



Original article

Genetic diversity of widespread moss-dwelling nematode species in German beech forests



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ABSTRACT

Molecular studies suggest that the number of microscopic animal species has been severely underestimated because of a high level of cryptic diversity. Using traditional methods of morphological species identification, a large number of species have remained undetected. In fact, many aquatic nematode morphospecies with an assumed widespread distribution instead may comprise cryptic species complexes. In terrestrial moss habitats, the diversity of nematode communities has yet to be evaluated in molecular surveys. Thus, the aim of this study was to assess the potential for cryptic diversity among the three dominant moss-dwelling nematode species (*Plectus parietinus*, *Plectus cirratus*, and *Chiloplectus andrassyi*) detected at five locations within four German beech forests. Analyses of the molecular variation in a mitochondrial (COI) gene and in two ribosomal (LSU and SSU) subunit genes were complemented by morphological identification of specimens. The morphological-based plectid species delineation was supported by the COI gene topology, but less by the analyses of nuclear marker genes. Furthermore, the results revealed a high level of high genetic diversity in terms of number of mitochondrial haplotypes ($n = 24$) detected overall for the three investigated morphospecies at the five locations, with no evidence of cryptic diversity. However, the large number of haplotypes only to be found at a single sampling location suggested a restricted level of gene flow even over short geographic distances (6 km).

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1. Introduction

Mosses are widespread in northern temperate zones and inhabit diverse locations, such as living or decaying trees, rocks, open mineral soil, and even water bodies. In addition to their ecological significance as water reservoirs mosses play an important role in the functioning of ecosystems [1]. However, mosses are also unstable environments, undergoing desiccation but also becoming inundated by rain.

The microscopic moss-dwelling faunal community, referred to as microfauna is strongly involved in ecological processes such as nutrient cycling and decomposition in addition to serving as a food source for higher trophic levels [2–5]. Generally, the moss-dwelling metazoan microfauna is dominated by mites, tardigrades, rotifers, and nematodes [6,7]. Amongst these, nematodes are the most abundant and diverse group, with densities as high as 1446

individuals per 100 ml of moss [8]. As many as 52 species have been detected in a single habitat [9]. Interestingly members of the family Plectidae are generally very common and numerous in moss cushions in the northern temperate zone with shares up to 53% of the moss-dwelling nematode communities. By contrast, they are rather less abundant in freshwater ecosystems [6,10–14].

Similar to tardigrades and rotifers, a key feature of plectids is their ability to tolerate desiccation events, by means of anhydrobiosis. This metabolically inactive state is triggered by water scarcity and it allows plectids to thrive even in unstable moss habitats [15–17]. Additionally, during their active and dormant phase, nematodes might be passively transported over long distances by vectors such as wind or birds [18–21] which probably contributes to the stated widespread or even worldwide occurrence of some plectid species [22].

Molecular surveys of free-living nematodes have thus far been mostly restricted to aquatic species and they have often confirmed the existence of cryptic species [23,24]. By contrast similar studies on moss-dwelling nematodes are to our knowledge extremely rare. Cryptic species cannot be distinguished morphologically, whereas genetic analyses reveal the presence of distinct taxonomic entities

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