysis of variance, genetic coefficient of variance, phenotypic coefficient of variance, heritability, genetic advance as percent of mean, correlation analysis and path analysis.

## RESULT AND DISCUSSION

Statistical ranking of genotypes with respect to individual traits is done for identifying best genotypes with desirable traits. Pooled Analysis of variance was carried out according to the standard statistical method to establish the level of significance among the genotypes. Correlation coefficients were determined as described by Singh and Chaudhary, 1979 [1]. The correlation coefficients were partitioned into direct and indirect effects using the path coefficient analysis according to Dewey and Lu, 1959 [2]. The results obtained from various statistical and biometrical analysis of the present investigation are presented.

### Pooled analysis of variance

Analysis across spacing (Table 1a and 1b) indicated that the spacing mean square was significant to highly significant for the traits *viz*., anthesis silking interval, 100 kernel weight, leaf area index at 90 DAS, harvest index and grain yield per plant. The genotype mean square across spacing was significant to highly significant for all the traits except ears per plant. The mean square due to genotype x spacing was

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significant to highly significant for the trait's days to 50% silk, ears per plant, leaf area index at 60 DAS, leaf area index at 90 DAS, harvest index and grain moisture. It was supported by V. Ram Reddy ~~[3], M.R. Sudarshan [3] and A.Seshagiri Rao,~~et al 2012 [3].

**Table 1a. Pooled analysis of variance for different morphological and physiological traits for across spacings**

| Source | df | Mean squares | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|
| | | D50%PS | D50%S | ASI | D100%DH | PH | EH | E/P | EL | ED | KR/E |
| **Spacing (S)** | 1 | 6.00 | 5.35 | 1.50 | 2.67 | 365.51 | 102.55 | 0.000 | 5.61 | 0.14 | 3.94 |
| **Replication within spacing** | 4 | 5.28 | 1.85 | 0.04 | 1.98 | 781.14** | 277.63** | 0.004 | 2.22 | 0.13** | 2.32 |
| **Genotype (G)** | 8 | 133.71** | 127.56** | 1.52** | 142.73** | 1,544.34** | 601.42** | 0.005 | 10.10** | 0.45** | 9.81** |
| **G X S** | 8 | 5.29 | 13.48* | 0.25 | 0.88 | 82.79 | 87.99 | 0.015** | 1.46 | 0.03 | 1.00 |
| **Pooled Error** | 3 | 2.44 | 5.62 | 1.50 | 1.77 | 158.72 | 49.64 | 0.003 | 1.19 | 0.03 | 1.01 |

***Significant at 5% level of significance; **Significant at 1% level of significance**

**Table 1b. Pooled analysis of variance for different morphological and physiological traits for across spacings**

| Source | df | Mean square | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|
| | | K/R | CHLC | LAI (60 DAS) | LAI (90 DAS) | HI | GMC | 100 KW | GY/P | GY/HA |
| **Spacing (S)** | 1 | 17.15 | 0.002 | 12,613.66 | 22,176.53** | 196.38** | 4.17 | 12.69** | 2,914.62** | 2,86,608.29 |
| **Replication within spacing** | 4 | 7.67 | 0.004 | 1,872.22 | 652.40 | 6.10** | 0.96** | 1.14 | 159.66 | 12,57,101.21 |
| **Genotype (G)** | 8 | 105.81** | 0.611** | 77,975.14** | 92,256.87** | 23.62** | 1.33** | 13.56** | 1,138.88** | 8,127,492.68** |
| **G X S** | 8 | 6.80 | 0.21 | 4,261.63* | 10,754.55** | 31.25** | 1.15** | 0.01 | 240.84 | 14,64,693.44 |
| **Pooled Error** | 3 | 4.60 | 0.004 | 1,881.04 | 2,060.01 | 0.91** | 0.11 | 3.85 | 183.82 | 9,79,571.32 |

***Significant at 5% level of significance; **Significant at 1% level of significance**

**[D50%PS-Days to 50% pollen shed; D50%S-Days to 50% silk; D100%DH-Days to 100% dry husk; ASI-Anthesis silking interval; PH-Plant height; EH-Ear height; E/P-Ears per plant; EL-Ear length; ED-Ear diameter; KR/E-Kernel rows per ear; K/R-Kernels per row; CHLC-Chlorophyll content; LAI60DAS-Leaf area index at 60 days after sowing;**

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**LAI90DAS-Leaf area index at 90 days after sowing; HI-Harvest index; GMC-Grain moisture content; 100 KW-100 kernel weight; GY/P-grain yield per plant; GY/HA-Grain yield per hectare]**

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## Mean performances of the hybrids.

The comparison of genotype means between two spacings *i.e.* 60 cm x 20 cm and 50 cm x 20 cm (Table 2.1a and 2.1b) revealed that the genotype grand means differed from spacing to spacing for the traits namely, EL, ED, LAI(60DAS), LAI(90DAS), HI, GM% and GY/P. Genotype grand means were similar between the two spacings for the traits D50%PS, D50%S, D100%DH, ASI, PH, EH, E/P, KR/E, K/R, CHLR, 100 KW and GY/HA.

For grain yield per plant, the hybrids which acquired the three best superior positions (with statistical ranks within parentheses) in the spacing 60 cm x 20 cm (Table 2d) were ADV 756(1), PAC 751 (2), ADV 759(2) and CP 333(3). The hybrids which acquired any of the top three positions for grain yield per plant in 50 cm x 20 cm were CP 838(1), PAC 751 (1), ADV 757(1), ADV 756(2), PAC 751 ELITE (2), ADV 759(2) and CP 333(3). For the trait grain yield per plant, the best three hybrids common to both the spacings were ADV 756, PAC 751, ADV 759 and CP 333. From pooled analysis, it was evident that the following hybrids topped the list with any of the three superior positions: ADV 756(1), PAC 751(2), ADV 759(2), ADV 757(3) and PAC 751 ELITE (3). These superior hybrids also exhibited superiority for the following traits in both the spacings as well as across the spacings: ADV 756 for EL, K/R, GM, GY/P and GY/HA, PAC 751 for EH, E/P, ED, KR/E, K/R, CHLR, LAI 60DAS, LAI 90DAS, GY/P and GY/HA and ADV 759 for EL, ED, K/R, LAI 60 DAS, LAI 90 DAS, GMC, GY/P, GY/HA,

For grain yield per hectare, the top three best positions in 60 cm x 20 cm (Table 2d) were acquired by ADV 756(1), PAC 751(2), ADV 759(2), PAC 751 ELITE (3) and CP 333(3). The hybrids which acquired any of the top three positions for grain yield per hectare in 50 cm x 20 cm were PAC 751(1), PAC 751 ELITE (2), ADV 757(2), ADV 756(3) and CP 838(3). For the trait GY/HA, the best hybrids common to both the spacings were PAC 751, PAC 751 ELITE, ADV 756, ADV 759 and ADV 757. From pooled analysis, it was evident that the following hybrids topped the list with any of the three superior positions: PAC 751 (1), ADV 756 (2), PAC 751 ELITE (2), ADV 759 (3) and ADV 757 (3).

These superior hybrids for grain yield per hectare also exhibited superiority for the following traits in both the spacings individually as well as across the spacings: PAC 751 for EH, E/P, ED, KR/E, K/R, CHLR, LAI 60DAS, LAI 90DAS, GY/P and GY/HA, PAC 751 ELITE for EH, E/P, KR/E, K/R, GMC, LAI 90DAS, GY/P and GY/HA.ADV 756 for EL, K/R, GM, GY/P and GY/HA, ADV 759 and ADV 757 for EL, ED, K/R, LAI 60 DAS, LAI 90 DAS, GY/P, GY/HA.

**Comment [i2]:** Please give a table of Attribute vs Ranking to summarise these results properly. The other tables following are okay and can be retailed as it is.

The hybrids VMH 53, CP 838 and CP 333 had lower estimates for either one or more of the phenological traits viz., D50%PS, D50%S and D100%DH in both the spacings. Out of these, CP 838 and CP 333 were also superior performers for grain yield and yield contributing positive traits along with one or few earliness traits. CP 838 is the only hybrid with relative earliness, high grain yield and other yield attributing traits mentioned above. This hybrid also exhibited superiority for these traits in the pooled analysis.

Each of the hybrids responded similarly from spacing to spacing for the traits D50%PS, D100%DH, ASI, PH, EL, ED, KR/E, K/R, 100KW and GY/HA. One or more hybrids responded differently in the two spacings for the traits D50%S, EH, E/P, CHL, LAI 60, LAI 90, HI, GM and GY/P. The hybrids which differed between the spacings were: ADV 757 for D50%S; CP 838 for EH; ADV 756, CP 838, VMH 53, 91A21, ADV 757 for E/P; VMH 53, PAC 751, 91A21, ADV 759, ADV 757 for CHL; CP 838, ADV 759, ADV 757 for LAI 60; CP 838, ADV 759 for LAI 90; CP 838, VMH 53, PAC 751 ELITE, PAC 751, CP 333, 91A21, ADV 757 for HI; VMH 53 for GM and ADV 756 for GY/P.

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**TABLE 2a. Mean performance of hybrids**

| GENOTYPE/ CHAR | Days to 50% pollen shed(days) | | | Days to 50% silk(days) | | | Days to 100% dry husk(days) | | | Anthesis silking interval(days) | | | Plant height(cm) | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | 60X20 | 50X20 | POOLED | 60X20 | 50X20 | POOLED | 60X20 | 50X20 | POOLED | 60X20 | 50X20 | POOLED | 60X20 | 50X20 | POOLED |
| **ADV756** | 106(3) | 107(5) | 107(4) | 109(3) | 109(5) | 107(3) | 174(7) | 175(7) | 175(7) | 2(2) | 2(1) | 2(1) | 150(4) | 160(5) | 155(7) |
| **CP838** | 104(3) | 101(2) | 103(2) | 107(3) | 103(2) | 105(2) | 166(2) | 166(2) | 166(2) | 2(2) | 2(1) | 2(1) | 154(5) | 173(7) | 164(7) |
| **VMH53(C)** | 96(1) | 97(1) | 96(1) | 98(1) | 99(1) | 99(1) | 159(1) | 160(1) | 160(1) | 3(2) | 2(2) | 2(1) | 105(1) | 111(1) | 108(1) |
| **CP333** | 109(5) | 107(5) | 108(4) | 111(4) | 109(5) | 110(4) | 167(3) | 168(2) | 168(3) | 2(2) | 2(1) | 2(1) | 128(2) | 127(2) | 128(2) |

| | | | | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| **PAC751ELITE** | 107(4) | 105(4) | 106(3) | 111(5) | 108(4) | 109(3) | 173(6) | 174(7) | 174(6) | 4(3) | 3(4) | 4(2) | 141(4) | 131(2) | 136(4) |
| **PAC 751** | 109(5) | 108(5) | 109(5) | 112(5) | 110(5) | 111(4) | 170(4) | 171(5) | 170(4) | 2(2) | 2(2) | 2(1) | 128(2) | 132(2) | 130(3) |
| **91A21** | 103(2) | 102(3) | 103(2) | 105(2) | 104((3) | 105(2) | 171(5) | 170(4) | 170(4) | 2(1) | 2(1) | 2(1) | 141(4) | 148(4) | 144(5) |
| **ADV759** | 112(7) | 110(6) | 111(6) | 114(6) | 113(7) | 113(6) | 174(7) | 174(7) | 174(6) | 2(2) | 3(2) | 3(2) | 132(4) | 137(3) | 135(3) |
| **ADV757** | 110(6) | 113(8) | 111(6) | 109(3) | 115(8) | 112(5) | 172(5) | 173(6) | 173(5) | 2(2) | 3(2) | 3(2) | 133(3) | 140(4) | 136(4) |
| **Spacing Mean** | 106 | 106 | 106 | 108 | 108 | 108 | 170 | 170 | 170 | 2 | 2 | 2 | 135 | 140 | 137 |
| **CD (G)** | **3** | **3** | **2** | **5** | **4** | **3** | **3** | **2** | **2** | **1** | **1** | **1** | **24** | **24** | **15** |
| **CD (S)** | | **0.87** | | | **4.04** | | | **0.74** | | | **0.36** | | | **6.99** | |
| **CD (GXS)** | | **3** | | | **4** | | | **2** | | | **1** | | | **21** | |

[CD (G)- Critical Difference (Genotype); CD(S)- Critical Difference (Spacing); Critical Difference (Genotype x spacing)]

**TABLE 2b. Mean performance of hybrids**

| **GENOTYPE/ CHAR** | **Ear height(cm)** | | | **Ears per plant** | | | **Ear length(cm)** | | | **Ear diameter(cm)** | | | **Kernel rows per ear** | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | **60X20** | **50X20** | **POOLED** | **60X20** | **50X20** | **POOLED** | **60X20** | **50X20** | **POOLED** | **60X20** | **50X20** | **POOLED** | **60X20** | **50X20** | **POOLED** |
| **ADV756** | 66(6) | 68(7) | 67(8) | 0.9(1) | 0.8(5) | 0.9(2) | 17(2) | 17(1) | 17(2) | 5.5(3) | 5.3(3) | 5.4(4) | 16.1(2) | 15.1(5) | 15.5(4) |
| **CP838** | 51(3) | 68(8) | 60(7) | 0.9(2) | 0.8(5) | 0.9(2) | 16(2) | 18(1) | 17(2) | 5.9(1) | 5.9(1) | 5.9(1) | 17.8(1) | 17.7(1) | 17.8(1) |
| **VMH53(C)** | 32(1) | 31(1) | 31(1) | 0.9(2) | 0.8(6) | 0.9(2) | 14(4) | 14(4) | 14(4) | 5.1(6) | 5.0(5) | 5.0(6) | 14.5(4) | 12.8(8) | 13.7(8) |
| **CP333** | 55(4) | 52(4) | 54(5) | 0.8(5) | 0.9(3) | 0.8(4) | 15(3) | 15(2) | 15(4) | 5.8(2) | 5.6(2) | 5.7(2) | 16.1(2) | 15.2(3) | 15.7(3) |
| **PAC751ELITE** | 52(3) | 44(2) | 48(3) | 0.9(2) | 0.9(1) | 0.9(1) | 16(2) | 15(3) | 15(4) | 5.6(2) | 5.4(3) | 5.5(3) | 15.9(2) | 16.5(2) | 16.2(2) |
| **PAC 751** | 46(2) | 48(3) | 47(2) | 0.8(3) | 0.9(2) | 0.9(2) | 15(3) | 16((2) | 15(4) | 5.6(2) | 5.6(2) | 5.6(3) | 16.1(2) | 16.3(2) | 16.1(3) |
| **91A21** | 46(2) | 57(4) | 52(4) | 0.8(6) | 0.9(2) | 0.8(3) | 15(3) | 17(2) | 16(3) | 5.3(5) | 5.2(4) | 5.2(6) | 14.7(2) | 13.5(6) | 14.1(7) |
| **ADV759** | 46(2) | 51(3) | 49(3) | 0.8(5) | 0.8(4) | 0.8(4) | 17(2) | 18(1) | 18(1) | 5.4(4) | 5.4(3) | 5.4(4) | 14.1(5) | 14.1(6) | 14.2(7) |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| **ADV757** | 59(4) | 59(5) | 59(6) | 0.8(6) | 0.9(3) | 0.8(3) | 18(1) | 18(1) | 18(1) | 5.5(3) | 5.6(2) | 5.5(4) | 15.7(3) | 14.5(5) | 15.1(4) |
| **Spacing Mean** | 50 | 53 | 52 | 0.8 | 0.9 | 0.9 | 16 | 16 | 16 | 5.5 | 5.4 | 5.5 | 15.7 | 15.1 | 15.4 |
| **CD (G)** | **12** | **14** | **8** | **0.08** | **0.12** | **0.06** | **2** | **2** | **1** | **0.3** | **0.3** | **0.2** | **2.4** | **1.1** | **1.2** |
| **CD (S)** | | **3.91** | | | **0.03** | | | **0.6** | | | **0.09** | | | **0.56** | |
| **CD (GXS)** | | **12** | | | **0.1** | | | **2** | | | **0.3** | | | **1.7** | |

[CD (G)- Critical Difference (Genotype); CD(S)- Critical Difference (Spacing); Critical Difference (Genotype x spacing)]

**TABLE 2c. Mean performance of hybrids**

| **GENOTYPE/ CHAR** | **Kernels per row** | | | **Chlorophyll content (mg g$^{-1}$)** | | | **Leaf area index at 60 days after sowing(cm$^2$)** | | | **Leaf area index at 90 days after sowing(cm$^2$)** | | | **Harvest index (%)** | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | **60X20** | **50X20** | **POOLED** | **60X20** | **50X20** | **POOLED** | **60X20** | **50X20** | **POOLED** | **60X20** | **50X20** | **POOLED** | **60X20** | **50X20** | **POOLED** |
| **ADV756** | 39(1) | 38(2) | 38(1) | 3.3(4) | 3.2(4) | 3.3(4) | 631(2) | 569(7) | 600(5) | 642(3) | 692(2) | 667(2) | 36(9) | 34(5) | 35(8) |
| **CP838** | 29(6) | 33(5) | 31(5) | 3.6(3) | 3.6(2) | 3.6(2) | 506(6) | 598(6) | 552(7) | 524(7) | 692(2) | 608(7) | 37(7) | 44(1) | 41(2) |
| **VMH53(C)** | 27(7) | 24(8) | 26(6) | 3.7(2) | 3.0(5) | 3.3(4) | 309(7) | 323(8) | 316(9) | 343(9) | 271(7) | 307(9) | 43(2) | 39(2) | 41(1) |
| **CP333** | 31(4) | 32(5) | 32(4) | 3.5(3) | 3.6(2) | 3.5(3) | 680(1) | 699(2) | 690(2) | 751(1) | 687(1) | 719(1) | 43(3) | 37(3) | 40(2) |
| **PAC751ELITE** | 35((2) | 35(3) | 35(2) | 3.2(5) | 3.3(4) | 3.3(4) | 631(2) | 630(4) | 630(4) | 641(3) | 690(3) | 665(3) | 39(6) | 33(7) | 37(7) |
| **PAC 751** | 34(3) | 36(3) | 35(2) | 3.9(1) | 3.7(1) | 3.8(1) | 682(1) | 703(1) | 692(1) | 684(2) | 715(2) | 699(2) | 41(4) | 34(6) | 38(6) |
| **91A21** | 28(6) | 30(7) | 29(5) | 2.9(6) | 3.4(3) | 3.1(5) | 576(4) | 580(6) | 578(6) | 591(5) | 572(6) | 581(8) | 39(6) | 33(7) | 36(8) |
| **ADV759** | 36(2) | 39(1) | 38(1) | 3.5(3) | 3.2(4) | 3.3(4) | 607(3) | 702(2) | 654(2) | 587(5) | 741(1) | 664(4) | 40(5) | 38(3) | 39(4) |
| **ADV757** | 36(2) | 37(2) | 37(2) | 2.5(7) | 2.9(4) | 2.7(6) | 579(3) | 673(3) | 626(4) | 618(4) | 683(3) | 653(4) | 43(1) | 34(6) | 38(5) |
| **Spacing Mean** | 33 | 34 | 33 | 3.3 | 3.3 | 3.3 | 578 | 609 | 593 | 598 | 639 | 618 | 40 | 36 | 38 |
| **CD (G)** | **4** | **4** | **3** | **0.1** | **0.1** | **0.1** | **68** | **93** | **51** | **99** | **69** | **53** | **1.4** | **2.2** | **1.1** |
| **CD (S)** | | **1.19** | | | **0.04** | | | **24.06** | | | **25.18** | | | **0.53** | |

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|  |  |  |  |  |  |
|---|---|---|---|---|---|
| **CD (GXS)** | **4** | **0.1** | **73** | **76** | **2** |

[CD (G)- Critical Difference (Genotype); CD(S)- Critical Difference (Spacing); Critical Difference (Genotype x spacing)]

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**TABLE 2d. Mean performance of hybrids**

| **GENOTYPE/CHAR** | **Grain moisture content (%)** |  |  | **100 kernel weight (g)** |  |  | **grain yield per plant(g)** |  |  | **Grain yield per hectare(kg)** |  |  |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
|  | **60X20** | **50X20** | **POOLED** | **60X20** | **50X20** | **POOLED** | **60X20** | **50X20** | **POOLED** | **60X20** | **50X20** | **POOLED** |
| **ADV756** | 27(7) | 26(3) | 26(5) | 35(3) | 35(3) | 35(3) | 134(1) | 98(2) | 116(1) | 9393(1) | 8206(3) | 8800(2) |
| **CP838** | 26(3) | 26(7) | 26(6) | 37(1) | 36(2) | 37(1) | 100(5) | 108(1) | 104(4) | 6889(6) | 8499(3) | 7694(5) |
| **VMH53(C)** | 27(6) | 25(1) | 26(3) | 37(2) | 37(1) | 37(2) | 79(7) | 61(7) | 70(9) | 5357(9) | 5135(9) | 5246(9) |
| **CP333** | 27(5) | 26(6) | 26(6) | 35(5) | 34(5) | 34(5) | 112(3) | 90(3) | 101(4) | 7997(3) | 7401(5) | 7699(4) |
| **PAC751ELITE** | 26(2) | 25(2) | 25(1) | 33(7) | 32(7) | 32(7) | 113(3) | 98(2) | 106(3) | 8151(3) | 8567(2) | 8359(2) |
| **PAC 751** | 26(1) | 26(4) | 26(2) | 35(5) | 34(4) | 34(5) | 120(2) | 108(1) | 114(2) | 8538(2) | 9809(1) | 9173(1) |
| **91A21** | 26(3) | 27(9) | 27(8) | 37(2) | 36(2) | 36(2) | 108(4) | 86(3) | 97(6) | 7331(5) | 6614(7) | 6973(7) |
| **ADV759** | 26(2) | 25(3) | 26(2) | 36(3) | 35(3) | 36(3) | 119(2) | 102(2) | 111(2) | 8415(2) | 8068(4) | 8241(3) |
| **ADV757** | 27(5) | 26(7) | 27(7) | 34(6) | 34(4) | 34(6) | 107(4) | 108(1) | 108(3) | 7731(4) | 8815(2) | 8273(3) |
| **Spacing Mean** | 26 | 26 | 26 | 35 | 35 | 35 | 110 | 95 | 103 | 7756 | 7902 | 7829 |
| **CD (G)** | **0.8** | **0.4** | **0.4** | **4** | **4** | **2** | **26** | **26** | **16** | **1715** | **2001** | **1165** |
| **CD (S)** |  | **0.18** |  |  | **1.09** |  |  | **7.52** |  |  | **548.98** |  |
| **CD (GXS)** |  | **1** |  |  | **3** |  |  | **23** |  |  | **1647** |  |

[CD (G)- Critical Difference (Genotype); CD(S)- Critical Difference (Spacing); Critical Difference (Genotype x spacing)]

**Table 2.1a. Environment wise mean performance for the various traits**

| | D50%PS (days) | D50%S (days) | ASI (days) | D100%DH (days) | PH (cm) | EH (cm) | E/P | EL (cm) | ED (cm) | KR/E |
|---|---|---|---|---|---|---|---|---|---|---|
| **S1 (60 X 20)** | 106 | 108 | 170 | 2.5 | 135 | 50 | 0.86 | 16 | 5.5 | 15.7 |
| **S2 (50 X 20)** | 106 | 108 | 170 | 2.2 | 140 | 53 | 0.85 | 17 | 5.4 | 15.1 |
| **CD (Spacing)** | 0.87 | 1.32 | 0.74 | 0.36 | 6.99 | 3.91 | 0.03 | 0.60 | 0.09 | 0.56 |

**Table 2.1b Environment wise mean performance for the various traits**

| | K/R | CHLC (mg $g^{-1}$) | LAI (60DAS) ($cm^2$) | LAI (90DAS) ($cm^2$) | HI (%) | GMC (%) | 100 KW(g) | GY/P(g) | GY/HA (kg) |
|---|---|---|---|---|---|---|---|---|---|
| **S1 (60 X 20)** | 33 | 3.3 | 578 | 598 | 40 | 26.31 | 35.58 | 110 | 33 |
| **S2 (50 X 20)** | 34 | 3.3 | 609 | 639 | 36.16 | 25.76 | 34.61 | 96 | 34 |
| **CD (Spacing)** | 1.19 | 0.04 | 24.06 | 25.18 | 0.53 | 0.18 | 1.09 | 7.50 | 1.19 |

**Genetic parameters for morphological and physiological traits across spacing**

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From the analysis across the two spacings, the genotypic coefficient of variation (GCV) ranged from 19.98% for leaf area index at 90 DAS to 1.79% for grain moisture (Table 3). The traits namely, plant height, ear height, kernels per row, leaf area index at 60 DAS, leaf area index at 90 DAS, grain yield per plant and grain yield per hectare had moderate GCV while days to 50% pollen shed, days to 50% silk, days to 100% dry husk, ear length, ear diameter, kernel rows per ear, 100 kernel weight, chlorophyll content, harvest index and grain moisture had low estimate of GCV. On the other hand, phenotypic coefficient of variation (PCV) ranged from 20.43% for leaf area index at 90 DAS to 1.93% for grain moisture. The traits viz., ear height and leaf area index at 90 DAS had high PCV while plant height, kernels per row, leaf area index at 60 DAS, grain yield per plant and grain yield per hectare showed moderate estimates of PCV. All the remaining traits exhibited low PCV. The characters with high or moderate estimate of GCV indicated prospect for genetic improvement in the material under study.

High heritability coupled with high genetic advance as per cent of mean observed for the traits plant height, ear height, kernels per row, leaf area index at 60 DAS, leaf area index at 90 DAS, grain yield per plant and grain yield per hectare indicate the preponderance of additive gene action in controlling the above-mentioned traits. Simple selection methods such as mass selection or simple recurrent selection without progeny testing will be of helpful for improving a population through the exploitation of genes showing additive gene action. However, the progress of selection will be better if a breeder resorts to apply methods with progeny testing such as progeny selection or recurrent selection with general combining ability. Similar studies were reported by Bhalla, 1980[4] and Debnath, 1981 [5]. Other traits viz., days to 50% pollen shed, days to 50% silk, days to 100% dry husk, ear diameter, 100 kernel weight, harvest index and grain moisture were found to have high heritability along with low genetic advance as per cent of mean indicating that these characters were under preponderant non-additive gene action and genes responsible in the inheritance of these traits do not show phenotype stably across generations resulting from selfing or intermating. Thus, population with respect to such characters can be improved using recurrent selection for specific combining ability and hybrid breeding approach.

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**Table 3. Estimates of genetic parameters for different morphological and physiological traits across spacings.**

**Comment [i3]:** Good Table

| Traits | RANGE | Genotypic coefficient of variation (GCV) (%) | Phenotypic Coefficient of variation (PCV) (%) | Heritability board sense ($h^2_{bs}$) (%) | Genetic advance percent of mean (%) |
|---|---|---|---|---|---|
| **Days to 50% pollen shed** | 96-111 | 4.44 | 4.53 | 96.45 | 8.99 |
| **Days to 50% silk** | 99-113 | 4.24 | 4.42 | 91.79 | 8.36 |
| **Days to 100% dry husk** | 160-175 | 2.87 | 2.90 | 97.57 | 5.83 |
| **Anthesis silking interval** | 106-164 | 11.48 | 12.64 | 82.45 | 21.48 |
| **Plant height** | 31-67 | 19.08 | 20.63 | 85.49 | 36.33 |
| **Ear height** | 14-18 | 7.86 | 8.77 | 80.36 | 14.52 |
| **Ears per plant** | 5.0-5.9 | 4.94 | 5.23 | 89.35 | 9.62 |
| **Ear length** | 14-18 | 8.18 | 9.00 | 82.50 | 15.30 |
| **Ear diameter** | 26-38 | 12.53 | 13.07 | 91.90 | 24.74 |
| **Kernel rows per ear** | 32.32 - 36.88 | 4.08 | 5.20 | 61.48 | 6.58 |
| **Kernels per row** | 70-116 | 13.03 | 15.09 | 74.56 | 23.18 |
| **Chlorophyll content** | 5246-9173 | 14.56 | 16.29 | 79.93 | 26.82 |
| **Leaf area index at 60 days after sowing** | 2.7-3.8 | 9.59 | 9.65 | 98.70 | 19.62 |
| **Leaf area index at 90 days after sowing** | 316-692 | 19.14 | 19.60 | 95.36 | 38.50 |

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|  |  |  |  |  |  |
|---|---|---|---|---|---|
| **Harvest index** | 307-719 | 19.98 | 20.43 | 95.69 | 40.27 |
| **Grain moisture content** | 35.16-40.67 | 5.18 | 5.38 | 92.75 | 10.27 |
| **100 kernel weight** | 25.33-26.70 | 1.79 | 1.93 | 85.95 | 3.41 |
| **Grain yield per plant** | 70-116 | 13.03 | 15.09 | 74.56 | 23.18 |
| **Grain yield per hectare** | 5246-9173 | 14.56 | 16.29 | 79.93 | 26.82 |

## Correlation Analysis

### Genotypic and phenotypic correlation coefficient across the two spacings during *rabi* 2019-20

For across the two spacings, correlation studies revealed that grain yield per plant had either significant or highly significant positive correlation with days to 50% pollen shed, days to 50% silk, days to 100% dry husk, kernels per row, leaf area index at 60 DAS, leaf area index at 90 DAS and grain yield per hectare at both phenotypic and genotypic levels while it had positive correlation with plant height, ear height and ear length only at genotypic level. Grain yield per plant had significant to highly significant negative correlation with 100 kernel weight at genotypic level (Table 4). It was supported by Saleem et al., 2008 [6], Rafiq et al., 2010 [7], Noor et al., 2010 [8], Golam, 2011 [9], Reddy et al., 2013 [10], Kashiani et al., 2014 [11], Nzuve et al., 2014 [12] and Rani et al., 2017 [13]. On the other hand, grain yield per hectare had either significant or highly significant positive correlation with days to 50% pollen shed, days to 50% silk, days to 100% dry husk, kernels per row, leaf area index at 60 DAS and leaf area index at 90 DAS at both phenotypic and genotypic levels while it had positive correlation with ear height only at genotypic level (Table 4). It was supported by Patil et al., 2016 [14] and Singh et al., 2020 [15] also obtain similar result. Grain yield per hectare had highly significant negative correlation with 100 kernel weight at genotypic level. The genotypic correlation might have arisen due to genetic linkage or pleiotropy between the characters or both. The traits which were genetically correlated to grain yield per plant and which also had high heritability need to be considered for indirect selection leading to improvement of the population for grain yield as grain yield is a highly complex character. Thus, results revealed the scope for simultaneous improvement of these traits through selection.

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**Table 4. Genotypic (above diagonal) and phenotypic (below diagonal) correlation coefficients between yield and yield attributing characters for across spacings**

| | D50% PS | D50%S | D100% DH | ASI | PH | EH | E/P | EL | ED | KR/E | K/R | CHL C | LAI (60DAS) | LAI (90DAS) | HI | GM | 100KW | GY/P | GY/H A |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| **D50%PS** | | $0.99^{**}$ | 0.19 | $0.82^{**}$ | 0.28 | 0.58 | -0.24 | $0.84^{**}$ | 0.52 | 0.23 | $0.90^{**}$ | -0.16 | $0.92^{**}$ | $0.89^{**}$ | -0.32 | 0.03 | -0.77 | $0.90^{**}$ | $0.91^{**}$ |
| **D50%S** | $0.97^{**}$ | | 0.20 | $0.87^{**}$ | 0.27 | 0.55 | -0.09 | $0.78^{*}$ | 0.52 | 0.21 | $0.93^{**}$ | -0.07 | $0.96^{**}$ | $0.93^{**}$ | -0.36 | -0.09 | -0.90 | $0.92^{**}$ | $0.93^{**}$ |
| **D100%DH** | 0.17 | 0.26 | | 0.32 | -0.21 | -0.14 | $0.72^{*}$ | 0.22 | 0.09 | 0.13 | 0.45 | -0.36 | 0.07 | 0.05 | -0.09 | $-0.72^{*}$ | $-0.99^{**}$ | 0.16 | 0.00 |
| **ASI** | $0.76^{*}$ | $0.76^{*}$ | 0.19 | | 0.48 | 0.65 | 0.20 | $0.76^{*}$ | 0.23 | 0.08 | $0.91^{**}$ | -0.28 | $0.79^{**}$ | $0.81^{**}$ | $-0.82^{**}$ | 0.00 | $-0.82^{**}$ | $0.86^{**}$ | $0.91^{**}$ |
| **PH** | 0.19 | 0.13 | -0.28 | 0.39 | | $0.85^{**}$ | 0.14 | $0.73^{*}$ | 0.57 | $0.68^{*}$ | 0.42 | 0.03 | 0.36 | 0.50 | -0.38 | 0.47 | 0.08 | 0.53 | 0.68 |
| **EH** | 0.46 | 0.38 | -0.26 | 0.54 | $0.84^{**}$ | | 0.00 | $0.88^{**}$ | 0.60 | 0.57 | 0.62 | -0.19 | 0.57 | $0.70^{*}$ | -0.46 | 0.61 | -0.22 | $0.71^{*}$ | $0.84^{**}$ |
| **E/P** | -0.19 | -0.15 | 0.43 | 0.17 | 0.09 | -0.05 | | -0.47 | 0.16 | 0.57 | 0.22 | 0.31 | -0.05 | 0.05 | $-0.77^{*}$ | $-0.68^{*}$ | $-0.99^{**}$ | 0.30 | 0.12 |
| **EL** | 0.53 | 0.45 | -0.03 | 0.46 | 0.45 | 0.48 | -0.20 | | 0.33 | 0.23 | $0.83^{**}$ | -0.48 | 0.48 | 0.61 | -0.16 | 0.34 | -0.11 | 0.61 | $0.74^{*}$ |
| **ED** | 0.44 | 0.44 | 0.07 | 0.22 | 0.43 | 0.44 | 0.00 | 0.39 | | $0.92^{**}$ | 0.39 | 0.39 | 0.65 | $0.74^{*}$ | 0.18 | 0.05 | -0.56 | 0.62 | 0.60 |
| **KR/E** | 0.13 | 0.17 | 0.19 | 0.12 | 0.46 | 0.38 | 0.30 | 0.23 | $0.84^{**}$ | | 0.30 | 0.49 | 0.36 | 0.50 | 0.09 | -0.11 | -0.52 | 0.51 | 0.47 |
| **K/R** | $0.81^{**}$ | $0.78^{**}$ | 0.10 | $0.81^{**}$ | 0.35 | 0.53 | 0.05 | $0.65^{**}$ | 0.31 | 0.23 | | -0.11 | $0.72^{**}$ | $0.77^{**}$ | $-0.52^{**}$ | -0.19 | $-0.70^{**}$ | $0.93^{**}$ | $0.95^{**}$ |
| **CHLC** | -0.14 | -0.08 | -0.26 | -0.26 | 0.03 | -0.17 | 0.12 | -0.30 | 0.36 | 0.38 | -0.09 | | 0.14 | 0.14 | 0.25 | -0.48 | 0.15 | 0.16 | 0.09 |
| **LAI (60DAS)** | $0.83^{**}$ | $0.82^{**}$ | -0.05 | 0.71 | 0.35 | 0.52 | -0.06 | 0.41 | 0.60 | 0.31 | $0.69^{*}$ | 0.13 | | $0.99^{**}$ | -0.41 | 0.05 | $-0.88^{**}$ | $0.91^{**}$ | $0.91^{**}$ |
| **LAI (90DAS)** | $0.83^{**}$ | $0.81^{**}$ | -0.02 | $0.74^{**}$ | 0.47 | 0.63 | -0.02 | 0.38 | 0.64 | 0.40 | $0.71^{*}$ | 0.14 | $0.95^{**}$ | | -0.44 | 0.09 | $-0.81^{**}$ | $0.95^{**}$ | $0.97^{**}$ |
| **HI** | -0.31 | -0.35 | -0.06 | $-0.68^{*}$ | -0.30 | -0.35 | -0.25 | -0.17 | 0.12 | 0.10 | -0.47 | 0.23 | -0.40 | -0.42 | | -0.05 | $0.71^{*}$ | -0.55 | -0.59 |
| **GMC** | 0.04 | -0.05 | -0.41 | 0.00 | 0.33 | 0.47 | -0.48 | 0.25 | 0.06 | -0.07 | -0.15 | -0.43 | 0.03 | 0.06 | -0.02 | | 0.48 | -0.15 | 0.03 |
| **100KW** | -0.39 | -0.38 | -0.26 | -0.42 | 0.09 | -0.15 | -0.26 | 0.00 | -0.17 | -0.09 | -0.39 | 0.09 | -0.36 | -0.42 | 0.29 | 0.23 | | $-0.87^{**}$ | $-0.68^{*}$ |
| **GY/P** | $0.77^{*}$ | $0.76^{*}$ | 0.09 | $0.74^{*}$ | 0.42 | 0.52 | 0.17 | 0.54 | 0.56 | 0.47 | $0.85^{**}$ | 0.17 | $0.80^{**}$ | $0.82^{**}$ | -0.48 | -0.11 | -0.37 | | $0.97^{**}$ |
| **GY/HA** | $0.74^{*}$ | $0.73^{*}$ | 0.00 | $0.76^{*}$ | 0.54 | 0.60 | 0.09 | 0.63 | 0.54 | 0.44 | $0.83^{**}$ | 0.10 | $0.79^{*}$ | $0.82^{**}$ | -0.47 | 0.02 | -0.28 | $0.96^{**}$ | |

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**(D50%PS-Days to 50% pollen shed; D50%S-Days to 50% silk; D100%DH-Days to 100% dry husk; ASI-Anthesis silking interval; PH-Plant height; EH-Ear height; E/P-Ears per plant; EL-Ear length; ED-Ear diameter; KR/E-Kernel rows per ear; K/R-Kernels per row; CHLC-Chlorophyll content; LAI60DAS-Leaf area index at 60 days after sowing; LAI90DAS-Leaf area index at 90 days after sowing; HI-Harvest index; GM-Grain moisture; 100 KW-100 kernel weight; GY/P-grain yield per plant; GY/HA-Grain yield per hectare)**

## Path Analysis

### Genotypic and phenotypic path coefficient across the two spacings during rabi 2019-20

Path coefficient analysis provides better means for selection by partitioning the correlation coefficient of grain yield with independent traits into direct and indirect effects. Path analysis is a straightforward extension of multiple regressions and its aim is to provide estimates of the magnitude and hypothesize casual connections between sets of variables. Considering all these facts, path coefficient analysis was carried out at genotypic levels taking grain yield per plant as a dependent character.

For across the two spacings, path analysis revealed that considering high to very high positive direct effects, the traits *viz*., days to 100% dry husk, days to 50% pollen shed, ear length and kernel rows per ear were the important component traits of grain yield per plant while plant height and ear height had moderate direct effect on grain yield per plant (Table 5). Thus, selection of plants with higher values of these component traits i.e. more days to 100% dry husk as well as 50% pollen shed, larger ear length and more kernel rows per ear would enhance the grain yield per plant. These traits also had high heritability. The high direct effects of these traits appeared to be the main reason for their strong association with grain yield. Hence, direct selection for these traits would be effective. Similar results were found by Choudhary and Choudhary, 2002 [16], Venugopal *et al*., 2003 [17], Rani *et al.*, 2017 [13], Sandeep *et al.*, 2017 [18] and Verma *et al.*, 2020 [19]. However, in path analysis, plant height and ear height had the moderate and low negative direct effect on grain yield per plant which was in contradiction

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with the correlation results. High negative indirect effects of various traits on grain yield per plant might have nullified many of the positive indirect effects of many other independent traits resulting in a low estimate of correlation coefficient of plant height and ear height on grain yield per plant despite having a high direct effect of plant height and ear height on grain yield. This might be the reason of non-significant association. On the other hand, the traits namely, days to 50% silk and kernels per row had high negative direct effects on grain yield per plant. Thus, selection of plants with lower values of these component traits i.e., early silking and fewer kernels per row, will improve the grain yield per plant. Plant selection will be easy for these traits as the traits had high heritability. However, there were positive correlation between the phenological traits such as days to 50% pollen shed, days to 50% silk and days to 100% dry husk reflecting conflict when taken together. As for example, days to 50% silk had negative direct effect and days to 50% pollen shed as well as 100% dry husk had positive direct effect on grain yield. Selecting plants with higher values of days to 50% pollen shed as well as days to 100% dry husk and lower values of days to 50% silk might create conflict. To resolve it, selection of plants with higher values of days to 50% pollen shed as well as days to 100% dry husk and moderate values of days to 50% silk might give high grain yield. The residual was found to be very low (0.0745) across spacing reflecting that the independent characters under study contributed to the variation in grain yield per plant to a great extent, which inherently suggested the characters taken in the investigation contributed a large extent of the variability in the population.

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**Table 5. Direct (bold) and indirect effects of various component traits on grain yield at genotypic level for across the spacings**

| | **D50%PS** | **D50%S** | **D100%DH** | **PH** | **EH** | **E/P** | **EL** | **ED** | **KR/E** | **K/R** | **$r_{iy}^{\pm}$** |
|---|---|---|---|---|---|---|---|---|---|---|---|
| **D50%PS** | **0.802** | -0.471 | 0.878 | -0.074 | -0.071 | -0.052 | 0.442 | 0.032 | 0.111 | -0.688 | $0.910^{**}$ |
| **D50%S** | 0.800 | **-0.473** | 0.928 | -0.072 | -0.067 | -0.020 | 0.408 | 0.031 | 0.102 | -0.711 | $0.926^{**}$ |
| **D100%DH** | 0.659 | -0.410 | **1.070** | -0.127 | -0.079 | 0.044 | 0.398 | 0.014 | 0.037 | -0.695 | $0.910^{**}$ |

| | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|
| **PH** | 0.224 | -0.128 | 0.512 | **-0.266** | -0.104 | 0.029 | 0.382 | 0.035 | 0.323 | -0.323 | $0.684^{*}$ |
| **EH** | 0.463 | -0.258 | 0.690 | -0.226 | **-0.122** | 0.001 | 0.462 | 0.037 | 0.273 | -0.477 | $0.842^{**}$ |
| **E/P** | -0.193 | 0.044 | 0.214 | -0.036 | 0.000 | **0.218** | -0.246 | 0.009 | 0.273 | -0.169 | 0.115 |
| **EL** | 0.675 | -0.366 | 0.809 | -0.193 | -0.107 | -0.102 | **0.526** | 0.020 | 0.108 | -0.636 | $0.735^{*}$ |
| **ED** | 0.420 | -0.243 | 0.244 | -0.153 | -0.074 | 0.034 | 0.173 | **0.061** | 0.437 | -0.298 | 0.601 |
| **KR/E** | 0.186 | -0.101 | 0.082 | -0.180 | -0.070 | 0.125 | 0.119 | 0.056 | **0.477** | -0.230 | 0.465 |
| **K/R** | 0.720 | -0.438 | 0.970 | -0.112 | -0.076 | 0.048 | 0.436 | 0.024 | 0.143 | **-0.767** | $0.947^{**}$ |

Residual=0.0745

$r_{iy}^{\pm}$ = Genetic correlation coefficient of grain yield and its *i*th component trait

**(D50%PS-Days to 50% pollen shed; D50%S-Days to 50% silk; D100%DH-Days to 100% dry husk; PH-Plant height; EH-Ear height; E/P-Ears per plant; EL-Ear length; ED-Ear diameter; KR/E-Kernel rows per ear; K/R-Kernels per row)**

**Comment [i4]:** Conclusions ?

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