FREQUENCY OF ALLELES CONFERRING RESISTANCE TO *BT* PROTEINS IN *HELICOVERPA ZEA* IN TEXAS AND THE MID-SOUTH

José Santiago González
Fei Yang
David Kerns
Department of Entomology/Texas A&M University
College Station, TX

Abstract

F_2 screens were conducted from 2018-2020 to determine the resistant allele frequency of *H. zea* from Texas and the Mid-South to Cry1Ac, Cry2Ab2, and Vip3Aa proteins. 128 neonates per F_2 family were exposed to diagnostic concentrations of Cry1Ac (10 µg/cm^2), Cry2Ab2 (10 µg/cm^2) and Vip3Aa39 (3 µg/cm^2) using diet over-lay bioassays. Chi-square analysis was used to determine the number of resistant alleles for each family using theoretical monogenic models based on the 7-day survivorship. 93.4% F_2 families collected from Texas (99 out of 106) and 92.7% from the Mid-South (178 out of 192), survived the diagnostic concentration of Cry1Ac, resulting in an estimated resistance allele frequency of 0.4150-0.4975 and 0.6458-0.6953 respectively. Likewise, 35% F_2 families in Texas (42 out of 120) and 39% in the Mid-South (74 out of192) survived on Cry2Ab2 with an estimated resistance allele frequency of 0.1097-0.1228 and 0.2526-0.2656, respectively. For the Vip3Aa39 protein, only 1.6% F_2 families from Texas (2 out of 126) and 2.6% from the Mid-South (5 out of 192) survived on Vip3Aa39, generating a resistance allele frequency of 0.0042 and 0.0130, respectively. These data suggest that the resistant allele frequency in *H. zea* is high for Cry1/Cry2 proteins and not rare for Vip3Aa in the fields in both Texas and the Mid-South. Since the efficacy of Cry proteins against *H. zea* is largely diminished, more selection pressure is expected on the Vip3Aa. Appropriate resistance management strategies must be adopted to sustain the efficacy of Vip3Aa against *H. zea*.