Die Nematodenpopulationen von sechs kommerziell genutzten Bananenplantagen in der Region Guapilles, Costa Rica wurden bestimmt. Dazu wurden Bodenproben von Standorten mit jeweils guten, mittleren und schwachen Fruchterträgen entnommen. Die Nematoden wurden mit der modifizierten Bearmann Methode extrahiert, quantifiziert, und die jeweils ersten hundert so isolierten Nematoden bis zur Ordnung identifiziert. Generelle für diese Nematoden geeignete Indices wurden errechnet und mit dem Ertrag sowie chemischen, physikalischen und biologischen Faktoren der Plantagen in Beziehung gesetzt.

127 – Metge, K.[1]; Braasch, H.[2]; Gu, J.[3]; Burgermeister, W.[1]

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Phylogenetic relationships among *Bursaphelenchus* species (Nematoda: Aphelenchoididae) of different groups

In Europe and Asia, main interest in species of the genus *Bursaphelenchus* Fuchs, 1937 is related to the phytopathogen *Bursaphelenchus xylophilus* (Steiner & Buhrer, 1934) Nickle, 1970, which is the causal agent of the pine wilt disease. Since the detection of *B. xylophilus* in Portugal 1999 (Mota et al., 1999), great effort was made in finding, identification and differentiation of *Bursaphelenchus* species (Burgermeister et al., 2005; Metge & Burgermeister, 2005; Matsunaga & Togachi, 2004; Kang et al., 2004; Braasch et al., 1999). Molecular genetic studies were carried out to determine phylogenetic relationships of these species. We compared sequences of ITS1, 5.8S and ITS2 of rDNA from members of the xylophilus group, the fungivorus group and the recently described species *B. arthuri*, *B. doui*, *B. rainulfi*, *B. singaporensis*, *B. thailandae, B. willibaldi* sp. n. and *B. yongensis* sp. n. as well as *B. eremus* to determine their phylogenetic status within the genus *Bursaphelenchus*.

The phylogenetic analysis using neighbour–joining (NJ) and maximum parsimony (MP) algorithms resulted in trees with similar topologies (Figure). Nineteen Bursaphelenchus isolates representing 17 species examined can be separated in two main branches: the first one includes the seven members of the xylophilus group, and the second one is divided in two clusters, one including the five species of the fungivorus group, the other one the four *Bursaphelenchus* species, *B. eremus*, *B. hofmanni*, *B. rainulfi* and *B. yongensis sp.* n. , which are considered as members of additional subgroups.

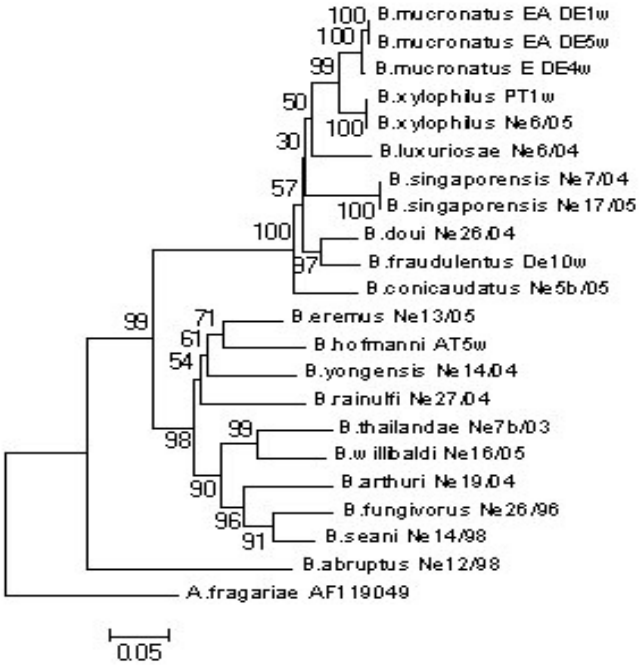

Figure Phylogenetic relationships of *Bursaphelenchus* species. Aphelenchoides fragariae is included as an outgroup. The global alignment matrix of rDNA sequences was calculated by neighbour–joining (NJ) algorithms. Bootstrap values [%] are given for each node.