Aflatoxin Production in an Array of Peanut Lines Selected to Represent a Range of Linoleic Acid
Contents.

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Resistant cultivars should be a component of an integrated program of aflatoxin management, but to
date no successful Aspergillus-resistant peanut (Arachis hypogaea L.) cultivar has been released.
High-oleate (low-linoleate) backcross-derived variants of virginia-type cultivars were previously
found to develop significantly more aflatoxin than their recurrent parents. In order to determine if
linoleate level could be used to predict aflatoxin production level, 16 lines were sampled from the
NCSU peanut breeding project’s collection of germplasm to represent a broad range of linoleate
content. Data from a prior evaluation of fatty acid content defined a range of 36 to 461 g kg-1 of
linoleate among 611 lines in the collection. The 16 lines were selected to represent roughly equal
increments of linoleate within that range. Fifty to 100 seeds of each line were sampled for fatty acid
analysis, and the seeds closest to the mean for the line were used for the experiment. The
distribution of oleate levels among lines in the seeds actually used was not uniform. One line had an
oleate level of 43 g kg-1, the other 15 ranged from 215 to 385 g kg-1. Approximately 5 g of seeds of
each entry were manually blanched, quartered and inoculated with spores of A. flavus Link ex Fries
strain NRRL 3357, placed on moistened filter paper in 10 cm petri dishes, and incubated for 8 d at
28ºC. Linoleate levels of the seeds used in each experimental unit were recorded. The 16 petri
dishes in each rep were arranged in 4 rows and 4 columns on a tray enclosed in a large plastic bag,
using a 4x4 balanced lattice design with columns as blocks within reps. Stacked trays were
separated by short sections of PVC pipe to eliminate pressure on petri dishes in lower trays. After
incubation, samples were dried, ground, and tested for aflatoxin content by HPLC. Multiple
regression was used to build a linear model to account for the variation among lines using the mean
fatty acid contents as independent variables. Linoleate content accounted for 39% of the variation
among lines for aflatoxin B1 (26% of variation when log-transformed), and total aflatoxin (27% of
variation when log-transformed), and 44% for aflatoxin B2 (27% when log-transformed). Oleate
content accounted for substantial additional variation among lines (27% for B1, 21% for log-
transformed B1, 29% for B2, 23% for log-transformed B2, 27% for total aflatoxin, and 20% for
transformed total). Other fatty acids accounted for statistically but small fractions of among-line
variation. There was significant residual variation among lines for all aflatoxin traits. Because most
of the variation in aflatoxin production among lines was due to the contrast between the single high-
oleic line and the other 15 lines from the normal range, the data were reanalyzed with the high-oleic
line removed. Oleate and linoleate level accounted for 20 to 25% of the variation among lines with
eicosenoate (20:1) and stearate (18:0) accounting for additional small, statistically significant
increments. Although fatty acids accounted for significant portions of the genetic variation, it does
not appear to be practical to use fatty acid level as a predictor of aflatoxin, especially for lines in the
normal range for oleate and linoleate.