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Evaluation of sorghum populations for morphological traits related fodder yield and stem borer resistance

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Abstract
Evaluation of segregating populations for stem borer resistance is one of the best ways to select RILs that mitigate adverse effect of stem borer. The present study was initiated to evaluate sorghum segregating populations, estimate the genetic variability, and identify the best performing genotypes for yield and stem borer resistance. The study was conducted during 2017 at Forage Research area of Department of Genetics & Plant breeding CCS Haryana Agricultural University, Hisar. F_3 population was obtained from crossing two parents HJ513 (susceptible) and IS 2205(resistance) with contrasting morphological traits for stem borer resistance. A total of 202 RILs were evaluated using augmented design. RILs 3, 4, 13, 21, 26, 54, 55, 56, 60, 83, 85, 86, 89, 90, 91, 96, 99, 100, 104, 108, 109, 118, 119, 189, 129, 139, 151 were recorded as top performing among F_3 population for green fodder yield. The less no. of dead heart and stem-tunneling were registered in RIL s 47, 48, 49, 72, 74, 144, 154, 155, 160, 166, 169. High heritability coupled with genetic advance as percent of mean was noted for green fodder yield and plant height. Good pogress is expected from selection of morphological traits for borer resistance in sorghum population. These RILs appear well suited for further specific area for stem borer resistance breeding and research.

Keywords: Sorghum, stem borer, selection, heritability

Introduction
Sorghum [*Sorghum bicolor* (L.) Moench] is the 5th most important cereal in the world after wheat, maize, rice and barley. India contributes 9.45% of the world's sorghum production covering 5.82 million ha, producing 5.39 million tones with a productivity of 926 kg/ha (Gite *et al.*, 2015) [9]. In Haryana 72,000 ha areas is under sorghum cultivation with a production of 40,000 tonnes and productivity of 550 kg/ha of grain yield (Anon. 2016) [1]. Besides being a source of staple food for humans, it serves as an important source of cattle feed and fodder. It is a major *kharif* fodder crop of north India. The use of sorghum as fodder has increased in recent years due to its high water use efficiency and wide adaptation as compared to maize.

Sorghum production especially in tropical Africa is curtailed by a number of important anthropod pests, with the stem borers belonging to Lepidoptera playing the most significant role. Chilo partellus is highly invasive, and has partially displaced some indigenous stem borers in India attacking all cereals (Kfir *et al*., 2002) [11]. Damage symptoms of C. partellus in sorghum include leaf feeding, deadhearts, exit holes, stem tunneling and chaffy grain and stem tunneling (Jose *et al*., 2001; Kfir *et al*., 2002; Kishore *et al*., 2007; Sally *et al*., 2007) [10, 11, 12, 22]. Cultural pest management practices such as early planting, destruction of stover, biological control, developing insect-resistant cultivars, and the use of chemical insecticides are being used (Ofomata *et al*., 2000; Rwomushana, 2005; Sharma *et al*., 2006) [17, 21, 25]. Push and pull technology is a relatively new cultural technique of managing stem borers where by a repellent crop, in this case desmodium spp (Fabaceae) is planted around the cereal crop while Napier Grass (Pennisetum Purpureum) is utilized as a trap plant to the borers (Zeyaur *et al*., 2007) [30]. The efficacy of pesticides is however limited especially when the larvae are feeding inside the stalks (Kfir *et al*., 2002) [11].

Therefore, it is important to identify sorghum genotypes with higher levels of resistance with diverse mechanisms of resistance to diversify the bases of resistance to this pest. Progress in breeding for resistance to this pest has been slow due to the complex inheritance of the trait and the strong influence of environmental factors on expression of resistance to stem borers.

Screening for resistance to stem borer under natural conditions is ineffective because of non-uniform pest pressure over time and space, and thus, it is necessary to employ artificial infestation to identify sources of resistance to this pest (Songa *et al*., 2001) [29]. Marulasiddesha *et al*. (2007) [16] evaluated 20 sweet sorghum and three grain sorghum genotypes under artificial infestation in the field, and found SSV 7073 to be the most resistant with respect to

leaf feeding, deadheart formation, and peduncle and stem tunneling. Several other authors have screened sorghum under artificial infestation and genotypes with varying levels of resistance identified (Sharma *et al*., 2005, 2006: Dhillon *et al*., 2006; Kishore *et al*., 2007; Singh, 2011) [12, 5, 25]. Improvement for resistance to C. partellus requires identification of new sources of resistance to diversify the bases of resistance to this pest (Songa *et al*., 2001; Kishore *et al*., 2007) [29, 12].

In India, a number of stem borer species have been reported as serious pests of sorghum of which spotted stem borer, *Chilo partellus* (Swinhoe) (Lepidoptera: Pyralidae) is the most damaging insect pest which causes 35% infestation and cause huge loss in fodder yield of sorghum (Divya *et al*., 2009) [6] during *kharif* and *rabi* seasons. Hisar has been identified as hot spot for stem borer infestation and screening. Several morphological and biochemical factors also associated with stem borer resistance like plant height, stem length, number of leaves, leaf length and width are negatively whereas trait like number of plants per unit area are positively associated with it. Several bio-chemicals such as tannin content, lignin, total phenols were found to be responsible for resistance against stem borer. Stem borer (*Chilo partellus*) attacks from about 4 weeks after germination and causes 'Dead hearts' at the early stages and 'stem tunneling' at the later stages resulting in reduction of yield.

Materials and Methods

The investigation was carried out at CCS HAU, Hisar. The following experiments was conducted for the study in *kharif* season of the year 2017 for evaluation of F_3 populations of cross HJ513 X IS 2205.

The experimental material consists of F_3 Populations of cross HJ 513 X IS 2205.

The crop was planted at Forage Section, Department of Genetics and Plant Breeding CCSHAU, Hisar for the evaluation of Morphological traits related to stem borer incidence and its related traits. The sowing was done on July 12,2017. Checks were repeted after 20 lines. The details of materials and techniques followed for recording different observations during the course of this investigation have been described as under:

Experiment site and location

The crop was planted at Research Area of Forage Section, Department of Genetics and Plant Breeding, CCS Haryana Agricultural University, Hisar. It is situated in semi-arid sub-tropical region at 29.09^{0}N latitude and 75.43^{0}E longitude with elevation of 215 m (705 ft) above mean sea level.

Experimental Design and Layout plan: Augmented

Experimental material	: 200 lines
Parents	: HJ 513 and IS 2205 used as checks
Plot size	: 2 rows of 2m length
Plant to Plant spacing	: 15 cm
Row to row spacing	: 45 cm

All the recommended cultural package of practices was followed from sowing to harvesting of the crop.

Morphological observations recorded

Plant population /row
Days to 50% flowering
Plant height (cm)
Numbers of tillers/plant
Leaf length (cm)
Leaf breath (cm)
Stem diameter (mm)
Leaf: Stem ratio
Green fodder yield in kg/plot
Dry fodder yield in kg/plot
Dead heart-at 35 and 45 days after sowing
Stem tunnelling at the time of harvesting

All the observations were recorded as per according to agronomical practices. The green fodder yield was recorded from each of the randomly selected plant of each replication at the time of 50% flowering**.**

Dry fodder yield in kg/plot

The dry fodder yield was recorded after oven drying of plants of the plants selected for green fodder/plant.

Observation recorded on insect attack

1. Dead Hearts (%)

Observation were recorded for stem borer (*Chilo partellus*) attack as set by Mathur *et al.* (1991). For stem borer data were collected at 35 and 45 days after germination and per cent dead hearts were calculated using the following formula:

$$\% \text{ Dead heart} = \frac{\text{Number of dead heart/ plot}}{\text{Number of plants/plot}} \times 100$$

2. Stem Tunnelling (%)

Observations were recorded at the time of cutting by measuring the length of tunnel produced by stem borer. And then calculating the percentage of total plant height damaged by stem borer.

$$\% \text{ damage} = \frac{\text{Length of tunnel produced/ plant (cm)}}{\text{Height of plant (cm)}}$$

Statistical analysis

Statistical analysis involves analysis of variances for augmented block-II design, estimation of genetic variability, heritability, genetic advance, genetic advance as percent of mean, morphological characters. All these estimations were worked out using MS Excel 2019, SPSS 16.0v INDOSTAT and OPSTAT. Augmented block II ANOVA

An augmented design-II (Federer, 1956) [7], serves effective means for evaluation of large number of breeding material through accommodation of single replication of each of the treatments over the blocks (b) with a set of checks (c) replicated in each block. Randomization of checks was done in such a way that all the checks (c) and part of test genotypes fall only once in each block. Number of test genotypes in each block were kept equal in number for effective statistical analysis. Analysis of variance for trials 2017 was done by using the augmented design as prescribed by Federer and Ragavarao (1975) [8].

Table 1: The structure of ANOVA for augmented design-II

Source of variation	D.F.	SS	MSS	F
Blocks (b)	b -1	SS_b	MS_b	MS_b / MS_e
Genotypes (g)	g -1	SS_g	MS_g	MS_g / MS_e
Checks (c)	c – 1	SS_c	MS_c	MS_c / MS_e
Varieties (v)	v – 1	SS_v	MS_v	MS_v / MS_e
Checks vs Varieties Error	1 (c-1) (b-1)	SS_{cv} SS_e	MS_{cv} MS_e	MS_{cv} / MS_e
Total	N-1	TSS		
Where,				

b= No. of blocks, c= No. of checks, v= No. of test varieties, e= c + v, N= bc + v

Different ANOVA components can be worked out as follows. As only the checks (c) are replicated in this design and not the test varieties (v), hence adjustment of means of 'v' should be done before ANOVA by using the effects as given below:

Block effects (bj) = 1/c (T b_j –c − Tv b_j) (j= 1 to b) Counter check: $\sum b\ b_j \approx 0$

Mean effect (m) = 1/e (GT-(b-1) c -$\sum b\ n_j\ b_j$) $\sum n_j\ b_j$)

Where,
n_j is the number of varieties occurring in j^{th} block Check effects (c_i) = c_i- m {i = 1 to c}
GCF (General correction factor) = GT^2 /N

$$\mathbf{SSb} = \sum_{j=1}^{b} Tb_j^2/(c + nj) - GCF$$

MSb = SS_b/ (b-1)

$$\mathbf{TSS} = \sum_{i=1}^{c}\sum_{j=1}^{b} c_{ij}^2 + \sum_{i=1}^{v} v_i - GCF$$

CF_c (Check correction factor) = Tc^2/bc

$$\mathbf{SSc} = \sum_{i=1}^{c} Tc_i/b - cCF$$

MSc = SS_c/ (c-1)

$$\mathbf{SSg} = (m \times GT) + \sum_{j=1}^{b} b_j (Tb_j) + \sum_{i=1}^{c} Tc_i (C_i) + \sum_{i=1}^{v} v_i(v_i) - [\sum_{j=1}^{b} Tb^2_j / (c+n_j)]$$

MSg = SS_g / (g-1)

CFv = Tv^2 / **v**

$$\mathbf{SS_v} = \sum_{i=1}^{v} v^2 - vcF$$

MSv = SS_v / (v-1)

SScv = $MS_{cv} = SS_e - SS_c - SS_v$

SSe = TSS – SS_g –SS_b

MSe = SS_e / (c-1) (b-1)
If the block effect was significant, then conclusion could be drawn with the help of following four standard errors.

SEd_1 (between any two-check means) = $\sqrt{\frac{2EMS}{b}}$

SEd_2 (between any two means of test varieties) = $\sqrt{2EMS}$

SEd_3 (between any two entries of the same block) = $\sqrt{f2EMS(1 + 1/c)}$

SEd_4 (between means of a check and a test variety)

= $\sqrt{f EMS(1 + 1/b + 1/c + 1/bc)}$

CDi is then obtained through Sed_i ×'t' at 5% or 1% levels. {i=1 to 4}

Estimation of variability and genetic parameters

Mean

$$\textbf{General mean (X)} = \frac{\text{Sum of observations of all the genotypes}}{\text{Number of genotypes}}$$

Range = Minimum and maximum values for each trait within population.

Coefficient of variability
Both genotypic and phenotypic coefficient of variability of each trait was computed as per method described by Burton and Devane (1953) [3].

$$\text{Genotypic Coefficient of Variation (GCV)} = \frac{\sigma g}{X} \times 100$$

$$\text{Phenotypic Coefficient of Variation (PCV)} = \frac{\sigma p}{X} \times 100$$

Where, σ_g = genotypic standard deviation.
σ_p = phenotypic standard deviation.
X = General mean of the character

GCV and PCV values were categorized as low, moderate and high as indicated by Sivasubramanian and Menon (1973).

>20%-high 10-20%-moderate 0-10%-low

Heritability (h2)
Heritability (broad sense) was estimated by using following formula as given by Lush (1940)

$$h^2(\%) = \frac{\sigma_g^2}{\sigma_p^2} \times 100$$

Where,
σ_g^2 = Genotypic variance σ_p^2 = Phenotypic variance
The heritability was categorized as low, moderate and high as given by Robinson *et al*. (1949) [4].

>60%-high 30-60%-moderate 0-30%-low

Genetic advance
Genetic advance (GA) for each character was computed by using the formulae suggested by Johnson *et al.* (1955):

Genetic advance = $h^2.K.\sigma_p$

Where,

h^2 = Heritability of the character.

K = Selection differential which is equal to 2.06 at 5% selection intensity (Lush, 1949) [13]

σ_p = Phenotypic standard deviation of the character.

1. Genetic advance as percent of mean (GAM)
Genetic advance as per cent of mean was categorized as low, moderate and high as given by Johnson *et al.* (1955).

>20%-high 10-20%-moderate 0-10%-low

Result and Discussion
The mean sum of squares for all the fourteen quantitative traits evaluated during the trial (2017), has been presented in Table 1 Perusal of the table revealed highly significant mean sum of squares due to RILs entries for most of the traits except leaf: stem ratio which mean sum of squares was not significant for checks and checks vs varities. For check varieties mean sum of squares were observed as highly significant for most of the characters except leaf:stem ratio, plant polulations/row, total tillers per plant, no. of leaves per plant, leaves width, srem diameter and green fodder yield, plant height, dry fodder yield, dead heart and stem tunneling were significant only at 5% level of significance. However, for days to 50% flowering mean sum of squares was significant at 1% level of significance.

Table 1: Analysis of variance for quantitative morphological and biochemical traits evaluated in sorghum during year 2017

Source of Variation	DF	P.P/ROW	NOD	PH	NOT	NOL	L.L	L.W
Block	9	22.56**	146.24**	6662.13**	0.09**	26.65**	485.39**	4.87**
Entries	201	3.46**	34.94**	817.1*	0.04**	3.93*	77.53**	0.91**
Checks	1	0.11*	151.25**	4836.05**	0.03*	4.9*	583.2**	1.52**
Varities	199	4.19**	27.42**	1042.26**	0.05**	5.1*	70.57**	1.08**
Checks vs. Varities	1	139.79*	1415.31**	18022.09*	0.66*	228.91*	956.02**	34.98*
Error	9	0.779	5.92	237.61	0.01	1.33	8.87	0.18

DF= Degree of freedom
P.P/ROW= Plant Populations/row
NOD= No of days 50% flowering
P.H= Plant height
NOT= No. of tiller
NOL= No. of leaves
L.L= Leaves length
L.W= Leaves width
S.D-= Stem diameter
L.S = Leaf stem ratio
GFY/PLOT= Green fodder yield kg/ plot
DFY/PLOT= Dry fodder yield kg/ plot
D.H (35) = Dead heart at 35days after sowing
DH (45) = Dead heart at 45days after sowing
S.T= Stem tunneling at the time of harvesting

Source of Variation	DF	S.D	L.S	GFY/PLOT	DFY/PLOT	DH(35)	DH(45)	S.T
Block	9	67.03**	0.01**	179.12**	12.4**	218.6**	37.02**	136.75**
Entries	201	20.32*	0.01*	35.87**	2.48**	63.59**	13.24**	36.94*
Checks	1	94.05**	0.01	0.02*	0.02*	0.02*	0.32*	160.06**
Varities	199	22.76**	0.02*	41.8**	2.89**	69.21**	10.68*	38.90*
Checks vs. Varities	1	538.92*	0.02	1108.78*	76.81*	992.68*	535.35**	476.30*
Error	9	4.91	0.01	5.06	0.35	2.16	2.48	10.94

*,**Significant at 5%, and 1% level of significance

Plant damage and morphological traits
The results of mean of plant damage and morphological traits are presented in Table no.2. The results for plant populations/row, no. of days of 50% flowering, plant height, no. of tiller/plant, leaf length, leaf breath, stem diameter, leaf: stem ratio, green fodder yield, dry fodder yield deadheart and stem tunneling were significantly different and are presented in Table 2.
Plant population ranged from 6.72 to 17.23 in RILs having general mean 13.03. Days to 50 % flowering ranged from 53.75 - 82 days, plant height having mean 232.75cm, no. of tiller range1.26-2.83.other traits leaf length, leaf breath, stem diameter, leaf: stem ratio having the mean 62.94,5.62,16.77and 0.40 respectively. For green fodder yield and dry fodder yield in RILs have range 9.85 to23.90 kg per plot and 2.59 to0.6.55kg per plot. General mean for green and dry fodder yield is 22.68 and 5.97.
Plant had the damage by stem borer in case of deadheart 1.89 to 46.32 after 35 days of sowing and 0.30 to 19.79 after 45 days of sowing with the general mean 21.35 and 8.35 respectively.
For the stem tunneling having the general mean 11.05 range is 0.66 to 35.33.

Fig 1(A): Dead heart damage in crop (B) Stem tunneling in sorghum

Table 2: Mean performance of 200 sorghum RILs along with two checks for different traits

S. No.	Traits	General mean	Range
1	Plant Population/row	13.03	6.72-17.23
2	Days to 50% flowering	67.19	53.75-82
3	Plant height(cm)	232.75	126.65-381.85
4	Number of tillers/plant	2.27	1.26-2.83
5	No. of leaves/plant	12.75	7.40-21.06
6	Leaf length (cm)	62.94	40.10-85.20
7	Leaf breadth (cm)	5.62	2.19-8.32
8	Stem diameter(mm)	16.77	8.10-39.55
9	Leaf : Stem ratio	0.40	0.29-0.51
10	Green fodder yield(kg/plot)	22.68	9.85-23.90
11	Dry fodder yield(kg/plot)	5.97	2.59-06.55
12	Dead heart at 35days after sowing	21.35	1.89-46.32
13	Dead heart at 45days after sowing	8.20	0.30-19.79
14	Stem tunneling at the time of harvesting	11.05	0.66-35.33

Genetic parameters for morphological traits

In case of among genetic parameters GCV and heritability were maximam in green fodder yield which is 26.07 and 0.87 respectively. PCV was seen maximam in stem diameter among traits which is 27.85.for genetic advance plant height show maximam 49.66 and again green fodder yield show maximam GAM 50.18 as shown in table no 3.

Table 3: Genetic parameters for morphological traits in sorghum RILs

Genetic parameters	P.P/ROW	NOD	PH	NOT	NOL	L.L	L.W	S.D	L.S	GFY/ PLOT	DFY/ PLOT
GCV	13.83	6.73	11.87	8.55	14.81	12.18	16.49	24.52	7.97	26.07	26.07
PCV	15.40	7.64	13.59	9.37	17.36	13.07	18.12	27.85	9.32	27.90	27.90
h^2(bs)	0.81	0.77	0.76	0.83	0.72	0.86	0.82	0.77	0.73	0.87	0.87
GA	3.33	8.18	49.66	0.36	3.32	14.67	1.73	7.46	0.05	11.35	2.98
GAM (%)	25.58	12.20	21.35	16.07	26.04	23.38	30.93	44.48	14.05	50.18	50.18

Conclusion

- Analysis of variance (ANOVA) revealed that mean sum of squares due to checks and RILs were significant for all studied morphological traits related to stem borer resistance except leaf stem ratio.
- All the F_3 population exhibited wide range of mean values for almost all the characters.
- For Green fodder yield per plot RILs (3, 4, 13, 69, 74, 85, 86, 91, 93, 100, 108, 109, 118, 128, 129, 131, 133, 134, 136, 137, 138, 139, 145, 146, 155, 165, 16) were recorded as top performers.
- Estimates of selection parameters indicates high values of PCV, GCV, heritability and genetic advance over mean for fodder yield per plot, dry fodder yield per plot, stem diameter plant height, stem tunneling and dead hearts.

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