

Nuclear ribosomal DNA diversity of a cotton pest (*Rotylenchulus reniformis*) in the United States

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Abstract

The reniform nematode (*Rotylenchulus reniformis*) has emerged as a major cotton pest in the United States. A recent analysis of over 20 amphimictic populations of this pest from the US and three other countries has shown no sequence variation at the nuclear ribosomal internal transcribed spacer (ITS) despite the region's usual variability. We investigated this unexpected outcome by amplifying, cloning and sequencing two regions of the nuclear ribosomal DNA (18S, ITS1) to ascertain whether any variation occurred within and among populations of reniform nematodes in Alabama, US. Both the nrITS1 and the relatively conserved 18S region showed a fairly substantial amount of variation among populations. The identity among ITS sequences ranged from 1.00 to 0.86, while sequence identity at the 18S ranged from 1.00 to 0.948. We conclude that variation does exist in these sequences in reniform nematodes, and the earlier report showing no ribosomal ITS variation in this pest might have been caused by preferential amplification of a conserved ITS paralog. Current and future application towards resistance in cotton varieties to this pest requires reliable information on the molecular variability of the nematode in cotton-growing areas.