Resistance of Peanut Genotypes to Seed Infection by *Aspergillus Flavus* in Field Trials in India[1]

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ABSTRACT

Eleven peanut genotypes, six resistant and five susceptible to *in vitro* seed colonization by *Aspergillus flavus* Link (IVSCAF), were evaluated for field resistance to seed infection by *A. flavus* and other soil fungi, and for aflatoxin contamination, in seven environments in southern India. Five of the IVSCAF-resistant genotypes had significantly greater resistance to infection of seed by *A. flavus* in the field and had lower aflatoxin contamination than the IVSCAF-susceptible genotypes. Resistance to field infection of seed by *A. flavus* was stable across the seven environments. Significant interactions were found between environments and IVSCAF-susceptible genotypes for infection by *A. flavus, Aspergillus niger* van Tiegh. and *Macrophomina phaseolina* (Tassi.) Goid. Genotypes with field resistance to *A. flavus* also had significantly less seed infection by *A. niger, M. phaseolina,* and *Fusarium* spp. than had the *A. flavus*-susceptible genotypes. Significant positive correlations were found between IVSCAF-resistance and field resistance to *A. flavus* seed infection, and between the seed infection and aflatoxin B1 contamination. The field resistant genotypes J 11, Ah 7223, UF 71513, U 4-7-47 have yield levels and pod and seed characters acceptable in India.

Key Words: Groundnut, *Arachis hypogaea* L., resistance, *Aspergillus flavus,* mycotoxin.

Aflatoxin contamination of peanuts is a serious problem in many areas of the world. Peanuts are invaded by aflatoxigenic strains of the *Aspergillus flavus* Link group fungi, and subsequently contaminated with aflatoxin, while they are in the ground, during postharvest drying, and/or in storage (5). In the semi-arid tropics (SAT) aflatoxin contamination of peanuts is mainly preharvest in origin (8). Late season drought stress, common in this environment, is an important contributing factor to seed infection (3,4,8).

Researchers in the USA (1,13,14), West Africa (17,18), and India (9,11) have found several peanut genotypes resistant to *in vitro* colonization by *A. flavus* of rehydrated, undamaged, mature, stored seed (IVSCAF). But their resistance to infection by the aflatoxigenic fungi in the field is not established. For example, in Georgia, Davidson *et al.* (3) failed to show preharvest seed-resistance in the IVSCAF-resistant cultivar, Sunbelt Runner, and Blankenship *et al.* (2) found that Florunner and four IVSCAF-resistant genotypes grown under late season drought stress were all highly susceptible to aflatoxin contamination. In North Carolina, Kisyombe *et al.* (7) demonstrated a linkage between IVSCAF-resistance and preharvest-resistance in one of 14 genotypes. Zambettakis *et al.* (18) reported several IVSCAF-resistant genotypes having field resistance to *A. flavus* infection in Senegal. Mehan *et al.* (12) at ICRISAT, India, found that several IVSCAF-resistant genotypes had significantly less preharvest seed infection with *A. flavus* than IVSCAF-susceptible genotypes. Genotypes having resistance to preharvest seed infection by *A. flavus* or *A. parasiticus* Speare are known (7,12,18), but evaluations have been limited to one or two sites. The objectives of the present study were (1) to evaluate IVSCAF-resistant genotypes in the field for *A. flavus* infection and subsequent aflatoxin contamination, and (2) to evaluate stability of field resistance over environments.

Materials and Methods

Eleven genotypes (Table 1) were selected for testing based on their resistance or susceptibility *in vitro* to seed colonization by *A. flavus.* PI 337394F, UF 71513, Ah 7223, J11, Var. 27, and U4-47-7 are resistant to *in vitro* seed colonization by *A. flavus* (IVSCAF-resistant) (1,9,11,14), and TMV 2, Gangapuri, NCAc 17090, F1-5 x NCAc 17090, and EC 76446(292) are susceptible (IVSCAF-susceptible) (9,11). NCAc 17090 and F1-5 x NCAc 17090 have shown tolerance to drought at ICRISAT Center (6), and were included because of drought being implicated in seed infection by *A. flavus* (3,4,8).

Table 1. Details of peanut genotypes used.

Genotype ICG No.	Identity	Botanical variety	Country of origin	Seed coat color[3] Description	RHS color code
IVSCAF[1]-resistant genotypes					
4749	PI 337394F	fastigiata	Argentina	dark salmon	27A
7633	UF 71513	fastigiata	USA	salmon	27B
1326	J 11[2]	vulgaris	India	salmon	27B
3700	Ah 7223	vulgaris	Nigeria	salmon	27B
4601	Var.27	fastigiata	Australia	red	178A
3263	U4-47-7	vulgaris	Uganda	light salmon	27C
IVSCAF-susceptible					
221	TMV 2[2]	vulgaris	India	light salmon	27C
751	Gangapuri[2]	fastigiata	India	red	178A
	F1-5 X NCAc 17090	fastigiata	India	light salmon	27C
1697	NC Ac 17090	fastigiata	Peru	salmon	27B
2716	EC 76446(292)	fastigiata	Uganda	plum purple	79A

[1]IVSCAF = In vitro Seed Colonization by A. flavus of rehydrated, undamaged, mature, stored seed.

[2]Released Indian cultivars

[3]As per the Royal Horticultural Society, London, Color Chart

The genotypes were evaluated for field infection of seeds by *A. flavus* and subsequent aflatoxin contamination, at three locations in 1984 and four locations in 1985; all locations were in Andhra Pradesh State, India. Three locations, Tirupati, Bapatla, and ICRISAT Center, were common to both years. The fourth location, Anantapur, was added in 1985. All locations were in drought-prone areas. Different fields were used at each location in 1984 and 1985, all fields had light, sandy loam soils (Alfisols) except at Bapatla which had Inceptisol soils.

The trials were conducted in the 1984 and 1985 rainy seasons, sowing dates being normal (June-July) for the locations. Sowing dates were – ICRISAT Center (2 July 1984, 24 June 1985), Bapatla (5 July 1984, 29 June 1985), Tirupati (7 July 1984, 22 July 1985), Anantapur

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(22 July 1985). Forty Kg/ha P_2O_5 fertilizer was applied during land preparation. A randomized block design with four replications was used and plots were 10 m long by 2.1 m (7 rows) wide with seeds sown singly at 10 cm spacing along the rows. The trials were all rainfed. All genotypes were harvested at maturity (approximately 110-114 days after sowing) and the plants were arranged in windrows with pods exposed for 3 days to facilitate drying. Pods were then harvested and sun-dried to a seed moisture content of 7-8%. From each plot, 200 seeds from undamaged, mature, dried pods were tested for fungal infection (9). Two 50 g samples of seed from each plot were tested for aflatoxin content (15).

Using arc sine transformed values, analyses of variance were performed separately for seed infection by *A. flavus* and by each of the other fungi over the seven environments. Genotype x environment interactions were computed separately for IVSCAF-resistant and IVSCAF-susceptible genotypes. An analysis of variance was also performed for aflatoxin B_1 content of seed of the genotypes, using $\log_e$ transformed values. The locations used in 1984 and 1985 were regarded as seven environments : 1 (Tirupati), 2 (Bapatla), 3 (ICRISAT Center), 4 (Tirupati), 5 (Anantapur), 6 (Bapatla), and 7 (ICRISAT Center). An analysis was carried out for correlation between IVSCAF-resistance and field resistance to seed infection by *A. flavus*, using mean percentages of seed colonized (IVSCAF tests - data from previous experiments on the genotypes at ICRISAT Center in the 1981, 1982, 1983, and 1984 rainy seasons and from the environments 4, 5, and 7 in the present study) and the mean percentages of seed infected by *A. flavus* (data from the present study in seven environments).

Results

Conditions were conducive for seed infection by *A. flavus* in all environments (locations and seasons) as moderate to severe drought stress occurred during pod maturation. There was considerable variation in rainfall between environments (Fig. 1). Air temperatures were similar in environments 1, 2, 4, 5, and 6, maximum temperatures ranging from 28-37 C and minimum temperatures from 17-28 C. In environments 3 and 7 temperatures were slightly lower (26-36 C max., 11-25 C min.).

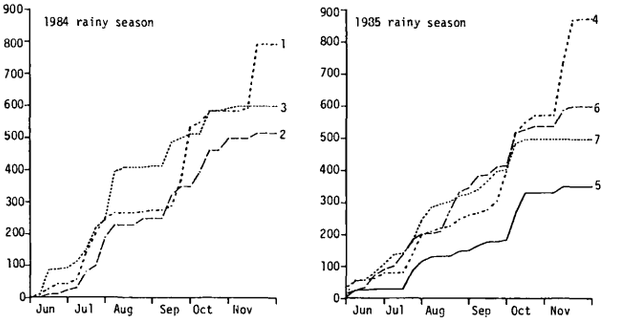

Fig. 1. Weekly cummulative rainfall in seven environments. ICRISAT Center (3,7 -----), Tirupati (1,4-----), Bapatla (2,6 -----), Anantapur (5 ———).

Significant genotypic differences were found for seed infection by *A. flavus* in all environments (Table 2). All IVSCAF-resistant genotypes except PI 337394F and Var. 27 had significantly lower percentages of seed infected by *A. flavus* than the IVSCAF-susceptible genotypes. Var. 27 and PI 337394F had percentages of seed infected by *A. flavus* similar to those of the IVSCAF-susceptible genotypes TMV2 and F1-5 x NCAc 17090. The IVSCAF-resistant genotypes Ah 7223, J 11, U 4-47-7, UF 71513, and PI 337394F did not differ significantly from one another for *A. flavus* infection in any environment. No significant interactions were found between IVSCAF-resistant genotypes and environments for seed infection by *A. flavus* (Tables 2 and 4), but there were significant interactions between IVSCAF-susceptible genotypes and environments for seed infection. Infection levels were significantly higher in environments 4 and 5 than in the other environments. This was most pronounced in the IVSCAF-susceptible genotypes EC 76446 (292), NCAc 17090 and Gangapuri.

Table 2. Seed infection of peanut genotypes with *Aspergillus flavus* in seven environments.

	Seed Infected (%)						
	Environments[2]						
Genotype	1	2	3	4	5	6	7
Ah 7223	0.8 (5.2)[1]	0.8 (5.2)	0.5 (4.1)	0.5 (4.1)	0.7 (4.9)	0.3 (2.9)	0.5 (4.1)
J 11	1.0 (5.6)	0.6 (4.5)	0.5 (4.1)	0.8 (5.2)	0.9 (5.3)	0.1 (2.0)	0.3 (3.0)
U4-47-7	1.1 (6.1)	1.6 (7.3)	0.2 (2.0)	0.7 (4.9)	0.7 (4.9)	0.0 (0.0)	0.5 (4.1)
UF 71513	1.3 (6.5)	0.9 (5.3)	1.1 (6.1)	1.8 (7.8)	1.1 (6.1)	0.5 (4.1)	0.6 (4.5)
PI 337394F	2.0 (8.2)	1.6 (7.3)	1.1 (6.1)	2.1 (8.4)	1.6 (7.3)	0.7 (4.9)	0.7 (4.9)
Var. 27	2.4 (8.9)	3.1 (10.1)	3.8 (11.3)	3.6 (10.9)	4.6 (12.4)	1.9 (8.0)	2.5 (9.0)
TMV 2	4.5 (12.2)	3.3 (10.5)	3.5 (10.7)	6.5 (14.7)	4.0 (11.6)	2.7 (9.4)	4.2 (11.8)
F1-5 x NCAc 17090	6.3 (14.5)	4.2 (11.8)	3.5 (10.7)	8.4 (16.8)	4.5 (12.2)	4.4 (12.1)	4.2 (11.8)
Gangapuri	13.7 (21.7)	4.7 (12.5)	6.0 (14.1)	15.8 (23.4)	12.2 (20.4)	5.2 (13.2)	8.0 (16.4)
NCAc 17090	19.1 (26.0)	4.0 (11.6)	5.2 (13.2)	20.0 (26.5)	20.9 (27.2)	4.9 (12.7)	16.0 (23.6)
EC 76446 (292)	10.4 (18.8)	6.5 (14.8)	10.4 (18.8)	21.3 (27.5)	40.8 (39.7)	6.2 (14.4)	25.3 (30.2)
SE				(±1.453)			

[1] Values in parentheses are arc sine transformations.

[2] Environments : 1=Tirupati, 2=Bapatla, 3=ICRISAT Center, 4=Tirupati 5=Anantapur, 6=Bapatla, 7=ICRISAT Center.

Correlation between resistance to seed colonization by *A. flavus* (IVSCAF) and field resistance to seed infection by the fungus was significant ($p = 0.01$) and positive. The correlation coefficient (r) was 0.837.

Significant differences were observed between genotypes for aflatoxin B_1 contamination of seed in all environments (Table 3). The IVSCAF-resistant genotypes Ah 7223, J 11, U 4-47-7, and UF 71513 had significantly lower levels of aflatoxin B_1 than the IVSCAF-susceptible genotypes EC 76446 (292), NCAc 17090, Gangapuri, and TMV 2 across all environments. Among the IVSCAF-resistant genotypes, Ah 7223, J 11 and U4-47-7 had the lowest levels of aflatoxin B_1 across environments, and did not differ significantly from one another. No significant interactions were observed between environments and IVSCAF-resistant or IVSCAF-susceptible genotypes in respect of aflatoxin B_1 content of seed (Tables 3 and 4).

The correlation between *A. flavus* seed infection and

Table 3. Aflatoxin B_1 content (ug kg^{-1} seed) of seeds of peanut genotypes in seven environments.

Genotype	Environments[2] 1	2	3	4	5	6	7
Ah 7223	14 (2.7)[1]	4 (1.5)	5 (1.8)	2.7 (1.0)	2.0 (0.7)	1.5 (0.4)	3.3 (1.2)
J 11	9 (2.3)	10 (2.4)	3 (1.4)	4.5 (1.5)	3.7 (1.3)	1.6 (0.5)	1.6 (0.5)
U4-47-7	10 (2.4)	2 (1.1)	4 (1.6)	1.6 (0.5)	3.7 (1.3)	1.6 (0.5)	1.6 (0.5)
UF 71513	23 (3.2)	2 (1.0)	2 (1.1)	2.4 (0.9)	4.1 (1.5)	0.0 (0.0)	2.7 (1.1)
PI 337394F	39 (3.7)	15 (2.8)	10 (2.4)	4.9 (1.6)	6.7 (1.9)	6.7 (1.9)	2.4 (0.9)
Var. 27	32 (3.5)	17 (2.9)	26 (3.3)	12.2 (2.5)	18.2 (2.9)	14.9 (2.7)	6.7 (1.9)
TMV 2	120 (4.8)	53 (4.0)	220 (5.4)	33.1 (3.5)	33.1 (3.5)	11.0 (2.4)	14.9 (2.7)
F1-5 X NCAc 17090	80 (4.4)	36 (3.6)	98 (4.6)	7.4 (2.0)	7.4 (2.0)	3.3 (1.2)	8.2 (2.1)
Gangapuri	120 (4.8)	73 (4.3)	163 (5.1)	40.4 (3.7)	90.0 (4.5)	12.2 (2.5)	24.5 (3.2)
NCAc 17090	180 (5.2)	44 (3.8)	269 (5.6)	33.1 (3.5)	33.1 (3.5)	27.1 (3.3)	18.2 (2.9)
EC 76446 (292)	200 (5.3)	120 (4.8)	199 (5.3)	66.7 (4.2)	181.3 (5.2)	-	33.1 (3.5)
SE				(±0.46)			

[1] Values in parentheses are $\log_e$ transformations.

[2] Environments : 1=Tirupati, 2=Bapatla, 3=ICRISAT Center, 4=Tirupati 5=Anantapur, 6=Bapatla, 7=ICRISAT Center.

Table 4. Analysis of variance showing genotype x environment interactions for seed infection by *A. flavus* and for aflatoxin content.

Source of variation	df	Mean square: Seed Infection by A. flavus	Mean square: Aflatoxin content
Environment	6	253.877	27.859
Reps/Environment	21	15.393	1.967
R vs. S	1	9579.412**	345.285**
R	5	150.213**	12.467**
S	4	687.874**	10.175**
(R vs. S) x Environment	6	160.387**	3.293**
R x Environment	30	4.382	0.685
S x Environment	24	73.114**	0.685
Residual	210	8.446	0.843

** Significance at P = 0.001

R = IVSCAF-resistant genotypes.

S = IVSCAF-susceptible genotypes.

aflatoxin B_1 content was significantly positive in all environments except for environment 6. The correlation coefficients were r = 0.67, 0.83, 0.60, 0.83, 0.87, 0.26, and 0.60 in environments 1, 2, 3, 4, 5, 6, and 7 respectively.

Significant differences between genotypes were also found for seed infection by fungi other than *A. flavus* in all environments. These fungi included *Aspergillus niger, Fusarium* spp., *Macrophomina phaseolina,* and *Botryodiplodia* spp. The IVSCAF-resistant genotypes Ah 7223, J 11 and U 4-47-7 consistently had low percentages of seed infected (1.0-4.0%) by these fungi while the IVSCAF-susceptible genotypes F1-5 x NCAc 17090, Gangapuri, NCAc 17090 and EC 76446(292) had higher percentages of seed infected (5.4-44.9%) across environments. The genotypes UF 71513, PI 337394F, Var. 27 (IVSCAF-resistant) and TMV 2 (IVSCAF-susceptible) had low to moderate levels of seed infection (2.5-13.1%). There were no significant interactions between IVSACAF-resistant genotypes and environments for seed infection by these fungi. Significant interactions occurred between environments and IVSCAF-susceptible genotypes. *A niger* was the most common colonizer of seed of most genotypes in environments 1, 4, and 5 whereas *M. phaseolina* was most common in environments 2 and 6. *Fusarium* spp. also occurred commonly in seeds of all genotypes in all environments. *Botryodiplodia* spp. were found only in seeds in environments 2 and 3.

The genotypes that expressed both IVSCAF and field resistance to seed invasion by *A. flavus* had yields comparable or greater than the *A. flavus*-susceptible cultivars TMV 2 and Gangapuri in all environments (Table 5). The genotype EC 76446 (292) had the lowest yield across environments, probably because of the high levels of seed and seedling rots caused by *A. niger* and *A. flavus.* Significant interactions between genotypes and environments were found for pod yield.

Table 5. Pod yield (kg ha^{-1}) of peanut genotypes in seven environments.

Genotype	Environments[1] 1	2	3	4	5	6	7
Ah 7223	821	617	702	1104	1269	239	798
J 11	988	704	686	1226	1340	262	775
U4-47-7	925	604	696	1157	1210	233	850
UF 71513	958	688	676	1119	1357	162	756
PI 337394F	833	445	411	1019	1179	179	632
Var.27	808	623	636	1162	1325	151	836
TMV 2	815	565	623	1024	1283	156	590
F1-5 X NCAc 17090	905	546	745	1013	1252	181	946
Gangapuri	695	517	441	752	1255	133	687
NCAc 17090	1049	690	731	821	1355	148	885
EC 76446 (292)	554	207	163	262	749	57	305
SE				±39.31			

[1] Environments : 1=Tirupati, 2=Bapatla, 3=ICRISAT Center, 4=Tirupati 5=Anantapur, 6=Bapatla, 7=ICRISAT Center.

Discussion

In field trials in the U.S. (2,3,7), Senegal (18), and in the present trials in India, 46 genotypes of known reaction to *in vitro* seed colonization by *A. flavus* have been examined for field resistance to seed infection by *A. flavus* and/or aflatoxin contamination. Only three of the 46 IVSCAF-resistant genotypes were tested in more than one country. Of these, J 11 was found to have resistance to *A. flavus* seed infection in North Carolina and at ICRISAT, India (7, 12). PI 337409 had resistance

to field infection in Senegal (18) but was susceptible in North Carolina (7). The cultivar Lampang, susceptible to IVSCAF, showed field resistance to seed infection by *A. flavus* in North Carolina (7). Perhaps conditions in the field trials in Georgia (2, 3) were so favorable for *A. flavus* infection that no useful resistance was detected, or the genotypes used may not have significant resistance to preharvest seed invasion, as was the case with genotype Var. 27 in the present study. Five of the six selected IVSCAF-resistant genotypes (Ah 7223, J 11, UF 71513, U4-47-7, and PI337394F) in the present trials had resistance to field infection by *A. flavus,* and the low levels of infection by this fungus were matched by low levels of aflatoxin B_1 contamination. Resistance to field infection of seed by *A. flavus* in these genotypes was stable across all seven environments. The existence of significant varietal resistance to *A. flavus* in the field is most important as much of the aflatoxin contamination of peanuts in the SAT is thought to take place before harvest (3, 8).

It should be borne in mind that the ability of a genotype to support aflatoxin production in an *A. flavus* colonized seed is a factor in determining the level of aflatoxin contamination. The genotype J 11 was reported to have *in vitro* resistance to aflatoxin production (16) but it was subsequently found that autoclaved seeds had been used in this work. Recent work in ICRISAT, India (10) has shown that high levels of aflatoxin B1 are produced when surface damaged seeds of J 11 are inoculated with an aflatoxigenic strain of *A. flavus* and incubated under conditions optimal for fungal growth and aflatoxin production. The low levels of aflatoxin B1 found in undamaged seed of J 11 under natural field conditions in the present study indicates that field resistance to *A. flavus* infection is important in conferring resistance to aflatoxin contamination.

Significant interactions between environments and IVSCAF-susceptible genotypes, especially genotypes EC 76446 (292), NCAc 17090, and Gangapuri, reflected a strong influence of environment on levels of seed infection by *A. flavus* in these genotypes. EC 76446 (292) and NCAc 17090 had significantly higher levels of infection by *A. flavus* in environments 4 and 5 than in other environments (Table 2). This can be attributed to severe drought stress, particularly during pod development, in these environments. Relatively lower levels of seed infection by *A. flavus* in most genotypes in environments 2, 3, and 6 may be explained by the dominance of *M. phaseolina* in these environments.

A. flavus seed invasion and aflatoxin contamination can also occur during postharvest drying and in storage (5), and in this connection the IVSCAF-resistant genotypes could have an advantage in minimizing the risk of aflatoxin contamination. The combination of postharvest testa resistance (IVSCAF-resistance) and resistance to invasion of pods and seeds in the field should be particularly useful in minimizing aflatoxin contamination in areas where this may occur either preharvest or postharvest or at both stages. However, it should not be assumed that all IVSCAF-resistant genotypes will have resistance to pod and seed invasion by fungi in the field. For example, the IVSCAF-resistant genotype Var. 27 showed similar susceptibility to *A. flavus* infection in the field to that of the IVSCAF-susceptible genotypes TMV 2 and F1-5 x NCAc 17090. These results are supported by the findings of Kisyombe *et al.* (7). The mechanism(s) of resistance in the developing pod is likely to be complex, involving physical and biochemical factors. Environmental factors such as drought and soil types may influence competition and antagonisms between *A. flavus* and other microbes in the geocarposphere. We note that variety *fastigiata* (valencia) type peanut genotypes EC 76446(292), NCAc 17090, and Gangapuri tended to show considerably higher levels of seed infection by *A. flavus* and other fungi than did the variety *vulgaris* (spanish) IVSCAF-resistant or IVSCAF-susceptible genotypes (Tables 1, 2 and 3). It is interesting to note that the drought-tolerant genotype NCAc 17090 and hybrid F1-5 x NCAc 17090 were highly susceptible and susceptible, respectively, to *A. flavus* seed infection in the field. Combining resistance to *A. flavus* with drought tolerance will be important in peanut cultivars for use in the SAT.

The IVSCAF-resistant genotypes Ah 7223, J 11 and U4-47-7 also appeared to have resistance to other fungi such as *Fusarium* spp. and *A. niger.* These genotypes have previously been found resistant to pod rot diseases at ICRISAT (11). Resistance to seed infection by fungi other than *A. flavus* is also important for maintaining seed quality for planting and consumption.

Of the resistant genotypes, J 11, Ah 7223, and UF 71513, have acceptable yields and commerical quality, and should be tested under farmers' conditions to determine whether the resistance can confer a definite advantage in terms of low aflatoxin contamination in comparison with currently grown peanut cultivars.

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