Original Research Article

Genetic variability, correlation and path coefficient analysis in Hybrid Maize (*Zea mays* L.)

[Article would be more useful if the introduction said what characteristic of maize, whether a particular nutrient content or some other character would be more useful to emphasize in breeding than others. Maize, for example, varies in starch quality and protein content. In Bangladesh, what characters would help in human nutrition? And what characters would help in animal nutrition? Or is it more important for maize's future utility to work on yield? Genetic studies without such thinking ahead of time may not be useful.

In general, the article would be improved by more specifics, such as those mentioned in the interlinear comments by the reviewer.]

Abstract

[First sentence needs to refer to the overall purpose of the study and its theoretical background. This abstract is merely descriptive.] The present study was carried out to investigate the correlation coefficient, path analysis and genetic variability among twenty four [too few; sample should be at least 100 in order to have statistical significance] maize hybrids for ten charactersin a Randomize Block Design (RBD) with three replications at the research field of Plant Breeding Division, Regional Agricultural Research Station, Barisal, Bangladesh Agricultural Research Institute (BARI), Bangladesh during rabi season of 2014-15. The measured traits were Days to 50% tasseling (DT), days to 50% silking (DS), Anthesis silking interval (ASI), plant height (PH), ear height (EH), days to maturity (DM), cob length (CL), cob diameter (CD), thousand seed weight (TSW) and yld(yield t/ha). Here yield was considered as dependent variable and the rest parameters were independent variable. The data were submitted to analysis of variance and mean values were compared by DMRT test at both 5% and 1% of probability. Positive and significant genotypic, phenotypic correlation coefficient were recorded for yield with cob diameter($r_{g=}0.75^{**}$, $r_p=0.61^{**}$), cob length ($r_g=0.66^{**}$and $r_p=0.42^{**}$), plant height ($r_g=0.62^{**}$and $r_p=0.55^{**}$), ear height ($r_g=0.66^{**}$and $r_p=0.55^{**}$) and thousand seed weight ($r_g=0.36^{**}$and $r_p=0.44^{**}$). High genotypic coefficient of variation (GCV) were obtained from anthesis silking interval (17.26), yield (15.17), ear height (13.80) and thousand seed weight (9.43). The highest phenotypic coefficient of variation (PCV) were observed in anthesis silking interval (26.49) followed by yield (20.51), ear height (16.19) and the lowest in days to maturity (0.70). The difference between GCV and PCV of yield indicated that the characters had some environmental influence. The highest heritability was observed for plant height (73.78) followed by ear height (72.67), thousand seed weight (59.52) and days to maturity (55.97) but the lowest heritability identified for days to silking (18.98). The characters with higher values high GCV and higher of heritability of the aforementioned traits were indicative for selection. The plant height had the highest positive direct effect (1.34) on yield followed by days to silking (0.75), cob diameter CD (0.46) and thousand seed weight (0.41), days to maturity (0.21**)** and cob length (0.20**)** indicating the effectiveness of direct selection**.** Direct negative effect on yield was shown by ear height (-1.03), days to tasseling (-0.52) and anthesis silking interval (-0.50) was indicating the effectiveness of indirect selection.

Key words: Genetic variability, correlation, path co-efficient, maize productivity

Introduction

Maize*(Zea mays* L.) is C_4 plant having higher yield potential comparied~~ng~~ with rice and wheat (Gong *et. al*., 2015). It is the second most abundant crop produced in the world (Ort and Long, 2014). Thus, i~~I~~t is an important crop throughout the world and its characteristics have~~has~~ both social and economic repercussions. It is widely used for various applications, but mainly as animal feed. Demand for maize, for both human and animal consumption, is expected to increase. It is also the cereal that is most produced in the world, due to its wide scope and utilization in human and animal diet. (Barbosa *et. al*., 2019). [The writing in this introduction is not well organized. The author should think how to order the sentences to make a clearer exposition of their points.]

[The next two sentences are in a larger point size.] Maize is the basis for food security in some of the world's poorest regions in Africa, Asia, and Latin America. The crop provides over 20% of total calories in human diets in 21 countries, and over 30% in 12 countries that are home to a total of more than 310 million people. (You *et. al*., 2012). Maize breeding researchers seek to combine increased grain yield with improved nutritional quality, especially regarding protein and energetic content. It is, therefore, of fundamental importance to identify the agronomic and nutritional traits of maize genotypes (Alves and Filho, 2017). ~~It is also the cereal that is most produced in the world, due to its wide scope and utilization in human and animal diet. (Barbosa *et. al*., 2019).~~

Presently maize is cultivated in 165 countries on 184 million hectares (ha), and has a production of 1,016 million tons (t) and productivity of 5.52 t/ha globally. (Yadav*et. al*., 2014). In Bangladesh its area and production increasing rapidly due to wide adaptability and versatile uses. According to DAE (2019) the production in Bangladesh was 25.16, 23.61, 27.59, 35.78, 38.93 lac metric ton in the year of 2013-14, 2014-15, 2015-16, 2016-17, 2017-18 with an area occupying 3.64,3.55, 3.95, 4.34, 4.47 lac ha. The yield was 6.91, 6.65, 6.98, 8.25, and 8.71 t/ha respectively.

Maize is one of the most important human food grains in the world, especially ~~as well as~~ in developing countries like Bangladesh. The food produced in Bangladesh is not adequate to meet domestic requirements. Cropping intensity [of maize?] is already more than 155%, and approaching 200% wherever intensification is possible. [Clarify what those percentages refer to.] Maize could be good source of nutrition for under nourished and malnourished population in Bangladesh. It is now widely used in the poultry farms, fisheries and animal feeding, ~~as well as~~ and the people consume roasted and fried maize in Bangladesh, as well.

Knowledge of the linear association between agronomic and nutritional maize traits could lead to significant advances in genetic breeding programs, especially when defining crossings, with the aim of targeting animal feed to increase efficiency and cut production costs. Associations between traits can be studied by analyzing a linear correlation coefficient ranging from -1 to 1. However, this coefficient measures the degree of relatedness between two traits and does not allow direct and indirect influences to be quantified (Cruz *et.al*., 2012).

Path coefficient and correlation analyses are used widely in many crop species by plant breeders to define the nature of complex interrelationships among yield components and to identify the sources of variation in yield. Knowledge derived in this way can be used to develop selection criteria to improve grain yield in relation to agricultural practices (Board *et al*., 1997; Finne *et al*., 2000; Gravois and McNew, 1993; Samonte*et al*., 1998; Sinebo, 2002).

Considering the above facts, the present investigation was undertaken with following objectives:

i) to identify the relationship between grain yield and other morphological traits and

ii) to estimate the direct and indirect effects on yield

Materials and Methods

The experiment was conducted at the research field of Plant Breeding Division, Regional Agricultural Research Station, Barisal, Bangladesh Agricultural Research Institute (BARI), Bangladesh during rabi season of 2014-15. Twenty one locally developed hybrids along with three check varieties (BARI hybrid maize 7, BARI hybrid maize 9 and NK40) were evaluated in this study. The experiment was laid out in Randomized Complete Block Design having three replications. The twenty one hybrids were developed from seven parental lines using the diallel mating design excluding the reciprocals in rabi season in 2012-

2013. Seven inbred lines collected both from BARI and CIMMYT were used as source materials such as E1=BIL20, E2 =BML36, E3= BIL77, E4= BIL106, E5 = CLQRCY44, E6 = BIL79 and E7 = BIL 31. The parents were selected based on their combining ability performance such as general combining ability (GCA) and specific combining ability (SCA). The hybrids developed through diallel mating design were as follows E1×E2, E 1× E3, E1×E4, E1×E5, E1×E6, E1×E7, E2×E3, E2×E4, E2×E5, E2×E6, E2×E7, E3×E4, E3×E5, E3×E6, E3×E7, E4×E5, E4×E6, E4×E7, E5×E6, E5×E7 and E6×E7.

Seeds of each entry were sown in two rows, four meters long plots with 60×20 cm spacing between rows and hills, respectively. Seeds were sown on 20 November, 2014. One healthy seedling per hill was kept after thinning. Fertilizers were applied at the rate of 250, 55, 110, 40, 5 and 1.5 kg/ha of N, P_2O_5, K_2O, S, Zn and B respectively. Standard agronomic practices were followed (Quayyum, 1993) and plant protection measures were taken as required. Two border rows at both end of each replication were used for minimize the border effect. Data on days to 50% tasseling (DT), days to 50% silking (DS), and anthesis silking interval (ASI), plant height (PH), ear height (EH), days to maturity (DM), cob length (CL), cob diameter (CD), thousand seed weight (TSW) and yield (t/ha) were measured. All the plants in two rows were considered for plot yield and finally converted to t/ha.

Path co-efficient analysis estimated by Dewey and Lu (1959). All the data were processed and analyzed according to Sheoran *et*. *al*. (1998).

Results and Discussion

Mean sum of squares from pooled analysis recorded significant effects for yield. All the characters identified significant treatment effects indicating sufficient variability among them(Table 1).

Table 1. Pooled analysis of variance using ten characters in maize

S.V	d.f	DT	DS	ASI	PH (cm)	EH(cm)
Replication	2	48.667	27.167	2.181	405.941	152.012
Treatment	23	8.783**	6.429ns	1.418**	947.609**	771.800**
Error	46	3.623	3.775	0.441	100.377	85.992

* indicates significant at 5% level and ** indicates significant at 1% level
Days to 50% tasseling (DT), days to 50% silking (DS), Anthesis silking interval (ASI), plant height (PH), ear height (EH), days to maturity (DM), cob length (CL), cob diameter (CD), thousand seed weight (TSW) and yld (yield t/ha)

Table 1. Contd.

S.V	d.f	DM	CL(cm)	CD (cm)	TSW(gm)	Yld (t/ha)
Replication	2	5.014	4.188	0.034	381.056	4.284
Treatment	23	2.229**	6.013**	0.245**	5,125.318**	7.143**
Error	46	0.463	1.333	0.057	947.157	1.543

The highest σ^2g (1392.72) and σ^2p (2339.88) variance were found for TSW (Table2) which was in agreement with Matin *et. al.* (2017). The lowest magnitude ofσ^2g (0.06), σ^2p (0.12) variance were observed inCD. High genotypic coefficient of variation (GCV) were obtained from ASI (17.26), Yld(15.17), EH(13.80) and TSW (9.43). Al-Amin *et. al.*(2019) observed high GCV in PH, CD and Yld/plant. The characters with high GCV indicated high potential for selection. Alam *et. al.* (1988) selected some traits with high GCV in *B juncea*. The lowest GCV recorded in DM (0.52) that was identical with DS (1.03) and DT(1.49). The highest phenotypic coefficient of variation (PCV) were observed in ASI (26.49) followed by Yld (20.51), EH(16.19) and the lowest in DM(0.70). The difference between GCV and PCV of yield indicated that the characters might have been influenced by the environment. [The next sentence is unclear.] Most of the traits showed high heritability except DS and DT indicating lower influence of environment which also observed in the study of Begum *et. al.* (2016). The highest Hb was observed for PH (73.78) followed by EH (72.67), TSW (59.52) and DM (55.97) but the lowest Hb identified for DS (18.98). That the~~The~~ higher values of heritability of aforementioned traits could be considered for selection are consistent with~~that corroborates~~ the findings of Matin *et. al.* (2017). Ali *et. al.* (2012) and Moulin *et. al.* (2009). Hb was recorded higher in EH and Yld in the study of Al-Amin *et. al.* (2019). The highest GA was reported in TSW (59.31) followed by PH (29.74), EH (26.55).The highest GAPM observed in EH (24.23), Yld (23.13), ASI (23.16), TSW (14.99)and PH (14.28) but the lowest in DM (0.80) that was followed by DS (0.92). Al-Amin *et.al.* (2019) observed higher GAPM in CD, PH. According to~~,~~ Panse (1957), the characters having high Hb value coupling with high GA was due to additive gene effects that was observed in TSW, PH, EH. Matin *et. al.* (2017) stated similar findings in TSW, PH, EH and CD. High heritability coupled with low GA observed in PH, EH, CL and CD indicating the exploitation of these traits in hybrid maize development as stated and observed in the findings of Munawar*et.al.* (2013) in PH, EH, CL, CD and grain weight. Begum *et. al.* (2016) also showed that high heritability accompanied with low genetic advance revealed nonadditive gene action that was identified in CD, Yld, DM, CL, respectively.

Table 2. Estimates of genetic parameters for ten characters in maize

Characters	σ^2g	σ^2p	GCV (%)	PCV (%)	Hb (%)	GA	GAPM
DT	1.72	5.34	1.49	2.62	32.19	1.53	1.74
DS	0.88	4.66	1.03	2.36	18.98	0.84	0.92
ASI	0.33	0.77	17.26	26.49	42.44	0.77	23.16
PH	282.41	382.79	8.07	9.40	73.78	29.74	14.28

EH	228.60	314.59	13.80	16.19	72.67	26.55	24.23
DM	0.59	1.05	0.52	0.70	55.97	1.18	0.80
CL	1.56	2.89	6.59	8.97	53.92	1.89	9.96
CD	0.06	0.12	5.05	6.98	52.23	0.37	7.52
TSW	1392.72	2339.88	9.43	12.23	59.52	59.31	14.99
Yld	1.87	3.41	15.17	20.51	54.75	2.08	23.13

σ^2g, σ^2p -Genotypic variance and phenotypic variance, GCV, PCV-Genotypic and phenotypic coefficient of variation, Hb- Heritability, GA- Genetic advance, GAPM- Genetic advance as percentage of mean

Genotypic and phenotypic correlation coefficients with yield

The genotypic (upper diagonal) and phenotypic (lower diagonal) correlation coefficients were presented in Table 3. The yield had the highest positive significant genotypic (r_g) and phenotypic (r_p) correlation coefficient with CD ($r_{g=}0.75^{**}$, $r_p=0.61^{**}$), CL($r_{g=}0.66^{**}$, $r_p=0.42^{**}$), PH ($r_g=0.62^{**}$and $r_p=0.55^{**}$) and EH ($r_g=0.66^{**}$and $r_p=0.55^{**}$). Positive correlation coefficient with yield was recorded with CD and EH in an study of Matin *et. al*. (2017), Nataraj *et. al*. (2014), Ojo *et. al*., (2006) and Batool *et. al*. (2012). Positive correlation with yield also estimated in the studies of Al-Amin *et. al*. (2019), Bello*et. al*. (2010) and Sadek *et. al*. (2006). PH and EH had positive correlation with yield in the study of Bankole *et. al*. (2019). Barosa *et. al*. (2019) mentioned positive correlation on yield by TSW. TSW had moderate significant and positive correlation with yield ($r_{g=}0.36^{**}$, $r_p=0.44^{**}$), at both genotypic and phenotypic levels. The study revealed that that genotypic correlation was higher than phenotypic correlationrepresenting the association was due to genetic reason (strong coupling phase) (Sharma,1988).

Negative significant correlation was found in DT ($r_{g=}$ $-0.21^{NS}$and $r_p= -0.35^{NS}$), DS ($r_{g=}$ $-0.19^{NS}$and $r_p= -0.36^{**}$) with yield at both genotypic and phenotypic levels but ASI ($r_p= -0.01^{NS}$) only at phenotypic levels. Similar findings were also recorded in the observation of Sadek *et. al*. (2006).

Table 3. Genotypic (upper diagonal) and phenotypic (lower diagonal) correlation with yield

	DT	DS	ASI	PH	EH	DM	CL	CD	TSW	Yld.
DT		0.82^{**}	-0.79^{**}	-0.26^{*}	-0.19^{NS}	-0.22^{NS}	0.01^{NS}	-0.41^{**}	-0.77^{**}	-0.21^{NS}
DS	0.90^{**}		-0.25^{*}	-0.43^{**}	-0.29^{*}	-0.19^{NS}	0.21^{NS}	-0.16^{NS}	-0.74^{**}	-0.19^{NS}
ASI	-0.29^{*}	0.09^{NS}		-0.16^{NS}	-0.07^{NS}	0.19^{NS}	0.23^{NS}	0.49^{**}	0.49^{**}	0.09^{NS}
PH	-0.15^{NS}	-0.19^{NS}	-0.11^{NS}		0.96^{**}	0.08^{NS}	0.19^{NS}	0.54^{**}	0.17^{NS}	0.62^{**}
EH	-0.11^{NS}	-0.14^{NS}	-0.07^{NS}	0.94^{**}		0.20^{NS}	0.30^{*}	0.68^{**}	0.20^{NS}	0.66^{**}
DM	-0.12^{NS}	-0.09^{NS}	0.02^{NS}	0.06^{NS}	0.12^{NS}		0.44^{**}	0.41^{**}	0.11^{NS}	0.31^{**}
CL	0.08^{NS}	0.14^{NS}	0.17^{NS}	0.07^{NS}	0.15^{NS}	0.23^{NS}		0.59^{**}	0.31^{**}	0.66^{**}
CD	-0.31^{**}	-0.18^{NS}	0.29^{*}	0.38^{**}	0.42^{**}	0.22^{NS}	0.46^{**}		0.53^{**}	0.75^{**}
TSW	-0.60^{**}	-0.51^{**}	0.27^{*}	0.11^{NS}	0.13^{NS}	0.19^{NS}	0.23^{NS}	0.54^{**}		0.36^{**}

Yld.	-0.35^{**}	-0.36^{**}	-0.01^{NS}	0.55^{**}	0.55^{**}	0.16^{NS}	0.42^{**}	0.61^{**}	0.44^{**}	

* indicates significant at 5% level and ** indicates significant at 1% level

Days to 50% tasseling (DT), days to 50% silking (DS), Anthesis silking interval (ASI), plant height(PH),ear height (EH), days to maturity (DM), cob length (CL), cob diameter (CD), thousand seed weight (TSW) and yld (yield t/ha)

Table 4. Direct (bold) and indirect effect of different traits at genotypic level on yield

Characters	DT	DS	ASI	PH	EH	DM	CL	CD	TSW	r_g with Yld.
DT	**-0.52**	0.61	0.40	-0.34	0.19	-0.05	0.00	-0.19	-0.31	-0.21^{NS}
DS	-0.43	**0.75**	0.13	-0.57	0.30	-0.04	0.04	-0.07	-0.30	-0.19^{NS}
ASI	0.41	-0.19	**-0.50**	-0.21	0.07	0.04	0.05	0.22	0.20	0.09^{NS}
PH	0.13	-0.32	0.08	**1.34**	-0.98	0.02	0.04	0.25	0.07	0.62^{**}
EH	0.10	-0.22	0.03	1.28	**-1.03**	0.04	0.06	0.31	0.08	0.66^{**}
DM	0.12	-0.14	-0.10	0.11	-0.21	**0.21**	0.09	0.19	0.04	0.31^{**}
CL	0.04	0.15	-0.12	0.25	-0.31	0.09	**0.20**	0.27	0.12	0.66^{**}
CD	0.21	-0.12	-0.24	0.73	-0.70	0.08	0.12	**0.46**	0.21	0.75^{**}
TSW	0.40	-0.55	-0.25	0.23	-0.21	0.02	0.06	0.24	**0.41**	0.36^{**}

Days to 50% tasseling (DT), days to 50% silking (DS), Anthesis silking interval (ASI), plant height(PH),ear height (EH), days to maturity (DM), cob length (CL), cob diameter (CD), thousand seed weight (TSW) and yld(yield t/ha)

Residual effect (R^2) = 0.241

Path coefficient analysis

Correlation coefficient analyses are useful tools for selecting the traits that influence grain yield simultaneously (Menkir, 2008). Normally it exploits the degree of association among continuous traits (Malik *et al*., 2005). Despite the usefulness of these estimates in the understanding of complex traits such as grain yield, direct and indirect effects of these traits on productivity are not well defined (Baretta *et.al*., 2016). In this regard, Wright (1921) proposed a method to partition the correlation coefficients into components of direct and indirect effects known as path coefficient analysis. The analysis not only partitions the correlation coefficient into direct and indirect effects, but also provides the information on the actual contribution of a trait on the yield (Dewey and Lu, 1959).

Being a dependent variable and complex, trait yield is often affected by several factors. So, if selection is made considering the correlations only, avoiding the cause and effect relationship, it may mislead the interpretation (Uddin *et. al*., 2015).

Association of characters assessed by correlation co-efficient may not always express the exact view of the relative importance of direct and indirect influence of each of the independent variable on dependent variable. [Poor paragraphing. Sentences should not be paragraphs.]

So, to represent the inter-relationship between yield and its components, direct and indirect effects were worked out using path analysis both at genotypic and phenotypic level that also measured the relative importance of each components. Yield being considered as a resultant variable other characters estimated as causal or independent variable (Shahidul *et. al*., 2015). [Close up space]

Here, the genotypic correlation coefficients were partitioned into direct and indirect effects through path coefficient analysis in Table 4.

Among environmental variables, t~~T~~he PH had the highest positive direct effect (1.34) on yield followed by DS (0.75), CD (0.46) and TSW (0.41), DM (0.21) and CL (0.20) which was corroborated with Matin *et. al*., (2017), Kumar *et al*., (2015) and Pavan *et.al*. (2011). Direct positive effect on yield by PH, CL, CD and 100 seed weight was notice by Jakhar *et. al*. (2017).Al-Amin *et. al*. (2019) identified direct positive effect on yield/plant by CD and thousand kernel weight (TKW). Munawar*et.al*. (2013) cited that CL and CD showed positive effect on yield. Direct positive effect on yield by PH also cited in the investigation of Barosa *et. al*. (2019) and Adesoji *et. al*. (2015).

Direct negative effect on yield was shown by EH (-1.03), DT (-0.52) and ASI (-0.50) which were in agreement with Begum *et. al*. (2016).EH showed negative direct effect on yield mentioned by Jakhar *et. al*. (2017). Direct negative effect indicating the effectiveness of indirect selection. Among them EH (0.66^{**}) and ASI (0.09^{NS}) showed positive correlation with yield while DT (-0.21^{NS}) exhibited negative correlation.

The residual effect was 0.241indicating there were also some other characters which although not studied but might have influenced the seed yield.

Conclusion

High genotypic coefficient of variation (GCV) were obtained from anthesis silking interval, yield, ear height and thousand seed weight. The highest phenotypic coefficient of variation (PCV) were observed in anthesis silking interval followed by yield, ear height and the lowest in days to maturity. The highest heritability was observed for plant height followed by ear height, thousand seed weight and days to maturity but the lowest heritability identified for days to silking. The characters with higher values high GCV and higher of heritability of aforementioned traits were could be considered for selection. Positive and significant genotypic, phenotypic correlation coefficient were recorded for yield with cob diameter, cob length, plant height, ear height and thousand seed weight. The plant height had the highest positive direct effect on yield followed by days to sulking, cob diameter and thousand seed weight, days to maturity and cob length indicating the effectiveness of direct selection. Direct negative effect on yield was shown by ear height,days to tasseling and anthesis silking interval that indicated the effectiveness of indirect selection. [Conclusion would be clearer if the nature of the associations were specified. So, if pH was imporant in yield, say how: was higher or lower pH better? Maize in general is a plant tolerant of lower pH and more aluminum than other cultigens. And say if shorter plants were more productive or taller ones when you say plant height was correlated with yield.]

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