TRANSCRIPT ANALYSIS OF SEDENTARY FEMALE RENIFORM NEMATODES IDENTIFIES POTENTIAL TARGETS FOR RNAI-MEDIATED RESISTANCE

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Abstract

RNA-interference (RNAi) has become an attractive avenue of research in the development of crop resistance to sedentary plant-parasitic nematodes. A prerequisite for this type of research is the availability of high quality gene sequence data for the nematode in question. The reniform nematode (*Rotylenchulus reniformis*) is a damaging pest of Upland cotton that may be vulnerable to an RNAi-based control strategy; however, there is currently an extremely limited amount of gene sequence data available for this pest. In this report, we describe the construction and analysis of a cDNA library that was created using total RNA isolated from sedentary female reniform nematodes. A total of 2,784 cDNA clones were sequenced which produced 555 unique non-overlapping *R. reniformis* expressed sequence tags (ESTs). Bioinformatic analyses of these ESTs identified >60 sequences that showed significant homology ($P<1.0e-15$) to *Caenorhabditis elegans* genes that present lethal phenotypes following RNAi. A number of *R. reniformis* ESTs also showed homology to sequences derived from sedentary and migratory plant-parasitic nematodes and some animal parasites. The details of these analyses and their implications for the development of RNAi-mediated reniform nematode resistance in cotton will be discussed.