



***Anguina paludicola* sp. n. (Tylenchida: Anguinidae): The nematode associated with *Rathayibacter toxicus* infection in *Polypogon monspeliensis* and *Lachnagrostis filiformis* in Australia**

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Abstract

Anguina paludicola sp. n. is described from *Polypogon monspeliensis* from southeastern South Australia and *Lachnagrostis filiformis* from northern New South Wales, following an examination of nematode populations by allozyme electrophoresis and morphological analysis. Genetic differences were consistent with those expected from conspecific allopatric populations and were based on geography rather than host. Morphological differences between nematodes from *P. monspeliensis* and *L. filiformis* were inconsistent and varied between different gall types on the same host plant. The new species is characterised by adults with irregular and variable tail termini, which appear lobed; females may have a process of vestigial ovary extending from the post uterine sac towards the tail; males are dorsally curved with a single reflexed testis; and the haploid chromosome complement is n=18.

Key words: Anguinidae, allozyme electrophoresis, flood plain staggers, morphology, new species, Australia

Introduction

Flood plain staggers is a livestock poisoning generally associated with flood prone pastures dominated by either *Polypogon monspeliensis* (L.) Desf. or *Lachnagrostis filiformis* (Forst.) Trinius. These grasses become infected by the toxigenic bacterium *Rathayibacter toxicus* (Riley & Ophel) Sasaki, Chijimatsu & Suzuki (McKay & Ophel 1993) as a result of colonisation by nematodes belonging to the genus *Anguina* (McKay *et al.* 1993). McKay *et al.* (1993) used allozyme electrophoresis to show that the nematodes infesting *P. monspeliensis* and *L. filiformis* were different from other described seed-gall forming species of *Anguina* known from Australia and New Zealand. However, they did not speculate on whether the nematodes from *L. filiformis* and *P. monspeliensis* were the same species, even though the genetic variation they found between populations was within the variation expected for conspecific allopatric populations (Richardson *et al.* 1986). This is possibly due to the limited number of populations they examined. More recently, Powers *et al.* (2001) and Subbotin *et al.* (2004) examined relationships within the *Anguina* based on molecular analyses of the first and second rDNA internal transcribed spacer regions. While data from both studies indicate that the nematodes infesting *P. monspeliensis* and *L. filiformis* are clearly different from other described species of *Anguina* and closely related, they provide no measure of genetic variation between nematode populations, as only a single nematode population from each host was examined.

This paper reports a new species of *Anguina* based on allozyme analysis of nematode populations infesting *L. filiformis* and *P. monspeliensis* from throughout their known range, morphological analysis to