CLASSIFICATION OF SORGHUM GENOTYPES FOR LEAF BLIGHT RESISTANCE

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ABSTRACT

Sorghum hybrids of 20 cytoplasmic-male steriles and six restorers and the parents were evaluated in 1996 and 1997 for leaf blight disease resistance parameters. On the basis of disease damage score the cluster analysis identified four major clusters corresponding to the disease reaction exhibited by the parents and the hybrids. Of the four clusters, Cluster I is considered to be the most important cluster as the progeny was found to be resistant irrespective of the disease reaction of the parents involved. The hybrids viz., MS 11 x R 3 and MS 9.x R 3 involving resistant and moderately resistant parents exhibited hypersensitive reaction.

Index Words: Exserohilum turcicum, leaf blight, sorghum.

Exserohilum turcicum (Pass.) Leonard and Suggs (1974) is extensively distributed (Tarumoto et al., 1997), and at times most damaging foliar pathogen of sorghum (Fredericksen, 1980). The safest and the most economical way of combating diseases was through the development of the resistant varieties. Although variation was measured in genotypes for various disease-related characters, overall disease damage score was used as a criterion in cluster analysis to identify the groups of related cultivars. The objective of our analysis was to categorize the genotypes into different groups on the basis of overall disease damage score.

MATERIAL AND METHODS

Materials and field evaluation

In the present study, 20 CMS (cytoplasmic male-sterile i.e., A) lines were crossed with six restorer (testers i.e., R) lines in a line x tester fashion during the rainy seasons of 1996 and 1997. The resultant 120 cross combinations (A x R hybrids),

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along with their respective parents and checks, were sown in a randomized complete block design replicated three times during the post rainy seasons of 1996 and 1997, to evaluate for leaf blight disease related parameters and yield contributing characters under artificial disease epiphytotic conditions at ICRISAT Asia Center, Patancheru, Hyderabad, Andhra Pradesh, India. Plot size in both the seasons consisted of 2 rows each of 4m length with 75 cm between rows and 12 cm spacing within the row. Spraying with fungicides was avoided immediately after the inoculation to prevent its adverse effect on the spread of the inoculum. Plant protection measures were applied as required at the initial stages of the crop from the incidence of shoot fly. Genotypes highly susceptible to leaf blight such as Kundi Jowar and H 112 were planted in two rows as infestor, all round the field and after every 10 rows and 12 rows of the test material.

inoculum preparation

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% mercuric 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. Sorghum grains covered with mycelia and the conidia of the fungus were removed from the flasks, allowed to air dry and separated as far as possible.

Inoculation

Sorghum plants were artificially inoculated following the shorl-drop method of inoculation (Frederiksen & Franklin, 1978). The inoculation was carried out 21 and 30 days after emergence of the coleoptile during the post rainy seasons of 1996 and 1997, respectively. The second inoculation was given one week after the first inoculation. All the plants in each entry were inoculated by placing two or three grains of seed inoculum in the whorl. High humidity conditions were created by providing overhead sprinklers on the day after inoculation until the disease has spread. It took 40 days for the disease to spread.

Observations

The observations were taken on disease damage score (DDR) (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 (cm²), number of lesions, number of flecks, days to 50% flowering, plant height (cm), agronomic

desirability (scored on a 1-5 scale on plot basis where 1 = excellent and 5 = poor), grain yield plant (g) and testweight (g 100 grain). The genotypes were grouped into six disease reaction groups viz., highly resistant (HR) resistant (R), moderately resistant (MR), less susceptible (LS), susceptible (S), and highly susceptible (HS) reaction groups taking overall disease damage score as the basis for presentation of the data. Cluster analysis is carried out using Hierarchical, Euclidean, Average Link Method following SAS. One hundred and forty six genotypes included in the study are grouped into different clusters following the abovde method.

RESULTS AND DISCUSSION

The present investigation have revealed, on the basis of the total leaf area damage, that all the genotypes could be clustered in to four groups (Table 1). Cluster I consists of 24 genotypes with a disease score ranging from 2.7 to 3.3. Parents with resistant reaction and the crosses involving R x R, R x MR, R x LS, MR x MR, LS x MR, and S x MR parents fall in the category of cluster I. It is evident that all the crosses involving either resistant female parent or moderately resistant male parent with disease score ranging from 2.7 to 3.3 fall in cluster*I indicating that resistance has exhibited no dominance in R x R, dominance in R x MR, R x LS and overdominance in MR x MR, LS x MR and S x MR combinations.

Thirty-six genotypes with overall disease damage score ranging from 3.7 to 4.7 fall in cluster II. The moderately resistant parents and the crosses involving R x R, R x LS, R x S, MR x R, MR x MR, MR x LS, MR x S, LS x R, LS x MR, LS x LS, S x R parents fall in second category. Though the hybrids involving resistant parents and the crosses involving R x LS, MR x MR, LS x MR were also reported in cluster I, the disease reaction of these hybrids is found to be moderately resistant while the disease reaction of the hybrids falling in cluster I is resistant. In this group, moderate resistance is found to be partially dominant in R x R, R x LS, R x S, LS x R and S x R combinations, dominant in MR x MR combination and overdominant in LS x MR combinations. The exception to this clustering pattern is resistant hybrids involving susceptible and less susceptible female parents and resistant male parents (S x R and LS x R) because one parent in these two hybrids is from cluster I.

Cluster III consists of 21 genotypes with overall disease damage score ranging from 6.7 to 8.0. The susceptible parents and the hybrids involving R x LS, MR x LS, MR x S, LS x LS, LS x S, S x LS, S x S parents occurred in this category. Though an overlapping of the hybrids viz., R x LS, MR x LS, MR x S, and LS x LS with the hybrids falling in category II is noticed, the progeny exhibited susceptible reaction in this cluster unlike moderately resistant reaction in cluster II. The disease reaction i.e., susceptibility is found to be resistant in MR x S, LS x S and S x LS,

Table 1. Cluster, genotype, disease damage score and the disease reaction of different genotypes of sorghum for R x R R x B LS x MB MR x LS LS x LS MR x LS LS x LS MR x S MR S×S S×LS MR × MR MR x LS MR x LS MR x LS LS x R S LS×S MR x LS LS x LS MR x S R x LS LS×R MR×R R x LS Reaction S x MR S•x R S S S R x LS R×S Parents Disease Hybrid Σ Damage Disease 6.7 6.7 MS 14 x R 2 MS 25 x R 5 MS 24 x R 5 MS 16 x R 6 MS 11 x R 4 MS 11 x R 2 MS 22 x R 2 MS 4 x R 1 9 MS 16 x R·11 MS 24 x R 3 MS1×R4 MS 3 x R 4 MS 22 x R 4 MS 16 x R 5 MS 14 x R 1 MS 6×R3 MS 17 x R 4 **MS 296 x B** MS 7 x R 4 MS 9 x R 1 MS 1 x R 1 MS 6 x R5 MS 10 x B MS 14 x R MS 13 x R α MS 17 x R MS 16 x R MS 12 x R Genotype MS 13 MS 16 MS 25 x MS 1 MS 22 x S α Cluster \equiv Ξ 60 62 63 63 64 65 **55** MR x MR LS x MR MR × MR MR x MR MR x MR MR x MR R×S. LS x B MR x MR R × MR S × LS S × MR S × MR RxLS MR x R R x MR Reaction **Parents** R x MR R R R x LS RxS E X E F E E R x LS ₩ ₩ ₩ ₩ α œ m m m m Disease Hybrid leaf blight (Exserohilum turcicum) EΣ α Damage Score Disease MS 22 x R 3 MS 10 x R 1 R·t MS 19 × R 3 MS 21 × R 3 **MS x 17 x R 3** MS 9 × H 4 MS 4 × R 2 MS 7 × R 6 MS 11 x R 5 3 MS 13 x R 3 MS 11 x R 1 MS 15 x R 1 MS 16 x R 3 MS 11 x R 3 MS 12 x R 1 MS 1 x Rv3 MS 10 x R 1 MS4×R3 MS1×R5 S Genotype MS 7 x R 1 MS 19 x R α MS 9 x B MS 9 x B MS 21 R 3 MS 15 MS 7 x R MS 4 MS 7 MS₉ ဖ × MS 10 Cluster 27 28 29 30 31 32 33 34 35 တ်

Disease Reaction	Parents		Y × Y	E X S	R x S	MR×R	LS x LS	MR×S	MRX	LS×LS	S×LS	LS x LS	MR×S	S	ĽS	R×LS	R x S	LS×MB	SIX	LS×S	SXLS	S S		LS	rs	S T	R×LS	LS×LS	MR x LS	LS x LS	S × S	MR x S	MRxS	S X S	MR x LS	MRXS	LS×S	S× P	S×MR
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Disease	Damage	1 2	7.1	5.7	5.7	5.7	5.7	5.7	5.7	5.7	5.7	5.7	5.7	6.3	6.3	6.3	6.3	6.3	6.3	6.3	6.3	6.3		0.9	0.9	0.9	0.9	0.9	0.9	0.0	6.0	6.0	0.9	0.9	6.0	0.9	6.0	0.9	0.9
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no dominance in S x S comibination and over dominance in R x LS, MR x LS and LS x LS combinations. The exceptional case to this cluster is highly susceptible hybrids involving less susceptible and susceptible (LS x S) parents. The less susceptible parents fall in cluster IV and susceptible parent in cluster III.

Cluster IV consists of moderately resistant parents and less susceptible parents. The hybrids viz., $R \times MR$, $R \times LS$, $R \times S$, $R \times R$,

Thus, the cluster analysis identified four major clusters corresponding to the disease reaction exhibited by the parents and the hybrids. Of the four clusters, cluster I is considered to be the most important cluster as the progeny was found to be resistant irrespective of the disease reaction of the parents involved. The hybrids viz., MS 11 x R 3 and MS 9 x R 3 involving resistant and moderately resistant parents and falling in cluster I and exhibiting hypersensitive reaction can be utilised further.

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