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Quality associated traits based biochemical diversity in maize (*Zea mays* L.)

Muhammad Umair Khalid[1], Muhammad Sheraz[*1], Shaham Hamayoun Khan[1], Ali Anwaar[1], Tayyab Nawaz Khan[1], Ramala Masood Ahmad[1,3], Muhammad Sufyan Tahir[2]
[1]Department of Plant Breeding and Genetics, University of Agriculture, Faisalabad, Pakistan
[2]Department of Biology, University of Western Ontario, London, Canada
[3]State Key Laboratory of Crop Genetics and Germplasm Enhancement, Nanjing Agricultural University, Nanjing, China
[*]Corresponding author: sherazahmad861@gmail.com

Abstract

Billions of people in the world are affected by malnutrition. The effects of malnutrition in developing countries are more common as compared to developed countries because they cannot afford supplementation. The micro nutrients deficiency is the 5th major cause of diseases in children and women. They mostly depend on cereals-based foods. To overcome this deficiency, we need to explore the genetic variability associated with quality and yield associated traits. Maize is staple food in many countries worldwide. This research was conducted following RCBD to explore the variability for agronomic traits and essential nutrients among twenty-five accessions of maize. The diversity of nutrients was determined by using Atomic Absorption Spectrophotometer (AAS) Perkin Elmer Analyst 400, well equipped with air-acetylene flame. Data were recorded for quality and yield associated traits including plant height (cm), cob length (cm), bad husk, days to 50 % silking, days to 50% tasseling, anthesis-silking interval (ASI), ears per plant, grains per ear, grain per row, rows per ear, cob diameter (cm), 100 grain weight (g) and mineral extraction. Significant diversity was found for all traits among all accessions, but genotype PEARL showed high concentrations for Fe and Zn in addition to having high yield.

Keywords: Zinc, iron, maize, diversity micronutrients and yield traits.

Introduction

In Pakistan maize (*Zea mays* L.) is the third major cereal growing crop in tropical and subtropical areas. It is grown in both spring and winter seasons and it accounts for 4.8% of the total cropped area and 3.5% of the value of agricultural output. Maize originated in Central America and then in 10th century it was familiarized to West Africa by Portuguese (Iken and Amusa, 2004). This cereal crop has diploid chromosome number (2n = 20) and belongs to the family *Poaceae.* Maize is tall, monoecious, annual grass that has wide leaves. Staminate flowers are present on the top in the form of long spike, and pistillate flowers that have 8-16 rows of ovaries, the length of each row is about 30cm on wood like cob. The whole structure is covered by the long bracts and collection of silky threads project from the tip (Sleper and Poehlman, 2006).

It is the most important cereal crop and is the primary staple food in many developing countries. It is one of the world's main value crop, with a multibillion dollar annual support to agriculture sector (Baloch *et al*., 2015). According to an estimate it is considered that by 2020, the world will have nearby 7.7 billion people and by 2050 this digit will be around 9.3 billion, thus the demand for maize in developing world will be doubled. In 94 developing countries maize delivers about 30% of diet calories to almost 4.5 billion people and in low income countries it contributes nearly 67% of whole maize production (Shiferaw *et al.*, 2011).

All over the world area under maize cultivation was 177.76 million hectares with 961.10 million metric tons during 2016-17 in which approximately 60% contribution was of USA and China (United States Department of Agriculture). In Pakistan it covers an area of 1,334 thousand hectares with annual production of 6,130 thousand tones (Govt. of Pakistan, 2017). In sum production the contribution of Punjab and Khyber Pakhtunkhwa is 97% while contribution of Baluchistan and Sindh is 3%. Its contribution in agriculture is 2.7% and 0.5% in GDP (Govt. of Pakistan, 2017).

Due to its nutritional value maize have diversified uses like it provides food for human, fodder for animals, fuel for domestic use and raw material for industrial use (Hassan *et al*., 2017). Grain contains oil contents that are very useful for human consumption because it contains lesser unsaturated fatty acid (Khan *et al., 2011*).

The mineral elements (micronutrients and macronutrients) which are most commonly deficient in human diets are Zn and Fe while other nutrients, such as Ca, Se, Cu and Mg, can be lacking in the diets of some populations. According to an estimation, out of the world's 6 billion people, 30% are Zn deficient, 60–80% are Fe deficient, 30% are I deficient and about 15% are Se deficient (White and Broadley, 2005). Ca, Se, Zn, I and Fe are important elements for productivity and health of human beings and their deficiency can cause harmful effects in children, infants and poor women (Graham *et al.,* 2001).

The genetic improvement of any crop depends upon the crop genetic resources. This is due to the contribution of these resources into the new varieties of present day. However, the disadvantage of alteration in the genetic basis of the crops is that the most desirable alleles have been lost (Karp, 1995). Several improved varieties of different crops have been developed through the selection by narrowing the genetic basis of the crops. On the other hand replacement of native landraces with better-quality varieties of narrow inherited bases caused in genetic erosion and rapid decrease in genetic diversity (Keneni *et al*., 2012).

The diversity in the concentration of traits like minerals has great importance to attain achievement in plant breeding. To cope with these types of problems a study was conducted to observe the mineral concentrations in different maize cultivars. These mineral concentration results will help to the researchers to adopt the new breeding strategies that will be useful for the enhancement and improvement of these nutrients into the new varieties. Therefore, present study's objective is to check the genetics of yield and quality associated traits (micronutrients) in different maize cultivars.

Materials and Methods

Twenty-five genotypes were sown in the research area of the Department of Plant Breeding and Genetics, University of Agriculture, Faisalabad. To check the genetic diversity of different genotypes quality and yield related traits were analyzed. All were analyzed in the field and then in the laboratory under normal conditions. Maize accessions were collected from Maize and Millet Research Institute (MMRI), Yousuf Wala, Sahiwal and Ayub Agricultural Research Institute (AARI), Faisalabad as given in Table 1.

Field experiment was conducted by following randomized complete block design (RCBD) and using two replications. In each replication randomly three plants were selected for observation and measuring the traits associated with quality and yield. Average mean of selected plants was calculated. The selected plants were harvested at full maturity and data was analyzed by following statistical analysis.

Data were recorded for these traits plant height (cm), cob length (cm), bad husk, days to 50 % silking, days to 50% tasseling, anthesis-silking interval (ASI), ears per plant, grains per ear, grain per row, rows per ear, cob diameter (cm), 100 grain weight (g), and mineral extraction. Steps of digestion for minerals (Fe and Zn) were done by following wet-ashing technique drawn by the Pinta and DeWele, 1975. Zinc and iron were determined by using Atomic Absorption Spectrophotometer (AAS) Perkin Elmer Analyst 400, well equipped with air-acetylene flame.

Variability for trait of interest among genotypes was calculated by using Analysis of variance (ANOVA) and appropriate average mean analysis were showed by using the procedure of (Steel *et al*., 1997). Results were obtained by using analysis of variance (ANOVA) and Microsoft Excel was used for the graphical presentation.

Results and Discussion

Significant diversity was found among all maize genotypes for all traits under normal environmental conditions from analysis of variance (ANOVA) technique given by Steal *et al.* (1997) and Latin Square Design was used for mean comparison.

Variety of differences were found for plant height by analysis of variance (Table 2) between maize genotypes. Latin square used for mean comparison which showed maximum height (215.50cm) produced by genotype 31R88 and minimum height (116.50cm) by P4040. The value for coefficient of variance 0.36 was noted in analysis of variance. For cob length the value (0.88) of coefficient of variance was noted. Average mean comparison showed maximum and minimum cob length showed by genotypes 31R88 (135.5cm) and 25W87 (49.50cm). Analysis of variance showed extremely significant variation for bad husk and coefficient valued showed 46.91. The genotype 31R88 showed extreme bad husk (2.50) while least bad husk (0) showed by 6103. For days to 50% tasseling analysis of variance showed significantly variation. The accession P4040 (54.5) showed maximum days to 50% tasseling while the accession 9108 (43.5) showed minimum days. Analysis of variance showed 1.29 value for coefficient of variance. Findings showed dissimilarity for days to 50% silking among all genotypes. Analysis of variance showed 1.29 magnitude for coefficient of variance. Maximum days (54.5) to 50% tasseling was recognized by the accession P4040 and minimum days for 9108 (43.5). Analysis of variance showed that the performance of all genotype for anthesis silking interval was highly variable and the value for coefficient of variance was noted 24.80. Maximum days for anthesis silking interval was showed by the genotype 9108 (5.50) and minimum days for the C905 (0.5).

Ear per plant was found extremely significant by analysis of variance. Different accessions showed different number of ears per plant. Mean comparison showed that maximum number of ears produced by 30T60 (1.97) and minimum by accession 8441 (1.46). Number of grains per ear was varied from genotype to genotype. Mean comparison showed that extreme number of grains per ear produced by accession MMRI YELLOW (355.5) and least number of grains was produced by 30T60(220.5). A lot of dissimilarity was found in grains per row in each genotype and mean comparison showed that maximum number of grains per row was produced by accession DK6789 (32.5) minimum grains per row was recognized by the accession P3939 (6.5). Analysis of variance for row per ear showed highly differences among all genotypes and value for CV 5.99 was noted. Maximum number of rows per ear was produced by the accession 626 (17.5) and lowest number of kernels per ear was produced by P3939 (8.5). Significant diversity was found was found by accessions for cob diameter. Latin square design showed maximum diameter of cob was produced by accession 25W87 (4.39 cm) followed by 8441 (4.25 cm) and lowest diameter of cob was detected in DK6714 (3.37 cm). Analysis variance showed dissimilarity for 100 grain weight. Mean comparison showed that maximum hundred grain weight was produced by accession MMRI YELLOW (40.95 g) followed by GAUHER (37.85 g) and minimum hundred grain weights were detected in 626 (21.1 g).

Iron and zinc

All the accessions showed different concentrations for iron and zinc. The average mean comparison showed that maximum concentration iron content was produced by accession DK6789 (42.62 ppm) followed by PEARL (41.93 ppm) and minimum iron concentration content was detected in 31R88 (4.30 ppm) as shown in Figure 1. Maximum zinc (Zn) concentration content was showed by the maize accession SAHIWAL-2002 (8.8584 ppm) followed by PEARL (4.9120 ppm) and lowest zinc concentration content was produced by DK 6714 (1.63 ppm) as shown in Figure 2. Four accessions 25W87, DK6789, PEARL and YAM123A were found with satisfactory iron concentrations and their levels were matched by the iron levels in maize given by Harvest Plus. These genotypes can be used for further studies to compete hidden hunger.

Abbreviations: PH= Plant height, **BD**= Bad husk, **DT**= Days to 50% tasseling, **DS**= Days to 50% silking, **ASI**= Anthesis silking interval, **EPP**= Ears per plant, **GPE**= Grains per ear, **GPR**= Grains per row, **RPE**= Rows per ear, **CD**= Cob diameter, **HGW**= Hundred grain weight, **I**= Iodine, **Fe**= Iron, **Zn**= Zinc and **AAS**= Atomic absorption spectrophotometer.

Conclusion

Yield and nutrient management are the most important factors in successful crop production. In this study, genetic diversity was studied to find out the more diverse accessions in maize which might be used in hybridization program.

The genotypes DK6789, SAHIWAL-2002, PEARL, 25W87 and YAM123A showed greater concentrations for Fe and Zn while the genotypes MMRI YELLOW, GAUHER, PEARL, 31R88, 27W87, SUNHERI and YUM123A identified as the best yielders among all genotypes.

The genotype PEARL showed higher yield and higher concentrations Fe and Zn and is therefore suggested for further breeding programs.

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Table 1. Genotypes used in study

Sr. No.	Genotypes	Sr. No.	Genotypes
1	DK 6789	14	HIC 339
2	P4040	15	DK 6714
3	YH 5536	16	GOLDEN
4	626	17	PEARL
5	30T60	18	GAUHER
6	31R88	19	YH5427
7	SUNEHRI	20	YAM123A
8	30Y87	21	MMRI YELLOW
9	9108	22	SAHIWAL-2002
10	FH 1046	23	8441
11	P3939	24	C905
12	6103	25	619
13	25W87		

Table. 2 Analysis of Variance for studied traits

SOV	PH	CL	BH	DT	DS	ASI	EPP	GPE	GPR	RPE	CD	HGW	Fe	Zn
SS	21984.0	15639.1	39.120	638	482.42	73.22	1.56	71258.7	1188.82	194.82	4.16	1032.64	7833.60	85.72
MS	919.76	653.54	4.38	27.27	20.22	13.11	0.06	7298.39	61.93	8.08	0.16	47.44	326.53	3.62
F	2410.53**	1302.09**	3.46*	60.99*	41.02**	7.76**	25.62**	1691.88**	116.70**	14.48**	34.03**	57.92**	520.65**	323.11**
CV	0.36	0.88	46.91	1.29	1.29	24.80	2.81	0.14	5.37	5.99	1.86	2.68	4.04	3.06

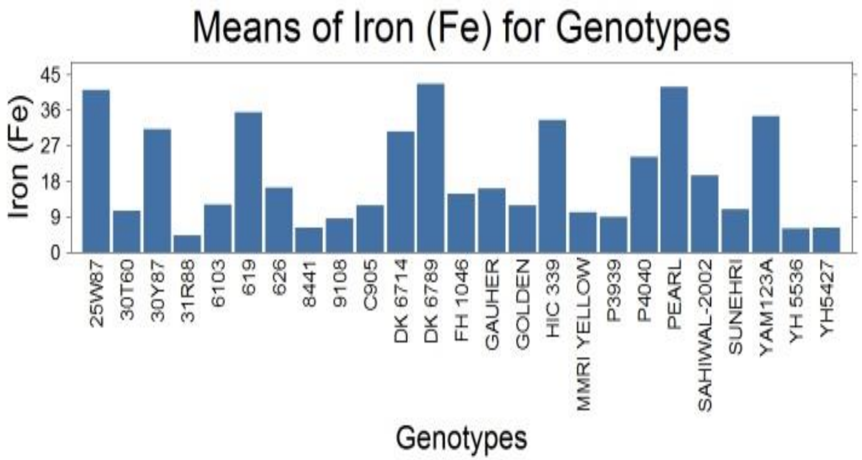

Figure 1. Iron contents (ppm) among studied genotypes

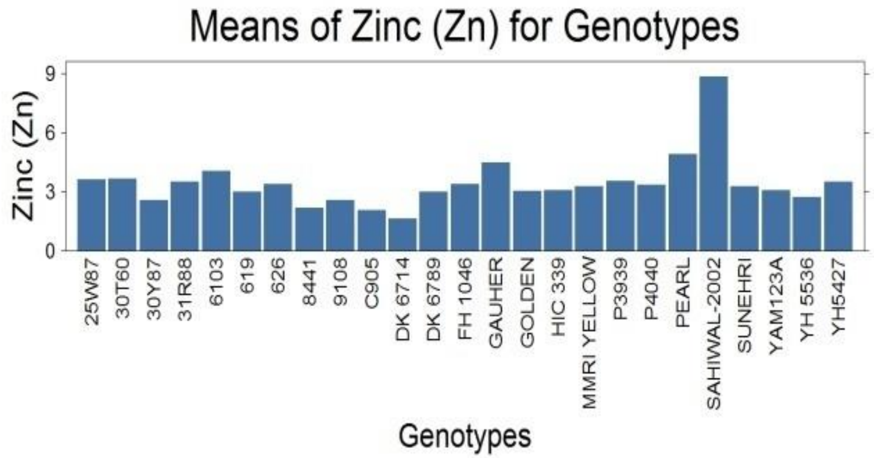

Figure 2. Zinc contents (ppm) among studied genotypes