MORPHOMETRIC VARIATION OF RENIFORM NEMATODE GEOGRAPHIC POPULATIONS FROM COTTON-GROWING REGIONS IN THE UNITED STATES

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RESEARCH PROBLEM

Reniform nematode (*Rotylenchulus reniformis*, Linford & Oliveira 1940) is considered the most damaging nematode in many cotton-producing areas of the southeastern United States. The diversity of this nematode in the U.S., however, has not been studied. The objective of this research was to measure the morphometric variation among thirteen populations from different cotton-growing regions.

BACKGROUND INFORMATION

Management practices of *R. reniformis* in cotton include the use of nematicides and rotation with nonhost crops. The most effective and profitable means of control would be the use of crop resistance, but no commercial upland cotton cultivars with resistance to reniform nematode are available. For resistant cultivars to be developed, breeders need to know if differences exist among populations of nematodes for preferred host range and reproduction and other information concerning the life cycle of the nematode. Unfortunately, information on the genetic variability among nematode populations for these parameters does not exist. This study is part of a research project to characterize diversity among reniform nematode populations based on their morphometric characteristics, their reproduction on selected hosts, and on nuclear and mitochondrial molecular markers.

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RESEARCH DESCRIPTION

Thirteen geographic populations from the main cotton regions where reniform nematode has been reported were included in this study as follows: Alabama (2), Arkansas (2), Florida (1), Georgia (1), Louisiana (1), Mississippi (1), North Carolina (1), South Carolina (1), and Texas (1). In addition, Hawaii (2) was included because it is the origin of the first report of the reniform nematode (Linford and Oliveira, 1940) and represents a more tropical environment than the other locations. Specimens for measuring were extracted from soil by the centrifugal flotation technique (Jenkins, 1964) and mounted in water. The main morphological characters (body length, stylet length, vulva position, spicule length, tail length, length of hyaline portion of tail, dorsal oesophageal-gland orifice position, excretory pore position, maximum width, oesophageal length, anal width, ratios a, b, c and c') were measured on 20 immature females and 20 adult males from each population. Multivariate analysis of variance (MANOVA) was used to determine if significant differences existed among populations. The DISCRIM procedure in SAS version 8.2 was used to perform discriminant analysis. Canonical variable scores were also generated and plotted to indicate how populations differed.

RESULTS AND DISCUSSION

The MANOVA indicated that significant differences exist across populations. The first two canonical variables were generated and plotted for both the immature female and the male data. Tables 1 and 2 interpret the canonical variables in their correlation to the original morphological characters. For females, canonical variable 1 is most highly correlated with body length, vulva position, and excretory pore, while canonical variable 2 is mostly defined by stylet, dorsal oesophageal gland orifice, and oesophageal length. For males, canonical variable 1 is most highly correlated to body length, excretory pore, and anal width, while canonical variable 2 is defined by a combination of body length, spicule, tail length, oesophageal length, and maximum body width.

The plot of the means of the first two canonical variables for females (Fig. 1) illustrates how the population from Hawaii (HWP) differs from the others in terms of the first canonical axis. The populations from Pine Bluff, Arkansas (ARP) and Mississippi (MS) differ from the others in terms of the second canonical axis, and are highly similar to each other. Figure 2, a plot of the mean canonical variable scores for the male, illustrates how the Hawaiian population (HWP) also differs from the others in terms of the first axis. Additionally, the population from Limestone, Alabama (ALL) differs from the others on the second canonical axis.

There was considerable fluctuation of size and shape within all the populations. This polymorphism of reniform nematode has been documented for populations in Japan (Nakasono, 1983) and also is consistent with variation reported within populations from Florida, Louisiana, and Texas (Lehman and Inserra, 1989). Overlapping morphometric values in our results suggest a more diverse composition of the reniform

populations in Hawaii covering a wider range of body sizes than is found in the populations from the continental U.S. The notably larger body size (body length >500 m) that we observed in the Hawaiian populations has been reported only from Cape Verde Islands (Germani, 1978) and in the original description of the species based on a Hawaiian population (Linford and Oliveira, 1940). Studies on population genetics should further elucidate the composition of populations of reniform nematode present in the U.S.

PRACTICAL APPLICATIONS

The development of cotton cultivars with wide genetic resistance to reniform nematode depends upon knowledge of and availability to the range of genetic diversity present within the nematode itself. Also, the development of effective management strategies is directly related to the ecological significance of the morphological variations of *R. reniformis* and their correlation with the genetic diversity of the nematode.

LITERATURE CITED

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Table 1. Correlations between the first two canonical variables and the original variables in immature females. The highlighted values correspond to the characters that contribute the most to distinguishing populations.

	Pooled within canonical structure	
Variable	Can1	Can2
Stylet	0.292833	**-0.426942**
Body length	**0.807854**	0.178108
Vulva	**0.747700**	0.246445
Tail length	0.319306	-0.110217
Hyaline portion	0.155569	0.142758
Dorsal oesoph. gl.	0.153402	**0.369677**
Excretory pore	**0.702242**	-0.102214
Max. width	0.480224	-0.298169
Oesophagus	0.621896	**0.473667**
Anal width	0.377200	-0.234497

Table 2. Correlations between the first two canonical variables and the original variables in adult males. The highlighted values correspond to the characters that contribute the most to distinguishing populations.

	Pooled within canonical structure	
Variable	Can1	Can2
Stylet	0.388348	0.013193
Body length	**0.586365**	**0.681958**
Spicule	0.242949	**0.393726**
Tail length	-0.066639	**0.467467**
Hyaline portion	-0.139429	0.073713
Excretory pore	**0.646651**	0.046112
Max. width	0.166736	**0.459137**
Oesophagus	0.377026	**0.404948**
Anal width	**0.591245**	-0.092283

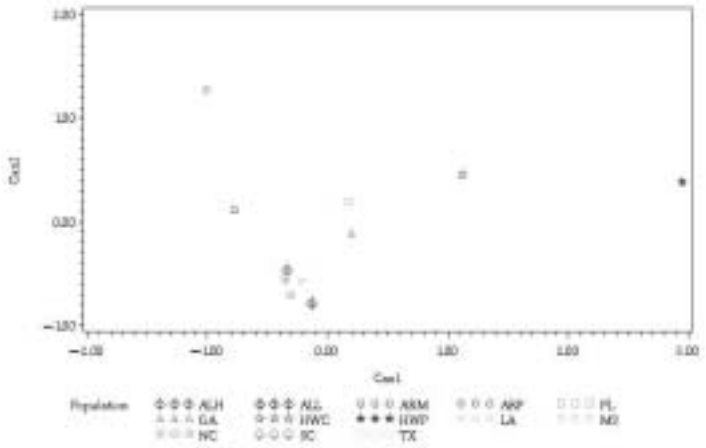

Fig. 1. Plot of the means of canonical variables for the immature female. (ALH: Alabama-Huxford, ALL: Alabama-Limestone, ARM: Arkansas-Mississippi Co., ARP: Arkansas-Pinebluff, Fl: Florida, GA: Georgia, HWC: Hawaii-Cowpea, HW: Hawaii-Pineapple, LA: Louisiana, MS: Mississippi, NC: North Carolina, SC: South Carolina, TX: Texas).

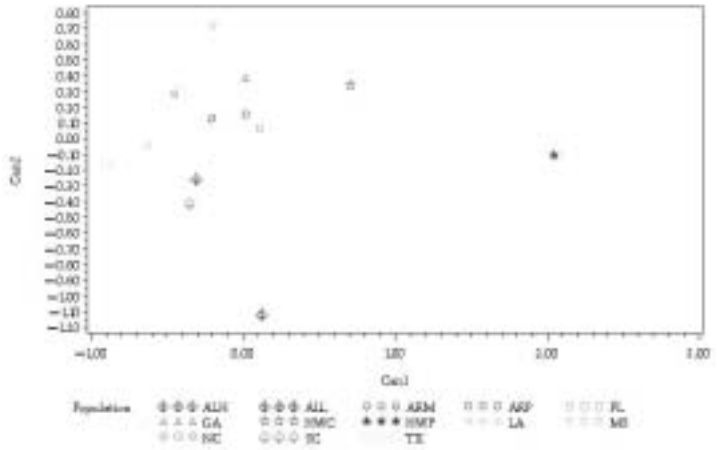

Fig. 2. Plot of the means of canonical variables for the immature female. (ALH: Alabama-Huxford, ALL: Alabama-Limestone, ARM: Arkansas-Mississippi Co., ARP: Arkansas-Pinebluff, FL: Florida, GA: Georgia, HWC: Hawaii-Cowpea, HW: Hawaii-Pineapple, LA: Louisiana, MS: Mississippi, NC: North Carolina, SC: South Carolina, TX: Texas).