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The objective of this study was to determine if *H. armigera* is present in some of the most important cotton-growing regions of northwestern Texas, namely the panhandle, high plains, and rolling plains.

Materials & Methods

Samples of adult moths collected during a 2003 Helicoverpa pheromone sampling program conducted in northwestern Texas were received from collaborators with the Texas Department of Agriculture and Texas Cooperative Extension Service. The samples represented at least 43 separate localities from 19 counties of the northwestern cottongrowing regions of Texas, namely the panhandle (3 counties), the high plains (12 counties), and the rolling plains (4 counties) (see Map 1, and complete sample data in Appendix 1). Sample collection dates varied from locality to locality, but ranged from the earliest on June 2, 2003 to the latest on October 9, 2003. Most counties were sampled from July through September (or early October). Samples had been frozen after field collection and, during the present study, were continually maintained in a laboratory freezer except when under examination. Each of the 362 samples received was given a unique sample number, and a tag with that number was placed in each sample bag. The sample numbers were entered into a Microsoft Excel spreadsheet along with sample collecting data as recorded on the sample bag or from slips of paper added to the samples by the original collectors. The number of Helicoverpa moths present in each sample was also recorded on the spreadsheet.

A definitive species-level identification was made on every male *Helicoverpa* specimen in each sample by examination of its genitalic structures using the following methods. Using fine-tipped forceps, the abdomen of each moth was removed from the remainder of the body and macerated in a solution of 10% KOH. During maceration, moth abdomens were maintained separately in individually numbered shell vials of KOH, and moth bodies were maintained dry in correspondingly numbered spot plate wells. If a specimen was ultimately saved as a permanent voucher specimen, the moth body and genitalia were re-associated and preserved, otherwise all moth bodies, abdomens, and genitalia were discarded after identification.

Each abdomen was soaked/macerated in a 10% KOH solution for 18 to 24 hours to soften and dissolve the non-chitinous portions of the abdomen. The valves and vesica of the male genitalia were extracted from the abdomen with fine-tipped forceps. The eighth abdominal segment and the hairs arising from the external face of the valves were separated and removed by grasping with a fine-tipped forceps. Once cleaned and fully visible, the valves were measured at 12X magnification using an Olympus SZ60 stereo-zoom microscope equipped with a calibrated ocular reticle. Valves were measured from base to apex as shown in fig. 1. Following Pogue (in press), valves measuring 4.9 mm or longer were identified as *Heliocoverpa zea*. Specimens with valve lengths less than 4.9 mm were set aside for study of the aedeagal vesica (figs. 3, 4, 5, & 6).

Specimens with valve lengths <4.9 mm could represent specimens of *H. armigera* or small specimens of *Helicoverpa zea*. Examination of the basal pouch of the everted vesica is required to distinguish these species. To evert the vesica from the shaft of the aedeagus, the basal portion of the sclerotized aedeagus was torn off. Using fine-tipped forceps, approximately one-half of the membranous vesica was removed through the opening in the base of the aedeagus. To inflate the remaining portion of the vesica, a 27.5

gauge hypodermic needle was inserted into the open basal end of the aedeagus, and the walls of the aedeagal shaft were clamped with forceps against the outside of the needle. Application of light pressure on the syringe attached to the needle easily everted the remaining portion of the vesica, exposing its basal lobes (figs. 5 & 6). Following Pogue (in press), the number of small membranous lobes or diverticula on the basal pouch of the vesica was used to distinguish *H. zea* (three lobes – fig. 5) from *H. armigera* (one lobe – fig. 6).



Map 1. County map of Texas showing the counties surveyed during the 2003 pheromone trapping for *Helicoverpa armigera* in northwestern Texas (counties included in survey: Bailey, Castro, Cochran, Gaines, Hale, Hartley, Hockley, Jones, Lamb, Lubbock, Mitchell, Moore, Nolan, Parmer, Scurry, Sherman, Swisher, Terry, Yoakum)

Twenty-seven *Helicoverpa* specimens, represented by either moths with male genitalia fully prepared or fully prepared male genitalia only, were pinned and labeled and saved as voucher specimens in the Texas A&M University Insect Collection (TAMUIC). Each voucher specimen was labeled with its sample data, a determination label, and a green-colored TAMUIC voucher label bearing the number 649.

Results

A total of 14,256 specimens of male *Helicoverpa* moths were examined, representing a total of 362 samples from 19 Texas counties (Appendix 1). The examined moths represent the total *Helicoverpa* catch from the 2003 pheromone trapping program in northwestern Texas. The male genitalia of each moth was examined. All moths were identified as *H. zea*. No specimens of *H. armigera* were found. Thirteen thousand two hundred and seventy (13,270) specimens were identified as *H. zea* based on valve length alone (i.e., specimens having a valve length of 4.9 mm or greater). Nine hundred and eighty six (986) specimens having value lengths of less that 4.9 mm were identified as *H. zea* by vesica inflation and counting of the membranous lobes on the basal pouch of the vescia. Female *Helicoverpa* moths and moths representing non-*Helicoverpa* species were found mixed in the samples but only at very low numbers (their numbers were not recorded). Detailed sample collection information is given in Appendix 1, together with the number of male *Helicoverpa zea* moths identified in each sample, and the number identified by vesica inflation in each sample.

Discussion

We examined 100% of the *Helicoverpa* moths collected during the 2003 *Helicoverpa* pheromone trapping program. We found no evidence of the presence of *H. armigera* in the cotton-growing regions of northwestern Texas that were covered in these samples. Given that no *H. armigera* were identified in these samples, it seems likely that *H. armigera* is not currently established in these regions. This conclusion is further supported by the extensive nature of the sampling and the concerted specimen identification effort reported upon here. Specifically, the large number of samples examined (362), the number and distribution of sample sites (at least 43 sites in 19 counties), the wide-range of sample dates (from July through September for most counties), and the large number of moths (14,256) definitively identified as *H. zea*.

Literature Cited

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