MOLECULAR DETERMINANTS OF HELICOVERPA ZEA FLIGHT CAPACITY RESPOND TO BODY WEIGHT, NUTRITION, AND BT CORN Howard W. Fescemyer The Pennsylvania State University, Department of Biology University Park, PA John J. Adamczyk, Jr. USDA, ARS, KSARC Weslaco, TX Ryan Jackson USDA, ARS, SIMRU Stoneville, MS James H. Marden The Pennsylvania State University, Department of Biology University Park, PA

Abstract

Alternative splicing (AS) is creates distinct transcripts from single genes, thereby amplifying functional genomic diversity. Force and power of insect muscle is affected by AS of the contractile gene troponin-t. Powerful muscles improve flight ability and are necessary to counteract body weight, but nutrition may also be important because power is energetically expensive. Therefore, we tested the hypothesis that AS of troponin-t is a mechanism by which Helicoverpa zea modulates flight muscle power in relation to three corn varieties, thereby influencing development of flight phenotypic variation among individuals. Conventional field and sweet corn differ in nutritive quality and the Cry1Ab Bt-toxin in GM field corn acts on larval digestive cells, thereby decreasing efficiency of nutrient acquisition. Body weight and corn variety together explained 95% of the variation in troponin-t isoform composition. Moths from larvae that ate Bt-corn were smallest and had troponin-t isoform composition and peak flight metabolic rates associated with reduced flight muscle performance. Moths from larvae that ate conventional field and sweet corn had peak flight metabolic rates significantly higher than the Bt-corn treatment, and sweet corn moths had a troponin-t isoform composition that suggested they had the most powerful flight muscles. Alternative splicing responds in a precise way to organism-level traits, is an epigenetic mechanism carrying effects of past nutritional history, and is a central component of phenotypic plasticity and life history variation. The cost of surviving the affect of Bt may be poor dispersal capability, which could impact the efficacy of spatial refuges in diluting Bt-resistant genotypes.