

Phylogenetic study of some *Aporrectodea* species based on molecular markers

(Oligochaeta: Lumbricidae)

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Abstract. The *Nicodrilus* genus is not accepted in the nomenclature according to ICZN; *Aporrectodea* term is used. However, according to Bouché, *Aporrectodea* and *Allolobophora* genera are not homogeneous and are supposed as polyphyletic genera. The aim is to study the phylogenetic structure of *Aporrectodea* genus in order to verify its cladistic nature and its taxonomical validity. In this work, five species, belonging to the *Aporrectodea* genus, as the most common in France are studied. First, we use usual morphological characteristics to identify each species. Species life history traits are included among morphological characteristics (e.g. clitellum, puberculum and pores position, Morren's gland, body size). Then, we pursue a molecular approach on individuals sampled in France. Molecular phylogenetic analyses are based on the sequences of nuclear (rDNA 28S) and mitochondrial (COI, rDNA 16S) gene regions and performed with maximum likelihood and bayesian inference. Phylogenetic analyses revealed two deep sister clades, *Aporrectodea caliginosa* species complex in one hand, and *A. giardi*, *A. longa* and *A. nocturna* in the other hand. The status of *A. nocturna* is recognized instead of *A. longa* and *A. giardi* ones. Our study cannot confirm the validity of *Aporrectodea* genus but highlights different lineages within species such as *A. longa* and *A. caliginosa*. Markers characterization ensures a molecular genotyping in lumbricids and begins to reveal intraspecific variabilities degrees unsuspected.

Key words. Phylogeny, evolution, COI, rDNA16S, rDNA28S, *Aporrectodea*.

Introduction

Most of the available phylogenetic classifications of Lumbricidae are based on morphological studies (BOUCHÉ 1972, SIMS & GERARD 1985). Although the morphology constitutes the base of species identification, these classifications have such particularities like a low resolution of phylogenetic relationship leading to uncertain grouping. Taking into account the important role which earthworms play as key organisms in terrestrial ecosystems functioning, the lack of knowledge in phylogenetic relationship among species can compromise interpretations in studies applied in functional ecology, biodiversity and evolution (King et al. 2008). DNA taxonomy and associated molecular tools are a good way to reveal the true level of biodiversity (Chang et al. 2009), but the use of molecular tools to study earthworm taxonomy has only recently started. Molecular markers, mitochondrial and nuclear, are thus developed (PÉREZ-LOSADA et al. 2009). Lumbricids represent a taxonomical diversified group of terrestrial Oligochaeta. Among the five families within Lumbricoidea, Lumbricidae family counts around 30 genera; some of them provide very diverse species based on their ecological functions. Molecular approaches realized for a few years on *Lumbricidae* confir-