



# Variability, Heritability and Genetic Advance for Yield and Shoot Fly Resistance Associated Traits in Recombinant Inbred Lines (RILs) of Sorghum [*Sorghum bicolor* (L.) Moench]

Babita Bhatt <sup>a\*</sup>, P K Pandey <sup>a</sup>, Rubina Khan <sup>b</sup>,  
Sivendra Joshi <sup>a</sup>, Amit Kumar <sup>a</sup> and Tushadri Singh <sup>a</sup>

<sup>a</sup> Department of Genetics and Plant Breeding, College of Agriculture, G.B. Pant University of Agriculture and Technology, Pantnagar, 263145, Uttarakhand, India.

<sup>b</sup> Department of Genetics and Plant Breeding, Sri Karan Narendra College of Agriculture, Sri Karan Narendra Agriculture University, Jobner, 303328, Jaipur, Rajasthan, India.

## Authors' contributions

This work was carried out in collaboration among all authors. All authors read and approved the final manuscript.

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\*Corresponding author: E-mail: [babita44379@gmail.com](mailto:babita44379@gmail.com);

## ABSTRACT

The present investigation was carried out with 210 Recombinant Inbred Lines (RILs) at the Instructional Dairy Farm of the Govind Ballabh Pant University of Agriculture and Technology, Pantnagar, Uttarakhand, India and the experiment was conducted during kharif season, 2018-19 in augmented design with three replications with the objective to assess variability, heritability and genetic advance for 18 traits studied to select suitable shoot fly resistance RILs. The analysis of variance revealed highly significant differences for the trait viz., seedling height, days to 50 per cent flowering, plant height, stem diameter, number of nodes per plant, leaf length, leaf width, 1000 grain weight, dry fodder yield and green fodder yield, while significant differences were found in case of oviposition and dead heart per cent at 21 days after emergence. Eleven traits showed higher value of Genotypic coefficient of variation (GCV) than environment coefficient of variation (ECV). Total soluble solid (TSS) percent showed highest GCV followed by green fodder yield while dead heart per cent at 14 days after emergence showed highest ECV followed by days to emergence and Hydrocyanic acid content. Among the traits with high heritability, only plant height, dry fodder yield, and green fodder yield exhibited high genetic advance suggesting the additive gene action, making these traits suitable targets for effective selection in the RIL population. Further, molecular markers can be identified for key traits used in marker-assisted selection, and selected RILs can be evaluated in multi-environment trials for stability and adaptability.

*Keywords: Recombinant Inbred Lines (RILs); shoot fly; variability; heritability; genetic advance.*

## 1. INTRODUCTION

Sorghum, [*Sorghum bicolor* (L.) Moench]  $2n=2x=20$ , is one of the most important cereal crops in the world. It belongs to family Poaceae. It is the fifth most important cereal crop after wheat, rice, maize, and barley in terms of production and utilization at the global level. During 2023-24, the preliminary world acreage of sorghum was 40.16 million hectares with the production of 58.22 million metric tons and productivity of 1.45 metric tons per hectare respectively [1]. It is chiefly grown in tropical and subtropical areas, where agro-climatic conditions like soil, rainfall and temperature are variable. It is originated in semi-arid tropics but it has also been adapted to temperate regions through selection. It is staple food crop in Africa and Asia, and is a major feed crop in Argentina, Australia, Mexico, South Africa, and the USA. It is probable place of domestication is considered to be the North-eastern Africa, an area extending from the Ethiopian-Sudanese border to Chad [2]. From this area, it was further spread to India, China, the Middle East, and Europe. Harlan and de Wet [3] have recognized five primary races viz., bicolor, kafir, guinea, caudatum, durra and ten intervening races originating from all the possible hybrid combinations among the primary races [4]. Sorghum is an often-cross-pollinated crop with 5-25 per cent cross-pollination [5]. Sorghum is characterized by C4 photosynthetic pathway so it is a physiologically very efficient crop in solar conversion and use of water, thus it is

known as a high-energy, drought tolerant crop that is environment-friendly. Sorghum is a versatile crop with variable uses as food, fodder, fiber, and fuel thus it is of different types as grain sorghum, forage sorghum and sweet sorghum. Its various alternative uses consist production of poultry feed, jaggery, glucose, alcohol, and industrial raw material. In India, it has been considerably used for feeding animal as dried stalks, which are stacked or preserved after removal of earheads. Along with dry fodder sorghum, green sorghum is also fed to a large extent. The whole grain sorghum has 13-14 per cent protein content making sorghum one of the richest sources of protein among the major cereal grains and also high in lysine content (2.7-3.0 per cent). For forage view point, HCN content is found to be high in a crop harvested before 30-35 days after sowing yet it is below the toxic limit if harvested after 50 days of sowing.

In spite of rapid development in innovative technologies to increase and improve production, the high yielding varieties are subjected to many constraints, the major of which are insects-pests. The occurrence of insect pests has increased considerably in almost all sorghum growing areas due to intensive cropping and the introduction of high yielding susceptible hybrids/varieties. This has resulted in restraining the productivity of sorghum, which otherwise would have been very high. Over 150 insect species have been reported which damage sorghum plants from sowing to crop harvest

[6,7]. Sorghum shoot fly (*Atherigona soccata* Rondani) is one of the most important insect pests, is widely distributed in sorghum growing areas of the world which influences both fodder and grain yield. It is one of the most destructive pests in Asia, Africa and Mediterranean Europe resulting in limiting the sorghum production. In all the sorghum growing countries like Asia, Africa, and Mediterranean Europe, the shoot fly is practically a serious pest [8]. Its incidence is found to be higher in crops sown late during the rainy season, and in the early-sown crops during the post-rainy season [9]. Yield losses of sorghum grain up to 50 per cent have been reported in India [10] but sometimes the extent of yield loss due to this pest varies from 39 to 94 per cent in different agroclimatic conditions [11-15].

The ultimate aim of a breeder is to utilize the existing variability for crop improvement considering economically important traits. Thus, a crop improvement program in any crop involves thorough evaluation and screening for desirable characteristics and understanding the genetic make-up of the germplasm to be handled. Success through selection depends on the extent of genetic variability present in the base material. Improvement in sorghum yield by genetic manipulation depends on quality and magnitude of genetic variability, heritability and genetic advance in the population as well as the nature of the association between yield and its component traits. This leads to the simultaneous selection for many traits associated with yield [16]. In general sorghum crop possesses a wide range of genetic variability. Adequate variability provides enough options from which desirable selections are made for crop improvement and possible hybridization. Proper exploitation of available variability with the primary objective is to identify and select superior genotypes with desirable traits. Heritability is of prime importance in determining its response to selection. Estimates of heritability assist breeders to allocate resources necessary to effectively select for desired traits and to achieve maximum genetic gain with little time and resources [17]. Once heritability is known, the genetic advance through selection can be predicted. Looking into the relevance of sorghum crop and importance of shoot fly, the present research was conducted with the objectives to assess the extent of genetic variability, estimate the heritability and to determine the genetic advance achievable through selection, which will guide breeding strategies.

## 2. MATERIALS AND METHODS

### 2.1 Experimental Materials and Site

The research included a set of 210 Recombinant Inbred Lines (RILs) sourced from the Indian Institute of Millet Research (IIMR). These lines were derived from a cross between a shoot fly susceptible parent (27B) and a resistant parent (IS 2122). Further, six varieties—SPV1616, SSG-59-3, Pant Chari-5, Pant Chari-6, IS18851 (resistant), and Swarna (susceptible)—were included as checks. This experimental material was planted in an augmented block design during the 2018 monsoon season. The study region experiences a semi-humid subtropical climate in the Tarai belt of the Indian Himalayan foothills. The predominant soil is of the medium to heavy-textured category of Tarai soil. It has high organic matter content, high cation exchange capacity, and nutrient retention capacity; however, it shows poor to moderate drainage and a high-water table. Two hundred ten recombinant inbred lines were sown in seven blocks, with 30 lines in each block along with six standard checks replicated in each block along with resistance and susceptible check for shoot fly resistance. Each RIL was accommodated in 2 rows of 3-meter length with a row to row spacing of 50 cm. Data were recorded on 18 traits viz., days to emergence, seedling height (cm), number of plants with eggs, oviposition number/number of eggs per plant, dead heart percent at 14, 21 and 28 days after emergence (DAE), days to 50 per cent flowering, plant height (cm), stem diameter (cm), number of nodes, leaf length, leaf width, hydrocyanic (HCN) acid content (ppm), total soluble solid (TSS) percent, 1000 grain weight, dry fodder yield per plant (g/plant), green fodder yield per plant (g/plant). Five competitive plants were randomly selected for data collection of each trait, and the average of their trait values was used for subsequent statistical analysis.

### 2.2 Statistical Analysis

The variability was estimated as per procedure for analysis of variance suggested by Federer [18] for augmented design. Both genotypic and phenotypic coefficient of variability was computed for each trait as per the method suggested by Burton [19]. Heritability in broad sense Heritability in a broad sense ( $h^2$ ) by Burton and De Vane [20] and Genetic advance (GA) under selection and genetic advance

expressed as percent of the population mean was calculated by the formula outlined by Johnson et al. [21].

### 3. RESULTS AND DISCUSSION

#### 3.1 Analysis of Variance

The analysis of variance for 210 Recombinant Inbred lines, (RILs) including 6 checks in Augmented Block Design was done considering eighteen measurable traits. The results (Tables 1 & 2) showed highly significant differences among checks for thirteen different traits viz., days to emergence, seedling height, dead heart per cent at 28 DAE, days to 50 percent flowering, plant height, stem diameter, number of nodes per plant, leaf length, leaf width, TSS percent, 1000 grain weight, dry fodder yield and green fodder yield, while a significant difference was observed in case of hydrocyanic (HCN) acid content. Among recombinant inbred lines highly significant difference were observed for eleven traits viz., seedling height, days to 50 per cent flowering, plant height, stem diameter, number of nodes per plant, leaf length, leaf width, TSS percent, 1000 grain weight, dry fodder yield and green fodder yield, while significant difference was observed in case of oviposition and dead heart percent at 21 DAE. The ANOVA results showed the existence of sufficient genetic variability among both checks and RILs for several agronomically important traits, including yield components, phenological traits, and resistance to shoot fly. There was considerable genetic variability among RILs based on shoot fly damage, morphological traits and some of the biochemical composition. To develop cultivars with stable resistance to shoot fly, there is need to use sorghum genotypes with different combinations of factors associated with shoot fly resistance. Therefore, we need to have a comprehensive understanding of the biochemical constituents that influence the expression of resistance to shoot fly. The present studies based on a diverse array of sorghum RILs with different levels of resistance to shoot fly provided a rational comparison of the contribution of different traits associated with shoot fly resistance, and pinpoint those that can be used as markers to screen and breed for resistance to this insect. These findings were in accordance with the findings of Khandelwal et al [22] and Chaudhary et al [23]. The presence of this kind of extensive genetic variability gives an ample scope to a plant breeder to utilize its

variability for crop improvement in population by applying specific and directed breeding approaches.

#### 3.2 Coefficient of Variation

Analysis of variance provides estimates of phenotypic, genotypic and environmental variances (Table 2). Dead heart percent at 14 DAE showed the highest phenotypic coefficient of variation (PCV) followed by days to emergence, oviposition / number of eggs per plant, HCN content, green fodder yield, TSS percent. Trait with moderate PCV included dead heart per cent at 21 DAE, dry fodder yield, egg percentage/ number of plants with egg, 1000 grain weight, stem diameter, seedling height, leaf width, dead heart per cent at 28 DAE, plant height. Lower PCV values were observed for number of nodes/ leaves per plant, leaf length and days to 50 percent flowering. TSS percent showed the highest genotypic coefficient of variation (GCV), followed by green fodder yield, dead heart percentage at 14 DAE, oviposition /number of eggs per plant, dry fodder yield, 1000-grain weight, HCN content, days to emergence, dead heart per cent at 21 DAE, stem diameter, leaf width, seedling height and plant height. Relatively lower GCV values were exhibited by dead heart percentage at 28 DAE followed by egg percentage/number of plants with eggs, leaf length, nodes/leaves per plant, and days to 50 percent flowering. Dead heart percentage at 14 DAE also exhibited the highest environmental coefficient of variation (ECV), followed by days to emergence, HCN content, oviposition/number of eggs per plant, green fodder yield, and dead heart percentage at 21 DAE. Moderate ECV was revealed by dead heart percentage at 28 DAE followed by dry fodder yield, and seedling height. Lower ECV values were observed for stem diameter, 1000-grain weight, TSS percent, plant height, and other traits, number of nodes/ leaves per plant, leaf width, days to 50 percent flowering and leaf length.

Coefficients of variation analysis revealed that phenotypic coefficient of variation (PCV) values were slightly higher than the corresponding genotypic coefficient of variation (GCV) values for all traits (Table 3). The high GCV and PCV values suggest potential for improvement through selection. The results highlight the significant influence of both genetic and environmental factors on trait variability. The

**Table 1. Mean sum of squares from analysis of variance of augmented block design for nine initial traits**

Source of Variation	df	DTE (days)	SH (cm)	E%	O	DH% @ 14 DAE	DH% @ 21 DAE	DH% @ 28 DAE	DTF (days)	PH (cm)
Blocks	6	29.165**	10.632**	269.937**	10.206**	137.543**	354.1150*	292.752**	194.352**	5060.070**
Entries	215	5.249	6.315**	77.28	1.387	53.006	114.352*	84.190**	99.747**	1785.087**
Checks	5	18.895**	18.567**	18.472	0.817	76.98	95.161	107.615**	135.867**	18296.414**
Varieties	209	5.345	5.039**	77.171	1.557*	54.461	115.447*	80.269	67.804**	1230.601**
Checks vs variety	1	-83.179	211.752**	394.035**	-31.198	-370.897	-18.593	786.547**	6595.305**	35115.945**
<b>Error</b>	<b>30</b>	<b>3.81</b>	<b>1.494</b>	<b>51.995</b>	<b>0.92</b>	<b>34.051</b>	<b>62.492</b>	<b>35.404</b>	<b>8.681</b>	<b>139.605</b>

\*Significant at 5 %; \*\* significant at 1%

DTE- Days to Emergence, SH-Seedling Height, E %-Egg Percentage/ Number of Plants with Eggs in Per Cent O-Oviposition Number / Number of Eggs Per Plant, DH%-Dead Heart Per Cent, DTF-Days to 50 % Flowering, PH-Plant Height

**Table 2. Mean sum of squares from analysis of variance of augmented block design for other nine traits**

Source of Variation	df	SD (cm)	NN	LL (cm)	LW (cm)	HCN (ppm)	TSS (%)	TGW (g)	DFY (g/plant)	GFY (g/plant)
Blocks	6	0.600**	24.448**	598.105**	8.923**	726.608	21.849**	65.196**	3774.792**	72392.002**
Entries	215	0.087**	2.856**	87.742**	1.742**	701.242*	23.208**	29.395**	616.909	5360.152*
Checks	5	0.196**	3.867**	351.203**	2.711**	4244.540*	4.285**	88.747**	4755.192**	20400.810**
Varieties	209	0.087**	2.653**	68.101**	1.607**	612.402	23.412**	26.865**	576.851**	6672.732**
Checks vs variety	1	-0.568	40.247**	2875.403**	25.060**	1552.37	75.151**	261.344**	-11702.331	-344172.435
<b>Error</b>	<b>30</b>	<b>0.013</b>	<b>0.292</b>	<b>2.392</b>	<b>0.075</b>	<b>388.779</b>	<b>0.659</b>	<b>2.239</b>	<b>118.435</b>	<b>2670.361</b>

Significant at 5 %; \*\* significant at 1%

SD-stem Diameter, NN-Number of Nodes, LL-Leaf Length, LW-Leaf Width, HCN –Hydrocyanic Acid Potential (ppm), T.S.S %-Total Soluble Solids in PerCent, TGW-Thousand Grain Weight, DFY-Dry Fodder Yield, GFY-Green Fodder Yield

**Table 3. Variability, heritability and genetic advance of different traits**

<b>Sl. No.</b>	<b>Trait</b>	<b>PCV (%)</b>	<b>GCV (%)</b>	<b>ECV (%)</b>	<b>Heritability (%)</b>	<b>Genetic advance</b>	<b>GA as Percent of Mean</b>
1	Days to emergence	43.12	21.81	37.20	25.60	1.19	22.72
2	Seedling height (cm)	20.73	16.96	11.92	66.90	2.93	28.57
3	Egg percentage/ number of plants with egg	24.27	13.12	20.41	29.20	5.16	14.61
4	Oviposition / No of eggs per plant	38.98	23.75	30.91	37.11	0.92	29.80
5	Dead heart % @ 14 DAE	45.82	26.11	37.65	32.47	4.75	30.65
6	Dead heart % @ 21 DAE	30.12	19.51	22.95	42.00	8.97	26.04
7	Dead heart% @ 28 DAE	18.96	13.66	13.14	51.90	9.19	20.28
8	Days to 50% flowering	9.73	8.99	3.73	85.30	13.51	17.10
9	Plant height (cm)	16.27	15.18	5.88	87.00	58.60	29.15
10	Stem diameter (cm)	21.29	19.45	8.67	83.40	0.47	36.59
11	No of nodes/ leaves per plant	13.18	12.31	4.69	87.33	2.73	23.71
12	Leaf length (cm)	12.95	12.69	2.62	95.91	15.10	25.59
13	Leaf width (cm)	17.65	17.16	4.10	94.60	2.29	34.39
14	HCN (ppm)	38.48	22.08	31.52	32.90	16.32	26.09
15	TSS (%)	34.84	34.26	6.31	96.72	8.93	69.42
16	1000 grain weight (g)	23.91	22.73	7.42	90.40	8.98	44.51
17	Dry fodder yield (g/plant)	26.58	23.29	12.82	76.75	35.69	42.03
18	Green fodder yield (g/plant)	35.80	26.82	23.72	56.11	90.17	41.39

higher magnitude of ECV compared to GCV for days to emergence, number of plants with eggs, oviposition number, dead heart percentage at 14 and 21 DAE, and HCN content indicates the significant role of the environment in their phenotypic expression. Conversely, the higher GCV for traits like seedling height, dead heart percent at 28 DAE, days to 50 percent flowering, plant height, stem diameter, and yield components suggests a predominant genetic control. The high GCV observed for TSS percent, green fodder yield, and certain resistance traits indicates promising potential for genetic improvement through selection. Conversely, the relatively lower GCV for traits like days to 50% flowering and some yield components suggests that selection for these traits might be less effective. These findings were in accordance with previous studies of Prabhakar [24], Chikkanaragund et al [25] and Chaudhary et al. [26] further supporting the importance of considering both genetic and environmental factors in sorghum breeding programs.

### 3.3 Heritability and Genetic Advance

Genetic variation alone is not sufficient for plant breeders; heritability estimates are important to understand the proportion of total variation that is heritable. Burton and de Vane [16dh] suggested that combining genotypic coefficient of variation (GCV) with heritability provides a clearer understanding of the expected advance from phenotypic selection. Additionally, heritability estimates, when combined with genetic advance, offer a more reliable prediction of selection response.

In this study, broad-sense heritability was estimated. Traits that exhibited high heritability (>60%) were leaf length followed by leaf width and TSS percent. Moderate heritability was found for seedling height, green fodder yield, and dead heart percentage at 28 DAE, while lower heritability was observed for dead heart percentage at 21 and 14 DAE, oviposition/number of eggs per plant, HCN content, egg percentage/number of plants with eggs, and days to emergence. Green fodder yield showed the highest genetic advance, followed by plant height and dry fodder yield. Moderate genetic advance was observed for HCN content, leaf length, and days to 50 percent flowering. Lower genetic advance was found for traits including egg percentage/ number of plants with eggs, dead heart per cent at 14 DAE, seedling height, number of nodes/ leaves per

plant, leaf width, days to emergence, oviposition / number of eggs per plant and stem diameter. When expressed as a percentage of the mean, TSS percent showed the highest genetic advance, followed by 1000-grain weight, dry fodder yield, and green fodder yield. Moderate genetic advance percent of mean was observed for stem diameter, leaf width, dead heart per cent at 14 DAE, oviposition / no of eggs per plant, plant height, seedling height, HCN content, dead heart per cent at 21 DAE and leaf length. Lower genetic advance percent of mean was found for number of nodes/leaves per plant, days to emergence, dead heart percentage at 28 DAE, days to 50 percent flowering, and egg percentage/number of plants with eggs. High heritability alone doesn't guarantee substantial genetic gain. In this study the combination of high heritability and high genetic advance for plant height, dry fodder yield, and green fodder yield indicates the predominance of additive gene action, making these traits prime targets for effective selection. Similar results were reported by Godbharle et al. [27] for fodder yield and Jimmy et al. [28] for grain yield per plant.

### 4. CONCLUSION

This study assessed the genetic variability in 210 sorghum RILs the vast potential for trait improvement through strategic selection. High values of PCV and GCV for several yield contributing and quality traits including green fodder yield, dry fodder yield, 1000 grain weight, HCN content, TSS percent indicates higher variability within the RIL population, offering scope for targeted breeding. High heritability coupled with high genetic advance for the traits like green fodder yield, dry fodder yield and plant height highlight their suitability as primary selection criteria for yield enhancement. However, the lower genetic advance observed for several resistance-related traits, despite high heritability, suggests a complex inheritance pattern likely involving non-additive gene action and environmental interactions necessitates the exploration of complementary strategies like marker-assisted selection or multi-trait selection indices to effectively enhance resistance. The variation in genetic advance among different traits indicates the importance of considering both heritability and genetic advance for selection. Therefore, targeted breeding approaches can be employed to select and develop superior sorghum lines with enhanced yield potential and improved resistance to shoot fly, contributing to more sustainable and

productive sorghum cultivation. Future research should include multilocation trials of identified lines for checking the adaptability under different agroclimatic zones. Besides, molecular characterization can also be done for identifying essential genes and markers associated with desirable traits to enhance breeding efforts through marker-assisted selection.

#### DISCLAIMER (ARTIFICIAL INTELLIGENCE)

Author(s) hereby declares that NO generative AI technologies such as Large Language Models (ChatGPT, COPILOT, etc) and text-to-image generators have been used during writing or editing of manuscripts.

#### COMPETING INTERESTS

Authors have declared that no competing interests exist.

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