



RESEARCH PAPER

Studies on genetic variability, heritability and genetic advance in sweet corn for green ear yield and yield related traits

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Abstract : A study was carried out in sweet corn to evaluate seven inbred lines, three checks and 42 experimental hybrids during *Kharif* 2019. This study revealed a significant difference among the genotypes for traits studied indicating the presence of abundant genetic variability. The phenotypic co-efficient of variation ranged from 4.57 (DFS) to 36.41 (GEWH) while the genotypic co-efficient of variation ranged from 3.72 (DFT) to 25.35 (GEWH). Green ear yield without husk (25.35, 36.41); green fodder weight (22.47, 29.20) and green ear yield (24.63, 33.31) recorded high PCV and GCV values. The traits plant height (0.73), ear girth (0.61) and TLB (0.69) displayed high heritability values and none of the traits showed low heritability. Genetic advance over mean ranged from 5.71 (DFT) to 37.53 (GEY). High genetic advance over mean was observed for the traits green ear weight without husk, and green fodder weight. Moderate heritability coupled with high genetic advance was observed for the traits green ear weight without husk, green fodder weight and green ear yield. Thus, traits like green ear yield, green ear weight without husk, green fodder weight, ear length and the number of kernels per row should be prioritized while selecting sweet corn genotypes for increased yield as they have a moderate to low range of genotypic co-efficient of variation, phenotypic co-efficient of variation, heritability, and genetic advance over mean.

Key Words : Genetic variability, Heritability, Genetic advance, Sweet corn, Green ear yield and yield

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INTRODUCTION

Maize is the most widely produced and consumed cereal crops in the world with a production of about 1.15 billion MT from an area of 197 million ha grown over 170 countries (Suresh *et al.*, 2021). It is a popular cereal grain that serves as a staple food crop for human consumption in many sub-tropical and tropical countries,

and used as a raw material for industrial products such as starch, corn syrup, protein, ethanol, and etc (Tippannavar *et al.*, 2019 and Reddy *et al.*, 2021). Among various maize types, sweet corn is popularly served as a vegetable in the USA and gaining popularity in Europe and Asia. This special corn is suitable for peri-urban agriculture with raising market value in India (Niji *et al.*, 2018). It is a natural mutant of field corn where

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one or more simply inherited mutant genes alter the carbohydrate composition in the endosperm (Tracy, 1994). Out of many mutants known for altering carbohydrate composition, fourteen mutants have been studied well in sweet corn and eight have been used to meet market demands. Mutant genes used for the quality improvement of sweet corn fall under two classes. Class 'I' mutants reduce carbohydrate concentration by increasing sugar content at the cost of starch accumulation. The mutants shrunken-1 (*sh1*), shrunken-2 (*sh2*), shrunken-4 (*sh4*), brittle-1 (*bt1*), brittle-2 (*bt2*) form class I mutants which accumulate 4 to 6 times more sugars than field corn. Class II mutants include amylose extender (*ae*), dull (*du*), sugary2 (*su2*) and waxy (*ex*) which alter the amount and type of starch accumulated. Commercially Class I mutants *viz.*, *sh2*, *bt1* and *bt2* are more popular than Class II mutants as they result in increased sugar content upto 35% (Boyer and Shanon, 1984). With an increase in the global market network of sweetcorn in recent times, overall export shoots upto 2% in volume *i.e.*, about 260 tonnes and 5% in value reaching more than 230 US\$ (Entringer *et al.*, 2017).

Plant disease outbreaks are increasing and threaten food security of the world. Global yield losses due to crop pests and diseases on food crops are large. Important diseases such as Turcicum leaf blight in maize (Vani Praveena *et al.*, 2021), downey mildew in sorghum, dry root rot in chickpea (Talekar *et al.*, 2017 and 2021), leaf spots in groundnut, wilt in pigeonpea and necrosis disease in sunflower (Sundaresha *et al.*, 2012), phyllody in chickpea (Balol *et al.*, 2021), bud blight caused by Groundnut bud necrosis virus (Balol and Patil, 2014) etc are contributing for the yield loss. Plant disease outbreaks are increasing and threaten food security of the world

The efficiency of plant breeding is affected by the amount of genetic variability available in the species and the degree of heritability for disease resistance and important yield contributing traits (Hussain *et al.*, 2011). Information on genotypic variance, phenotypic variance, genotypic co-efficient of variation (GCV) and phenotypic co-efficient of variation (PCV) gives a better understanding of the extent of variability and influence of environment on yield, since total variation or phenotypic variation includes both genotypic and environment components (Vikas *et al.*, 2015). Apart from knowledge of variability, heritability and genetic gain (genetic advance) are two other important selection

parameters. The amount of phenotypic variance explained by genotype is called heritability. Heritability is related to the population but not to an individual as such. It is a good indicator of trait inheritance from one generation to the next generation. Plant breeders use heritability estimates to select elite genotypes from a variety of genetic populations. The degree of gain observed in a trait under a given selection pressure is called a genetic advance.

Estimates of heritability and genetic advance together help to predict gain under selection rather than heritability alone. High heritability and genetic advance offer the best condition for selection as they indicate the presence of additive gene action for the trait and crop improvements by selecting for such traits are rewarding (Ogunniyan and Olakojo, 2015). Thus, knowledge of available genetic variability, heritability and genetic gain in selection will help the breeder arrive at yield improvement. Thus, the present study was conducted to determine genetic parameters that support sweet corn breeding programmes in developing hybrids and selecting superior inbreds for hybrid development.

MATERIAL AND METHODS

Seven diverse sweet corn inbred lines were crossed in diallel fashion (7×7) during *Rabi* 2018 as a result 42 hybrids were produced. All the 42 experimental hybrids along with 7 parents and three checks (Central Maize VL Sweet corn 1, Madhuri and Misti) were evaluated in Randomized Block Design in three replications during *Kharif* 2019 at Main Agriculture Research Station (MARS), University of Agricultural Sciences, Dharwad.

Biometrical data on days to 50% tasseling, days to 50% silking, plant height (cm), ear height (cm), ear length (cm), ear girth (cm), number of kernel rows per ear, number of kernels per row, ear weight without husk (t/ha), green fodder weight (t/ha), resistance to turcicum leaf blight (%), total soluble solids (%) and green ear yield (t/ha). Mean values from five representative plants for each trait from each genotype/replication were considered for statistical analysis. The intensity of turcicum leaf blight was recorded by scoring all randomly selected plants in each treatment at the silk drying stage as per the 1-9 scale. The total soluble solids (TSS) was measured from the seeds of the fresh ear immediately after harvest with the help of a hand refractometer and expressed in percentage.

Phenotypic and genotypic variances were calculated according to method suggested by Burton and Devane, 1953. Phenotypic and genotypic co-efficient of variation (Singh and Chaudhary, 1985); heritability (Johnson *et al.*, 1955); genetic advance (Burton, 1952); genetic advance as per cent of mean (Souza *et al.*, 2009) were calculated using formulas as given below :

$$\text{Phenotypic variance } (\sigma^2 p) = \sigma^2 g + \sigma^2 e$$

$$\text{Genotypic variance } (\sigma^2 g) = \text{MSg} - \text{MSe}/r$$

$$\text{GCV } (\%) = \{(\sqrt{\sigma^2 g}) / \bar{x}\} \times 100$$

$$\text{PCV } (\%) = \{(\sqrt{\sigma^2 p}) / \bar{x}\} \times 100$$

$$\text{Heritability } (h^2) = \sigma^2 g / \sigma^2 p$$

$$\text{Genetic advance (GA)} = K \cdot \sigma^2 p \cdot h^2$$

$$\text{Genetic advance percentage of mean} = (\text{GA} / \bar{x}) \times 100$$

Where, $\sigma^2 g$ = genotypic variance, $\sigma^2 p$ = phenotypic variance, \bar{x} = grand mean for the trait, MSg = genotype mean sum of square, MSe = error mean sum of square, r = No. of replications, GA = genetic advance, K = selection differential, δp = phenotypic standard deviation and h^2 = broad sense heritability.

The data was analysed in R software version 4.1.2 to draw valid conclusions.

RESULTS AND DISCUSSION

Significant variation among the genotypes for all the traits was observed and presented in Table 1. This indicates the availability of accountable variability in the generated experimental material which signifies the improvement of different quantitative and qualitative traits of sweet corn through selection (Kandel *et al.*, 2018).

Phenotypic and genotypic (PCV and GCV) co-efficient of variation as suggested by Sivasubramanian

and Menon (1973) were categorized as 0-10% (low), 10-20% (moderate) and > 20% (high). The estimates of different genetic parameters were presented in Table 2. In general, PCV is higher than GCV for all the traits under study which indicate these traits are least affected by the environment and direct phenotypic selection may be rewarding for these traits. Similar observations of high PCV than GCV was observed by Niji *et al.*, 2018, Abe and Adelegan, 2019 and Magar *et al.*, 2021. Phenotypic co-efficient of variation ranged from 4.57 (Days to 50% silking) to 36.41 (green ear weight without husk) while the genotypic co-efficient of variation ranged from 3.45 (Days to 50% silking) to 25.35 (green ear weight without husk).

Low PCV and GCV were observed for the traits days to 50% tasselling (3.72, 4.99); days to 50% silking (3.45, 4.57); ear height (5.56, 8.47); ear girth (7.30, 9.28); number of kernel rows (4.63, 8.44) and TSS (6.81, 9.48). Moderate values of co-efficient of variation were observed for ear length (10.65, 14.09) and number of kernels per row (12.68, 17.04). High PCV and GCV were observed for green ear yield without husk (25.35, 36.41); green fodder weight (22.47, 29.20) and green ear yield (24.63, 33.31). These results were supported by Bhusal *et al.*, 2017; Sharma *et al.*, 2018 and Magar *et al.*, 2021. Low GCV and moderate PCV were observed for plant height (9.72, 11.35) while moderate GCV and high PCV were observed for TLB (6.81, 22.57). Even with a high co-efficient of variation values for green ear yield without husk, green fodder weight and green ear yield the difference between GCV and

Table 1 : Estimates of mean sum of square, grand mean and range for green ear yield and its attributing traits in sweet corn

Characters	Mean sum Sq (Df=51)	Grand mean	Range
DFT	19.027**	60.52	54.67-63.67
DFS	17.31**	63.86	58.00-65.67
PH	494.46**	116.00	108.80-147.87
EH	9.32**	51.42	38.47-76.13
EL	10.06**	13.97	13.10-19.01
EG	0.36**	4.13	3.88-4.86
NKR	2.28**	13.64	12.00-16.64
NKPR	62.40**	28.04	27.00-41.22
GEWH	2.47**	5.18	4.06-9.34
GFW	3.65**	8.06	6.25-14.25
TLB	293.5**	54.01	35.26-64.76
TSS	2.38**	11.34	9.43-13.00
GEY	4.324**	7.26	6.25-12.48

PCV is significant for these traits indicating direct phenotypic selection for these traits may lead to the spurious selection. On contrary to this Nzube *et al.*, 2014 and Sesay *et al.*, 2016 reported a high difference between the co-efficient of variation values for plant height.

Heritability and genetic advance :

To realize genetic gain under selection estimates of the genetic component of variation and heritability will be more helpful. To derive a conclusion on the degree of heritable variation both heritability and genetic advance need to be worked out. Johnson *et al.*, 1955 categorized heritability as <30% (low), 30-60% (moderate) and >60% (high). GAM *i.e.*, genetic advance as per cent of mean was categorized (Johnson *et al.*, 1955) into 0-10% (low), 10-20% (moderate) and more than 20% (high).

In the present study moderate heritability was observed for days to 50% tasselling (0.55), days to 50% silking (0.57), ear length (0.57), ear height (0.43), number of kernel rows (0.30), number of kernels per row (0.55), green ear weight without husk (0.48), green fodder weight (0.59), TSS (0.51) and green ear yield (0.54). High heritability was observed for the traits plant height (0.73), ear girth (0.61) and TLB (0.69). Similar observations were reported by Ghimire and Timsina, 2019; Baratula *et al.*, 2019; Magar *et al.*, 2021. None of the traits showed low heritability. However, selection for these traits is not rewarding as broad sense heritability includes both additive and non-additive variance. So, to arrive at a reliable selection criteria estimates of genetic

advance along with heritability need to be understood.

Traits namely days to 50% tasselling (5.71), days to 50% silking (5.38), ear height (7.53) and number of kernel rows (5.24) showed low GA as per cent of the mean. Plant height (17.14), ear length (16.58), ear girth (11.83), number of kernels per row (19.43) and TSS (10.08) manifested moderate genetic advance as per cent of mean, while high genetic advance estimates were observed for green ear weight without husk (36.35), green fodder weight (35.61), TLB (32.48) and green ear yield (37.53).

Out of thirteen traits analyzed in current study, days to 50% tasselling, days to 50% silking, ear height and number of kernel rows manifested moderate heritability coupled with a low genetic advance over the mean which suggested that these traits were under non-additive gene action and response to selection will be poor where heterosis breeding or hybridization is rewarded. High heritability coupled with high GA over mean was observed for TLB which explains most of the heritability is due to additive gene action and selection might be effective. The traits green ear weight without husk, green fodder weight, and green ear yield recorded moderate heritability together with high genetic advance. This offers a situation where the role of additive gene action can be predicted with minute environmental influence as moderate heritability is observed which facilitates fixation of these traits and direct selection for yield improvement. Similar results were reported by Bartaula *et al.*, 2021; Begum *et al.*, 2016 and Niji *et al.*, 2018.

Thus, while selecting the genotypes of sweet corn

Table 2 : Estimates of genetic parameters for green ear yield and its attributing traits in sweet corn

Characters	GV	PV	EV	GCV	PCV	ECV	Heritability broad sense	GA	GA (%) of mean
DFT	5.00	9.00	4.00	3.72	4.99	3.32	0.55	3.43	5.71
DFS	4.61	8.07	3.46	3.45	4.57	2.99	0.57	3.34	5.38
PH	146.97	200.51	53.54	9.72	11.35	5.86	0.73	21.38	17.14
EH	2.15	5.00	2.84	5.56	8.47	6.39	0.43	1.98	7.53
EL	2.68	4.69	2.01	10.65	14.09	9.22	0.57	2.55	16.58
EG	0.10	0.16	0.06	7.30	9.28	5.72	0.61	0.51	11.83
NKR	0.42	1.42	0.99	4.63	8.44	7.06	0.30	0.74	5.24
NKPR	16.39	29.62	13.22	12.68	17.04	11.39	0.55	6.20	19.43
GEWH	0.61	1.25	0.64	25.35	36.41	26.14	0.48	1.12	36.35
GFW	0.99	1.67	0.68	22.47	29.20	18.65	0.59	1.57	35.61
TLB	85.53	122.48	36.95	18.86	22.57	12.40	0.69	15.92	32.48
TSS	0.60	1.17	0.56	6.81	9.48	6.59	0.51	1.15	10.08
GEY	1.12	2.06	0.93	24.63	33.31	22.43	0.54	1.61	37.53

for enhancing yield, importance should be given to traits like green ear yield, green ear weight without husk, green fodder weight, ear length and number of kernels per row as they manifested moderate to low range of genotypic co-efficient of variation, phenotypic co-efficient of variation, heritability and genetic advance over mean.

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