

$$\frac{\% \text{ stem-nematode-resistant plants}}{= \frac{\text{No. of symptomless plants at 16 weeks}}{\text{No. of plants present in stand at 2 weeks}} \times 100.$$

An analysis of variance was applied to the percentage data.

RESULTS AND DISCUSSION

Levels of resistance ranged widely among the varieties tested (Table 1). Ranger and Vernal had the lowest mean percentage of resistant plants (12.2 and 15.1%, respectively). Saranac was significantly better (34.9% resistant). Washoe and Lahontan were significantly better than Saranac (63.7 and 67.8% resistant, respectively). Apalachee (90.1%) was significantly more resistant than all other varieties tested.

These results agreed with known field resistance of the varieties. Lahontan and Washoe are more resistant than Ranger and Vernal; Apalachee is highly resistant; Saranac shows the low level of resistance characteristic of Flemish varieties.

Maximum variation of variety means among the three trials was about 10%; except for Vernal and Ranger in trial 3, mean separations within trials were similar.

The major advantages of our method are its ease of application and ability to differentiate clearly between the stem-nematode-resistant and susceptible alfalfa varieties. This method should appeal to many workers.

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DIFFERENTIAL RESPONSE OF COTTON VARIETIES TO INFECTION BY *ASPERGILLUS FLAVUS*¹

C. M. Brown, L. J. Ashworth, Jr., and J. L. McMeans²

ABSTRACT

Ten cultivars of upland-type cotton (*Gossypium hirsutum* L.) tested in the Imperial Valley of California were susceptible to infection by *Aspergillus flavus*. But two cultivars were more severely affected than the others, based upon the amount of aflatoxins occurring in seeds at harvest. Seeds of 'Paymaster 54-B' had about 800 ppb aflatoxins and seeds of 'Stoneville 3209' had about 125 ppb aflatoxins while seeds of the other cultivars contained a trace to 6 ppb aflatoxins.

Additional index words: Aflatoxins, *Gossypium hirsutum* L.

INFECTION of cotton (*Gossypium hirsutum* L.) by *Aspergillus flavus* Link was first reported by Bollenbacher and Marsh in 1954 (3). Subsequent work has shown that boll infection by *A. flavus* can result in discoloration and weakening of cotton fibers and in seed damage (5). Infected seeds are a source of aflatoxins and it is the aflatoxin phase of the disease syndrome with which this report is concerned.

The fibers and seeds of 100-boll samples, taken from each of five cultivars, were examined for infection in an initial experiment. Infection was based upon occurrence of a bright greenish yellow fluorescence exhibited by infected fibers when viewed in ultraviolet light (5). A second, more extensive, experiment was made in which 10 cultivars planted in a randomized block were compared. In this case, a 2.27 kg sample of seed cotton, from each of four replications, was collected from the lowermost third of the crop, where the bulk of infections occur (4). Seed cotton samples were oven dried from 4 to 6% moisture (wet weight basis) and ginned. Then determinations were made for the amount of infection, as described above, and for the aflatoxin content of seeds (2).

Relatively few seeds were damaged by *A. flavus* to the extent that they fluoresced in ultraviolet light (Table 1), a finding that agrees with earlier observa-

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² Research technician, Western Region, ARS, USDA, Imperial Valley Conservation Research Center, Brawley, CA 92227; plant pathologist (presently plant pathologist, Dept. of Plant Pathol., U. of Calif., Berkeley, CA 94721); and plant physiologist, Crops Res. Div., U. S. Cotton Res. Stn., Shafter, Calif., respectively.

Table 1. Occurrence of greenish yellow fluorescent seeds and aflatoxins in seeds of cotton cultivars grown in an experiment at Brawley, Calif.

Cultivar	GYF [†] seeds no. / 1,000	Aflatoxins [‡]		Total
		B ₁	B ₂	
		ppb		
Carolina Queen	1.3	Tr [§]	Tr	Tr
DPL-SL	1.5	Tr	Tr	Tr
Arizona 6024	2.3	Tr	Tr	Tr
Acala SJ-1	2.1	4.9	1.5	6.4
Acala Imperial	2.2	1.3	0.1	1.4
Acala 4-42	4.3	Tr	Tr	Tr
Stoneville 7A	3.4	Tr	Tr	Tr
Hopcala	4.6	Tr	Tr	Tr
Stoneville 3209	6.7*	96	29	125
Paymaster 54-B	6.4	409	290	799

* These values differ significantly from the low value of 1.3 at 9.1 level of confidence but not at 0.05 level of confidence. [†] Greenish yellow fluorescent. [‡] Aflatoxins G₁ and G₂ not observed. [§] Trace amounts of aflatoxins.

tions (1, 2). This characteristic, while being useful for estimating whether toxins are likely to occur in seed lots collected at random (2), can only be used for estimating the extreme differences that may occur between cultivars (Table 1).

In both experiments, the cultivars 'Paymaster 54-B' and 'Stoneville 3209' had more fluorescent seeds than the other cultivars with which they were compared. The green fluorescing aflatoxins (G_1 and G_2) were not observed in these samples; instead only aflatoxins B_1 and B_2 (which always occurred together) were observed here as in other studies of cotton seeds (2). Stoneville 3209 and Paymaster 54-B were severely affected with aflatoxins, having respectively 125 and 800-ppb total toxins. The amount of toxins in the other cultivars was negligible.

These results indicate that some genotypes of *G. hirsutum* are more likely to have toxic seeds than others. On the other hand, differences in the amount of infection occurring between cultivars are quite small. This observation suggests that innate susceptibility of commercial cottons may be similar but that some genotypes are more prone than others to having significant amounts of toxins for one or more reasons, such as boll morphology. For instance, bolls of Paymaster 54-B generally do not open fully at Brawley, California, even when air dry. Instead of the carpel walls being at approximately right angles with the penduncle when fully dried, the boll only partially opens and thus is similar to storm proof-type cotton cultivars in this regard. The fibers and seeds of such bolls dry slowly compared to bolls that quickly expand to the fully opened position (unpublished data, Ashworth, et al.) and thus remain prone to infection for a relatively long time. In this regard, most bolls of the cultivar 'DPL-SL' are fully opened when dried instead of being only partially opened like Paymaster 54-B under Brawley conditions, and under these conditions, DPL-SL seeds contained only a trace of aflatoxins while seeds of Paymaster 54-B contained 800 ppb toxins (Table 1).

No similar comparisons were made between these and other cultivars so the possible cause for differences in the toxin content of the others can only be supposed. Besides being more prone to infection by *A. flavus*, seeds of certain cotton cultivars may be more favorable substrates for aflatoxin elaboration by the fungus. Results of our experiments do not distinguish between these possibilities, nor to possible differences in the innate susceptibility that may exist between genotypes of the host. Therefore other experiments are being made in an attempt to settle these questions.

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HERITABILITY OF GROAT-PROTEIN PERCENTAGE OF HEXAPLOID OATS¹

K. J. Frey²

ABSTRACT

Standard-unit and realized heritabilities were computed for groat-protein percentage using data collected from F_2 or F_3 oat (*Avena* spp.) plants from intra and interspecific hexaploid oat crosses and their progenies grown in nonreplicated hills (25 to 30 plants/hill). Nitrogen percentages were determined on groat samples by the Kjeldahl procedure. The pooled standard-unit heritability percentage for inter and intraspecific crosses was 43.0%. In one experiment, the realized and expected gains from selection were 1.0 and 1.2% groat-protein, respectively.

Additional index words: *Avena sativa* L., *Avena sterilis* L., Standard-unit heritability, Gain from selection.

IN the recent intense effort to increase groat-protein percentage of hexaploid oats (*Avena* spp.), large numbers of N analyses have been conducted on seed samples from individual oat plants. This report gives estimates of heritability for groat-protein based on data from spaced plants and nonreplicated plots of their progenies grown in consecutive years in the field in Iowa.

LITERATURE REVIEW

Heritability percentages for protein concentration in caryopses vary widely, even within the same cereal crop. Specific crosses used and methods of computation both contribute to varying heritability estimates. Using three methods of estimation, Stuber, Johnson, and Schmidt (1962) found protein percentage of wheat (*Triticum aestivum* L.) seeds to be 82, 83, and 68% heritable. Davis, Middleton, and Hebert (1961), studying four wheat crosses, found the ranges of broad and narrow-sense heritabilities were from 54 to 69 and 23 to 35%, respectively. Other studies with wheat grain have shown heritabilities ranging from 15 to 103% (Kaul and Sosulski. 1965; Lofgren et al., 1968; Sunderman, Wise, and Sneed, 1965). Frey, Hall, and Shekeleton (1955) found broad-sense heritabilities of 88, 89, and 90% for seed-protein percentage in three oat crosses, and Campbell and Frey (1972b), using segregates from 10 crosses of *Avena sativa* L. \times *A. sterilis* L., obtained mean per-plot, per-experiment, and standard-unit heritabilities for groat-protein percentage of 41, 57, and 30%, respectively. Generally, heritabilities for protein percentage in grain are relatively high, which indicates that good progress from selection should be expected for this trait.

MATERIALS AND METHODS

All materials used in this study were segregates from oat (*Avena* spp.) crosses. The parental generation was always represented by an individual plant in the F_2 to F_6 generation, and its respective progeny line was always represented by an unreplicated hill sown with 25 to 30 seeds. Except in group I (see

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² C. F. Curtiss distinguished professor of Agriculture.