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GENETIC DIVERSITY OF RENIFORM NEMATODE GEOGRAPHIC POPULATIONS

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The purpose of this study was to analyze the genetic variation of global reniform nematode populations. DNA sequences of the nuclear ribosomal first internal transcribed spacer region (rDNA-ITS1) were used. Among the populations collected from the U.S., Alabama, Arkansas, Hawaii, Louisiana, Mississippi, North Carolina, South Carolina, Texas, Georgia, and Florida, no polymorphic nucleotide sites were observed for the ITS1 marker. Populations from Colombia, Brazil, Honduras, and Japan were also included. The only population differentiable with the genetic marker used was a parthenogenic population from Japan, with 5.3% sequence divergence. Among all the amphimictic populations subjected to DNA sequence analysis, no polymorphic nucleotide sites were observed for the ITS1 marker. These results are consistent with observations from reproduction tests on selected hosts and morphometric variation of specimens, where no phenotypic maker, other than parthenogenesis, has been successfully used to identify variation among geographic populations. The lack of genetic distinction observed in the amphimictic populations suggests a recent geographical expansion from a relatively small base of origin.