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Evaluation of A_1, A_2, A_3, $A_{4(M)}$, $A_{4(G)}$ and $A_{4(VZM)}$ cytoplasms in iso-nuclear backgrounds for grain mold resistance

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Abstract

Breeding for resistance to grain mold, an economically important disease of sorghum, has been only partially successful. Hybrid technology is well developed in sorghum due to the availability of CMS system and at present almost all commercial hybrids are based on A_1 CMS system. To compare the available alternate CMS systems for grain mold resistance, 72 hybrids produced by crossing 36 A-lines (six CMS systems; A_1, A_2, A_3, $A_{4(M)}$, $A_{4(G)}$, $A_{4(VZM)}$ each in six nuclear backgrounds) with two common restorers, were evaluated during 2006 and 2007 rainy seasons in grain mold nursery at ICRISAT. ANOVA indicated influence of cytoplasm on the responses of hybrids to grain mold infection as measured by PGMR (Panicle grain mold resistance) score. The A_1 cytoplasm seemed to contribute to grain mold resistance followed by $A_{4(VZM)}$ and A_2 cytoplasms. The $A_{4(M)}$ cytoplasm had superior GCA effects while the A_1 and $A_{4(VZM)}$ cytoplasm based hybrids had superior SCA effects for PGMR score. Almost all the hybrids had significant *per se* mid-parent heterosis. A_1 cytoplasm is best suited for the development of sorghum hybrids for the rainy season adaptation with grain mold resistance. However, use of alternate cytoplasms (A_2 and $A_{4(VZM)}$) for hybrid development should not increase the risk of grain mold in commercial grain production.

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1. Introduction

Sorghum (*Sorghum bicolor* (L.) Moench) is an important crop grown in the arid and semi-arid regions of the world. Grain mold, a highly destructive disease of sorghum cultivated in the rainy season, is widely distributed in the semi-arid tropics of Africa, Americas and Asia including India (Stenhouse et al., 1997). Grain mold is broadly defined as pre-harvest grain deterioration caused by several fungal genera interacting parasitically and/or saprophytically with developing grain (Thakur et al., 2006). In India, *Fusarium verticillioides*, *Curvularia lunata* and *Alternaria alternata* are more pathogenic than others (Thakur et al., 2003). The disease is particularly important on improved, short- and medium duration sorghum cultivars that mature during rains in humid tropical and sub-tropical climates. Grain mold results in reduction of seed mass, seed germination, and storage and food/feed processing quality and hence reduce the market value. Production losses due to grain mold range from 30% to 100% depending on the cultivar, time to flowering and prevailing weather conditions from flowering to harvesting (Singh and Bandyopadhyay, 2000). Grain mold resistance had been shown to be determined by several qualitative trait loci that include grain hardness, panicle compactness and shape, presence or absence of a pigmented testa, photoperiod sensitivity, glume coverage, production of phenols, antifungal proteins and other secondary metabolites. However, these loci do not account for all the variation observed for grain mold resistance in sorghum (Rooney and Klein, 2000).

Major efforts in breeding A_1 cytoplasmic-nuclear male sterility-based sorghum hybrid seed parents for grain mold resistance at International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Patancheru, India, and other locations in India as well as in the US have met with partial success. Cytoplasmic and nuclear genetic diversity of male-sterile (A-) as well as restorer (R-) lines in sorghum is important to avoid the disease outbreak as it happened in 1970 for turcicum leaf blight of corn hybrids possessing a uniform Texas (T) cytoplasm (Tatum, 1971). In India, while there was 37% reduction in area for sorghum production, yield increased by 80% (USDA, 1997) due to

concerted effort in the development and expansion of rainy season adapted sorghum hybrids. The commercial hybrids produced so far all over the globe are based on the single cytoplasm designated as *milo* or A_1 (Reddy and Stenhouse, 1994; Moran and Rooney, 2003). However, utilization of the non-*milo* CMS systems at commercial level depends on several factors such as influence of cytoplasm on responses to pests and diseases apart from stability of male-sterility, restorer gene frequency in the germplasm and availability of commercially viable heterosis (Reddy et al., 2005). In sorghum, type of cytoplasm (A_1 or A_2) does not affect grain mold severity and *Fusarium* head blight incidence (Stack and Pedersen, 2003) but has been shown to increase susceptibility to rust (*Puccinia purpurea*), zonate leaf spot (*Gloeocercospora sorghi*), and leaf blight (*Exserohilum turcicum*) (Rodriguez et al., 1994). However, a reliable comparison of different cytoplasms has not been possible since alloplasmic male-sterile lines with a common genetic background and common fertility restorers were not available. Hence the present study was conducted to determine the influence of cytoplasms, A_1, A_2, A_3, $A_{4(M)}$, $A_{4(G)}$ and $A_{4(VZM)}$, on grain mold resistance using a set of diverse iso-nuclear and allo-cytoplasmic sorghum hybrids.

2. Materials and Methods:

2.1. Genetic material

Six diverse sources of male-sterility inducing cytoplasms that include A_1, A_2, A_3, $A_{4(M)}$, $A_{4(G)}$ and $A_{4(VZM)}$ in the genetic backgrounds of ICSA 11, ICSA 37, ICSA 38, ICSA 42, ICSA 88001 and ICSA 88004 thus making a total of 36 A-lines were crossed with two varieties (as R-lines); IS 33844-5 and M 35-1-19 that restored fertility on all the six CMS systems to produce 72 hybrids. The A-lines used in the study were originally developed in A_1 cytoplasm through pedigree selection from segregating populations derived from the crosses between improved germplasm lines during 1980-1990 (Reddy et al., 2005). The R-lines were developed through direct selections from landraces during early 1990's. The A_1, A_2, A_3, $A_{4(M)}$, $A_{4(G)}$ and $A_{4(VZM)}$ versions of the 6 male-sterility maintainer (B-) lines were developed through repeated back crossing of the B-lines to the known cytoplasm source. Significant differences for grain mold resistance in the six nuclear genetic backgrounds were found in the earlier studies (Ramesh et al., 2008).

2.2. Experimental design and layout

A total of 84 entries including 72 hybrids, six B-lines (ICSB 11, ICSB 37, ICSB 38, ICSB 42, ICSB 88001 and ICSB 88004), two R-lines (IS 33844-5 and M 35-1-19) and four checks (296B-high yielding B-line susceptible to grain mold, RS 29-high yielding R-line, CSH 16-high yielding hybrid and IS 14384-grain mold resistant line) were evaluated in grain mold screening blocks at ICRISAT, Patancheru during the 2006 and 2007 rainy seasons. The 72 hybrids were planted in a split-split-plot design with three replications considering R-lines as main plots, A-lines as sub-plots and cytoplasms as sub-sub-plots so that the cytoplasms will be assessed with more precision (have more degrees of freedom). The 6 B-lines, 2 R-lines and 4 checks were evaluated in an adjacent block in randomized complete block design with three replications. Each entry was planted in two rows of 2 m length with a spacing of 75 cm between rows and 15 cm between plants in a row.

2.3. Grain mold nursery management and disease assessment

Sprinkler irrigation was provided twice a day on rain-free days for 30 min each during noon and evening from flowering to physiological maturity to create high humidity (>90% relative humidity) that is congenial for the development of mold on the developing grains. Ten uniformly flowered panicles were tagged in each replication for recording panicle grain mold rating (PGMR) at physiological maturity using a progressive 1-9 scale where 1= no mold, 2= 1-5%, 3= 6-10%, 4= 11-20%, 5= 21-30%, 6= 31-40%, 7= 41-50%, 8= 51-75% and 9=>75% molded grains on a panicle (Thakur et al., 2006).

2.4. Data analysis

Data of individual years were subjected to analysis of variance using split-split-plot model treating R-lines as main plots, A-lines as sub-plots and cytoplasms as sub-sub plots, with Genstat 12th edition. Separate analysis of variance (ANOVA) for individual years were done to test the significance of differences among the F_1s. The error variances in the trials conducted in two years were homogeneous, as revealed by Bartlett's test

(1937), providing statistical validity to carry out combined ANOVA. The genotypes were considered fixed while the years and replications were considered as random effects. A combined analysis was performed to test the significance of the hybrid × year interaction. Line × Tester analysis (Kempthorne, 1957) was used to study combining ability estimates using females as lines and males as testers. The mid-parent heterosis was worked out following Singh and Narayanan (1993). The main effects of CMS and restorer lines were equivalent to general combining ability (GCA), and the effects of a CMS line with a specific restorer were equivalent to specific combining ability (SCA) (Hallauer and Miranda, 1981). The significance of the rank correlation suggested cross over type of genetic interaction. The genotypes are specific to the year of evaluation and hence the results are presented for the individual years.

3. Results and Discussion

3.1. Analysis of variance

Individual analysis of variance (ANOVA) for 2006 and 2007 rainy seasons depicted highly significant differences between hybrids for PGMR score. Combined analysis of the data obtained over the years suggested differential responses to grain mold infection among the A-lines measured through PGMR. However, mean squares due to years were significant indicating resistance varied with the year of evaluation. The responses of A-lines to grain mold infection varied with the two experimental years as revealed from significant mean squares due to year × A-line interactions for PGMR. Influence of environmental variables, such as relative humidity and temperature, at grain maturity on infection by grain mold fungi and mold development has been well documented (Indira and Muthusubramanian, 2004; Navi et al., 2005). The significant mean squares due to year × A-line × R-line interactions suggested that the SCA effects are sensitive to seasonal changes over the years. The seasonal changes driven by variation in environmental variables cause differential responses of the hybrids to grain mold infection and thereby variation in SCA effects. The significant mean squares due to cytoplasms *per se* and their first-order interaction with A-line and second-order

interaction with A-line, R-line and year for PGMR scores suggested the overall influence of cytoplasm on the responses of hybrids to grain mold infection (Table 1).

3.2. Cytoplasm effects on hybrid mean performance

Since the PGMR score is inversely proportional to resistance, the low PGMR score implies more resistance. When overall mean of the hybrids in 12 nuclear backgrounds across six cytoplasms, is compared, hybrids based on A_1 cytoplasm had significantly lower PGMR score and thus more resistant than $A_{4(M)}$ cytoplasm; while the hybrids based on A_3 and $A_{4(VZM)}$ cytoplasms had significantly lower PGMR scores than $A_{4(M)}$ and $A_{4(G)}$ cytoplasms during 2006 rainy season while the A_1 and A_2 hybrids had significantly lower PGMR scores than those based on A_3, $A_{4(M)}$ and $A_{4(G)}$ cytoplasms during the 2007 rainy season (Table 2). Cytoplasmic influence on PGMR score varied with the nuclear background. Similar result was reported by Stack and Pedersen (2003) wherein the A_1 cytoplasm exhibited slightly lower grain mold incidence than A_2 (64 versus 70%). They observed that although the cytoplasm effect for grain mold incidence was statistically significant, most of the variation in grain mold incidence was attributable to nuclear genotype. However, in the present study, genetic backgrounds of ICSA 42 x IS 33844-5, ICSA/B 11 × M 35-1-19 and ICSA 42 × M 35-1-19 during 2006 rainy season, and the genetic backgrounds of ICSA 37 x IS 33844-5, ICSA 38 x IS 33844-5 and ICSA 88001 × M 35-1-19 during 2007 rainy season had significantly lower PGMR scores across the six cytoplasms than other cross combinations. Though the influence of the genetic background varied with the year of evaluation and with more grain mold incidence reported in 2007 rainy season, the contribution of A_1 cytoplasm towards resistance to grain mold cannot be ignored especially under higher incidence of grain mold as observed during 2007 rainy season (Table 2). The A_1 cytoplasm seemed to have some influence on grain mold resistance followed by $A_{4(VZM)}$ and A_2 cytoplasms in majority of nuclear backgrounds in both the 2006 and 2007 rainy seasons. Thus, the use of alternate cytoplasms (A_2 and $A_{4\ (VZM)}$) to incorporate genetic diversity into grain sorghum hybrids should not increase the risk of grain mold in commercial grain production.

3.3. Cytoplasm effects on GCA, SCA and heterosis

Since low PGMR score is desirable in sorghum hybrids, negative GCA and SCA effects are desired in the parents, and heterosis in the negative direction is desired for this trait. The $A_{4(M)}$ cytoplasm had superior GCA effects compared to A_1, A_2, A_3, $A_{4(G)}$ and $A_{4(VZM)}$ cytoplasms for PGMR scores during both 2006 and 2007 rainy seasons (Table 3). For SCA effects, the A_1 and $A_{4(VZM)}$ cytoplasm based hybrids had superior SCA effects compared to the A_2, A_3, $A_{4(G)}$ and $A_{4(M)}$ cytoplasm based hybrids for PGMR score during 2006 rainy season and during 2007 rainy season, the $A_{4(G)}$ cytoplasm marginally contributed to significant SCA effects compared to other cytoplasms (Table 4). A total of 69 of the 72 hybrids during 2006 and 68 hybrids during 2007 rainy seasons had significant negative *per se* mid parent heterosis for PGMR scores indicating the significance of heterosis for grain mold resistance. However, when mid-parent heterosis of all the six cytoplasm based hybrids, were compared as six groups among themselves by two-sample paired 't' test, the hybrids based on all the six cytoplasms were on par for mid parent heterosis during 2006 rainy season while the A_1 cytoplasm based hybrids had significantly superior mid parent heterosis compared to A_3, $A_{4(M)}$ and $A_{4(G)}$ cytoplasm based hybrids; and the A_2 cytoplasm based hybrids had significantly superior mid parent heterosis compared to $A_{4(M)}$ and $A_{4(G)}$ cytoplasm based hybrids during 2007 rainy season (Table 5).

3.4. Conclusions

For PGMR scores recorded as an indicative of grain mold resistance, the significant mean squares due to cytoplasms *per se* and their first-order interaction with A-line and second-order interaction with A-line, R-line and year for PGMR scores suggested the overall influence of cytoplasms on the responses of hybrids to grain mold infection. The A_1 cytoplasm followed by $A_{4(VZM)}$ and A_2 cytoplasms contributed to grain mold resistance in the hybrids. The $A_{4(M)}$ cytoplasm had superior GCA effects compared to other cytoplasms for PGMR score while the A_1 cytoplasm based hybrids were more resistant and had more SCA effects compared to other cytoplasm based hybrids. However, the hybrids based on all the cytoplasms were heterotic. Hence the widely exploited A_1 cytoplasm is best suited for the development of sorghum hybrids for the rainy season adaptation with grain mold resistance.

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Table-1. Combined analysis of variance of isonuclear alloplasmic A-lines and their hybrids for PGMR score in 2006 and 2007 rainy seasons

Source of variation	df	Mean Sum of Squares PGMR[a]
Year	1	1069.95**
Residual	2	4.25
R-line	1	0.08
Year × R-line	1	4.87
Residual	4	0.89
A-line	5	0.65*
Year × A-line	5	0.77**
R-line × A-line	5	0.13
Year × R-line × A-line	5	1.41**
Residual	40	0.21
Cytoplasm	5	1.22**
Year × Cytoplasm	5	0.84**
R-line × Cytoplasm	5	0.84**
A-line × Cytoplasm	25	0.74**
Year × R-line × Cytoplasm	5	0.59**
Year ×A-line × Cytoplasm	25	0.76**
R-line × A-line × Cytoplasm	25	0.73**
Year × R-line × A-line × cytoplasm	25	0.53**
Residual	240	0.11

*Significant at p=0.05; **Significant at p=0.01

[a]PGMR (panicle grain mold rating) taken on 10 panicles based on 1 to 9 scale, where 1= no mold, 2= 1-5%, 3= 6-10%, 4= 11-20%, 5= 21-30%, 6= 31-40%, 7= 41-50%, 8= 51-75%, 9= >75% grain colonized by grain mold fungi.

Table 2. Mean performance of iso-nuclear allo-plasmic hybrids for PGMR[1] score in 2006 and 2007 rainy seasons

	2006 rainy season							2007 rainy season						
Iso-nuclear crosses	**A_1**	**A_2**	**A_3**	**$A_{4(M)}$**	**$A_{4(G)}$**	**$A_{4(VZM)}$**	**Mean of genetic background**	**A_1**	**A_2**	**A_3**	**$A_{4(M)}$**	**$A_{4(G)}$**	**$A_{4(VZM)}$**	**Mean of genetic background**
ICSA 11x IS 33844-5	5.00	4.00^{ah}	4.00^{bk}	4.00^{cm}	5.00	4.00^{eo}	**4.33**	6.67^{c}	6.80^{g}	7.00	7.50	7.07	7.17	**7.03**
ICSA 37 x IS 33844-5	4.00^{e}	3.67^{i}	4.00^{l}	4.00^{n}	4.00^{o}	5.33	**4.17**	6.17^{de}	6.7	6.40^{l}	6.45^{n}	7.00	7.07	**6.63**
ICSA 38 x IS 33844-5	3.67^{a}	5.00	4.00^{f}	4.00^{g}	4.00^{h}	4.00^{i}	**4.11**	6.86^{b}	6.70^{f}	7.97	6.50^{j}	6.80^{k}	6.70^{l}	**6.92**
ICSA 42 x IS 33844-5	3.00^{abde}	4.00	4.00	3.67	4.00	4.00	**3.78**	6.33^{bcd}	6.40^{fgh}	8.41	7.67^{j}	7.07^{k}	6.50^{ln}	**7.06**
ICSA 88001 x IS 33844-5	4.00	4.00	4.00	4.00	3.00^{dhkmo}	4.00	**3.83**	6.89^{d}	7.10^{h}	7.40	7.30	7.73	6.53^{ilno}	**7.16**
ICSA 88004 x IS 33844-5	5.00	4.00^{a}	3.67^{b}	4.00^{c}	4.00^{d}	4.00^{e}	**4.11**	7.03	7.33	7.00	6.87	7.33	7.26	**7.14**
ICSA 11 x M 35-1-19	4.00	4.00	3.00^{bfjk}	4.00	4.00	3.33^{eino}	**3.72**	7.38	7.47	7.57	7.87	7.60	7.13^{n}	**7.50**
ICSA 37 x M 35-1-19	4.00^{c}	4.00^{g}	4.00^{j}	4.67	4.33	3.00^{eilno}	**4.00**	6.30^{bcde}	6.73^{fgi}	7.47	7.80	7.07^{m}	7.57	**7.16**
ICSA 38 x M 35-1-19	3.00^{abcde}	4.00	4.00	4.00	4.00	4.00	**3.83**	6.47^{bcde}	6.97^{f}	7.97	7.30^{j}	7.23^{k}	7.47	**7.23**
ICSA 42 x M 35-1-19	3.33^{bde}	3.00^{fghi}	4.00	3.67	4.00	4.00	**3.67**	7.28^{c}	6.70^{g}	6.60^{bjk}	7.97	7.30^{m}	7.00^{n}	**7.14**
ICSA 88001 x M 35-1-19	5.33	4.00^{a}	3.67^{b}	4.00^{c}	3.67^{d}	4.00^{e}	**4.11**	6.80	6.93	6.90	6.73^{m}	7.37	6.53^{o}	**6.88**
ICSA 88004 x M 35-1-19	3.00^{abcd}	4.00^{g}	4.00^{j}	5.00	4.33^{m}	3.00^{ilno}	**3.89**	7.07^{cde}	7.5	6.80^{fjkl}	7.87	7.80	7.80	**7.47**
Mean	3.94^{c}	3.97	3.86^{jk}	4.08	4.03	3.89^{no}	**3.96**	6.77^{bcde}	6.94^{fgh}	7.29	7.32	7.28	7.06^{nol}	**7.11**
LSD (between overall mean of hybrids) (P= 0.05)				0.12							0.18			
LSD (between cytoplasms at same levels of A-line and R-line) (P= 0.05)				0.42							0.62			
LSD (between genetic backgrounds) (P= 0.05)				0.17							0.59			

[1]PGMR (panicle grain mold rating) taken for 10 panicles on a scale 1 to 9, where 1= no mold, 2= 1-5%, 3= 6-10%, 4= 11-20%, 5= 21-30%, 6= 31-40%, 7= 41-50%, 8= 51-75%, 9= >75% panicle surface area colonized by grain mold fungi

Significant differences between [a]A_1 and A_2, [b] A_1 and A_3, [c]A_1 and $A_{4(M)}$, [d]A_1 and $A_{4(G)}$, [e]A_1 and $A_{4(VZM)}$, [f]A_2 and A_3, [g]A_2 and $A_{4(M)}$, [h]A_2 and $A_{4(G)}$), [i]A_2 and $A_{4(VZM)}$, [j]A_3 and $A_{4(M)}$, [k]A_3 and $A_{4(G)}$, [l]A_3 and $A_{4(VZM)}$, [m]$A_{4(M)}$ and $A_{4(G)}$, [n]$A_{4(M)}$ and $A_{4(VZM)}$, [o]$A_{4(G)}$ and $A_{4(VZM)}$ cytoplasms for a given hybrid

Table-3. Estimates of GCA effects of iso-nuclear allo-plasmic A-lines for PGMR score in 2006 and 2007 rainy seasons

	2006 rainy season						2007 rainy season					
A-lines	**A_1**	**A_2**	**A_3**	**$A_{4(M)}$**	**$A_{4(G)}$**	**$A_{4(VZ M)}$**	**A_1**	**A_2**	**A_3**	**$A_{4(M)}$**	**$A_{4(G)}$**	**$A_{4(VZ M)}$**
ICSA 11	0.54	0.04^{afi}	0.54	-0.13^{cjn}	0.04^{dko}	0.70	-0.38^{*a}	0.14	0.01	-0.68^{**gjn}	-0.68^{**hko}	-0.08
ICSA 37	0.37	0.04	0.04	-0.46^{**cgjn}	-0.13^{d}	0.04	-0.33^{d}	0.12^{h}	-0.36^{*k}	-0.74^{**gm}	0.93**	-0.33^{o}
ICSA 38	0.04^{c}	0.04^{g}	-0.46^{**bfjl}	0.54	-0.13^{m}	0.04^{n}	-0.12	0.24	0.02	0.07	-0.18	0.18
ICSA 42	0.04^{d}	-0.46^{**agh}	-0.30^{*bk}	0.04^{m}	0.37	-0.30^{*eo}	0.31	0.61**	0.26	$-0.59^{**cgjmn}$	0.52**	0.21
ICSA 88001	-0.46^{**abe}	0.04	0.04	-0.80^{**gjmn}	-0.13	0.04	-0.39^{*abd}	0.52**	0.24	-0.12^{g}	0.17	0.04
ICSA 88004	0.70	-0.13^{ah}	-0.13^{bk}	-0.46^{**cm}	0.54	-0.30^{*eo}	-0.24^{e}	-0.29^{hi}	-0.16^{l}	0.17^{n}	0.22	0.69**
SE± (gi)			0.15						0.18			
SE+ (gi-gj)			0.21						0.26			

[1]PGMR (panicle grain mold rating) taken for 10 panicles based on 1 to 9 scale, where 1= no mold, 2= 1-5%, 3= 6-10%, 4= 11-20%, 5= 21-30%, 6= 31-40%, 7= 41-50%, 8= 51-75%, 9= >75% grain colonized by grain mold fungi.

*Significant at p=0.05; **Significant at p=0.01

Significant differences between $^{a}A_1$ and A_2, $^{b}A_1$ and A_3, $^{c}A_1$ and $A_{4(M)}$, $^{d}A_1$ and $A_{4(G)}$, $^{e}A_1$ and $A_{4(VZM)}$, $^{f}A_2$ and A_3, $^{g}A_2$ and $A_{4(M)}$, $^{h}A_2$ and $A_{4(G)}$, $^{i}A_2$ and $A_{4(VZM)}$, $^{j}A_3$ and $A_{4(M)}$, $^{k}A_3$ and $A_{4(G)}$, $^{l}A_3$ and $A_{4(VZM)}$, $^{m}A_{4(M)}$ and $A_{4(G)}$, $^{n}A_{4(M)}$ and $A_{4(VZM)}$, $^{o}A_{4(G)}$ and $A_{4(VZM)}$ cytoplasms for a given hybrid

Table 4. SCA effects as influenced by male sterility inducing cytoplasm (A_1, A_2, A_3, $A_{4(M)}$, $A_{4(G)}$ and $A_{4(VZM)}$) for responses to grain mold infection in sorghum iso-nuclear hybrids during 2006 and 2007 rainy seasons

	2006 rainy season						2007 rainy season					
Iso-nuclear crosses	**A_1**	**A_2**	**A_3**	**$A_{4(M)}$**	**$A_{4(G)}$**	**$A_{4(VZ\,M)}$**	**A_1**	**A_2**	**A_3**	**$A_{4(M)}$**	**$A_{4(G)}$**	**$A_{4(VZ\,M)}$**
ICSA 11x IS 33844-5	0.52*	0.02	0.52*	0.19	0.02	-0.65**^{eilno}	-0.07	-0.25	-0.05	-0.27	-0.03	-0.04
ICSA 37 x IS 33844-5	-0.65**^{abde}	0.02	0.02	-0.48*^{m}	0.19	0.02	0.08	0.73**	0.05	-0.04^{g}	0.37	0.28
ICSA 38 x IS 33844-5	0.02	0.02	-0.48*^{j}	0.52*	-0.15^{m}	0.02	-0.11^{b}	0.05	0.60*	-0.15^{j}	0.06	0.04
ICSA 42 x IS 33844-5	0.02^{e}	-0.48*^{fi}	0.35	0.02^{n}	-0.31^{ko}	0.69**	-0.05	-0.15	0.23	-0.22	-0.17	-0.25
ICSA 88001 x IS 33844-5	-0.48*^{cd}	0.02	0.02	0.19	0.19	0.02	-0.25	0.33	-0.12	0.29	-0.69**^{hmo}	0.15
ICSA 88004 x IS 33844-5	0.69**	-0.15^{ai}	-0.15^{bl}	-0.48*^{cn}	-0.48*^{do}	0.69**	-0.07	0.08	0.41	-0.22	-0.54*^{k}	0.00
ICSA 11 x M 35-1-19	-0.52*^{e}	-0.02^{i}	-0.52*^{l}	-0.19^{n}	-0.02^{o}	0.65**	0.07	0.25	0.05	0.27	0.03	0.04
ICSA 37 x M 35-1-19	0.65**	-0.02	-0.02	0.48*	-0.19	-0.02	-0.08	-0.73**^{g}	-0.05	0.04	-0.37	-0.28
ICSA 38 x M 35-1-19	-0.02	-0.02	0.48*	-0.52*^{jm}	0.15	-0.02	0.11	-0.05	-0.60*^{bj}	0.15	-0.06	-0.04
ICSA 42 x M 35-1-19	-0.02	0.48*	-0.35^{f}	-0.02	0.31	-0.69**^{eino}	0.05	0.15	-0.23	0.22	0.17	0.25
ICSA 88001 x M 35-1-19	0.48*	-0.02	-0.02	-0.19^{c}	-0.19^{d}	-0.02	0.25	-0.33^{h}	0.12	-0.29^{m}	0.69**	-0.15^{o}
ICSA 88004 x M 35-1-19	-0.69**^{abcd}	0.15	0.15	0.48*	0.48*	-0.69**^{ilno}	0.07	-0.08	-0.41^{k}	0.22	0.54*	0.00
SE(Sij)				0.18						0.26		
LSD(Sij-Skj) (P= 0.05)				0.62						0.71		

1. PGMR (panicle grain mold rating) taken for 10 panicles based 1 to 9 scale, where 1= no mold, 2= 1-5%, 3= 6-10%, 4= 11-20%, 5= 21-30%, 6= 31-40%, 7= 41-50%, 8= 51-75%, 9= >75% grain colonized by grain mold fungi

*Significant at p=0.05; **Significant at p=0.01

Significant differences between $^{a}A_1$ and A_2, $^{b}A_1$ and A_3, $^{c}A_1$ and $A_{4(M)}$, $^{d}A_1$ and $A_{4(G)}$, $^{e}A_1$ and $A_{4(VZM)}$, $^{f}A_2$ and A_3, $^{g}A_2$ and $A_{4(M)}$, $^{h}A_2$ and $A_{4(G)}$), $^{i}A_2$ and $A_{4(VZM)}$, $^{j}A_3$ and $A_{4(M)}$, $^{k}A_3$ and $A_{4(G)}$, $^{l}A_3$ and $A_{4(VZM)}$, $^{m}A_{4(M)}$ and $A_{4(G)}$, $^{n}A_{4(M)}$ and $A_{4(VZM)}$, $^{o}A_{4(G)}$ and $A_{4(VZM)}$ cytoplasms for a given hybrid

Table 5. Male sterility inducing cytoplasm effects on heterotic responses to grain mold infection in sorghum iso-nuclear hybrids in A1, A2, A3, A4(M), A4(G) and A4(VZM) CMS backgrounds in 2006 and 2007 rainy seasons

	Mid-parent heterosis 2006 rainy season						Mid-parent heterosis 2007 rainy season					
Iso-nuclear crosses	**A_1**	**A_2**	**A_3**	**$A_{4(M)}$**	**$A_{4(G)}$**	**$A_{4(VZM)}$**	**A_1**	**A_2**	**A_3**	**$A_{4(M)}$**	**$A_{4(G)}$**	**$A_{4(VZM)}$**
ICSA 11x IS 33844-5	-9.09*	-27.27**	-27.27**	-27.27**	-9.09*	-27.27**	-24.50**	-23.03**	-20.77**	-15.11**	-19.98*	-18.85**
ICSA 37 x IS 33844-5	-27.27**	-33.27**	-27.27**	-27.27**	-27.27**	-3.09	-29.61**	-23.56**	-26.98**	-26.41**	-20.14**	-19.34**
ICSA 38 x IS 33844-5	-33.27**	-9.09*	-27.27**	-27.27**	-27.27**	-27.27**	-19.77**	-21.64**	6.78	-23.98**	-20.47**	-21.64**
ICSA 42 x IS 33844-5	-52.64**	-36.86**	-36.86**	-42.07**	-36.86**	-36.86**	-27.24**	-26.44**	3.33	-11.84**	-18.74**	-25.29**
ICSA 88001 x IS 33844-5	-38.46**	-38.46**	-38.46**	-38.46**	-53.85**	-38.46**	-19.88**	-17.44**	-13.95**	-15.12**	-10.12**	-24.07**
ICSA 88004 x IS 33844-5	-9.09*	-27.27**	-33.27**	-27.27**	-27.27**	-27.27**	20.25*	-16.85**	-20.59**	-22.06**	-16.85**	-17.64**
ICSA 11 x M 35-1-19	-17.27**	-17.27**	-37.95**	-17.27**	-17.27**	-31.13**	-14.88**	-13.84**	-12.69**	9.23*	-12.34**	-17.76**
ICSA 37 x M 35-1-19	-17.27**	-17.27**	-17.27**	-3.41	-10.44*	-37.95**	-26.74**	-21.74**	-13.14**	-9.30*	-17.79**	-11.98**
ICSA 38 x M 35-1-19	-37.95**	-17.27**	-17.27**	-17.27**	-17.27**	-17.27**	-22.84**	-16.88**	4.95	-12.94**	-13.77**	-10.91**
ICSA 42 x M 35-1-19	-41.27**	-47.09**	-29.45**	-35.27**	-29.45**	-29.45**	-14.70**	-21.50**	-22.67**	6.62	-14.47**	-17.98**
ICSA 88001 x M 35-1-19	-8.65**	-31.45**	-37.10**	-31.45**	-37.10**	-31.45**	-19.38**	-17.84**	-18.20**	-20.21**	-12.63**	-22.58**
ICSA 88004 x M 35-1-19	-37.95**	-17.27**	-17.27**	3.41	-10.44**	-37.95**	-18.27**	-13.29**	-21.39**	9.02*	9.83**	9.83**
Paired "t" test probability				NS						bcdgh		

1. PGMR (panicle grain mold rating) taken for 10 panicles based on 1 to 9 scale, where 1= no mold, 2= 1-5%, 3= 6-10%, 4= 11-20%, 5= 21-30%, 6= 31-40%, 7= 41-50%, 8= 51-75%, 9= >75% grain colonized by grain mold fungi

*Significant at p=0.05; **Significant at p=0.01

Significant differences between [a] A_1 and A_2, [b] A_1 and A_3, [c] A_1 and $A_{4(M)}$, [d] A_1 and $A_{4(G)}$, [e] A_1 and $A_{4(VZM)}$, [f] A_2 and A_3, [g] A_2 and $A_{4(M)}$, [h] A_2 and $A_{4(G)}$), [i] A_2 and $A_{4(VZM)}$, [j] A_3 and $A_{4(M)}$, [k] A_3 and $A_{4(G)}$, [l] A_3 and $A_{4(VZM)}$, [m] $A_{4(M)}$ and $A_{4(G)}$, [n] $A_{4(M)}$ and $A_{4(VZM)}$, [o] $A_{4(G)}$ and $A_{4(VZM)}$ cytoplasms for a given hybrid