



Heritability and correlation analysis of morphological and yield traits in Maize

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Abstract

Introduction: Breeders are interested in screening and development of the open-pollinated population in maize, especially high adaptability to the environment and high grain yield.

Method: Sixty maize (*Zea mays* L.) germplasm along with three check cultivars were evaluated in Augmented Design with three blocks. Analysis of variance manifested significant differences among genotypes for the majority of the traits.

Results: Regarding genetic potential of various genotypes; mean days to 90% maturity ranged from 77.00 to 103.00, days to 50% silking (47.00 to 68.00), days to 50% tasseling (45.00 to 65.00), plant height (37.18 to 212.40 cm), number of ears plant⁻¹ (1.00 to 4.00), tassel length (25.00 to 49.25 cm), number of grains cob⁻¹ (25.00 to 490.00) and number of rows cob⁻¹ (15.50 to 8.00). The GCV and PCV were absolutely low for a number of ears plant⁻¹ whereas it was high for a number of grains cob⁻¹, respectively. Majority of the traits under study had maximum values of broad-sense heritability estimates ranged from 0.88 to 1.00. On the other hand, days to 90% maturity and a number of rows cob⁻¹ exhibited respectively 0.37 and 0.58 values of heritabilities. A maximum number of grains cob⁻¹ were recorded for ACC-15276 (490.00) followed by ACC-14980 (400.60) with the potential to be used in future breeding programs for the development of new cultivars for a specific region of Pakistan.

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Introduction

Maize (*Zea mays* L.) belongs to the grass family Poaceae, is monoecious and protandrous, cross-pollinated crop with chromosome numbers of $2n=2X=20$. Synthetic variety is a variety which is developed by inter-mating in all possible combinations a number of inbred lines with good general combining ability and mixing their seeds (seeds of F₁s) in equal whereas composite variety is a variety which is developed by mixing the seed of

various genotypes (in equal quantity) which are similar in maturity, height, seed size, color etc. Synthetic varieties of maize (*Zea mays* L.) are used either as germplasm sources in breeding programs or, in developing countries, as better populations [1]. Maize or corn can be used as food for human and feed for cattle and poultry [2]. reported the various sub-species of maize on the basis of consumption as food including flour corn, popcorn,



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dent corn, flint corn and sweet corn. It has higher nutritional value for starch, valuable proteins and oils. Certain varieties of maize may contain a number of important vitamins (B, C), folic acid, and pro-vitamin A. Based on metric tons, maize is the #1 production grain crop in the world (<http://faostat.fao.org/>). This success is largely due to high productivity and commercial versatility [3]. The United States is the leading producer (42% of the world production) of maize (353,699 441 tons). The most widely-used maize lines are of exotic sources with growing regions of temperate such as Argentine, European, and South African germplasm [4]. Maize can be cultivated on rain-fed and irrigated areas. Due to its short-day photoperiod, it can be grown in tropical and sub-tropical regions of the world has a high temperature of thirty degree Celsius and plenty of sunshine from eight am in the morning to four pm in the afternoon. The study reveals that the pollen grain of the maize crop can remain viable for longer durations under favorable conditions [5]. For normal germination, sandy to clay soil with 6.5 to 7.5 pH is more suitable. Hot dry weather tends to speed the pollen shedding [6]. In Pakistan, the area under maize occupies the third position after wheat and rice of which 98% is grown in Punjab and Khyber Pakhtunkhwa. During the year 2013-14, maize was cultivated on 1,117 hectares and the production was 4,053 kg ha⁻¹. Punjab contributes 39% of the total cultivated area under maize crop and 30% of the total production. Similarly, Khyber Pakhtunkhwa contributes 56% of the total area with 63% of the production, however; only 5% of the total area with 3% of the total production has been reported as share of Sindh and Baluchista [7]. In order to increase the production of maize, it is essential to develop high yielding varieties and hybrids. Yield is the primary objective in breeding maize hybrids. During the last decade, crop yield in Pakistan has been declining despite increased inputs of fertilizers and pesticides, this is due to the sowing of synthetic or composite varieties, which have less potential as compared to hybrids [8]. Hybrids generally have higher yield potential than open-pollinated varieties. Hybrids maize has long ears; more grain rows ear⁻¹ and enhanced grain yield than the open-pollinated cultivars [9].

Almost 65% maize in Pakistan is cultivated on irrigated land, while the remaining is under rainfed conditions. The main problem with maize is its high sensitivity to drought; to avoid it somehow, it requires frequent irrigations for successful vegetative and reproductive growth [10]. Drought affects many physiological processes and hence causes a significant decrease in yield. The yield of maize is also greatly affected by different diseases and insects that mostly appear during later stages of the crop. The climate change is another recently emerging constraint to increased crop production. To deal with this issue the farmers have to alter the existing cropping pattern and farming practices [11]. This change in the climate is also becoming a major threat to the production of maize. Early maturing varieties and hybrids are needed in order to cope with these newly emerging constraints. The production of early maturing varieties and hybrids may avoid yield losses by escaping the terminal droughts, as well as disease and insect attacks to large extent. Cultivation of early maturing hybrids and varieties also promote the production of two or more crops per year and adjust easily in the existing cropping pattern [12].

In Pakistan, maize is the staple food for a large population, especially in hilly areas. This crop is capable of producing the huge quantity of grains per unit area [13] and can be grown twice in a year (spring and summer seasons).

According to Hallauer and Miranda Filho (1988) [14], the correlation estimated by the specific coefficient is important in plant breeding because it quantifies the degree of genetic and non-genetic association between two or more traits, allowing the indirect selection. Knowledge of heritability influences the choice of selection procedures used by the plant breeder to decide which selection method would be most useful to improve the character, to predict gain from selection and to determine the relative importance of genetic effects [15-17]. This experiment was conducted to study the association between yield and related traits alongwith heritability estimates for studied traits.

Material and methods

The experimental material comprised 60 maize genotypes and three check cultivars. The genotypes were obtained from the Gene-Bank of Plant Genetics Resource Institute (PGRl), National Agricultural Research Center (NARC)-Islamabad. The experiment was laid out in Augmented Design with three blocks. Each block consisted of twenty plots and each plot having ten plants of a single genotype. Each plot consisted of a single row of 2-meter length and 75 cm of row-row distance. Data were collected on days to 50% silking, days to 50% tasseling, days to 90% maturity, plant height, number of ears plant⁻¹, tassel length, number of grains cob⁻¹ and number of rows cob⁻¹. Data were subjected to analysis of variance (ANOVA) by using software 'SAS' analytics (Essential Statistics Using SAS University Edition). The means for each parameter were further separated by least significant difference (LSD) test at 5% level of probability. Genotypic and phenotypic variances, genotypic (GCV) and Phenotypic Coefficients of Variance (PCV), heritability (Broad-Sense) and genetic advance were computed according to Burton and Devane (1953), Johnson et al. (1955) and Singh and Chaudhary (1985) [18-20].

Data were recorded on days to mid-tasseling, silking, maturity, plant and ear height, a number of ear per plant, tassel length, grains per ear and rows per cob.

The genotypic, phenotypic and environmental variances and heritability were then calculated by using the following formulas.

$$\text{Environmental variance (Ve)} = \text{Error mean squares (EMS)}$$

$$(\text{Phenotypic Variance}) V_p = V_g (\text{Genotypic Variance}) + V_e (\text{Environmental Variance})$$

Heritability broad sense (H^2) on entry mean basis was calculated as:

$$\text{Heritability (BS)} = V_g / V_p$$

The expected response to selection (R_e) for each trait was calculated as under:

$$R_e = k\sqrt{V_p} H^2$$

Where:

$k = 1.40$ at 20% selection intensity for a trait.

V_p = Phenotypic variance for a trait.

H^2 = Broad sense Heritability for a trait.

Genotypic Coefficient of Variation

$$(\text{GCV}) = \sqrt{V_g} / \text{GM} \times 100$$

Phenotypic Coefficient of Variation

$$(PCV) = \sqrt{VP} / GM \times 100$$

Where:

V_g = Genotypic variance

V_p = phenotypic variance

GM= Grand mean of the trait

Correlations

The simple correlation of yield with other yield components was worked out according to the procedure outlined.

phenotypic correlation coefficients (r_p)

$$= \text{Covp}(X_1, X_2) / \sqrt{VP(X_1) \times VP(X_2)}$$

Where,

$\text{CovP}(X_1, X_2)$ = Phenotypic covariance for X_1, X_2

$V_p(X_1)$ & $V_p(X_2)$ = Phenotypic variances for traits X_1 and X_2

Results and Discussion

Days to 50% silking

For days to 50% silking, highly significant variation ($P \leq 0.01$) revealed by ANOVA within the blocks, treatments, checks, accessions and check vs test genotypes and block (for values see supp data). Days to 50% silking revealed highly significant positive correlation with days to maturity ($r=0.494$), days to tasseling ($r=0.914$), plant height ($r=0.389$), tassel length ($r=0.607$), and grains cob^{-1} ($r=0.495$) (Table 1). Broad-sense heritability for days to silking calculated was 0.98% (Table 2). Days to 50% silking ranged from 47.00 (Acc-14906) to 68.00 (Acc-15147) days (Table 3).

Days to 50% silking is an important trait, usually, determine earliness to maturity of the maize crop. Genetic diversity in the studied material for days to silking revealed highly significant differences among the genotypes; these results are in close agreement with the trait under discussion by [21]. Such diversity can be bitterly exploited for the improvement of maize germplasm for maturity characters. Heritability was found to be highest for days to 50% silking [22]. High values of GCV and PCV were observed for 50% days to silking, however, very low values of GCV and PCV have also been reported [23]. Days to 50% silking had a highly significant positive correlation with plant height [24].

Days to 50% tasseling

For days to tasseling, highly significant variation ($P \leq 0.01$) revealed by ANOVA within the blocks, treatments, accessions and check vs test genotypes and blocks (for values see supp data). Days to 50% tasseling revealed highly significant positive correlation with days to maturity ($r=0.502$), days to 50% silking ($r=0.914$), tassel length ($r=0.439$) and grains cob^{-1} ($r=0.421$) (Table 1). Broad-sense heritability for days to tasseling calculated was 0.91% (Table 2). Days to 50% tasseling ranged from 44.00 (Acc-14906) to 63.00 (Acc-15147) days (Table 3).

Tasseling beside with other maturity attributes is usually utilized by plant breeder as the basis of deciding maturity of maize. Nkomo *et al.* (2013) [25] stated that tasseling is one of the most important stages in maize production. Analysis of variance for days to tasseling revealed highly significant differences

among the genotypes [21]. We experienced a high heritability for days to 50% tasseling while; low heritability was originated as well [26]. High GCV and PCV for days to 50% tasseling were observed; obtained low value.

Days to 90% maturity

For days to 90% maturity, non-significant variation ($P \geq 0.05$) was observed for blocks, treatment, and accessions (for values see supp data). However, check the source of variation was highly significant ($P \leq 0.01$) while check vs test genotypes showed significant ($P \leq 0.05$) differences. Days to maturity revealed highly significant ($p \leq 0.01$) positive correlation with days to 50% silking ($r=0.494^{**}$), days to 50% tasseling ($r=0.502^{**}$), and significant differences ($p \leq 0.05$) with tassel length ($r=0.316^*$) and grains cob^{-1} ($r=0.267^*$). Broad-sense heritability for days to maturity calculated was 0.37% (Table 2). Day to 90% maturity ranged from 77.00 (Acc-14906) to 103.00 (Acc-15147) (Table 3).

Analysis of variance for days to 90% maturity revealed significant differences among the genotypes; however, similar results were manifested for the said attribute and heritability was found to be moderate for days to maturity [24,27]. Moderate values of broad-sense heritability have also been detected in maize accessions. The highly significant positive correlation was observed for days to 90% maturity with days to 50% tasseling and days to 50% silking [28]. Low heritability for this particular trait is an evidence of the influence of environment on this particular trait.

Plant height (cm)

For plant height, highly significant variation ($P \leq 0.01$) was observed for all sources of variation i.e. blocks, treatment, checks, accessions and check vs test genotypes (for values see supp data). Plant height revealed highly significant positive correlation with days to silking ($r=0.389$), tassel length ($r=0.621$), and showed significant correlation with ears plant^{-1} ($r=0.256$), grains cob^{-1} ($r=0.267$). Broad-sense heritability for plant height calculated was 0.97% (Table 2). Plant height ranged from 37.18 cm (Acc-14883) to 212.40 cm (Acc-15187) (Table 3).

Plant height plays an imperative role in plant lodging. Consequently, maize breeders give special attention to this trait in maize breeding. Analysis of variance pertaining to plant height revealed highly significant differences among different genotypes of maize crop [29,30]. High heritability estimates were observed for plant height coupled with a high range of GCV and PCV suggested that genetic improvement might be achieved through the simple selection process for the said trait [31-33]. A significant correlation was revealed between plant height and grains cob^{-1} [34].

Number of ears plant^{-1}

For ears plant^{-1} , highly significant variation ($P \leq 0.01$) was recorded for blocks, treatment, accessions and check vs test genotypes (for values see supp data), however, the variation was significant ($P \leq 0.05$) for checks only. Ears plant^{-1} revealed significant positive correlation with plant height ($r=0.256$). Broad-sense heritability for a number of ears plant^{-1} calculated was 0.99% (Table 2). Ears plant^{-1} ranged from 1.00 (Acc-14906) to 4.00 (Acc-15147) (Table 3).

Analysis of variance for ears plant^{-1} manifested significant differences for all the genotypes with low heritability [26]. High broad-sense heritability was also estimated for a number of ears plant^{-1} by Jigjiga and Gebrewahd (2014) [35]. The non-sig-

nificant negative correlation was observed between ears plant⁻¹ and grains cob⁻¹ while the significant positive association was demonstrated for the said attributes [36].

Tassel length (cm)

For tassel length, highly significant variations ($P \leq 0.01$) were observed for blocks, treatment, accession, checks and check vs test genotypes explained by ANOVA (for values see supp data). Tassel length revealed highly significant positive correlation with days to 50% silking ($r = 0.607$), days to 50% tasseling ($r = 0.439$), plant height ($r = 0.621$), number of grains cob⁻¹ ($r = 0.497$) showed significant correlation with days to 50% maturity ($r = 0.316$) (Table 1). While broad-sense heritability for tassel length calculated was 0.88% (Table 2). Tassel length ranged from 25.00 cm (Acc-14911) to 49.25 cm (Acc-15076) (Table 3).

Heritability was found to be high for tassel length with significant variation among the accessions [37,38]. Moderate heritability results are also displayed for the said characteristic by [39,40]. High GCV and PCV was observed for tassel length [41]. The highly significant positive correlation was found between tassel length and plant height; [42] described the non-significant positive correlation for the trait under debate.

Number of grains cob⁻¹

ANOVA for grains cob⁻¹ exhibited highly significant variation ($P \leq 0.01$) was observed for blocks, treatment, accession, checks and check vs test genotypes (for values see supp data). Grains cob⁻¹ revealed highly significant positive correlation with days to 50% silking ($r = 0.495$), days to 50% tasseling ($r = 0.421$), tassel length ($r = 0.497$), rows cob⁻¹ ($r = 0.355$) and significant correlation with days to 50% maturity ($r = 0.267$), plant height ($r = 0.267$), while broad sense heritability for number of grains cob⁻¹ calculated was 1.00% (Table 2). Grains cob⁻¹ ranged from 25.00 (Acc-15081) to 490.00 (Acc-15276) grains (Table 3).

The average mean squares for different characters revealed that the results were highly significant for all the characters and hence indicated the presence of significant genetic variability in the material providing sufficient scope for further selection [43]. Heritability in this study was high for a number of grains ear⁻¹ however; other researchers reported high to moderate heritability [43,44]. GCV and PCV for grains cob⁻¹ were almost similar in this particular study while Sharma *et al.* (2014) [43] reported high PCV as compared to GCV. Inamullah *et al.* (2011) [45] reported a maximum number of grains for Syngenta and lowest for Baber with negative correlation to ears plant⁻¹.

Number of rows cob⁻¹

ANOVA explained highly significant ($P \leq 0.01$) differences for rows cob⁻¹ for treatment and accessions and significant variation ($P \leq 0.05$) for checks whereas checks vs test genotypes and blocks showed non-significant results (for values see supp data). Number of rows cob⁻¹ revealed highly significant positive correlation with grains cob⁻¹ ($r = 0.355$) (Table 1), while broad-sense heritability for number of rows cob⁻¹ calculated was 0.58% (Table 2). A number of rows cob⁻¹ ranged from 15.50 for Acc-15047 to 8.00 for Acc-15059) (Table 3).

A number of rows ear⁻¹ is an important yield parameter, which can significantly contribute to the grain yield. Analysis of variance for a number of rows ear⁻¹ indicated that the differences among the genotypes were highly significant. Similar findings have been reported for this particular trait by Saleem *et al.* (2002) [21]. High to moderate heritability and GCV values

were observed for a number of rows cob⁻¹ [46]. The non-significant negative correlation was observed between a number of rows cob⁻¹ and plant height. The highly significant positive association has been explained for the said traits [47,48].

Conclusion

The research work comprising evaluation of 60 maize germplasm along with three check cultivars for agro-morphological characteristics and estimation of heritabilities was carried out during the year 2016 using Augmented design in three blocks at PGRI, NARC, Islamabad, Pakistan.

Most of the genotypes were identified as early maturing with a maximum number of ears plant⁻¹ and grains cob⁻¹. High broad-sense heritability estimates were recorded for days to 50% silking, days to 50% tasseling, plant height, ears plant⁻¹, tassel length and grains cob⁻¹ for the development and improvement of superior inbred lines. GCV for most of the traits was comparatively higher than that of PCV suggested that the variation is due to the genetic potential of the accessions and hence the existence of sufficient variability and potential for genetic improvement through selection will be possible. A number of grains cob⁻¹ were positively correlated with days to 50% silking, days to 50% tasseling, tassel length, rows cob⁻¹ at both genotypic and phenotypic level. However, grains cob⁻¹ had negative relationships with ears plant⁻¹ at a genotypic and phenotypic level reflecting the possibility of increasing productivity through selection for early maturity in areas with short rainfall period. The present investigation revealed that a wide range of genetic variability was exhibited by the tested genotypes for most of the traits under study.

1. Based on the present research, the following recommendations were drawn for use of these maize inbred lines in future breeding programs.
2. Almost all the traits were found high heritable by having high heritability range (0.88 to 1.00), which can guide the breeders for further improvement.
3. A number of grains cob⁻¹ manifested significant positive correlation with yield contributing traits i.e. days to 50% silking, days to 50% tasseling, tassel length, rows cob⁻¹, days to 90% maturity, plant height.
4. Almost all of the maize genotypes manifested highly significant differences in the majority of the traits and revealed greater genetic variability.

Maize genotypes Acc-15276, Acc-14980, Acc-15047, Acc-15179 and Acc-15029 were screened as best lines for their mean performance and maximum heritability and could be used in future breeding programs to enhance the grain yield in maize.

Tables

Table 1: The coefficient of phenotypic correlation among eight important traits of 60 maize genotypes along with three check cultivars evaluated during the year 2016 of Kharif crop season at PGRI, NARC-Islamabad, Pakistan.

Traits	Days to 90% maturity	Days to 50% silking	Days to 50% tasselling	Plant height	Tassel length	Number of ears plant ⁻¹	Number of grains cob ⁻¹
Days to 50% silking	0.494**						
Days to 50% tasseling	0.502**	0.914**					
Plant height	0.236NS	0.389**	0.231NS				
Tassel length	0.316*	0.607**	0.439**	0.621**			
Number of ears plant ⁻¹	0.095NS	-0.136	-0.167	0.256*	0.082NS		
Number of grains cob ⁻¹	0.267*	0.495**	0.421**	0.267*	0.497**	-0.031	
Number of rows cob ⁻¹	0.042NS	0.083NS	0.197NS	-0.13	0.050NS	0.103NS	0.355**

Significant = *, Highly Significant = **

Table 2: Genotypes means of important characteristics of 60 maize genotypes along with three check cultivars coupled with phenotypic, genotypic and environmental variances, the coefficient of variations, Broad-Sense Heritability and Standard error evaluated during the year 2016 of Kharif crop season at PGRI, NARC-Islamabad, Pakistan.

Traits	VE	GV	VP	GCV	PCV	H ²	SE
Days to 50% silking	0.44	33.28	33.87	84.77	78.53	0.98	0.66
Days to 50% tasseling	1.77	24.32	26.68	96.41	82.70	0.91	1.33
Days to 90% maturity	75.44	58.91	159.50	81.00	133.27	0.37	8.68
Plant height	24.70	1174.94	1207.88	296.29	293.60	0.97	0.03
Number of ears plant ⁻¹	0.00	0.28	0.28	40.94	40.83	0.99	4.97
Tassel length	3.31	32.68	37.10	100.42	94.27	0.88	1.81
Number of grains cob ⁻¹	30.03	11729.31	11769.36	733.12	724.3	1.00	5.48
Number of rows cob ⁻¹	1.1361	2.06	3.57	42.02	55.32	0.58	1.06

Ve: Error Mean Square; GV: Genotypic Variance; Vp: Phenotypic Variance; GCV: Genotypic Coefficient of Variance; PCV: Phenotypic Coefficient of Variance; H²: Broad Sense Heritability, SE: Standard Error.**Table 3:** Mean values of days to silking, days to tasseling, days to maturity, plant height (cm), number of ears plant⁻¹, tassel length (cm), number of grains cob⁻¹ and number of grain rows cob⁻¹

Accessions	DS	DT	DM	PH	NEPP	TL	NGPC	NGRC
Acc-14883	51	49	89	37.2	1.5	34	139.7	12.3
Acc-14886	47	44	89	114	1.7	31.6	189.3	12
Acc-14889	52	49	89	90	1.5	27.9	141.3	11.3
Acc-14899	47	44	89	90	2	25	115	10
Acc-14900	52	48	89	113	2	33	110	13
Acc-14903	48	45	77	94.3	1.8	27.8	171.3	12.7
Acc-14904	47	44	77	99.2	2.2	25.3	148.3	11.3
Acc-14906	47	45	77	88.7	1.3	28.2	121	11
Acc-14907	47	45	77	63.5	1.5	26.3	70	13
Acc-14909	47	44	77	113.3	1.6	30.5	110	10
Acc-14911	49	46	77	84	1.8	25	97.7	9
Acc-14914	55	51	89	90.3	1.3	33.7	297.3	12.7
Acc-14926	52	48	89	160	2	30	66	10.7

Acc-14966	62	56	89	188	1	42	290	10
Acc-14975	55	48	97	157.4	1.4	39.5	267.3	10.7
Acc-14979	52	47	97	184	4	41	276	12
Acc-14980	56	52	97	165	3.5	43.3	400.7	13
Acc-14982	61	55	97	135.3	1.3	37	218	11.3
Acc-15000	57	53	97	161	1.7	38.2	250	11.3
Acc-15002	66	61	103	161	1	46.5	223	10.3
Acc-15013	62	58	103	140.8	1	35.5	109.5	10.5
Acc-15026	53	47	77	155	1.6	37.6	146.3	11.7
Acc-15029	47	43	89	134.5	1.6	35.9	354.7	14.7
Acc-15040	62	56	89	184.3	2	43.3	293	11
Acc-15043	47	43	89	128.6	1.6	36.8	158.3	11.7
Acc-15047	62	56	89	120	2	41.3	396.5	15.5
Acc-15059	49	45	103	120	2	29.5	61.3	8
Acc-15068	62	57	103	140	1	28	247	13
Acc-15071	62	56	103	163.3	1.3	40	342	11.5
Acc-15074	47	43	97	142.2	2	34.3	80	12
Acc-15076	62	55	77	168	2	49.3	157.3	10.3
Acc-15081	48	44	89	112	2.7	38	25	14
Acc-15094	54	48	89	182.3	1.7	40.5	193.7	11.7
Acc-15096	53	48	97	150.2	1.6	39.4	175.3	10.7
Acc-15097	51	48	89	135.8	1.4	41.6	253	10.7
Acc-15099	52	48	89	147.2	1.8	33	243	11.7
Acc-15103	52	48	89	142	2	33.3	145	10
Acc-15106	56	53	97	153	2	35	48	12
Acc-15107	47	43	89	140	1.8	36.3	127.7	12.3
Acc-15108	57	48	89	153	2	41.5	184	8
Acc-15117	49	45	77	147.4	1	36.2	210.3	11.7
Acc-15118	49	46	89	111.5	1	40.3	175	10
Acc-15142	58	54	103	135.8	1.6	39.8	345.7	11.3
Acc-15147	68	63	103	134	2	40	174	13.5
Acc-15155	62	56	89	156	1	35	253	11
Acc-15161	51	49	77	130	1.3	35.3	174	12.3
Acc-15162	48	45	89	130.2	1.6	33.3	251	11.7
Acc-15179	66	62	97	158.5	1	38.8	358.5	13.5
Acc-15182	62	55	97	181.5	2.3	45.8	251.7	13.7
Acc-15187	62	55	97	212.4	2	41.1	219.3	10.3
Acc-15191	54	51	89	170.8	2	33.4	202.7	13
Acc-15227	53	50	89	127	2	29	140	14
Acc-15231	52	49	103	164.7	2	34	204	12
Acc-15236	55	51	89	152.3	2	34.3	50	10

Acc-15276	62	57	97	137	1.6	40.5	490	14
Acc-15280	58	55	89	142	2	38.5	327	13.5
Acc-15291	51	48	89	124	2	34.3	300	10
Acc-15302	55	52	89	170	2	28	276	12
Acc-15328	56	48	89	156.4	2	41.8	186	9.7
Acc-15330	61	56	97	136	2	40.5	305	10
Haq Nawaz-1	58	52	96	150.5	1.5	44.6	429.5	12.5
Haq Nawaz-1	60	54	98	152.5	1.5	46.6	431	14.4
Haq Nawaz-1	57	51	97	153.1	1.4	44.8	433.1	14.2
ISL-W	56	55	68	138.5	1.5	39	295	12
ISL-W	58	53	70	136.6	1.4	40	297.3	10.8
ISL-W	57	52	69	137.2	1.3	41	298.1	11.4
Azam	58	52	96	150.5	1.5	44.6	325	12.5
Azam	60	53	96	150.5	1.5	42.3	322.2	12.5
Azam	59	53	70	136.6	1.4	40	310.1	10.8

DS: days to 50% silking; DT: Days to 50% Tasseling; DM: Days to 50% Maturity; PH: Plant Height (cm); NEPP: Number of Ears Plant⁻¹; TL: Tassel Length (cm); NGPC: Number of Grains Cob⁻¹; NGRC: Number of Rows Cob⁻¹

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