

INHERITANCE OF FIELD RESISTANCE TO SORGHUM DOWNY MILDEW*

B.S. RANA, K.H. ANAHOSUR¹, M. J. VASUDEVA RAO², V.JAYA MOHAN RAO,
R. PARAMESHWARAPPA¹ and N. GANGA PRASADA RAO²

National Research Centre for Sorghum, Rajendranagar, Hyderabad 500030

ABSTRACT

Inheritance of SDM resistance was studied in a set of resistant \times susceptible crosses using both qualitative and quantitative genetic analysis techniques. Segregation ratios in the (R \times S) crosses clearly indicated the presence of three gene pairs which exhibited both complementary and duplicatory types of gene interaction among them. Quantitative genetic analysis of this character indicated similar results. SDM resistance was observed to be quantitative threshold character.

Incidence of sorghum downy mildew (SDM), caused by *Perenosclerospora sorghi* (Weston and Uppal) Shaw, is frequent in the humid areas of Karnataka, Maharashtra and Tamil Nadu. The level of incidence varies from year to year. The local cultivars of sorghum are more susceptible compared to the recently released hybrids and varieties. Although considerable progress has been made in breeding resistant hybrids and varieties, the nature of inheritance of SDM resistance is yet to be fully understood. The present study is an attempt in this direction.

MATERIAL AND METHODS

Two released varieties, CS-3541 and 148 (CSV-5), known for SDM resistance (R) were crossed to 296 and 303, two susceptible (S) but otherwise desirable varieties resulting in four R \times S crosses. Another cross was also made between the two resistant parents. Subsequently, backcrosses to both parents were attempted in all the five crosses. The five sets of parents, F₁'s, backcrosses, F₂'s and some F₃ progenies of each cross were raised in randomized complete block design with two replications at AICSIP, Regional Research Station, Dharwar during *kharif*, 1976 in a SDM sick-plot.

Data on systemically infected sorghum plants were recorded on 96 to 204 plants in parents, F₁'s and individual F₃ progenies and on 435 to 633 plants in different F₂ populations. There were 12 to 40 different progenies in F₃ in different crosses. SDM susceptibility was expressed as the number of systemically infected plants and also as percent of total number of plants. Percentages so obtained were transformed to angles for statistical analysis.

Proportions of resistant and susceptible plants in a population allowed the study of SDM resistance in the form of a qualitative character. The frequency of SDM susceptible plants expressed as percentages of population, were used to study this trait as a quantitative character.

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Present addresses : 1. UAS, Regional Research Station, Dharwad 580005. 2. ICRISAT, Patancheru, Hyderabad 502324.

RESULTS

QUALITATIVE GENETICS OF SDM RESISTANCE

The resistant (R) parents were completely free from infection while susceptible (S) parents showed different levels of infection (Table 1). The infection levels in F_1 's indicated that there was dominance of resistance over susceptibility in all the four crosses, though the levels of infection reached was not as much as the resistant parents. The F_2 ratios indicated that the two crosses involving 296 as one parent segregated into a 15 : 1 ratio of resistant and susceptible plants. In the other two crosses involving 303 as one parent, a segregation ratio of 57 : 7 was observed. It was interesting to note that the F_2 of the cross between the two resistant parents gave two susceptible plants out of 494 F_2 plants.

TABLE 1

Frequency of resistant (R) and susceptible (S) plants in different generations

Genera- tion	Disease Reaction	Cross				
		CS-3541 × 296	148 × 296	CS-3541 × 303	148 × 303	CS-3541 × 148
P ₁	R	153	184	153	184	184
	S	0	0	0	0	0
P ₂	R	145	145	96	96	153
	S	34	34	65	65	0
F ₁	R	148	105	—	99	88
	S	5	7	—	6	0
F ₂	R	414	563	528	566	492
	S	21	39	60	67	2
	ER	15:1	15:1	57:7	57:7	∞:0
	χ ²	1.50	0.05	0.33	0.08	0.016
	P	.20—.25	.80—.90	.50—.70	.70—.80	.90—.95

ER = Expected ratio

A 15 : 1 ratio observed in crosses with 296 indicated that two gene pairs which are duplicatory in action are controlling SDM resistance. However, the other two crosses involving 303 as a common parent exhibited a 57 : 7 ratio which is possible in a 3-gene control of SDM resistance in which the first two loci are segregating in a 9 : 7 complementary ratio, i. e., two genes are involved in conferring resistance. Presence of both together in dominant state conferred resistance while absence of either resulted in susceptibility. The third gene in this system was more powerful which alone can give resistance in dominant condition. Thus, this gene segregated in a 3 : 1 ratio.

Hence, together the three genes resulted in a 57 : 7 trigenic ratio. It is possible to show that the third gene can give a 14 : 2 ratio with one of the two complementary genes, which was very close to the 15:1 ratio obtained in the other two crosses involving 296. The two susceptible plants observed in the F_2 of the cross involving two resistant parents, CS-3541 \times 148, could be a chance occurrence, though segregation of some genes with minute modifying effects which were not in a homozygous conditions in the parents could not be ruled out.

QUANTITATIVE GENETIC ANALYSIS

A perusal of the means of various generations in different crosses (Tables 2) suggested that resistance to SDM was a quantitative threshold character. The differences between the resistant and susceptible parents, F_1 's F_2 's and F_3 's were significant. Higher susceptibility of F_2 's involving 303 as a susceptible parent indicated that 303 contributed more genes for susceptibility to its progenies. The F_1 hybrid between resistant parents was absolutely resistant while the (R \times S) hybrids showed partial dominance of resistance over susceptibility. However, there was no significant difference between F_2 and F_3 generations.

TABLE 2

Downy mildew susceptibility (%) in different generations of five crosses

Generation	Resistance reaction of parents	No. of crosses/parents	Average SDM susceptibility (%)
Parents	R	2	0.00
	S	2	28.43
F_1	R \times R	1	0.00
	R \times S	3	4.97
F_2	R \times R	1	0.56
	R \times S	4	7.95
Back Crosses	(R \times R) \times R	2	3.33
	(R \times R) \times S	3	3.23
F_3	(R \times S) \times S	4	18.00
	(CS-3541 \times 296)	14	5.71
	(148 \times 296)	12	8.12
	(CS-3541 \times 303)	18	7.25
	(148 \times 303)	37	7.26
(148 \times CS-3541)	R \times R	40	0.75

The F_2 generation of $R \times R$ cross showed less than one percent susceptibility. F_3 progenies of this cross showed a narrow range of susceptibility. The F_2 variation for susceptibility in $R \times S$ crosses ranged from 4 to 10 per cent, while F_3 differences were significant in $R \times S$ crosses and this provided an opportunity to select cross *per se* as well as selection of resistant progenies within the crosses.

Gene effects were estimated in two ($R \times S$) crosses, viz., 148×296 and 148×303 (Table 3 and 4). In the cross (148×296), resistance was governed by additive factors. The interaction effects varied in their magnitude as well as direction. Apart from additive gene effects, epistasis of duplicate nature was also involved the resistance. In

TABLE 3

Mean values (\sin^{-1} %) of the six generations of two crosses

Generation	148 × 296	148 × 303
P_1 (Res.)	1.000	1.000
P_2 (Susc.)	4.075	6.345
F_1	2.595	2.415
F_2	2.670	3.315
BC-1	1.905	2.335
BC-2	5.670	3.240
F_3	8.125	7.257
MP	2.537	3.672
Heterosis (%)	2.270	-34.24

TABLE 4

Estimates of gene effects for SDM resistance in two crosses

Parameter	148 × 296	148 × 303
m	2.670	3.315
d	-3.765	-0.905
h	4.527	-3.367
i	4.470	-2.110
j	-8.840	-9.155
l	-9.355	3.135
Epistasis type	Duplicate	Duplicate
$H = (\hat{h}-\hat{i} - \hat{d}-\frac{1}{2}\hat{j})$	-0.597	-2.415
Inbreeding depression (%)	2.89	37.27

the other cross, both heterosis and inbreeding depression were quite large and gene interaction of dominance \times dominance type increased the susceptibility. The epistasis in this cross was also of duplicate type. The R^2 values were high indicating high heritability of SDM resistance.

DISCUSSION

While extremely susceptible varieties of sorghum like DMS 652 may show near total incidence of downy mildew, several agronomically desirable varieties also show high levels of downy mildew susceptibility. In the present study the incidence of downy mildew in 296 was about 24 per cent while in 303 it was 66 per cent. Under such situations, classification into discrete classes of resistant and susceptible is possible as is frequently done, but it also presents problems. Strickberger (1968) states that "although lacking a continuous distribution with intermediate values, such characters may nevertheless be influenced by numerous polygenes. The relationship between polygenes and expression of discontinuous characters comes about through the establishment of 'thresholds'. That is, those polygenically determined genotypes which have values below the threshold show no expression of the character. Expression occurs only when the genotypes have values above this threshold". Since SDM appears to behave as a threshold character, both qualitative and quantitative analysis were attempted and attempts made to reconcile the findings.

Miller (1966) and Puttarudrappa, Kulkarni, Kaffari and Goud (1972) indicated qualitative inheritance with not more than two genes involved. It was clear in this study that there were three genes with major effects influencing SDM resistance in the parental material. When 296 was involved in crossing, only two of the three genes segregated giving a 15 : 1 duplicate dihybrid F_2 ratio; when 303 was involved, a 57 : 7 F_2 ratio was obtained indicating that two of the genes segregated in a 9 : 7 ratio and the third gene in a 3 : 1 ratio. Hence, SDM resistance in the crosses studied was controlled genetically by three pairs of genes with both complementary and duplicatory types of interactions involved in their genetics. Quantitative genetic analysis of this trait as threshold character corroborated the results of the qualitative genetic analysis. Resistance was governed by additive factors. Among the interaction types in the ($R \times S$) crosses, duplicatory interactions were predominant. Similar duplicatory gene interactions were noticed in the segregation ratios. Presence of modifying genes was suggested by the appearance of few susceptible segregates in the ($R \times R$) cross.

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