Effect of Rain-Fed Conditions on Yield of Mash Bean Genepool by Using Augmented Design

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Abstract
The augmented block design (ABD) is commonly used in breeding programs to evaluate the performance of large number of genotypes using non-replicated new test treatments and replicated check treatments. The purpose of this design is to determine which test treatment performs better than check treatments. The objective of this study is to identifying better genotype of Mash been than check treatment under rain feed condition of Pakistan. For this purpose, the data of 125 mash been genotypes included 5 check entries were analyzed. The experiment was conducted in augmented block design using 6 blocks in rain feed condition of Pakistan and data of different attribute were recorded. The analysis showed that the treatment effects (adjusted) are significant for all attributes. However, for all attribute other than the number of seeds/pod, the adjusted block effects are non-significant, indicating that the evaluated blocks are homogeneous. Only three principal components were considered, first component explained 33.85% of variation and 21.85%, 17.51% explained by PC2 and PC3 respectively for the first season whereas in the second season 33.62%, 23.43%, and 16.86% variation described with respect to the first, second, and third principal components. First PC designated as a component of productivity, second as component of pod appearance while third designed as a component of physical appearances. All attributes showed significant and positive association with other attributes, only significantly negative association was among number of pods/plant and 100-seeds weight.

Keywords Augmented block design · Check treatments · Principal Component Analysis (PCA) · Mash Been · Yield trial experiments
1 Introduction

Mash Been [Vigna mungo (L.) Hepper], being a cheapest source of protein is an important pulse crop in many Asian countries like Pakistan, India, Myanmar, Thailand, and Bangladesh. The mash been containing high nutritive values and contains amino acids, sulphur, cysteine, methionine and lysine. The peoples, in many developing countries, used it as an alternative of meet because it is a good source of iron, sodium, potassium, calcium magnesium, phosphorus, sulphur, copper and vitamins [16, 15]. It has a close relationship with humans just because of their easier-to-digest [18]. Along with high nutritional importance of Mash Been for human and animal, it is also very helpful for improving fertility of the soil [1]. Moreover, in recent years, requirements for a healthy diet have received the attention from all areas of life and legume seeds plays an important role in this regard [5].

Due to the importance of this crop, agricultural scientist, now a days, emphasizing on the large-scale cultivation of Mash and other pulses crops so that developing countries are self-sufficient in the production of pulses and less revenue is required for the import of these crops [5].

Mash bean is mostly farmed as a pulse crop, although it is used as an organic fertilizer to enhance soil fertility. This short-season crop required less water than most of the other summer crops, this makes it an excellent choice for rain-fed areas. In rain-fed regions, farmers will reap tremendous economic benefits from successful cultivation. This crop may be grown in marginal fields where many other crops have failed [14].

Like many other countries, Mash been in Pakistan is also least important crop and both cultivated area and production is decreasing every year. Mash been is grown all over the Pakistan, but the majority of its growing is in Punjab province [2]. In comparison to other grain legumes, mash bean productivity has remained low in the region [3].

In spite of large benefits of this crop, the yield of mash bean in all over the world specially in Pakistan is very poor. In Pakistan research on this crop is very limited due to which its area of farmland and production is constantly decreasing [15]. During 2021–22, mash crop was cultivated over an area of 8.00 (000) ha with a total production of 6.1 (000) tones which showed 27.27% and 11.6% decrease in area and production respectively (GOP, 2021–22).

Moreover, the production of mash is not sufficient for the domestic demand of the country and every year government has to spend a substantial amount of funds to import mash beans for domestic consumption. In only one year, 64.08 thousand tons of mash had imported with an amount of 7824.55 million rupees (AMIS, 2019–20). Therefore, high yielding and consistent mash genotypes are need of the hour.

In this study the high yielding mash genotypes have been found from 120 test treatments as compare to 5 check treatments and recommended for further studies to find the consistent ones.
2 Material and Methods

The yield trial experiment of Mash been which consists of 125 genotypes including 5 checks was conducted at Barani Agricultural Research Institute (BARI), Chakwal, for 2 consecutive years i.e., 2015 and 2016. Each year experiments were conducted using augmented design layout and 120 genotypes were divided into 6 blocks, each block contains 20 genotypes plus 5 check entries randomized in each block. Seeds were dibbled for each entry keeping 40 seeds per entry. The plot size was maintained at 1.2 m² (one row of 4-m length). The row spacing was 30 cm across rows and 10 cm within rows. The data regarding plants height (PH)-cm, days to 50% flowering (DF), days to maturity (DM), pods per plant (PPP), pod length (PL)-cm, seed yield per plot (SYPP), seeds per pod (SPP), 100 seed weights (100 SW)-g, primary branches (PB) and yield (SY)-kg/ha were recorded. The analysis of data as suggested by Federer [8], [9] were performed using R software [16]. After performing analysis of variance, all major components eigen values or latent roots were also displayed in the principal component analysis, which was based on the correlation matrix.

The linear model for Augmented Block design (ABD) is as follows

\[ Y_{ijk} = \mu + \beta_i + C_j + \tau_{k(i)} + \epsilon_{ij} \]  

where \( Y_{ijk} \) is the value of \( j \)th check or \( k \)th new entry in \( i \)th block. \( \mu \) is the over all mean, \( \beta_i \) is the effect of \( i \)th block, \( C_j \) is the effect of \( j \)th check treatment, \( \tau_{k(i)} \) is the effect of the \( k \)th new entry in the \( i \)th block and \( \epsilon_{ij} \) is the random error.[8]

3 Result and Discussion

In present study 120 tested genotypes and 5 check verities of mash bean for yield and yield components are included for 2015 and 2016 seasons under rain feed conditions. The list of checks and new genotypes considered in this study are reported in Table 1.

The descriptive statistics along with coefficient of variation (CV) of all traits under study of both years were presented in Tables 2 and 3 respectively. The highest CV was observed in case of Yields (kg/plot) in both years whereas in 2nd year seed yield per plot and pods per plant showed highest CV values as compared to other traits.

The analysis of variance (ANOVA) of all traits for both years are reported in Tables 4 and 5 respectively. The ANOVA reported in Table 4 revealed a significant results for all traits for different sources of variation. The Block effect (unadjusted) for the first season and the treatment effects (adjusted as well as unadjusted) are significant for all the traits. Similarly, the effects due to checks and varieties are also significant. However, the adjusted block effects are non-significant for all traits except pods per plant indicating homogeneity for evaluation of blocks. Similarly, the mean square due to checks v/s varieties is significant for
all traits except pod length, seed per plant, and seed yield per plot indicating that the test entries are significantly different from checks except for pod per plant. In Table 4 the block effect (unadjusted) for the first season and the treatment effects (adjusted as well as unadjusted) are significant for most of the traits. Similarly, the effects due to checks and varieties are also significant but not for day to 50% flowering, pod per plant, pod length, and primary branches. However, there
observed a non-significant adjusted block effects for most of the traits except pods per plant, day to maturity, pod length, and primary branches that indicates homogeneity of evaluation of blocks.

The second season results of all traits are reported in Table 5. Like first season both the block effect and treatment effects are significant for most of the traits. The traits, day to 50% flowering, pod per plant, pod length, and primary branches shows non-significant results in case of the effects due to checks and varieties. Moreover, only traits pods per plant, day to maturity, pod length, and primary branches shows significant adjusted block effects among all observed traits. Since the mean square due to checks v/s varieties is non-significant for many traits indicating that the test entries are not responding significantly different from checks. As compared to first season results it can be observed that in second season there are some noise factors that affect the productivity of all genotypes.

In order to compare the adjusted means of test entries in different blocks as well as in same blocks along with checks, the standard error of difference for both seasons are calculated and results of all attributes are reported in Tables 6 and 7 respectively. In order to select best genotypes as compared to best check variety, the Least significant increase (LSI) [13] is calculated for each season and also reported in Tables 6 and 7.

Based on LSI values, the number of genotypes that perform better as compared to the best check in the first season (Table 6) are 54 for 50% DF, 30 for DM, and 10, 69,14, 64, 47, 60, 9, 60 for PH, PPP, PL, SPP, 100SW, PB, SY and SYPP respectively. In case of check genotypes, the genotype 9CM-702, 10CM-703 was the best check for all features except DM, 50% DF and PH in the first season. Similarly, in the second season (Table 7) the number of genotypes that performed much better than all check varieties were 30 test treatments for 50% DF, 28, 42,11,37,50,19, 15,30, and 50 test treatments for DM, PH, PPP, PL, SPP, 100SW, PB, SY and SYPP surpass the check varieties. Similarly, the genotype 10CM-703 was considered as top check genotype as compared to others for all characteristics except PH. In the second season, 9CM-702 was likewise effective for all features except Day of maturity, days of flowering, primary branches, and plant height.

Table 3 Descriptive statistics of yield parameters for Mash bean genotypes (2nd season)

| Traits                  | Mean ± SD  | Range       | CV(%) |
|-------------------------|------------|-------------|-------|
| Plant height (PH)-cm    | 44.46 ± 0.84 | 18.93–65.41 | 13.89 |
| Days to 50% flowering (DF) | 46.79 ± 0.35 | 40.53–55.73 | 8.29  |
| Days to maturity (DM)   | 72.36 ± 0.22 | 67.9–79.30  | 1.66  |
| Pods per plant (PPP)    | 21.82 ± 0.54 | 9.19–35.57  | 24.97 |
| Pod length (PL)-cm      | 4.13 ± 0.05  | 2.72–5.47   | 9.68  |
| Seed yield per plot (SYPP) | 117.05 ± 3.08 | 52.57–226.17 | 20.57 |
| Seeds per pod (SPP)     | 6.55 ± 0.03  | 5.45–7.45   | 3.17  |
| 100 seed weight (100SW)-g | 4.33 ± 0.02  | 3.89–4.98   | 3.8   |
| Primary branches (PB)   | 2.00 ± 0.04  | 1.23–3.19   | 18.17 |
| Yield (SY)-kg/ha        | 967.75 ± 26.23 | 301.87–1885.07 | 21.43 |
Table 4 Augmented block design ANOVA for 10 traits of 125 genotypes of Mash bean (1st season)

| SOV                                | Df | PH     | DF     | DM     | PPP    | PL     | SYPP   | SPP    | 100SW  | PB     | SY-kg/ha |
|-------------------------------------|----|--------|--------|--------|--------|--------|--------|--------|--------|--------|---------|
| Blocks (ignoring treatments)        | 5  | 28.60***| 5.08** | 3.85***| 28.34***| 9.65***| 10.09***| 4.89** | 20.71***| 85.27***| 3.18*   |
| Treatments (eliminating blocks)     | 124| 7.21*** | 4.92***| 3.85***| 12.02***| 3.03** | 8.20***| 4.00***| 6.37***| 9.20***| 1.89*   |
| Checks                             | 4  | 41.11***| 6.6**  | 5.98** | 22.96***| 2.67*  | 27.47***| 1.18   | 22.53***| 11.76***| 4.43*** |
| Blocks (eliminating checks and varieties) | 5  | 1.67    | 0.46   | 1.83   | 5.48** | 1.07   | 2.03   | 0.99   | 1.53   | 1.18   | 1.47    |
| Entries (ignoring blocks)           | 124| 8.30*** | 5.10***| 3.90***| 12.93***| 3.37** | 8.53***| 4.16***| 7.15***| 12.59***| 1.96*   |
| Treatments (eliminating blocks)     | 119| 6.33*** | 4.98***| 3.67***| 9.15*** | 3.41** | 7.95***| 4.29***| 6.43***| 12.18***| 1.87*   |
| Checks v/s varieties                | 1  | 112.32***| 13.70**| 24.05***| 422.59***| 0.6   | 1.66   | 0.87   | 30.61***| 65.03***| 1.97    |
| Error                               | 20 | 4.19    | 3.723  | 1.45   | 3.96   | 0.04   | 157.43 | 0.02   | 0.01   | 0.01   | 46.38   |

* P < 0.05, * P < 0.01, ** P < 0.001
### Table 5  Augmented block design ANOVA for 10 traits of 125 genotypes of Mash bean (2nd season)

| SOV                                | Df | PH     | DF   | DM     | PPP    | PL     | SYPP   | SPP    | 100SW  | PB    | SY-kg/ha |
|------------------------------------|----|--------|------|--------|--------|--------|--------|--------|--------|-------|---------|
| Blocks (ignoring treatments)       | 5  | 4.33** | 1.33 | 9.79*** | 1.02   | 4.40** | 6.62*** | 1.94   | 4.44** | 6.17** | 6.42** |
| Treatments (eliminating blocks)    | 124| 1.35   | 1.01 | 3.73*** | 1.15   | 1.16   | 1.51    | 1.76*  | 2.15*  | 0.74   | 1.48    |
| Checks                             | 4  | 3.86*  | 0.52 | 2.43*  | 0.63   | 0.44   | 3.84*   | 0.85   | 1.95   | 0.19   | 4.14*   |
| Blocks (eliminating Treatments)    | 5  | 4.47** | 0.04 | 2.07   | 0.67   | 1.89   | 3.92*   | 1.29   | 2.76*  | 1.3    | 3.43*   |
| Entries (ignoring blocks)          | 124| 1.33   | 1.06 | 4.04*** | 1.16   | 1.26   | 1.62    | 1.79*  | 2.21*  | 0.94   | 1.60    |
| Treatments (eliminating blocks)    | 119| 1.26   | 1.08 | 3.85*** | 1.18   | 1.28   | 1.51    | 1.84*  | 2.23*  | 0.97   | 1.50    |
| Checks v/s varieties               | 1  | 0.03   | 1.27 | 32.36*** | 0.28   | 2.84   | 5.07*   | 0.13   | 1.24   | 0.42   | 4.21*   |
| Error                              | 20 | 38.07  | 14.96| 1.45   | 29.94  | 0.15   | 562.25  | 0.048  | 0.02   | 0.13   | 41,798.61 |

* P < 0.05, * P < 0.01, ** P < 0.001
Table 6  Different Standard Error (SE) of Means and LSI values based on 1st Season data

| Standard Error                          | Formula                        | PH  | DF  | DM  | PPP | PL  | SYPP | SPP | 100SW | PB  | SY-kg/ha |
|-----------------------------------------|--------------------------------|-----|-----|-----|-----|-----|------|-----|-------|-----|----------|
| Control treatment means (Sc)            | $\sqrt{2\text{MSE}/r}$       | 1.18| 1.11| 0.69| 1.15| 0.12| 7.24 | 0.08| 0.07   | 0.06| 124.34   |
| Two test treatments (Sb)                | $\sqrt{2\text{MSE}}$         | 2.89| 2.72| 1.7 | 2.81| 0.29| 17.74| 0.02| 0.17   | 0.16| 304.57   |
| Two test treatments (Db)                | $\sqrt{(2(C + 1)\text{MSE})/C}$| 3.17| 2.98| 1.86| 3.08| 0.32| 19.43| 0.23| 0.18   | 0.18| 333.64   |
| A test treatment and a control variety (Stc) | $\sqrt{(R + 1)(C + 1)\text{MSE}/R.C}$ | 2.42| 2.28| 1.42| 2.35| 0.24| 14.84| 0.17| 0.15   | 0.14| 254.82   |
| Least significant increase (LSI)        | $t \alpha$. Stc               | 4.17| 3.93| 2.44| 4.05| 0.41| 25.59| 0.29| 0.26   | 0.24| 439.49   |
| Standard Error                        | Formula                                  | PH  | DF  | DM  | PPP | PL  | SYPP | SPP | 100SW | PB  | SY-kg/ha |
|--------------------------------------|------------------------------------------|-----|-----|-----|-----|-----|------|-----|-------|-----|----------|
| Control treatment means (Sc)         | $\sqrt{2\text{MSE}/R}$                  | 3.56| 2.23| 0.69| 3.15| 0.23| 13.69| 0.12| 0.09  | 0.21| 118.03   |
| Two test treatments (Sb)             | $\sqrt{2\text{MSE}}$                    | 8.73| 5.47| 1.7 | 7.73| 0.56| 33.53| 0.29| 0.23  | 0.511| 289.13   |
| Two test treatments (Db)             | $\sqrt{(2(C + 1)\text{MSE})/C}$         | 9.56| 5.99| 1.86| 8.47| 0.62| 36.74| 0.32| 0.25  | 0.56 | 316.72   |
| A test treatment and a control variety (Stc) | $\sqrt{(R + 1)(C + 1)\text{MSE})/R.C}$ | 7.3 | 4.57| 1.42| 6.48| 0.47| 28.05| 0.24| 0.19  | 0.43 | 241.90   |
| Least significant increase (LSI)     | $t_\alpha \text{Stc}$                   | 12.59| 7.88| 2.44| 11.18| 0.81| 48.38| 0.41| 0.32  | 0.74 | 417.2    |
3.1 Principal Component Analysis

To perform principal components (PC) analysis, six important traits; pod per length, pod length, seeds per pod, seed yield per plot, yield (kg/ha) and 100 seed weight were selected. To select the appropriate PCs for further analysis, the criteria recommended by [10, 11, 17] is adopted. The PC analysis of both seasons are reported in Tables 8, 9, 10, and 11. In first season, the latent roots or eigen values are ranged from 2.031 to 0.012 for the six PCs and ranged from 2.017 to 0.010 for second seasons. Following above criterion, first three PCs are selected for both seasons as they accounted for 73.2% and 73.9% of the total variation respectively. In first season, first PC explained 33.85% of variation and 21.85%, 17.51% variation were explained by PC2 and PC3 respectively (see Table 8) whereas in the second season 33.62%, 23.43%, and 16.86% variation explained by PC1, PC2 and PC3 respectively (see Table 9).

3.2 Non-rotated Component Loadings

The important traits (for first season) in PC1 were seed yield per plot (SYPP) and yield (SY)-kg/ha, whereas pods per plant (PPP) and 100 seed weight (100SW)-g are important traits in PC2. In PC3, pod length and seeds per pod are important traits. The PC1 can be defined as a component of productivity because it consists of seed yield per plot (SYPP) and Yield (SY)-kg/ha, while the PC2 can be labelled as a
component of pod appearance because it contains pods per plant and 100SW. PC3 can be categorized as a component of physical appearances because it holds pod length and seed number as important traits. In the second season, the most important features in PC1 were seed yield per plot and yield in kg. The pods per plant, seeds per pod, and 100 seed weight in games are important traits in 2nd PC, while Pod length was the most important trait in PC3. As for season 1, the PC1 can be categorized as a component of productivity while PC2 can be regarded as a component of pod appearance and PC3 can be characterized as a component of physical appearances based on their important traits.

### 3.3 Correlation Coefficients

Information regarding trait associations in mash bean breeding material is important to achieve several objectives because it allows researcher to perceive variability in breeding material. It is very informative to select traits that plays very important role in the successful growth of a plant in any given ecological condition. The correlation among six important traits selected in PCA analysis were reported in Tables 12 and 13 for 1st and 2nd seasons respectively. The results from both seasons showed that there observed a strong and positive association with the Yield (SY)-Kg/ha and Seed Yield Per Plot (SYPP) in both seasons. Where as there observed a significantly and positively associated between Pod per plant (PPP) and seeds per pod (SPP) in 1st season only. There observed

#### Table 10 Non-rotated component loadings (1st season)

|                      | PC1     | PC2     | PC3     | PC4     | PC5     | PC6     |
|----------------------|---------|---------|---------|---------|---------|---------|
| Pods per plant (PPP) | 0.161   | −0.619  | 0.221   | −0.296  | 0.674   | −0.019  |
| Pod length (PL)-cm   | 0.0384  | −0.285  | 0.653   | 0.673   | 0.193   | 0.044   |
| Seeds per pod (SPP)  | 0.057   | −0.279  | −0.696  | 0.619   | −0.225  | −0.005  |
| Seed yield per plot (SYPP) | −0.696 | −0.094  | 0.011   | 0.007   | −0.062  | −0.708  |
| Yield (SY)-kg/ha     | −0.695  | −0.102  | 0.010   | 0.003   | −0.088  | 0.705   |
| 100 seed weight (100SW)-g | 0.015 | −0.661  | −0.198  | −0.280  | 0.666   | 0.008   |

#### Table 11 Non-rotated component loadings (2nd season)

|                      | PC1     | PC2     | PC3     | PC4     | PC5     | PC6     |
|----------------------|---------|---------|---------|---------|---------|---------|
| Pods per plant (PPP) | 0.066   | 0.534   | −0.357  | 0.686   | −0.334  | −0.009  |
| Pod length (PL)-cm   | −0.005  | 0.425   | −0.652  | −0.463  | 0.422   | 0.001   |
| Seeds per pod (SPP)  | −0.178  | 0.524   | 0.325   | −0.503  | −0.579  | −0.001  |
| Seed yield per plot (SYPP) | −0.693 | −0.037  | 0.043   | 0.098   | 0.071   | −0.707  |
| Yield (SY)-kg/ha     | −0.693  | −0.027  | −0.043  | 0.109   | 0.069   | 0.706   |
| 100 seed weight (100SW)-g | −0.031 | −0.507  | −0.581  | −0.198  | −0.603  | 0.004   |
a negative correlation was between pod per plant (PPP) and 100-seed weight (100SW) suggesting that a high number of pods per plant reduced seed weight. Similar results were observed by [4]. Where as in 2nd sesason there observed positive correlation among pod per plant (PPP) and 100-seed weight (100SW). Number of studies have been reported positive correlation between pod per plant, seed per pod as well as 100-seed weight [6, 7, 12] (Tables 12 and 13).

### 4 Conclusion

The Test genotype 3CM-705 for the first season is highly efficient for all traits but in second season this is working moderately. The genotype 12CM-707 is highly efficient for a number of pods/plant, pod length (cm), seeds/pod and Mash-88 is efficient for yield in kg and seed yield/plot (g). Based on different traits, the genotypes 3CM-705, 99CM-009, 11CM-705, 95CM-508, 97CM-056, and 11CM-704 are the best genotypes for yield production. The Check 9CM-702 is best for all traits. The genotype 10CM-703 is also the best one check for all traits except for days of maturity, days of flowering, and plant height in 1st season however in the second season 10CM-703 is the best check for all traits except plant height. The genotype, 9CM-702 also working efficiently for all traits except day of maturity, days of flowering, primary branches, and plant height. Overall the 60 and 30 test genotypes for first and second season respectively are surpassed check varieties for seed yield per plant.

| Table 12 | Correlation coefficients for six quantitative traits in Mash bean (1st season) |
|----------|-----------------------------------------------|
|          | PPP   | PL    | SPP   | SYPP  | SY-kg/ha | 100SW-g |
| PPP      | –     | 0.166 | 0.710 | −0.064| −0.049 | −0.106 |
| PL       | –     | –     | 0.086 | 0.006 | 0.001  | 0.003  |
| SPP      | –     | –     | –     | 0.381 | 0.141  | 0.190  |
| SYPP     | –     | –     | –     | –     | 0.987  | 0.046  |
| SY-kg/ha | –     | –     | –     | –     | –      | 0.038  |
| 100SW-g  | –     | –     | –     | –     | –      | –      |

| Table 13 | Correlation Coefficients for six quantitative traits in Mash bean (2nd season) |
|----------|-----------------------------------------------|
|          | PPP   | PL    | SPP   | SYPP  | SY-kg/ha | 100SW-g |
| PPP      | –     | 0.141 | 0.280 | 0.119 | 0.100  | 0.340  |
| PL       | –     | –     | 0.023 | 0.006 | −0.009 | 0.035  |
| SPP      | –     | –     | –     | 0.390 | −0.033 | 0.145  |
| SYPP     | –     | –     | –     | –     | 0.989  | 0.360  |
| SY-kg/ha | –     | –     | –     | –     | –      | 0.330  |
| 100SW-g  | –     | –     | –     | –     | –      | –      |
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Author Contributions MY carried out statistical analysis of the data and drafted the manuscript. MK carried out the results and discussion section and helped to write up the manuscript. HNT and RM participated in data arrangement and analysis of the data. JI and GR participated in the design of the study and data collection. MU and MK conceived of the study, and participated in its design and coordination and helped to draft the manuscript. All authors read and approved the final manuscript.

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Availability of Data and Material The data used in the study will be available on request.

Declarations

Conflict of interest There is no competing interests.

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