# VARIABILITY STUDIES FOR VARIOUS DISEASE RELATED PARAMETERS AND YIELD CONTRIBUTING CHARACTERS OF SORGHUM {SORGHUM BICOLOR (L.) MOENCH}

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#### ABSTRACT

Moderate coefficients of variability, very high to high heritability coupled with moderate genetic gain are reported for overall disease damage (score) in two consecutive years of 1996-97 and 1997-98 indicating the presence of non-additive gene action in the inheritance of this trait. High heritability is being exhibited due to favourable influence of environment rather, than the genotypes and selection for such traits may not be rewarding. Since the favourable genes (leaf diseases parameters) were dispersed in different genotypes, multiple crossing is suggested to accumulate all these favourable genes into one genotype.

In sorghum, leaf blight caused by Exserohilum turcicum (Pass.) Leonard and Suggs has resulted a loss of 45% in grain yield (Sharma, 1978). The significant yield losses due to diseases can be effectively controlled through the development of multiple-disease resistant varieties. However, most of the cultivars and hybrids, which are being grown on commercial scale, are found to be susceptible to leaf blight. The reasons for lack of resistance in the material may be attributed to presence of poor variability in the population. In order to develop the disease resistant and high yielding cultivars, it is imperative to analyse and understand the variability for various disease parameters and yield contributing characters. Hence, in the present investigation an effort has been made to study the variability parameters for various disease resistance and yield contributing characters of sorghum.

In the present study conducted at ICRISAT, Patancheru, India 20 CMS (cytoplasmic male-sterile i.e., A-lines) lines were crossed with six restorer (testers i.e., R-lines) lines in a line x tester fashion during *kharif* 1996 and *kharif* 1997 and the resultant 120 cross combinations (A x R hybrids) along with their respective parents and checks were sown in a randomized complete block design replicated thrice during rabi 1996 and rabi 1997 to evaluate for leaf blight resistance under artificial disease epiphytotic conditions for various disease related parameters and vield contributing characters. The recommended package of practices was followed to raise a healthy crop. Plot size in both the experiments consists of 2 rows of 4m length each (75 cm between rows and 12 cm within the row). Spraying with fungicides was avoided intermediately after the inoculation to prevent its adverse effect on the spread of the inoculum. However, need based plant protection measures were taken up at the initial stages of the crop to safeguard the crop from the incidence of shoot fly. Highly leaf blight susceptible entries such as Kundi Jowar and H 112 were planted in two rows each as infestor rows all round the field and after every 10 rows and 12 rows of the test material during first and second years, respectively.

Inoculum preparation: The inoculum was prepared as follows for artificial whorl-drop method of inoculation (Frederiksen and Franklin, 1978) in the field, The leaves affected with leaf blight, *Exserohilum turcicum* (Pass.), were collected from the field and cut into small pieces and surface sterilized with 0.1% mercu-

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ric chloride for one minute followed by washing with sterile distilled water. Leaf pieces were aseptically transferred to sterilized petri plates containing 20 ml of sterilized Potato Dextrose Agar media (PDA) and incubated at 20°C for encouraging the fungal growth. The fungal growth was aseptically transferred to flasks containing sterilized sorghum grains and incubated at 20°C for 15 days so that the sorghum grains were covered with mycelia and the conidia of fungus colonized grains were removed from the flasks, allowed to airdry and separated as far as possible.

Inoculation: The pathogen. Exserohilum turcicum (Pass.), causing leaf blight disease in sorghum was artificially inoculated following whorl-drop method of inoculation (Frederiksen and Franklin, 1978). The inoculation was carried out at 21 and 30 days after emergence of coleoptile during rabi 1996 and 1997, respectively. The second inoculation was given one week after the first inoculation. All the plants present were inoculated by placing two or three grains of seed inoculum in the whorl. The high humid conditions were created by providing overhead sprinklers on the same day after inoculation. It took 40 days from the day of inoculation for the spread of the disease.

The observations were recorded for the following characters: Disease damage score (scored on a 1-9 scale on plot basis, where 1= highly resistant and 9= highly susceptible), length of the lesion (cm), width of the lesion (cm), area of the lesion (cm<sup>2</sup>), number of lesions (no), number of flecks (no), lodging (%), days to 50% flowering (days), plant height (cm), agronomic desirability (scored on a 1-5 scale on plot basis where 1=excellent and 5=poor), grain yield plant-1 (g) and test weight (g for 100 grains). The genotypes were grouped into different disease reaction groups viz., highly resistant (HR), resistant (R), moderately resistant (MR), less susceptible (LS), susceptible (S) and highly susceptible (HS) reactions taking overall disease damage score as the basis for presentation of the data.

Moderate coefficients of variability was reported for overall disease damage (score) in two consecutive years (Table 1) are in contrary with the findings of Hughes and Hooker, (1971), Hooker, (1971), and Satyanarayana, (1995). They have reported high estimates of phenotypic coefficient of variability (PCV) and genotypic coefficient of variability (GCV) for disease damage score in maize for Helminthosporium turcicum leaf blight, suggesting that the selection based on this trait would facilitate a successful isolation of resistant types. Difference between PCV and GCV estimates for two years are very narrow indicating minor role of environmental factors in influencing the expression of disease inheritance and offering greater scope for selection of desirable resistant parents (Satyanarayana, 1995). Among the yield contributing characters, days to 50% flowering recorded very low variability followed by 100 seed weight and plant height. The low variability recorded for days to 50% flowering is in contrast with the findings of Raghu Ram Reddy et al. (1996) who reported the presence of high phenotypic variance indicating the influence of environment.

High heritability coupled with high genetic advance as per cent of mean recorded for area of the lesion, number of lesions and number of flecks in both the years indicated the importance of additive gene action.

High heritability coupled with moderate genetic advance as per cent of mean recorded for disease damage score, length of the lesion (first year), plant height and grain yield plant<sup>-1</sup> indicates ambiguous gene action. Selection on these traits may give conflicting results in the passing generations. Satyanarayana (1995) and Ramamurthy *et al.*, 1980 reports similar results of heritability for disease score

Characteristic	Year	Genotypic coefficient of variability (GCV)	Phenotypic coefficient of variability (PCV)	Heritability (H²)	Genetic advance (GA)	Genetic advance as % of mean (GG)
DISEASE PARAMETERS	,					
Disease score <sup>1</sup>	96 97	25.00 19.65	28.59 24.03	76.47 66 92	2.34 1.59	45.00 33.13
Length of the lesion (cm)	96 97	48.31	72.10	44.89	1.23	66.85 71.59
Width of the lesion (cm)	96 97	23.81	27.50	75.00	0.10	43.48
Area of the lesion (cm²)	96 97	45.73	48.09	95.10 84.38	13.59	1527.00
Number of lesions	96 97	68.98 52.02	70.17	96.64 93 75	12.04	139.68
Number of flecks	96 97	65.62	67.23	95.26 95.74	175.98	131.94
Lodging (%)	96	121.21	166.95	52.72	23.39	181.32
GRAIN COMPONENT CHA	RACTERS	5				
Days to 50% flowering	96 97	5.18 6.54	5.84 6.74	78.48 94.14	7.59 8.63	9.44 13.08
Plant height (cm)	96 97	15.99 20.15	16.33 20.42	95.84 97.37	48.40 78.62	32.25 40.95
Agronomic score <sup>2</sup>	96 97	16.22	24.78	42.86	0.66	21.85 29.73
Grain yield plant (g)	96 97	29.88	33.84	77.94	13.48	54.35 69.16
100 seed weight (g)	96 97	10.17 13.79	12.03 15.03	71.43 84.21	0.55 0.76	17.68 26.21

Table 1. Variability parameters for various disease resistant parameters and yield contributing characters of sorghum, post-rainy season, ICRISAT, Patancheru, 1996 and 1997.

<sup>1</sup> Scored on a (1-9) scale,

<sup>2</sup> Scored on a (1-5) scale.

in maize. On the contrary, high expected genetic advance was recorded for disease damage score in maize (Johnson *et al.*, 1955 and Panse, 1967) and plant height in sorghum (Patil and Thombre, 1983) owing to higher additive gene effects. High heritability accompanied with high expected genetic advance for grain yield plant<sup>-1</sup> in sorghum was reported by Kukadia *et al.* (1983), Patil and Thombre, (1983); and Cheralu and Rao, (1989) indicating that the selection would be effective for these characters.

High heritability coupled with low genetic advance as per cent of mean noticed for days to 50% flowering and 100 seed weight indicates the high influence of the environment on the genotypes leading to unstable expression of the genotypes. The gene action is governed by merely non-additive genes. Selection on such traits will lead to slippage of traits under investigation in the subsequent generations. The presence of high heritability and low genetic advance over mean indicates the presence of non-additive type of gene action. High heritability might be due to environment and the high heritability estimates may not necessarily mean an increased genetic advance as reported by Johnson et al. (1955) in soybean. Raghu Ram Reddy et al. (1996) also reported the presence of high heritability and low genetic advance for days to 50% flowering in sorghum. Similarly, high heritability and low expected genetic advance for days to 50% flowering, and 100 seed weight was also recorded by Kukadia *et al.* (1983). Patil and Thombre, (1983) noticed high heritability for days to 50% flowering, plant height, grain yield plant<sup>-1</sup> and 100 seed weight as reported in the present study. many of these traits it is expected that such breeding programme would be successful in realising the favourable alleles of various traits into a few genotypes.

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