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Assessment of genetic diversity in maize for microelements

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Abstract

Malnutrition of micro-nutrients is affecting billions of people in the world. Developing countries are more vulnerable to micronutrient deficiencies due to limited affordability because of low per capita income. Maize (*Zea mays* L.) is the third most important cereal and is used as source of food, feed, fodder and biofuel in addition to providing raw material for industrial products like corn oil, corn starch, glucose etc. This study was conducted to assess the genetic diversity in quality and yield contributing components under the normal environmental conditions among 40 maize genotypes. Data for the traits like plant height, cob length, ear per plant, grains per ear, grains per row, cob diameter, 100 grain weight, and iron, zinc, copper, and magnesium contents were recorded. Analysis of variance determined highly significant diversity among the genotypes for all traits except magnesium contents. This quality and yield based diversity provided a valuable source for developing high yielding and nutrient rich maize. Germplasm to overcome the issues of food security and malnutrition. The best performing genotypes with focus on both the issues could be used in different breeding programs to develop high yielding and micronutrient enriched hybrids/varieties.

Keywords: Genetic diversity, microelements, maize, micronutrients, yield

Introduction

Maize is an important cereal after wheat and rice and is used as staple food worldwide (Sleper and Poelhlman, 2006). It is a short duration versatile crop which is cultivated throughout the world specifically in tropical to temperate regions of Asia, America, Africa and Europe (Anonymous, 2012). USA is the largest producer of maize followed by China and Brazil; these countries cover 70% area of the world under the cultivation of the maize crop (FAO, 2012).

In the developing countries, almost 1 billion of people consume maize as food (Ndukwe *et al*., 2015). Many parts of maize plant including kernel are being used in industrial products as a raw material (Khan *et al*., 2011). During 2018-19, in Pakistan maize has been cultivated on an area of 1318 thousand hectares with a total production of 6.301 million tons (Pakistan Economic Survey, 2018-19). It plays important role in the GDP (0.40%) and agriculture of Pakistan, it contributes 2.1% in value addition in agriculture (Anonymous, 2014). Yield contributing traits are important because they contribute in the final volume as well as for estimating the crop plant yield capacity; they also form the basis of the plant. Yield is the magnitude of different yield contributing components and these components determine the capacity of the yield (Ion *et al.*, 2013). Deficiency of microelement in staple foods is the most important issue of the human being regarding hidden hunger (Goudia *et al.*, 2015).

Globally, 1/3rd of the population is affected by deficiency of micronutrients such as iron and zinc. In developing countries deficiency of micronutrients causes many diseases (Kanwal *et al.*, 2010). Deficiency of microelements is global issue and is more prevalent in developing countries, especially in those people who depend upon such staple food which is naturally deficient in microelement. In human staple food, iron and zinc are significantly deficient (Goudia *et al.*, 2015). Role of micronutrient is vital in human nervous system, cellular signaling, and function of reproductive health (Comertpay *et al.*, 2016). In the developing countries this problem is reported significantly high. It is verified in the review that significant magnitude of genetic diversity is present in available maize germplasm for the improvement of micronutrients (Welch and graham, 2002).

Genetic improvement in yield contributing traits of economic importance along with maintaining adequate amount of diversity is constantly the desired objective in corn breeding programs. To improve genetic variability of local genotypes, it is necessary to know the already existing genetic diversity in such material. Genetic diversity, which is an inherited difference among genotypes, is required in a considerable level among the population to make possible and carry on an effective plant breeding program (Ahmad *et al*., 2011). The development of effective breeding technique to enhance the micronutrient concentration in maize grain depends upon the existence of genetic diversity in different Germplasm (Menkir, 2008).

Materials and Methods

The experiment was carried out the normal condition to find out the diversity of the quality and yield contributing traits. The germplasm of maize was collected from different research center of the Pakistan PGRI, NARC, and Islamabad (Table 1). The studied parameters were recorded in the field and laboratory and analyzed. In field experiment, two rows of each genotype were sown following RCBD. Row to row distance 75cm and plant to plant distance 15 cm and row length 4m was maintained. Selected plants were tagged during different developmental stages of plants. At the maturity tagged plants were harvested and yield as well as quality characters were recorded, and data were analyzed by using Statistix 8.1. To achieve objectives, during experiment following parameters were recorded plant height, cob length, ear per plant, grain per ear, grain per row, cob diameter, 100 grain weight, iron, zinc, copper, and magnesium contents. The steps of digestion for microelements (Fe, Mg, Cu and Zn) were followed by following wet-ashing technique as proposed by (Pinta and DeWele, 1975).

Results and Discussion

Significant diversity was found among all maize genotypes for all related traits except magnesium under normal environmental conditions (ANOVA) and mean comparison. Statistical analysis showed that data recording plant height of 40 maize genotypes were submitted to analysis of variance and high level of variation among maize genotypes was identified. The value of coefficient of variation (CV) 9.4 % was recorded for plant height. Maximum plant height was produced by maize genotype 14882 (216 cm) followed by 14894 (215 cm) and minimum plant height was recorded in case of 14858 (116.5 cm). LSD test showed that there are 10 genotypes in which the means for plant height are not considerably different. Shakoor *et al.* (2007) published significant variation for plant height among maize genotypes. These results confirm the finding of Shakoor *et al.* (2007). Maximum cob length produced by the genotype 14906 (20.5 cm) followed by 14889 (15 cm) and minimum by genotype 14920 (9 cm) respectively. The CV value for cob height was recorded as (11.08%). Mean comparison for cob length of 40 maize genotypes was done by using LSD test. The results indicated that there are 15 groups which are not considerably different from one another at 5% probability level. Turi *et al*. (2007) conducted the experiment and reported highly considerable variation for cob length among maize genotypes. This high level of variation confirms that there are chances to improve this character by selection followed by breeding among good parents.

Regarding ear per plant results showed significance differences among maize genotypes under study. The CV value (1.64%) was recorded regarding the said traits. Maximum number of ears per plant was identified by the genotype 14855 (1.985) followed by 14882 (1.765) and lowest by genotype 14936 (1.23) respectively. LSD test was conducted for mean comparison for ear per plant of 40 genotypes. LSD information depicts that there are 15 groups which are not considerably different from one another. Lucchin *et al*. (2003) found considerable genetic differences for cob per plant among maize genotypes. The results testify the previous findings. Presence of significant genetic differences means differences at allelic level are present; therefore, there are chances to improve the character genetically. Qamar *et al*. (2007) published highly considerable differences for cob per plant among maize genotypes which is in accordance to the finding of the present study.

The maximum number of grains per ear was identified in case of the genotype 14855 (479.5) followed by 14924 (296) and minimum by genotype 14870 (208) respectively. LSD test was applied for mean comparison of grain per ear of 40 genotypes. Total 15 groups were observed which are not significantly different from one another by mean comparison.

The results indicated that grains per row of 40 maize genotypes were significantly different from one another. The genotype 14855 developed highest grains per row (34.5) followed by 14930 (13) and minimum by the genotype 14897 (7.5). There are 12 groups which are not significantly different from one another. Vafa *et al.* (2014) observed a significant genetic diversity among all the accessions under study based on number of grains per row. The present study confirmed the findings of Vafa *et al*. (2014). The existence of this diversity can be exploited to improve the character.

The result showed that highest cob diameter was produced by the genotype 14895 (4.545 cm), followed by 14906 (3.785 cm) and the least value was recorded in case of 14902 (3.37 cm). Means for this character were compared following LSD test. LSD test comparison indicated that there are 18 groups in which the means are not comparatively different. Andrade *et al*. (2008) reported significant differences among the genotypes for diameter of cob which is similar to our results. Alaei *et al* (2012) revealed significant diversity between the genotypes for diameter of cob which is similar to our study.

The result showed that maximum 100 grain weight was produced by the genotype 14897 (47.25 g), followed by 14857 (33.9 g) and minimum by 14866(21.1 g). LSD test was used for pair wise comparison of mean in 40 maize genotypes based on diversity. LSD test comparison indicated that there were 21 groups in which the means was not different. Aghdam *et al*. (2014) published comparatively significant differences for 100 grains weight. Present findings are contradictory than the findings of Aghdam *et al.* (2014) but confirms the results of Murtza *et al*. (2014) who reported significant difference among different genotypes for 100 grains weight.

Highest iron contents were produced by genotype 14856 (43.626 ppm), followed by 14906 (43.434 ppm) and least value for iron contents was recorded in case of genotype 14861 (6.013 ppm). For pair wise comparison regarding iron contents, LSD test was followed among 40 maize genotypes. According to results based on LSD test 12 groups did not significantly different from each other. Oilkeh *et al*. (2003) showed highly significant variations for iron concentration in grains. Results did not agree with the report of Oilkeh *et al*. (2003) and Mi *et al*. (2004 reported significant variation among genotypes under study. This contradiction might be due to different genotypes under study. Genotypes with more genetic distances or with variable origins might have different level of iron contents as compared to genotypes of lesser genetic distances. The genotype 14923 showed highest contents of zinc (38.29 ppm) followed by 14863 (27 ppm) and lowest value was recorded in case of genotype 14902 (19.649 ppm). LSD test based mean comparison for zinc contents among 40 genotypes exhibited that there are 9 groups which are not considerably different from one another by comparison of mean. Harvestplus (2006) found statistically significant differences for zinc concentration in 40 maize accessions. These published results are not in accordance with the findings of present study. The results do agree with the publication of Queiroz *et al*. (2006) who reported significant differences for cob zinc content among different maize genotypes.

The result showed that highest zinc concentration (3.95 ppm) was identified in the genotype 14931 followed by 14901 (2.5 ppm) and lowest by genotype 14893 (0.9635 ppm). There are 12 groups which are not significantly different from one another. Ziarati *et al*. (2015) and Manasek (2013) did not found considerable difference in maize genotypes based on zinc contents. The difference in the findings of present study than mentions earlier is due to different genotypes under study in all the three studies.

Based on magnesium contents, there are no significant differences among maize genotypes under study. The result showed that highest magnesium concentration was identified in the genotype 14863 (3.5404 ppm) followed by 14933 (3.367 ppm). The lowest value for magnesium contents was recorded in case of genotype 14861 (2.0847 ppm). The results of present study are contradicting the findings of Drinic *et al*. (2015) who reported significant differences among the maize genotypes with variable origin.

Conclusion

All growth attributes under study showed significant genotypic differences. Therefore, the characterized maize germplasm based on several quantitative and qualitative characters can be used for further maize improvement especially in development of biofortified maize hybrids which ultimately contribute to alleviate hidden hunger.

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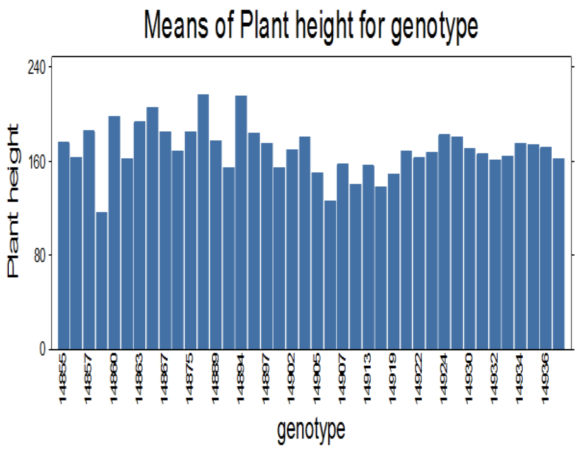
Table 1: List of procured Germplasm under study

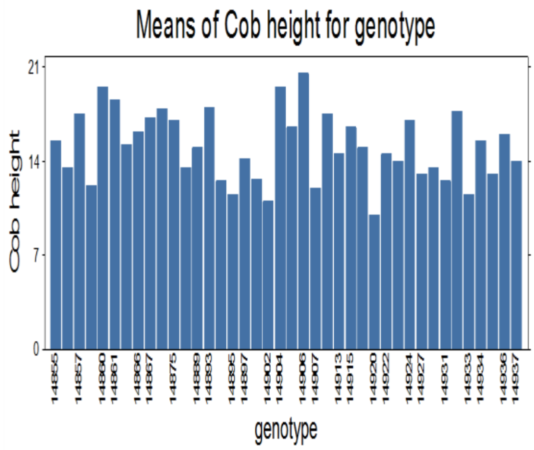
Sr. No.	Genotypes	Sr. No.	Genotypes
1	14855	21	14905
2	14856	22	14906
3	14857	23	14907
4	14858	24	14911
5	14860	25	14913
6	14861	26	14915
7	14863	27	14919
8	14866	28	14920

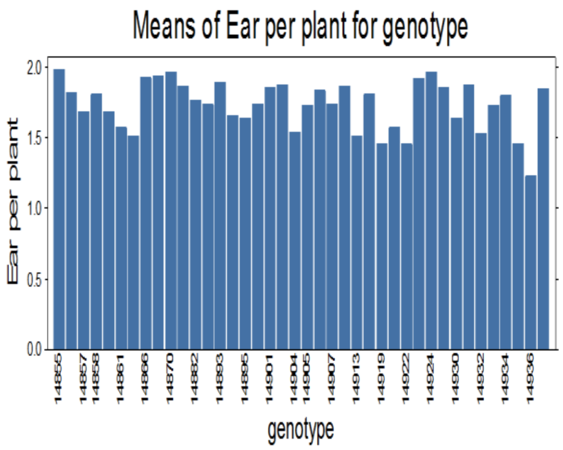
9	14867	29	14922
10	14870	30	14923
11	14875	31	14924
12	14882	32	14927
13	14889	33	14930
14	14893	34	14931
15	14894	35	14932
16	14895	36	14933
17	14897	37	14934
18	14901	38	14935
19	14902	39	14936
20	14904	40	14937

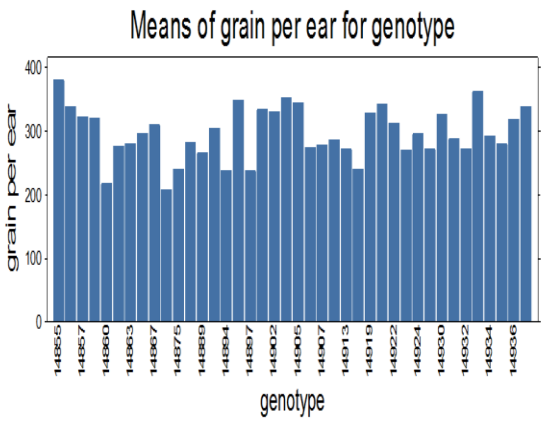
Table 2: Statistical description of the traits under study

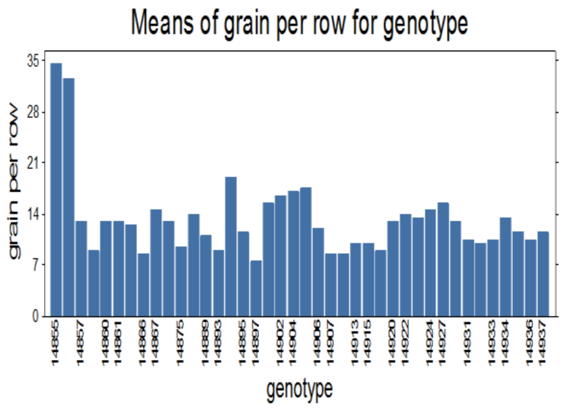
SOV	PH	CL	EPP	GPE	GPR	CD	100GW	Fe	Zn	Cu	Mg
SS	33517.4	517.58	2.415	128823	2304.95	7.297	1962.01	9745.3	2505.9	42.705	6.032
MS	859.42	13.271	0.061	3303.15	59.101	0.187	50.307	249.88	64.253	1.095	0.154
F	3.32**	4.76**	76.28**	7.19**	14.7**	13.28**	77.99**	22.94**	7.3**	306.77**	1.05^{ns}
CV	9.48	11.08	1.64	7.23	15.1	3.14	2.41	12.77	10.45	2.49	11.69

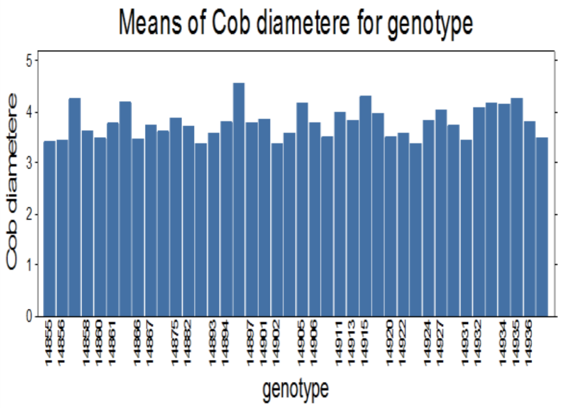


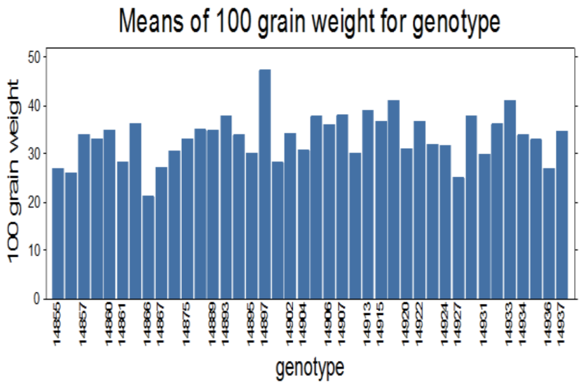


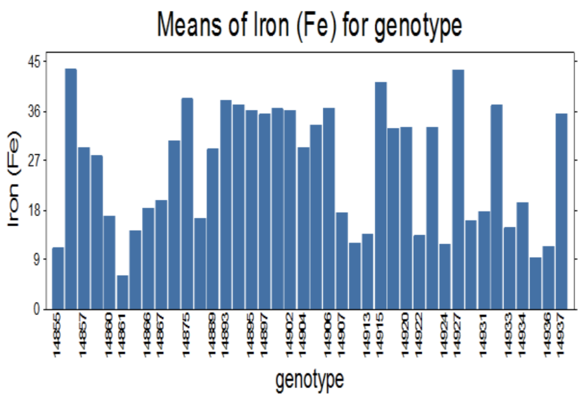


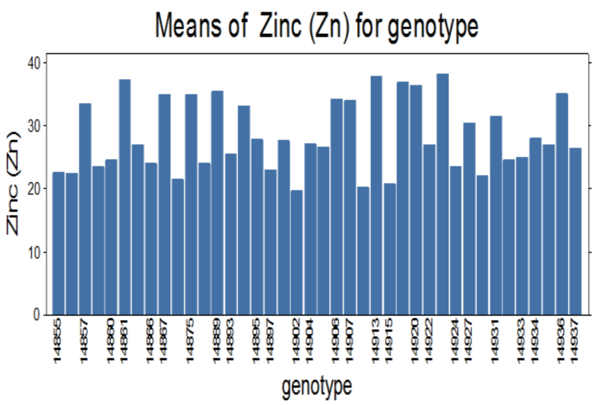


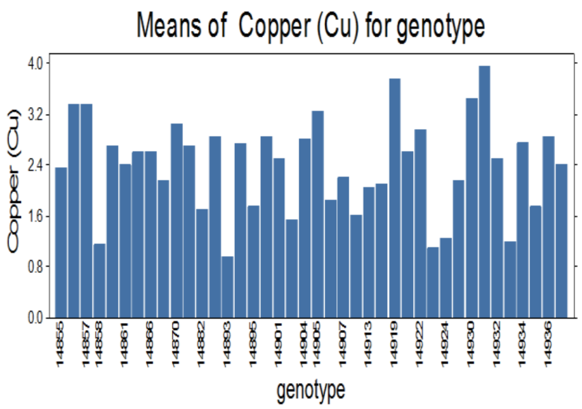

Means of grain per row for genotype
grain per row
genotype

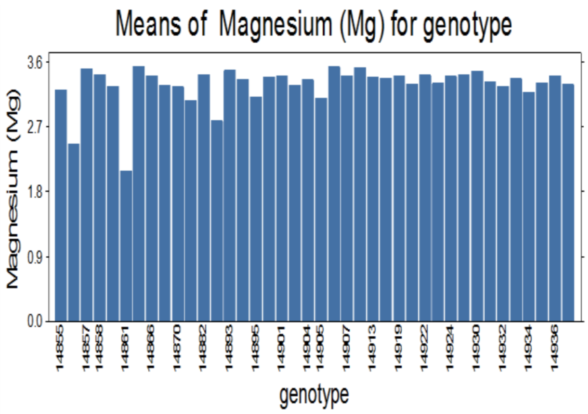

Means of Cob diametere for genotype
Cob diametere
genotype


Means of 100 grain weight for genotype
100 grain weight
genotype


Means of Iron (Fe) for genotype
Iron (Fe)
genotype


Means of Zinc (Zn) for genotype
Zinc (Zn)
genotype


Means of Copper (Cu) for genotype
Copper (Cu)
genotype


Means of Magnesium (Mg) for genotype
Magnesium (Mg)
genotype