

MICROSATELLITES REVEAL GENETIC DIVERSITY IN RENIFORM NEMATODE POPULATIONS**Renee S. Arias****USDA-ARS Genomics and Bioinformatics Research Unit****Stoneville, MS****Salliana R. Stetina****Jennifer L. Tonos****Jodi A. Scheffler****USDA-ARS Crop Genetics Research Unit****Stoneville, MS****Brian E. Scheffler****USDA-ARS Genomics and Bioinformatics Research Unit****Stoneville, MS****Abstract**

Reniform nematode (*Rotylenchulus reniformis*) is the predominant parasitic nematode of cotton in the Mid South area of the United States. To document genetic variability within this species, we developed microsatellite-enriched libraries and designed 192 simple sequence repeats (SSR) markers for reniform nematode. The markers were tested on six reniform nematode cultures that originated in Texas, Louisiana, Mississippi and Georgia. Based on performance we selected 156 SSR markers for reniform nematode, 88 of which were polymorphic across the six reniform nematode populations. The most frequent motif was the dinucleotide AG. The polymorphic information content of the markers ranged from 0.00 to 0.82, and the percentage of multiallelic loci of the isolates ranged from 40.9 to 45.1%. Among the three Mississippi isolates, 22 SSR markers were polymorphic. Significant differences were found between the Texas and Georgia isolates with respect to the level of infection on six cotton genotypes. Sixty-two polymorphic markers were able to distinguish these two populations, but further studies will be required to establish possible connections between markers and aggressiveness of the nematode. In addition to their utility in assessing the genetic diversity of this nematode, the SSR markers identified might also be used in research on the origin and spread of reniform nematode in the United States and in assessing the response of a reniform nematode population to host resistance or other management practices at the genotype level.