

Genetic analysis of *Aspergillus flavus* infection and aflatoxin accumulation in tropical yellow maize

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Abstract

Yellow maize, which is known to have high carotenoid levels, is susceptible to *Aspergillus flavus* infection and subsequent aflatoxin accumulation. This study examined the genetic basis of resistance to *A. flavus* and aflatoxin accumulation under laboratory conditions. The evaluation used grains from 19 inbred lines and their 171 diallel hybrids, which were grown in field trials across two locations. Grain was harvested from the lines, and hybrids and kernels were inoculated with toxigenic *A. flavus* artificially under laboratory conditions. Percent kernel infection (PKI) was recorded at seven, 14, and 21 days after inoculation (DAI). Aflatoxin content was determined using ELISA at 21 DAI. Significant genetic variation was observed for agronomic traits, PKI, and aflatoxin accumulation. Broad-sense heritability was moderate to high ($H^2 = 0.59$ to 0.80) for agronomic traits but low for aflatoxin resistance parameters ($H^2 = 0.28$) in hybrids. The magnitude of general combining ability (GCA) exceeded that of specific combining ability (SCA) for most traits, indicating that additive genetic effects were predominant. Five inbred lines showed significant ($P < 0.05$) negative GCA effects for kernel infection, while two lines (CML496 and CKL187031) showed significant ($P < 0.05$) GCA effects for reduced aflatoxin accumulation. The inbred line CKL187031 demonstrated favorable GCA effects for both reduced kernel infection and lower aflatoxin accumulation. The number of groups of genes controlling kernel infection and aflatoxin accumulation was estimated to be four and six, respectively. Among the inbred lines, TZSTR188 and CML226 showed the lowest kernel infection and aflatoxin accumulation. Aflatoxin content in the top 15 hybrids ranged from 2.89 to 5.35 ng/g. These findings suggest the existence of genetic variability in tropical yellow maize germplasm while highlighting potential parental lines for breeding programs targeting resistance to