



Ecological drivers influence the distributions of two cryptic lineages in an earthworm morphospecies



David J. Spurgeon^{a,1,*}, Manuel Liebeke^{b,1}, Craig Anderson^{a,c}, Peter Kille^d, Alan Lawlor^e, Jacob G. Bundy^b, Elma Lahive^a

^a Centre for Ecology and Hydrology, Maclean Building, Benson Lane, Wallingford OX10 8BB, UK

^b Department of Surgery and Cancer, Faculty of Medicine, Imperial College London, London SW7 2AZ, UK

^c Biological and Environmental Sciences, School of Natural Sciences, University of Stirling, Stirling FK9 4LA, UK

^d School of Biosciences, University of Cardiff, Main Building, Museum Avenue, Cardiff CF10 3AT, UK

^e Centre for Ecology and Hydrology, Library Avenue, Bailrigg, Lancaster LA1 4AP, UK

ARTICLE INFO

Article history:

Received 25 April 2016

Received in revised form 5 July 2016

Accepted 25 July 2016

Available online xxx

Keywords:

Biogeography

Earthworm

Cryptic species

pH

Soil organic matter

ABSTRACT

Substantial genetic diversity exists within earthworm morphotypes, such that traditional species designations may be incomplete. It is, however, currently not known whether these different genetic variants show ubiquity or specialty in their distribution across separated sites subject to different climatic, biotic or soil physicochemical factors. Here we report on the results of a survey in which individuals of the *Lumbricus rubellus* morphotype, a species known to comprise two deeply divergent genetic lineages in England and Wales, were sampled from 26 plots. Sequences from the mitochondrial cytochrome oxidase I gene were used to distinguish lineages for 787 individuals. In conjunction, a range of geographic, climatic, biotic and soil physicochemical variables were also collected for each locality.

Genotyping indicated that Lineage A was more common than Lineage B, comprising 58% of the collected *L. rubellus*. Six site populations comprised only Lineage A, while only a single site comprised entirely Lineage B. The remaining 20 sites contained both lineages. A multivariate ordination of site variables identified major difference between sites were associated with low pH, organic-rich soils in Western wet upland areas and pollutant levels associated with sites in the South. Earthworm genotype (as proportion of Lineage A) was not correlated with either of these major environmental axes. When individual variables of soil pH and the percentage of soil organic matter, which are known to be key driver of soil species distributions, were investigated as single variables significant relationship with lineage frequency were found. Soil organic matter content was significantly negatively correlated with Lineage A proportion, while pH was significantly positively correlated. This lineage preference may be related to lineage metabolism and/or behavioral differences.

Measurement of tissue metal concentrations in worms from 17 sites identified a significant site effect in all cases, but a lineage effect only for arsenic (higher Lineage B). Tissue arsenic concentrations varied between lineages, supporting previous observations that there are differences in the way the two lineages have adapted to manage exposure to this metalloid.

© 2016 Elsevier B.V. All rights reserved.

1. Introduction

Soils contain a wealth of invertebrate biodiversity recognised for their important contributions to ecological processes (Bardgett

and van der Putten, 2014; Fitter et al., 2005; Giller, 1996). One key group of species are the “ecosystem engineers”: those organisms that modify the physical state of the soil and resource availability for other species. Earthworms are known as a key group of ecosystem engineers in many habitats. They perform a range of physical (aeration, bioturbation, litter fragmentation) and biological (microbial interactions, exudate production) roles in soil (Blouin et al., 2013; Lavelle et al., 1997; Sackett et al., 2013; Umarov et al., 2008). Because of their functional importance, earthworms have emerged as a major taxon for biomonitoring and biomarker

* Corresponding author at: Centre for Ecology and Hydrology, Maclean Building, Benson Lane, Crowmarsh Gifford, Wallingford, Oxfordshire OX10 8BB, UK.

E-mail address: dasp@ceh.ac.uk (D.J. Spurgeon).

¹ Current address: Department of Symbiosis, Max Planck Institute for Marine Microbiology, Bremen, Germany.

assessments of human induced pressures on soil communities (Cluzeau et al., 2012; Rutgers et al., 2009).

As soil invertebrate species, including earthworms, have been shown to be sensitive to a range of land use change and pollution impacts (Bundy et al., 2007; Cluzeau et al., 2012), different soil taxa have become a natural focus for research on the relationships between environmental pressures, biodiversity and soil functioning (Bartlett et al., 2010; Leveque et al., 2015; Rutgers et al., 2016). For community studies, a major constraint relates to current uncertainties in earthworm taxonomy. Traditionally earthworm identification has relied on morphology, but the paucity of suitable local keys and problems with application to juveniles has also recently encouraged the use of molecular methods (Dominguez et al., 2015; Emerson et al., 2011; Klarica et al., 2012). These genotyping studies have begun to challenge current understanding of diversity through the identification of genetically distinct cryptic lineages within previously established morphospecies.

Earthworm species in which cryptic lineage diversity has to date been identified include *Eisenia fetida/andrei* (Römbke et al., 2016), *Lumbricus terrestris* (James et al., 2010), *Aporrectodea caliginosa* (PerezLosada et al., 2009), *Allolobophora chlorotica* (King et al., 2008), *Amyntas gracilis/Amyntas cortici* (Novo et al., 2015) and *Lumbricus rubellus*. For *L. rubellus*, genotyping studies based on mitochondrial cytochrome oxidase I and II markers have identified as many as 6 cryptic lineages across Europe (Giska et al., 2015), two of which are found in the UK (Andre et al., 2010; Kille et al., 2013). The two UK lineages have 10–15% divergence for the mitochondrial COI and COII sequences. While this implies they may actually be cryptic species, recent analysis of multiple nuclear markers using RADseq has not supported this interpretation, instead suggesting that different *L. rubellus* lineages may actually correspond to a single highly polymorphic species (Giska et al., 2015). Comparative studies of the two lineages in the UK have, nonetheless, identified physiological differences between them, including variation in pheromone production (Jones et al., 2016), maturation time (Anderson et al., 2013), metabolic profiles (Liebeke et al., 2014), mechanism of arsenic adaptation (Kille et al., 2013), trace element metabolism (Andre et al., 2010), and microbiome complement (Pass et al., 2015).

Despite known biological differences, the extent to which differences in distribution and physiology are related to different geographical, climate and soil physicochemical preferences between the two known UK lineages of *L. rubellus* is not established. The two lineages found co-occur at some, but not all, sites meaning that they have some likely niche divergence that facilitates coexistence (Andre et al., 2010; Giska et al., 2015; Kille et al., 2013). We aim to better understand the nature of the spatial and geochemical drivers of lineage relative abundance, and so here we test the hypothesis that the site distribution of the two cryptic *L. rubellus* lineages is based on one or more geographical, climatic, physicochemical or biotic drivers. We collected and genotyped morphotype *L. rubellus* at multiple well-characterized sites that differed in their properties to investigate the relationships that determine lineage distributions. Tissue metal concentrations were also measured to assess if trace metal levels could also influence distributions, as could be the case if the two lineages had different sensitivity to specific contaminants.

2. Methods

2.1. Site selection

Twenty six sites located across England and Wales (Fig. 1) were visited between four times (for Devon Great Consols Mine and Control, Shipham Mine and Control, Cwmystwyth Mine and Control) and a single visit (for Porton Down, Parys Mountain,

Castell, Clydach, Roman Gravel, Didcot) over four separate sampling events from Spring 2011 to Spring 2014. The chosen sites were selected to capture a range of the habitats and soil conditions under which morphotype *L. rubellus* can be collected. Land-uses covered included arable systems, broadleaf woodland, rough grassland and improved pasture habitats. Sites included both mineral and organic soils, although not true peats.

To allow the role of soil geochemistry and pollution status on lineage distribution to be addressed, sites of different known pollution history were sampled. Sites corresponded to three groups with respect to past land-use and associated expected contamination level. These were: 1) sites with no known pollution source (Unpolluted); 2) sites near to industrial facilities expected to be characterised by moderate pollution (Industrial polluted); and 3) sites at abandoned mining sites that can be expected to have high pollution (Mine polluted). For expected polluted sites from categories 2 and 3, a local control site was also sampled. This reference site was located outside of the area that was expected to be strongly influenced by the main pollution source and so was on soil expected to contain regional background pollutant concentrations.

2.2. Site geographical, biological and soil physicochemical characterisation

To allow the assessment of environmental drivers relating to lineage distribution, we used both publically available resources as well as our own analyses to gather data on each sites. Site geographical locations were collected as Easting and Northings from www.gridreferencefinder.com and site altitudes from www.freemaptools.com/elevation-finder.htm. A series of site climate conditions were also assembled from www.metoffice.gov.uk/. These were: annual average maximum temperature, annual average minimum temperature, average January minimum temperature, average July minimum temperature, average annual rainfall, average annual rain days and average annual frost days. Initial visits to each site recorded main land-use (arable, broadleaf woodland, rough grassland and improved pasture) and where present the average sward height of vegetation at collection locations. The site was identified according to the level of shade (open, part shaded, shaded) and the presence of livestock was noted.

An initial site survey identified points on the site where morphospecies *L. rubellus* could be found. Thereafter all collections were focussed on these locations. For any one sampling event at each site, between 6 and 25 fully clitellate *L. rubellus* were collected by digging and hand-sorting from the soil to 20 cm depth. Generally the required number of worms could be collected within a reasonable search period (approximately 2 h duration). There were, however, some locations where this was not possible for particular sampling events. Climate factors (notably dry soils), low frequency of adults in the population or the requirement to limit site damage caused by digging were the major constraints. During collection, the presence of other earthworm morphospecies was noted. Only common species were recorded (>5 individuals observed). In total 10 other species were found: *Aporrectodea caliginosa*, *Aporrectodea rosea*, *Aporrectodea longa*, *Allolobophora chlorotica*, *Lumbricus castaneus*, *Dendrobaena rubida*, *Lumbricus terrestris*, *Lumbricus festivus*, *Octolasion cyaneum*, and *Octolasion tyraeum*. At the end of sampling, the *L. rubellus* collected were washed and blotted dry on-site and then snap frozen in liquid nitrogen before being transferred to the laboratory under dry ice storage.

Triplicate soil samples from surface to 5 cm depth were collected from each site collection location. All soil samples were oven dried at 80 °C to constant weight and then sieved through a

Download English Version:

<https://daneshyari.com/en/article/6297423>

Download Persian Version:

<https://daneshyari.com/article/6297423>

[Daneshyari.com](https://daneshyari.com)