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Assessment of morphological and biochemical traits of early and late maturity maize (*Zea mays* L.)

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Abstract

The experiment under present investigation was conducted in a well prepared field during *Kharif* 2017 at Agriculture Farm, and Biochemical analysis was conducted in Biochemistry and Biotechnology Lab in the Department of Crop Sciences, Faculty of Agriculture, Nana Ji Deshmukh New Agriculture Campus, Mahatma Gandhi Chitrakoot Gramodaya Vishwavidyalaya, Chitrakoot, Satna (M.P.). High heritability coupled with high expected genetic advance in per cent of mean was observed for grain yield, plant height, days to 75% dry husk, ear height, shelling% and 100-seed weight.

Keywords: Maize, heritability and biotechnology

Introduction

Maize (*Zea mays* L.) is the most important versatile crop among cereals with respect to its adaptability, types and uses. It is cultivated in tropics, sub-tropics to temperate climate and has several types like- field corn, sweet corn, pop corn, baby corn. Within field corn, it has several types like quality protein maize (QPM), waxy maize, high-oil maize etc. Maize is used as the raw material for several food, feed and non-food based industries including as source of bio-fuel. The consumption pattern of maize (feed-64%, food-16%, industry-19%, seed and other miscellaneous 1%) in India largely matches with the global pattern (feed-61%. Food-17% and Industry-22%). It has attained a position of Industrial crop globally as 83% of its production in the world and 76% in India is used as feed, starch and bio-fuel industries and it provide wide opportunity for value addition more than 3000 products (AICRP on Maize Progress report, 2017-18) It is a source of basic raw material for a number of industrial products *viz.*, starch, oil, protein, alcoholic beverages, food sweeteners, cosmetics and bio-fuel etc. Maize being a C₄ plant is physiologically more efficient, has higher grain yield and wider adaptation over wide range of environmental conditions.

The all India maize productivity during 2016-17 was 25.90 Million MT t/ha. The average productivity during the period yield was 2689 kg/ha and area increased 9.6 million ha in 2017-18 based on advanced estimate. It is no longer capable of survival in the wild form and can be grown only under cultivation. Maize (*Zea mays*) is the only species in the genus *Zea*. Its diploid with chromosome number 2n=20. Maize (*Zea mays*) an agronomically versatile crop, is also known as corn in other countries.

The maize is cultivated throughout the year in all states of the country for various purposes including grain, fodder, green cobs, sweet corn, baby corn, pop corn in peri-urban areas. The predominant maize growing states that contributes more than 80% of the total maize production are Andhra Pradesh (20.9%), Karnataka (16.5%), Rajasthan (9.9%), Maharashtra (9.1%), Bihar (8.9%), Uttar Pradesh (6.1%), Madhya Pradesh (5.7%). Morphologically maize exhibits greater diversity of phenotypes than any other grain crop (Kuleshov, 1933) and is extensively grown in temperate, subtropical and tropical regions of the world. Yield of maize is considered as a complex inherited character and therefore, direct selection for yield *per se* may not be the most efficient method for its improvement, but indirect selection for other yield related characters with high heritability estimates will be more effective.

World-wide with its high content of carbohydrate, fats, proteins, some of the important vitamins and minerals, maize has acquired a well deserved reputation as a poor man's nutri cereal. It is estimated that several million people, particularly in the developing countries derive their protein and calorie (11.1 g and 342 Kcal/day) requirement from maize (Gopalan *et al.*, 1999) [3].

Maize is a good source of carbohydrates, fats, proteins and some of the important vitamins and minerals. Several million people, especially in the developing countries, derive their protein and calorie requirements from maize. However, in spite of several important uses, maize has an in-built drawback of being deficient in two essential amino acids, *viz.*, lysine and

tryptophan. This leads to poor net protein utilization and low biological value of traditional maize genotypes.

The selection criteria may be yield or one or more of the yield component characters. However, breeding for high yielding crops requires information on the nature and magnitude of variation in the available material, relationship of yield with other agronomic characters and the degree of environmental influence on the expression of these component characters. Since grain yield in maize is quantitative in nature and polygenically controlled, effective yield improvement and simultaneous improvement of yield components are imperative. To enhance the yield productivity, genetic parameters and correlation studies between yield and yield components are pre requisite to plan a meaningful breeding programmed.

Material and Methods

Heritability

Heritability in broad sense (h^2) was calculated using the formula suggested by Burton and de Vane (1953).

$$h^2 = \frac{\sigma^2_g}{\sigma^2_g + \sigma^2_e}$$

or

$$h^2 = \frac{\sigma^2_g}{\sigma^2_p} \times 100$$

Results and Discussion

Heritability (broad sense) and genetic advance along with biochemical characters studies

Heritability in broad sense was computed for all the characters and has been presented in Table 1. In general, high to low estimates of broad sense heritability were observed for all the characters. High estimates of broad sense heritability (h^2_b) ranged from (>75%), moderate (50-75%) estimation of broad sense heritability (h^2_b) and low (<50%) broad sense heritability (h^2_b).

The heritability values ranged from 14.80 per cent for cob count to 98.60 for days to 75% dry husk. The high heritability estimates were found for days to 75% dry husk (98.60), followed by soluble protein (98.21); days to 50% pollen shed (90.71%), days to 50% silking (89.91%) and 100-seed weight (75.98%) while moderate heritability estimates were found for ear height (70.79%), grain yield kg/ha (59.81%), moisture% (54.42%) and shelling% (53.58%) where as low heritability estimates were found for plant height (49.91%), oil% (49.15%), and cob count (14.80).

The expected genetic advance in per cent of mean ranged from 0.92 per cent for cob count to 44.82 per cent for soluble protein (Table 1). High estimates of expected genetic advance were found for soluble protein (44.82%), ear height (29.73%), days to 75% dry husk (23.87%), 100-seed weight (22.42%),

grain yield (20.94%) and oil% (20.62%) while moderate expected genetic advance were found for moisture% (17.24%) followed by days to 50% silking (14.36%), days to 50% pollen shed (14.24%), plant height (13.68%) and shelling% (9.38%) where as low estimates of expected genetic advance were found for cob count in this study.

High heritability coupled with high expected genetic advance in per cent of mean was observed for grain yield, plant height, days to 75% dry husk, ear height, shelling% and 100-seed weight.

Heritability estimate, that provides the assessment amount of transmissible genetic variability to total variability, happens to be most important basic factor that determines the genetic improvement or response to selection. However, the degree of improvement attained through selection is not only dependent on heritability but also on the amount of genetic variation present in the breeding material and extent of selection procedure applied by the breeder. The parameter, genetic advance in per cent of mean (GA) is a more reliable index for understanding the effectiveness of selection in improving the traits because its estimate is derived by involvement of heritability, phenotypic standard deviation and intensity of selection. Thus, heritability and genetic advance in per cent of mean, in combination, provide clear picture regarding the effectiveness of selection for improving the plant characters.

The heritability in broad sense values were ranged from 14.80 per cent for cob count to 98.60 for days to 75% dry husk. The high heritability estimates were found for days to 75% dry husk followed by soluble protein; days to 50% pollen shed, days to 50% silking and 100-seed weight while moderate heritability estimates were found for ear height, grain yield kg/ha, moisture% and shelling% where as low heritability estimates were found for plant height, oil% and cob count.

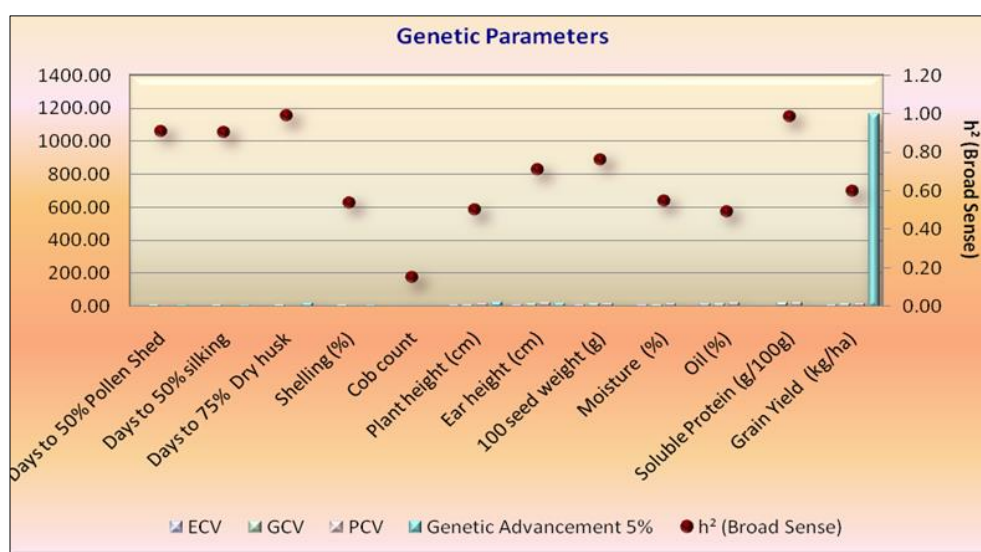
The expected genetic advance in per cent of mean ranged from 0.92 per cent for cob count to 44.82 per cent for soluble protein (Table 1). High estimates of expected genetic advance were found for soluble protein, ear height, days to 75% dry husk, 100-seed weight, grain yield and oil% while moderate expected genetic advance were found for moisture% followed by days to 50% silking, days to 50% pollen shed, plant height and shelling% where as low estimates of expected genetic advance were found for cob count in this study.

High heritability coupled with high expected genetic advance in per cent of mean was observed for grain yield, plant height, days to 75% dry husk, ear height, shelling% and 100-seed weight. These findings was found in accordance with the result of Singh (1990), Mahmood, *et al.* (2004)^[5] for grain yield, (Memon *et al.*, 2007; Mangi *et al.*, 2008)^[4], Ahmed *et al.*, (2007) for. high heritability value and low genetic advance, Reddy, *et al.* (2013) for ear height, grain yield per plant, plant height, number of kernels per row and ear length, Nzube, *et al.* (2014) for ear height and plant height, Reddy *et al.* (2016) and Beulah, *et al.* (2018)^[2] for anthesis- silking interval, grain yield per plant, plant height, cob height, days to maturity and grain row per cob.

Table 1: Heritability (%) in broad sense, genetic advance and genetic advance in percent of mean for 12 quantitative and biochemical characters in early and late maturity Maize.

S. No.	Characters/Traits	Heritability (broad sense)	Genetic advance	Genetic advance in percent of mean
1	Days to 50% Pollen Shed	90.71	8.01	14.24
2	Days to 50% silking	89.91	8.80	14.36
3	Days to 75% Dry husk	98.60	22.35	23.87
4	Shelling (%)	53.58	6.72	9.38
5	Cob count	14.80	1.08	0.92
6	Plant height (cm)	49.91	26.88	13.68
7	Ear height (cm)	70.79	20.63	29.73
8	100 seed weight (g)	75.98	5.70	22.42
9	Moisture (%)	54.42	1.06	17.24
10	Oil (%)	49.15	1.09	20.62
11	Soluble Protein (mg/g)	98.21	3.66	44.82
12	Grain Yield (kg/ha)	59.81	1161.19	20.94

* Significant at 5% probability level; ** Significant at 1% probability level;

**Fig 1:** Genetic Parameters

References

1. AICRP on Maize Progress Report All India Coordinated Research Project on Maize Director's Report, ICAR, IIMR, PAU Campus, Ludhiana, 2017-18, 1.
2. Beulah Grace, Marker Shailesh, Rajasekhar Duddukur. Assessment of quantitative genetic variability and character association in maize (*Zea mays* L.) Journal of Pharmacognosy and Phytochemistry. 2018; 7(1):2813-2816.
3. Gopalan C, Sastri RBV, Balasubramanian SC. Nutritive value of Indian foods. NIN, ICMR, Hyderabad, 1999.
4. Mangi SA, Sial MA, Ansari BA, Arain MA. Study of genetic parameters in segregating populations of spring wheat. Pakistan J Bot. 2008; 39(7):2407-2413.
5. Mahmood Zahid, Ajmal Saif Ullah, Jilani Ghulam, Irfan Muhammad, Ashraf Muhammad. Genetic Studies for High Yield of Maize in Chitral Valley. Int. J Agri. Biol. 2004; 6(5):788-789.
6. Mehmet A, Telat Y. Heritability of yield and some yield components in bread wheat (*Triticum aestivum* L.) genotypes. Bangladesh J Bot. 2006; 35(1):17-22.