Asian Journal of Plant Sciences

ISSN 1682-3974

science alert

ANSInet
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Asian Journal of Plant Science 3 (1): 11-13, 2004
ISSN 1682-3974

Genetic Analysis of Resistance to Head Bug *Eurystylus oldi* (Poppius) in Sorghum (*Sorghum bicolor* (L.) Moench)

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Abstract: Genetic analysis were carried out to determine heterotic effects, gene action and inheritance of resistance to head bug, *Eurystylus oldi* Poppius in four sorghum crosses. Resistance was found dominant over susceptibility. Significant negative heterotic effect above mid-parent and better parent for grain damage rating was detected for all crosses. Dominance gene action is more important for the three resistance traits: grain damage rating, floaters percentage and germination percentage. Inheritance to *E. oldi* is conditioned by one dominant gene in two F_2 populations, while resistance in the remaining two F_2 populations is controlled by two dominant genes and in part by genes at two or more loci.

Key words: Genetics, *Eurystylus oldi*, resistance, dominance, heterosis, sorghum

INTRODUCTION

Sorghum is cultivated under diverse agroecosystems and its production is influenced by various biotic and abiotic factors. The stability of sorghum production is threatened by several insect pests. *Eurystylus oldi* (Poppius) popularly known as head bug feed mainly on the developing grain and occasionally on tender parts of the plant. The nymphs and adults suck sap from developing grain, which remain unfilled and shrivel. *E oldi* causes severe yield losses due to its feeding and oviposition activities in Asia and Africa, particularly in Western Africa. Recommended chemical and cultural control methods to reduce yield losses are beyond the reach of the subsistence farmers. Genetic solution to the pest problems are desirable, since they are packaged with the seed and involves no further purchase of external in puts.

Some sorghum genotypes have been screened and found resistant to *E. oldi*[1-3]. The resistant genotypes that have shown consistent results under artificial infestation at Institute for Agricultural Research (IAR) Samaru are however, poor in yield and other agronomic traits and some lack adaptability to local conditions.

Incorporation of *E. oldi* resistance into improved genotype has proved difficult, mainly due to inadequate knowledge of the genetic basis of resistance. This study aims at giving information on heterosis, gene actions and mode of inheritance of resistance, which are important in order to develop a resistance breeding programme.

MATERIALS AND METHODS

The plant materials used are HRhb 94001 HRhb 94002 (both resistant to *E oldi*), HRhb 94001S and HRhb 94002S (both susceptible to *E. oldi*). They were crossed in all possible combinations (excluding reciprocals) using hand emasculation. The four F_1 hybrids were self-fertilized to produce F_2 seeds.

Parents, F_1 and F_2 populations of each cross were planted with three replications at IAR research field. The parental genotypes and F_1s were planted in two rows plots while F_2s were planted in four-row plots. Each row was 5 m long, spaced at 0.75 m between rows and 0.25 m between plants in a row. At soft dough stage, 10 pairs of adult *E. oldi* (i.e., male and female) were released into each head cage of the test materials (Artificial infestation) as recommended by Sharma *et al.*[4]. Each plant was evaluated for three resistance parameters: Grain damage rating on visual scale (1=grains fully developed without feeding punctures) to (9=grains highly shriveled and slightly visible outsides the glumes), floaters percentage and germination percentage.

Data for both floaters and germination percentages were transformed into arc sine values for analysis. Heterotic effects were computed from entry means, while

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the genetic component of variance was estimated using mean squares according to Kempthorne[5] narrow sense heritability was estimated using Grafius *et al.*[6] formula and chi-square method was used to determine the fit to expected F_2 segregation ratios for *E. oldi* resistance genes.

RESULTS AND DISCUSSION

Percent F_1 heterosis above mid-parent and better parent is shown in Table 1. All the F_1 hybrids showed high degree of resistance to *E. oldi*. Negative heterosis of F_1 mean above mid-parents value was significant for damage rating in all crosses, similar negative and significant heterosis in two crosses for the same trait above better-parent was obtained. Negative and significant heterosis for floaters percentage above mid-parent value was obtained in one cross. This suggests dominance of resistance over susceptibility, as a result of dominance and other non-additive gene action. Positive, low and significant heterosis for floaters percentage and germination percentage showed partial dominance of resistance over susceptibility in all crosses for germination percentage and two crosses for floaters percentage. Therefore, suggesting the importance of nonadditive gene action for these traits.

Components of variance (Table 2) revealed the preponderance of dominance variance (δ^2_D) over that of additive (δ^2_A) for the three parameters; grain damage rating, floaters percentage and germination percentage (δ^2_D=35.28, 2.73 and 29.9 respectively) and (δ^2_A=0.016, 1.949 and 1.764, respectively). The importance of dominance gene action was further confirmed by the δ^2_A/δ^2_D value that is less than unity for all the resistance traits, this result conform to those of Agrawal and Abraham[7] that reported resistance to shoot fly was predominantly controlled by non-additive gene action. Low narrow-sense heritability was obtained for F_1 generation thus supporting the non-additive or dominance gene action for all resistance traits.

From previous studies, grain damage rating is the most important resistance trait because it ultimately affects other *E. oldi* resistance traits[8-10]. Thus Table 3 shows mean grain damage rating, range and segregation in F_2 populations. Plants with scores of I to 4 were considered resistant, while plants with scores of 5-9 were considered susceptible. Resistant parents common in

Table 1: Percent F_1 heterosis above mid-parent and better parent for resistance to *E. oldi* in four sorghum crosses

	Grain damage rating (1-9)		Floaters percentage (arc sine)		Germination percentage (arc sine)	
Cross	MP	BP	MP	BP	MP	BP
$R_1 \times S_1$	-47.82*	5.88*	-6.98	14.67*	19.32*	0.42
$R_1 \times S_2$	-65.85*	-17.65*	12.35*	32.78*	26.56*	2.31
$R_2 \times S_1$	-6.49*	44.00*	3.34	21.15*	29.66*	17.5*
$R_2 \times S_2$	-48.89*	-8.00*	-12.75*	-1.79	37.92*	16.62*

*=Significance at 5% LSD

R_1=HRhb 94001; R_2=HRhb 94002; S_1=HRhb 940015 and S_2=HRhb 94002S, MP=Mid-Parent, BP=Better-Parent

Table 2: Components of variance and percent heritability for *E. oldi* resistance traits

Component	Grain damage rating (1-9)	Floaters percentage (arc sine)	Germination percentage (arc sine)
δ^2_m	0.044**	15.347	9.124**
δ^2_f	0.080**	0.242	4.989**
δ^2_{mf}	35.25**	2.73*	29.9**
δ^2_A	0.016	1.949	1.764
δ^2_D	35.25	2.73	29.90
δ^2_A/δ^2_D	0.0005	0.714	0.059
H^2(ns)	0.35	41.18	29.70

*, **=Significant at 5 and 1% probability levels

δ^2_m, δ^2_f and δ^2_{mf} =component of variance for males, females and males x females (Resistant genotypes=males and susceptible genotypes=females) δ^2_A=Average additive genetic variance; δ^2_D =Dominance genetic variance and h^2 (ns)=Narrow-sense heritability

Table 3: Grain damage rating, range and segregation ratios for resistance to *E oldi* among parents and their F_1 and F_2 generations

			Observed			Chi-square value at expected ratio		
Cross	Parent and progeny	Mean grain damage rating and range	R	S	Total	3:1	9:7	13:3
$R_1 \times S_1$	R_1 (HRhb 94001)	1.7 (1-2)	80	0	80			
	S_1 (HRhb 94001S)	5.2 (5-7)	0	78	78			
	F_1	1.8 (1-3)	80	0	80			
	F_2	2.0 (1-6)	122	37	159	0.25	23.93**	2.13
$R_1 \times S_2$	R_1 (HRhb 94001)	1.7 (1-2)	75	0	75			
	S_2 (HRhb 94002S)	6.5 (5-9)	0	77	77			
	F_1	1.4 (1-2)	78	0	78			
	F_2	2.4 (1-7)	112	48	160	2.133	12. 29**	13.29**
$R_2 \times S_1$	R_2 (HRhb 94002)	2.0 (1-3)	76	0	76			
	S_1(HRhb 94001S)	5.2 (5-7)	0	69	69			
	F_1	2.3 (1-4)	70	0	70			
	F_2	3.0 (1-9)	98	60	158	14.186**	2.14	38.33**
$R_2 \times S_2$	R_2 (HRhb 94002)	2.0 (1-3)	80	0	80			
	S_2 (HRhb 94002S)	6.5 (5-9)	0	71	71			
	F_1	2.3 (1-4)	79	0	79			
	F_2	2.7 (1-6)	109	51	160	4. 04*	13.04**	18.09**

* Indicates significance at P=0.05 **Indicates significance at P=0.01

different crosses showed consistency in reaction to *E. oldi* at their F_1. The hybrids for all combinations were resistant with the mean grain damage ratings equal to or near that of the resistant parent, thus indicating that one or more dominant genes controlled the resistance. In the F_2 population the chi-square values at expected ratio 13:3 (resistant: susceptible) are significant at the 1% level of significance for all the crosses except HRhb 94001 x HRhb 94001S (R_1 x S_1), thereby indicating poor fit of the observed segregations to this ratio. Similarly, highly significant chi-square value (P=0.01) was obtains for three crosses at the expected segregation ratio 9:7, therefore, poor fit of the observed segregation ratio. At the expected segregation ratio of 3:1 the cross HRhb 94002 x HRhb 94001S (R_2 x S_1) fit poorly (P=0.01) while HRhb 94002 x HRhb 94002S (R_2 x S_2) is significant at 5% significance level, also indicating poor fit of the observed segregation ratio.

In two F_2 populations involving the resistant genotype HRhb94001, the chi-square values at expected ratio 3:1 (resistant: susceptible) are not significant, indicating good fit of the observed segregation ratios. A population each of the F_2 populations gave the best fit of 9:7 and 13:3 ratio. The F_2 populations that segregated in 3:1 (resistant:susceptible) ratio suggests that resistance in conditioned by one dominant gene. Those F_2 populations that segregated at 9:7 ratios indicates two dominant genes are in control of resistance to *E. oldi,* while F_2 populations that fit into 13:3 revealed that resistance in controlled in part by genes at two or more loci.

In conclusion all the F_1 hybrids showed high degree of resistance to *E. oldi*. The component of variance revealed that dominance gene action is more important for the three resistance traits. Resistance to *E. oldi* is conditioned by one dominant gene in two F_2 populations, while a population each is being controlled by two dominant genes and in part by genes at two or more loci.

ACKNOWLEDGEMENTS

I am grateful to professor Jacob.P. Voh, the Director of IAR and DR. O. Ajayi formerly of ICRISAT for providing facilities, fund and encouragement to undertake this research.

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