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Identifying Lepidopteran resistance within *hcf* mutants

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Southwestern corn borer (SWCB) and fall armyworm (FAW) feeding on maize causes extensive crop damage in the United States. Previous proteomic analysis comparing resistant and susceptible lines of maize indicates genes found in the photosystem II pathway are highly expressed in the resistant line. The *high chlorophyll fluorescence (hcf)* mutants have defects in photosystem I or photosystem II genes. A preference test was performed comparing *hcf* mutants to their wild-type siblings. *Oy*, *pg*, and *g* mutants were also compared to their wild-type siblings to ensure that color was not a factor in feeding differences. SWCB preferred the wild-type over *hcf11-N1205A* and *hcf49-N1480* mutants, indicating these genes may be resistance factors. *Oy1-Andrew* and *hcf13-N1097B* mutants were preferred by SWCB compared to their wild-type siblings, indicating these genes increase susceptibility to feeding damage. *hcf49-N1480*, *hcf7-N1029D*, and *pg15-N340B* had reduced FAW damage compared to wild-type siblings, indicating they may increase resistance to feeding damage. *hcf44-N1278B* showed increased susceptibility to FAW feeding compared to its wild-type sibling. An antibiosis test was performed using *hcf* mutants. Photographs and larval weights were taken at the end of the four days. Tissue damage areas were analyzed using AlphaEaseFC software. From the data, *hcf7-N1029D* and *hcf50-N1481* had reduced larval weights for both FAW and SWCB indicating these genes have antibiotic properties and can reduce larval feeding damage. The mutants evaluated for effects of pigmentation displayed varying results indicating color differences associated with some *hcf* mutants are unlikely to be responsible for the differences in feeding behavior observed. These genes identified here may be useful in increasing resistance to FAW and SWCB in commercial hybrids.