

Molecular analyses of *Xiphidorus* species (Nematoda: Longidoridae) from Brazil.

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Introduction

Xiphidorus nematodes are indigenous to Latin America and have a more restricted distribution as compared with *Xiphinema*. The economic importance of these nematodes with respect to crop damage is unknown. Only eight *Xiphidorus* species have been identified from the following countries: Argentina, Brazil, Uruguay and Venezuela.



Figure 1 *Xiphidorus* populations from Brazil included in this study.

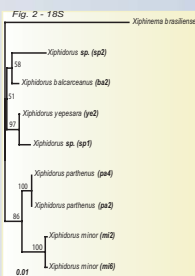
species	locality	host
1 <i>Xiphidorus balcarceus</i> (ba2)	Guia Lopes da Laguna, MS	Cerrado
1 <i>Xiphidorus minor</i> (mi6)	Guia Lopes da Laguna, MS	Cerrado
2 <i>Xiphidorus minor</i> (mi2)	Piracicaba, SP	Natural vegetation
3 <i>Xiphidorus parthenus</i> (pa4)	São Pedro, SP	Saccharum officinarum
4 <i>Xiphidorus parthenus</i> (pa2)	São Carlos, SP	Psidium guajava
5 <i>Xiphidorus</i> sp (sp1)	São José do Rio Preto, SP	Psidium guajava
6 <i>Xiphidorus yepesara</i> (ye2)	Bonito, MS	Palm
7 <i>Xiphidorus</i> sp. (sp2)	Dourados, MS	Natural vegetation
8 <i>Xiphinema brasiliense</i> (outgroup)	Cananéia, SP	Euterpes edulis

During a national survey (Oliveira *et al.*, 2003), six *Xiphidorus* species were recorded from two Brazilian States. We investigate the taxonomic relationships of these species using PCR RFLP, 18S rDNA and ITS-1 region sequences.

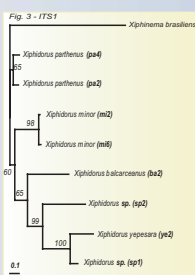
Phylogenetic analyses

Although not congruent, maximum likelihood phylogenetic trees derived from both 18S rDNA and ITS-1 sequences (Figs. 2 and 3) discriminated six *Xiphidorus* species (*X. balcarceus*, *X. minor*, *X. parthenus*, *X. yepesara*, and two undescribed *Xiphidorus* species) from Brazil.

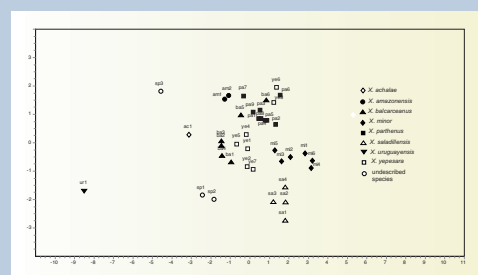
Divergence between *X. parthenus* and *X. yepesara* of both the 18S rDNA and ITS-1 sequences was noted. Based on this data we formally reject both the subspecies hypothesis of Decraemer *et al.* (1996) and the synonymization proposed by Chaves *et al.* (1999). Thus we recommend the retention of the original species proposed by Monteiro (1976) and Monteiro *et al.* (1981).



Phylogenetic trees showing relationships between *Xiphidorus* species based on sequences of 18S rDNA (Fig 2) and ITS1 (Fig 3). The trees were constructed using DNAML. The numbers indicate the bootstrap values higher than 50. Branch lengths are drawn to be proportional to the number of changes inferred. *Xiphinema brasiliense* is the outgroup.



PCA



A principal component analysis (PCA) based on eight morphometric characters from 39 South American populations clearly separated populations previously identified as *X. achalae*, *X. amazonensis*, *X. minor*, *X. saladillensis* and *X. uruguayensis* and three undescribed *Xiphidorus* species. However, populations identified as *X. balcarceus*, *X. parthenus* and *X. yepesara* did not form similar discrete groupings and exhibited either considerable morphological variability or have been incorrectly identified.

ITS1 RFLP

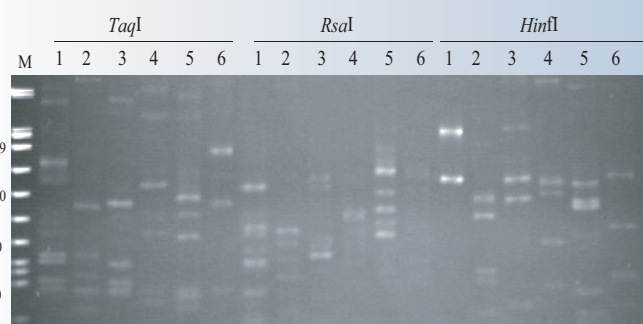


Fig. 4. Restriction Fragment Length Polymorphisms yielded by digestion of ITS-1 region from six *Xiphidorus* species with three restriction enzymes (*TagI*, *RsaI* and *HinfI*). Digested products were separated on a 10% non-denaturing polyacrylamide gel. 1: *X. balcarceus* (ba2); 2: *X. minor* (mi2); 3: *X. parthenus* (pa4); 4: *X. yepesara* (ye2); 5: *Xiphidorus* sp (sp1); 6: *Xiphidorus* sp. (sp2). M = molecular marker VIII

Conclusions

Our data confirms that *X. yepesara* and *X. parthenus* are distinct taxonomic species as originally described. In addition, the molecular analysis suggests that the populations from Dourados, MS and São José do Rio Preto, SP are two undescribed *Xiphidorus* species.

Acknowledgements

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