Original Research Article

Genotype x Environment Interaction and Stability Analysis for Yield and Quality Traits in QPM (Zea mays L.)

Hemlata Kumari1*, P. K. Singh1, R.B.P. Nirala1, Jai Prakash2, Rajkishor3 and Mukesh Kumar4

1Department of Plant Breeding & Genetics, BAC, 2Department of Plant Breeding & Genetics, BPSAC, 3Pulse Research Centre, 4Department of Seed Science and Technology, BAC, Bihar Agricultural University, Sabour, Bhagalpur-813210 (Bihar), India

*Corresponding author

Abstract

Maize is one of the most important grain crops in South Asia and is produced throughout the country under diverse environments. The grain of quality protein maize (QPM) varieties contain nearly twice as much lysine and tryptophan, amino acids that are essential for humans and monogastric animals. Evaluation of maize hybrids under different environments would be useful for identifying hybrids that combine stability with high yield potential for diverse environments. This study was conducted to evaluate 30 maize hybrids and 06 parents including two checks (Shaktiman-3 & Shaktiman-4) to study the stability parameters for grain yield per plant and quality parameters under varied environmental conditions. Among the different environments studied environment-5 (Rabi season) recorded the highest and positive environment index for the trait grain yield per plant. Hence, this trait appeared to be the most favourable for environment-5. The environment-2 (Kharif season) was favourable for the expression of lysine and tryptophan content in kernel protein since it had positive and high environmental index. Hence, these traits appeared to be the most favourable for environment-2. The hybrid CML161 x CML171 responded favourably under all environment, whereas the hybrid CML167 x CML171 suitable for rich environment (Rabi season) and the hybrid 167x161 suitable for poor environment (Kharif season) for higher grain yield per plant. The hybrid CML 161 x CML 171 and VL 1037 x VL1056 stable for all the six environments and it is adaptable to wider environments for yield and quality parameters. Therefore, these aforesaid maize hybrids are the promising genotypes in future for evolution of location specific superior maize hybrids for different maize growing situations.

Keywords
Quality protein maize, Stable variety, Six different environments, Superior hybrid 2020

Introduction

Maize (Zea mays L.) is the world’s most widely grown cereals and is the staple food in many developing countries (Morris et al., 1999). It is a miracle crop in view of its widespread use as food and nonfood items. Maize is also the third most important crop in the world, after wheat and rice, in terms of...
growing area, production and grain yield (Shiri et al., 2010).

The area, production and productivity of maize in India was 9.25 million ha, 23.70 million tones and 25.60 q/ha respectively (Annonymous, 2014) whereas in Bihar it was cultivated over 0.70 million ha with a production of 2.40 million tones having average productivity of 34.16 q/ha. (Annonymous, 2015-16). Maize is a good source of carbohydrates, fats, protein, important vitamins and minerals, providing food (25%), animal feed (12%), and poultry feed (49%), starch (12%), brewery (1%) and seeds (1%). Apart from normal maize, it has many other types viz., quality protein maize, sweet corn, baby corn, popcorn, waxy corn, high oil corn etc. It accounts for 15 to 56% of the daily total calories of people in many of the developing countries.

Maize is a potential source of protein for human food, cattle and poultry feed. However, it is deficient in several amino acids essential for monogastric animals in which lysine is the most limiting amino acid (Bhan et al., 2003). Main reasons for the poor quality of normal maize is the relatively high concentrations of prolamines or zeins storage proteins (50-60%) which are deficient in lysine and tryptophan causing maize to be nutritionally inferior in protein quality as compared with rice, wheat and other major cereals. The other storage proteins in the maize endosperm are albumins (3%), globulins (3%) and glutelins (30-45%) that have a relatively higher lysine content of 5-6%, 5-8% and 4-5%, respectively (Wilson,1991). The discovery of mutant alleles, opaque-2 (o2o2) (Mertz et al., 1964) by Purdue University researchers were found to alter the amino acid profile and the composition of maize endosperm protein and result in two fold increase in the levels of lysine and tryptophan compared to what is encountered in normal maize genotypes. Yet, it expresses negative pleiotropic effects on the grain quality such as lower density, susceptibility to pests and diseases and a floury appearance (Vasal, 2001). The International Maize and Wheat Research Center (CIMMYT) has developed quality protein maize (QPM) that improves kernel quality characteristics over opaque-2 (o2o2) soft genotypes, by introducing modifier genes and selecting for a hard, vitreous endosperm in opaque-2 (o2o2) germplasm (Vasal, 2001).

After the discovery of the nutritional benefits of the opaque-2 (op2) mutation, it has been incorporated into many breeding programs worldwide, with a major emphasis on conversion of normal endosperm populations and inbred lines to opaque-2 (op2) versions through a modified back crossing cum recurrent selection method.

The studies indicated that the QPM protein contains, in general, 55% more tryptophan, 30% more lysine and 38% less leucine than that of normal maize (Prasanna et al., 2001). The biological value of QPM protein is about 80% that of milk, which is about 90% and that of normal maize is only about 45% (FAO, 1992). QPM also provides better quality feed and fodder to poultry, cattle, swine, and fishmeal industries. Bressani (1991) stated that people eating QPM had significantly higher nitrogen retention than those who ate normal maize, indicating that QPM protein is more “bioavailable”. Besides the increased biological value, QPM has additional nutritional advantages, such as higher concentrations of niacin (vitamin B3) and improved absorption of potassium (Graham et al., 1980) and carotene (De Bosque et al., 1988). Substituting normal maize with high lysine maize on an equal weight basis can maintain proper amino acid balance (Wilson, 1991). The adoption of QPM can contribute immensely to alleviation of malnutrition in maize based economies in developing countries. The nutritional quality
of the protein in QPM grain approaches that of protein derived from cow’s milk.

In India in the 1970, three opaque-2 composites were developed and commercially released such as Shakti, Ratan and Protina. In 1997 Shakti-1 (OPV) was developed with modified endosperm and nutritionally superior opaque-2 composites. Later on in India several QPM hybrids were developed for different agroclimatic conditions like HQPM 4, HQPM 1, HQPM 5, HQPM 7, Vivek QPM 9, Shaktiman 1, Shaktiman 2, Shaktiman 3 and Shaktiman 4 (Dass et al., 2009a).

The ideal maize genotype could produce high yield regardless of environmental conditions. In reality, genotypes not performed equally well in all environments but some trend to be closer than others. Genotypes response to changing environments can be measured statistically by genotype x environment interaction. Stable genotypes would have a small genotypes x environment interaction, while those with large interaction could be called unstable. A reliable method of estimation of stability was proposed using regression analysis by Eberhart and Russell (1966). Further, its genotype x environmental interaction and stability of across environments help in identifying suitable QPM parents and its hybrid that are widely or specifically adapted to environments.

Keeping in view of aforesaid information, the present investigation is undertaken to explore the genetic potentiality of QPM inbred lines in view of the development of single cross QPM hybrids, with objectives to identifying productive, nutritionally superior and stable single cross hybrids.

**Materials and Methods**

The experimental material consist of six inbreed line with 2 checks (Shaktiman-3 and Shaktiman-4) as mentioned in table-1. The parents were evaluated and crossed during rabi 2016-17 in crossed in full diallel fashion [Griffing, 1956(b), method 1 model 1] to derived the single cross hybrid at Maize Section, BAC Sabour. The hybrid were evaluated for stability at three different locations such as sabour, purnea and mokama during kharif 2017 and rabi 2017-18 in randomized complete block design (RCBD) with three replications, 06 parents along with checks .The plots selected were uniform in topography, fertile and well drained soil. The experiment was laid out, with a row length of 4 m, with inter and intra row spacing of 75cm and 20cm respectively. Each genotype was sown with 2 rows. Five plants from each replication were randomly selected and tagged for recording observations in each genotype.

Data were recorded on different morphological and Quality parameters viz., Morphological data, namely, grain yield/plant were recorded on 5 randomly taken competitive plants from middle row of plot. Data for protein content in kernel, tryptophan content in kernel protein and lysine content in kernel protein were taken from the sample of bulk seeds. The stability of yield performance for each genotype was calculated by regressing the mean yield of individual genotypes on environmental index, similarly calculating the deviations from regressing the mean yield of individual genotypes on environmental index as suggested by Eberhart and Russell model (1966). Regression coefficient (bi) was considered as an indication of the response of the genotype to varying environment while the environment and genotype x environment interactions were partitioned into three components viz., environment (linear), genotype x environment (linear) and deviation from regression (pooled deviation over the genotypes).
Results and Discussion

Analysis of variance for stability showed significant mean squares for genotypes and environments (linear), indicating that the genetic variation was present and the environments were distinct from one another (Table 2). Variance due to environment plus interaction of genotype and environment and pooled deviation (nonlinear) were significant for grain yield per plant indicating presence of variation in the mean performance of all genotypes over environments i.e., differential behaviour of the genotypes under different environments except lysine content in kernel protein, tryptophan content in kernel protein and protein content in kernel. These findings are in consistent with Deshpande and Dalvi (2006), Panwar et al., (2008), Ramya and Senthilkumar (2008) and Krishnappa et al., (2009). The pooled analysis of variance revealed that genotype x environment (linear) interactions were highly significant for a character i.e., grain yield per plant implying differential response of genotypes under six locations for the character. Similar reports were earlier made by Panwar et al., (2008) and Ramya and Senthilkumar (2008). The genotype x environment (linear) interactions for the remaining 3 characters i.e., lysine content in kernel protein, tryptophan content in kernel protein and protein content in kernel were non-significant. Therefore, further analysis of stability was not carried out for these 3 characters.

The environmental indices computed for 4 characters are presented in the (Table 3) Environmental index directly reflects the environment by negative and positive values. Among the 6 environments, Environment-5 (Rabi seasons) recorded the highest and positive environmental index for the trait like grain yield per plant. Therefore, this environment appeared to be the most favourable for particular conditions. None of the traits had positive indices in Environment-5. The Environment-2(Kharif seasons) was favourable for the expression of high lysine content in kernel protein, tryptophan content in kernel protein and protein content in kernel, since it had positive and high environmental index. Hence, these traits appeared to be the most favourable for environment-2 conditions. Negative values of environmental index indicated the unfavourable nature of that particular condition.

In this study, the mean performance coupled with the regression coefficient (bi) and variance of deviation from regression (δ2di) of each genotype represented its stability (Table 4a and 4b). With these conditions, the parents and hybrids were classified and evaluated for their adaptability and stability in respect of yield and other component characters studied.

Eberhart and Russell (1966) described an ideal variety as one which should have high mean value over a wide range of environments, a regression coefficient around unity and non-significant deviation from regression coefficient. Genotypes based on their stability for different traits under the study were categorized in (Table 5). The ability to develop high yielding and stable cultivars is an ultimate goal in most breeding programs. The consistent performance of a genotype, both with high or low yield across different environments is referred as yield stability (Epinat-Le Signor et al., 2001). An ideal maize hybrid should have a high mean yield combined with a low degree of fluctuation under different environments (Annicchiarico, 2002).
Table 1. Details of QPM genotypes studied

| SN. | Inbred line | Pedigree | Colour | Source                      |
|-----|-------------|----------|--------|-----------------------------|
| 1   | CML161      | CML161   | Yellow | CIMMYT, HYD. (India)        |
| 2   | CML167      | CML167   | Yellow | CIMMYT, HYD. (India)        |
| 3   | CML171      | CML171   | Yellow | CIMMYT, HYD. (India)        |
| 4   | CML193      | CML193   | Yellow | CIMMYT, HYD. (India)        |
| 5   | VL1037      | CL 02450Q-B-B*6 | Yellow | CIMMYT, HYD. (India)        |
| 6   | VL1056      | CML 451Q-B*7-# | Yellow | CIMMYT, HYD. (India)        |
| 7   | Check-1     | Shaktiman-3 | Yellow | RAU, PUSA, Samastipur (Bihar)|
| 8   | Check-2     | Shaktiman-4 | Yellow | RAU, PUSA, Samastipur (Bihar)|

Table 2. Analysis of variance of Stability for different traits in QPM

| Source of Variations          | df  | Mean Square          |
|------------------------------|-----|----------------------|
|                              |     | Grain yield per plant| Lysine % in kernel protein | Tryptophan % in kernel protein | Protein % in kernel |
| Genotype                     | 37  | 5868.24**            | 0.41**                        | 0.02**                        | 0.28**            |
| Environment + Genotype x Environment | 190 | 669.86**            | 0.02                          |       | 0.01                          | 0.00            |
| Environment (Lin.)           | 1   | 101057.15**          | 0.16**                        | 0.01**                        | 0.03**            |
| Genotype x Environment.(Lin.)| 37  | 374.68**            | 0.02                          | 0.01                           | 0.01            |
| Pooled Deviation             | 152 | 81.27**             | 0.02**                        | 0.01                           | 0.01            |
| Pooled Error                 | 444 | 32.71               | 0.01                          | 0.01                           | 0.01            |

*, ** Significant at 5 % & 1 % level of probability, respectively

Table 3. Environmental indices for different characters in QPM

| Parameters                        | Kharif | Rabi |
|----------------------------------|--------|------|
|                                  | Sabour | Mokama | Purnea | Sabour | Mokama | Purnea |
| Grain yield/plant                | (E₁)   | (E₂)   | (E₃)   | (E₄)   | (E₅)   | (E₆)   |
| Lysine % in kernel protein       | -25.837| -14.935| -21.526| 18.178 | 22.982 | 21.138 |
| Tryptophan % in kernel protein   | -0.023 | 0.031  | -0.038 | 0.017  | -0.015 | 0.028  |
| Protein % in kernel              | -0.006 | 0.004  | -0.010 | 0.006  | -0.003 | 0.009  |
| Note: E: Environment             |        |       |        |        |        |        |

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### Table 4a: Estimates of stability parameters for different traits in QPM

| SN | Entry                  | Protein % in kernel | Lysine % in kernel protein |
|----|------------------------|---------------------|---------------------------|
|    |                        | $X_i$   | $b_i$   | $S^2d_i$ | $X_i$   | $b_i$   | $S^2d_i$ |
| 1  | CML161xCML167          | 9.883  | 2.693  | 0.0015   | 3.582  | 1.207  | 0.1252*** |
| 2  | CML161xCML171          | 9.724  | 1.555  | -0.0011  | 3.244  | -0.417** | -0.0010 |
| 3  | CML161xCML193          | 9.667  | 0.523  | 0.0023   | 3.183  | 1.223  | 0.0237*** |
| 4  | CML161xVL1037          | 9.492  | 3.626  | -0.0020  | 3.250  | 0.257  | -0.0008 |
| 5  | CML161xVL1056          | 9.183  | 0.977  | -0.0019  | 3.461  | 3.757  | 0.1421*** |
| 6  | CML167xCML161          | 9.379  | -1.296 | 0.0111** | 3.111  | 1.059  | 0.0002  |
| 7  | CML167xCML171          | 9.622  | 1.130  | -0.0020  | 3.133  | 0.547  | 0.0063*** |
| 8  | CML167xCML193          | 9.579  | 0.944  | -0.0025  | 3.156  | -0.929 | 0.0144*** |
| 9  | CML167xVL1037          | 9.267  | 1.446  | 0.0002   | 3.267  | -0.716* | -0.0001 |
| 10 | CML167xVL1056          | 9.811  | 3.063  | -0.0029  | 3.678  | -0.259 | 0.0063*** |
| 11 | CML171xCML161          | 9.994  | 0.549  | -0.0025  | 3.457  | 8.241  | 0.0367*** |
| 12 | CML171xCML167          | 9.761  | -0.027 | -0.0035  | 3.628  | 4.196  | 0.0543*** |
| 13 | CML171xCML193          | 9.739  | 0.353  | -0.0035  | 3.977  | -0.503* | -0.0005 |
| 14 | CML171xVL1037          | 9.239  | 5.454  | 0.0008   | 3.106  | 1.078  | 0.0011  |
| 15 | CML171xVL1056          | 9.317  | -1.647 | -0.0018  | 3.417  | 0.772  | 0.0058*** |
| 16 | CML193xCML161          | 9.417  | 1.056  | -0.0003  | 3.278  | 1.481  | 0.0080*** |
| 17 | CML193xCML167          | 9.433  | -1.021 | -0.0022  | 3.233  | -0.090 | -0.0001 |
| 18 | CML193xCML171          | 9.582  | 0.689  | -0.0015  | 3.139  | 1.634  | 0.0134*** |
| 19 | CML193xVL1037          | 9.294  | 6.206  | 0.0102** | 3.144  | 1.020  | 0.0136*** |
| 20 | CML193xVL1056          | 9.933  | 0.579  | -0.0033  | 3.328  | -2.974 | 0.0191*** |
| 21 | VL1037xCML161          | 9.194  | 3.176  | 0.0068*  | 3.106  | 1.692  | 0.0038*** |
| 22 | VL1037xCML167          | 9.571  | 2.554  | -0.0007  | 3.767  | 1.226  | 0.0444*** |
| 23 | VL1037xCML171          | 9.684  | -1.556 | -0.0022  | 3.272  | -0.472 | 0.0016  |
| 24 | VL1037xCML193          | 9.525  | -0.735 | 0.0191*** | 3.933  | 2.552  | 0.0258*** |
| 25 | VL1037xVL1056          | 9.692  | -2.322 | 0.0004   | 4.067  | -0.379 | 0.0003  |
| 26 | VL1056xCML161          | 9.552  | -1.764** | -0.0036 | 3.200  | 2.176  | 0.0021* |
| 27 | VL1056xVL1056          | 9.536  | 0.500  | -0.0024  | 3.272  | 0.676  | 0.0063*** |
| 28 | VL1056xCML171          | 9.723  | -3.324 | -0.0012  | 3.244  | 0.552  | 0.0000  |
| 29 | VL1056xCML193          | 9.818  | -2.415* | -0.0032 | 3.256  | 1.475  | 0.0013  |
| 30 | VL1056xVL1037          | 9.961  | 1.125  | 0.0006   | 3.350  | 3.063  | 0.0265*** |
| 31 | CML161                 | 9.787  | 1.571  | -0.0029  | 3.391  | -0.097 | 0.0349*** |
| 32 | CML167                 | 9.681  | 3.329  | -0.0005  | 3.322  | -0.763 | 0.0141*** |
| 33 | CML171                 | 9.647  | 1.141  | -0.0012  | 3.350  | -0.609 | 0.0122*** |
| 34 | CML193                 | 9.598  | 1.684  | -0.0022  | 3.294  | -0.439 | 0.0166*** |
| 35 | VL1037                 | 9.680  | 3.579  | -0.0005  | 3.277  | 6.544  | 0.0882*** |
| 36 | VL1056                 | 9.782  | 4.173  | -0.0015  | 3.449  | -4.507 | 0.0857*** |

37 Shaktimson-3(check) | 9.88 | -0.06 | -0.00 | 3.68 | 3.35 | 0.00 |
38 Shaktimson-4(check) | 9.87 | 0.69 | -0.00 | 3.89 | 1.37 | 0.00 |

General mean | 9.61 | 3.39 |
SEm (±) | 0.02 | 0.06 |
SE(b) | 1.94 | 2.34 |

*, ** Significant at 5 % & 1 % level of probability, respectively
Table 4b: Estimates of stability parameters for different traits in QPM

| S.N | Entry                   | X_i  | b_i    | S^2d_i     | X_i  | b_i    | S^2d_i     |
|-----|-------------------------|------|--------|------------|------|--------|------------|
| 1   | CML161xCML167           | 0.894| 1.889  | 0.0085***  | 164.876| 0.155*  | 59.264*    |
| 2   | CML161xCML171           | 0.803| -0.217**| 0.0000     | 146.839| 1.154  | -12.413    |
| 3   | CML161xCML193           | 0.787| 2.942  | 0.0013***  | 140.525| 1.308  | 5.323      |
| 4   | CML161xVL1037           | 0.803| 0.513  | 0.0000     | 143.486| 1.139  | 28.738     |
| 5   | CML161xVL1056           | 0.867| 3.547  | 0.0075***  | 138.506| 1.301  | 22.758     |
| 6   | CML167xCML161           | 0.764| 0.933  | 0.0001*    | 166.463| 0.333* | 43.684     |
| 7   | CML167xCML171           | 0.777| 0.756  | 0.0004***  | 137.479| 1.349**| -20.757    |
| 8   | CML167xCML193           | 0.787| -0.247 | 0.0011***  | 137.842| 1.098  | 7.658      |
| 9   | CML167xVL1037           | 0.817| 0.210  | 0.0001*    | 159.683| 0.701  | 272.389**  |
| 10  | CML167xVL1056           | 0.912| -0.810 | 0.0009***  | 152.578| 0.252  | 396.064**  |
| 11  | CML171xCML161           | 0.858| 8.916* | 0.0019***  | 136.518| 0.980  | 6.405      |
| 12  | CML171xCML167           | 0.901| 4.560  | 0.0035***  | 144.096| 1.049  | 61.352*    |
| 13  | CML171xCML193           | 0.996| 0.006  | 0.0000     | 124.630| 0.959  | 1.086      |
| 14  | CML171xVL1037           | 0.767| 1.028  | 0.0000     | 136.915| 1.320* | -8.718     |
| 15  | CML171xVL1056           | 0.850| 0.719  | 0.0007***  | 134.938| 1.354* | -4.800     |
| 16  | CML193xCML161           | 0.813| 0.837  | 0.0004***  | 143.045| 1.170  | 41.879     |
| 17  | CML193xCML167           | 0.813| 0.093  | 0.0001*    | 133.916| 1.304* | -2.595     |
| 18  | CML193xCML171           | 0.779| 1.618  | 0.0006***  | 135.542| 1.299  | 63.304*    |
| 19  | CML193xVL1037           | 0.781| 0.402  | 0.0006***  | 134.927| 1.251  | 91.249**   |
| 20  | CML193xVL1056           | 0.833| -1.831 | 0.0012***  | 124.905| 1.602* | 20.330     |
| 21  | VL1037xCML161           | 0.769| 1.776  | 0.0001*    | 131.609| 1.110  | 28.669     |
| 22  | VL1037xCML167           | 0.934| 2.226  | 0.0029***  | 137.380| 1.221  | 11.963     |
| 23  | VL1037xCML171           | 0.811| 0.017  | 0.0001     | 144.008| 1.492  | 63.329*    |
| 24  | VL1037xCML193           | 0.983| 2.183  | 0.0017***  | 138.327| 1.186  | 28.007     |
| 25  | VL1037xVL1056           | 1.033| 0.119**| -0.0001    | 134.690| 1.054  | 33.253     |
| 26  | VL1056xCML161           | 0.795| 1.038  | 0.0004***  | 123.683| 1.291* | -15.705    |
| 27  | VL1056xCML167           | 0.814| 0.961  | 0.0003***  | 156.361| 0.446  | 345.587**  |
| 28  | VL1056xCML171           | 0.809| 0.278  | 0.0000     | 114.611| 1.414  | 264.690**  |
| 29  | VL1056xCML193           | 0.808| 0.803  | 0.0000     | 127.028| 1.423**| -28.246    |
| 30  | VL1056xVL1037           | 0.833| 2.502  | 0.0013***  | 130.841| 0.804  | 6.484      |
| 31  | CML161                  | 0.849| -2.150 | 0.0021***  | 60.606 | 0.591* | 1.532      |
| 32  | CML167                  | 0.827| -1.115 | 0.0015***  | 62.715 | 0.987  | -10.104    |
| 33  | CML171                  | 0.829| -0.283 | 0.0007***  | 67.262 | 0.846  | -16.091    |
| 34  | CML193                  | 0.821| -0.875 | 0.0014***  | 64.534 | 0.742* | -28.288    |
| 35  | VL1037                 | 0.813| 3.837  | 0.0088***  | 62.108 | 0.614* | -9.536     |
| 36  | VL1056               | 0.863| -4.618 | 0.0058***  | 68.006 | 0.787  | -0.590     |
| 37  | Shaktimns-3(check)      | 0.92 | 3.12   | 0.0000**   | 135.3  | 0.53** | -12.65     |
| 38  | Shaktiman-4(check)      | 0.98 | 2.30   | 0.00**     | 139.7  | 0.33** | 82.60**    |
|     | General mean            | 0.84 |        |            | 129.1  |        |            |
|     | SE(b_i)                | 0.01 |        |            | 4.0    |        |            |

*, ** Significant at 5 % & 1 % level of probability, respectively
Table 5 Stable genotypes for different traits in Maize

| Parameters                  | Hybrids for all environments          | Hybrids for favourable environments (Rabi) | Hybrids for unfavourable environments (Kharif) |
|-----------------------------|---------------------------------------|------------------------------------------|-----------------------------------------------|
| Protein % in kernel         | CML171 x CML161                       | VL1056 x CML193                         |                                               |
|                             | VL1056 x VL1037                       |                                          |                                               |
|                             | CML193 x VL1056                       |                                          |                                               |
|                             | CML161 x CML167                       |                                          |                                               |
|                             | CML167 x VL1056                       |                                          |                                               |
| Lysine % in kernel protein  | VL1037 x VL1056                       | -                                        | CML171 x CML193                               |
| Tryptophan % in kernel protein| CML171 x CML193                      | -                                        | VL1037 x VL1056                               |
| Grain yield/plant           | CML161 x CML171                       | CML167 x CML171                         | CML167 x CML161                               |
|                             | CML161 x VL1037                       | CML171 x VL1037                         |                                               |
|                             | CML193 x CML161                       | CML171 x CML193                         |                                               |
|                             | CML161 x CML193                       | CML193 x VL1056                         |                                               |
|                             | VL1037 x CML193                       | CML171 x CML167                         |                                               |

From stability analysis studied, it can be inferred that the hybrid. For grain yield per plant showed high mean than the general mean (129.1), regression coefficient more than unity and non-significant deviation from regression were observed in the hybrids CML 167 x CML 171, CML 171 x VL 1037, CML 171 x VL1056 and CML 193 x CML 167 indicating that these hybrids responded to favourable conditions and can produce higher yields when provided with suitable environments. Similar reports were earlier reported by Kalla et al., (2001). The hybrid CML 161 x CML 171, CML 161 x VL 1037, CML 193 x CML 161, CML 161 x CML 193 and VL1037 x CML 193 appeared with high mean than the general mean, regression coefficient around unity and non-significant deviation from regression are considered to be stable for wider conditions. Similar findings were reported by Gouri Shankar et al., (2008).

Maize protein is highly characterized by high levels of glutamic acid, leucine and low levels of lysine and tryptophan. The QPM endosperm proteins showed significantly higher percentage of lysine and tryptophan. For protein content, high mean than the general mean (9.61), regression coefficient
more than unity and non-significant deviation from regression as reported by Kozubenko et al., (1990) were observed in the hybrids VL 1056 x CML 193. None of the hybrid showed high mean than the general mean, regression coefficient less than unity, non-significant deviation from regression. The hybrids CML 171 x CML 161, VL 1056 x VL 1037, CML 193 x VL 1056, CML 161 x CML 167 and CML 167 x VL 1056 showed with high mean than the general mean (9.61), regression coefficient around unity and non-significant deviation from regression. Therefore, these hybrids are recommended for cultivation across the tested environments for particular trait.

For lysine content, none of the hybrid showed high mean than the general mean (3.39), regression coefficient more than unity and non-significant deviation from regression. The hybrid CML 171 x CML 193 (3.39) showed high mean than the general mean, regression coefficient less than 1 and non-significant deviation from regression was specifically adapted to poor environments and suitable for kharif seasons. The hybrids VL 1037 x VL 1056 (3.39) showed high mean than the general mean, regression coefficient around unity and non-significant deviation from regression. Therefore, these hybrids are recommended for cultivation across the tested environments for particular trait.

None of the hybrid showed high mean for tryptophan content than the general mean (0.84), regression coefficient more than unity and non-significant deviation from regression. The hybrid VL 1037 x VL 1057 showed high mean than the general mean (0.84), regression coefficient less than 1 and non-significant deviation from regression was specifically adapted to poor environments and suitable for kharif seasons. The hybrids CML 171 x CML 191 showed high mean than the general mean (0.84), regression coefficient around unity and non-significant deviation from regression. Therefore, these hybrids are recommended for cultivation across the tested environments for particular trait.

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