

# *Molecular genetic differentiation in earthworms inhabiting a heterogeneous Pb-polluted landscape*

Article

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1     **Molecular genetic differentiation in earthworms inhabiting a heterogeneous Pb-polluted**  
2   **landscape**

3  
4     J. Andre<sup>1,2</sup>, R. A. King<sup>1</sup>, S. R. Stürzenbaum<sup>3</sup>, P. Kille<sup>1</sup>, M. E. Hodson<sup>2</sup> and A. J.  
5     Morgan<sup>1</sup>

6  
7     <sup>1</sup> Cardiff School of Biosciences, Cardiff University, Museum Avenue, Cardiff, CF10  
8     3TL, UK.

9  
10    <sup>2</sup> Department of Soil Science, School of Human and Environmental Sciences,  
11    University of Reading, Whiteknights, Reading, RG6 6DW, UK.

12  
13    <sup>3</sup> King's College London, School of Biomedical & Health Sciences, Pharmaceutical  
14    Sciences Division, London, SE1 9NH, UK.

15  
16    Corresponding Author: Dr Jane Andre, Cardiff School of Biosciences, Cardiff  
17    University, Museum Avenue, Cardiff, CF10 3TL, UK. Email:Andrej@cardiff.ac.uk

18  
19    Abstract

20  
21    Landscapes blighted by industrial activity but which accommodate seemingly resistant  
22    animal ecotypes provide an ideal opportunity to study evolution in action. We  
23    investigated the phylogenetic structure and molecular adaptation of the metal  
24    extremophile earthworm *Lumbricus rubellus* inhabiting a geochemically heterogeneous  
25    Pb/Zn mine. These worms prodigiously accumulate Pb (c.1.5% total-body dry mass),

26 trafficking most to Ca/PO<sub>4</sub>-rich organelles in chloragocytes. Infrared  
27 microspectroscopy (FTIR) of chloragocytes detected altered phosphate profiles in a  
28 putative tolerant population. Moreover, bioinformatic analysis of *L. rubellus* EST<sup>Pb</sup>  
29 libraries indicated that constituents of Ca-signalling and sequestration pathways were  
30 aberrantly elevated. Sequencing a gene central to this pathway, sarco/endoplasmic  
31 calcium ATPase (SERCA), revealed mutations clustered in the cytosolic domain that  
32 correlated with site-specific Pb-tolerant genotypes. Our findings present a mechanism  
33 that enables locally adapted earthworm populations to tolerate a novel habitat,  
34 potentially contributing to genetic differentiation and eventual speciation. Additionally,  
35 they indicate that extreme Pb tolerance mechanisms are evolutionary appropriations of  
36 intrinsic Ca molecular machinery: Inorganic mimicry begets biomolecular adaptive  
37 mechanisms.

38

39 Capsule: Landscapes punctuated by polluted islands are inhabited by Pb-adapted  
40 invertebrate extremophiles.

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42 Keywords: Calcium, lead, earthworms, phylogenetics, ecotoxicology

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49 Introduction

50

51 Occupational and environmental exposures to Pb continue to cause serious human  
52 health problems in developing and industrialised countries (Tong et al., 2000) and  
53 diverse disruptive effects on both ecological processes (Rantalainen et al., 2006) and  
54 wildlife (Chapman and Wang, 2000). Intriguingly some field populations (ecotypes) of  
55 invertebrates have evolved resistance to metal stressors in their native habitats (Morgan  
56 et al., 2007), with the earthworm *Lumbricus rubellus* representing an extreme example  
57 of a complex organism that can manifest Pb tolerance in mine-associated soils  
58 contaminated to a degree exceeding by an order of magnitude the exposure level that  
59 severely compromises reproduction in spiked laboratory soils (Spurgeon et al., 1994). *L.*  
60 *rubellus* is an acid-tolerant species inhabiting litter on soils ranging from pH 3.8 to 8.4  
61 (Sims and Gerard, 1985), thereby indicating that this early pioneer of mine-associated  
62 and industrial ‘soils’ may possess the genetic amplitude to become a locally-adapted  
63 population with the inherent ability to cope with site-specific extremes in contaminant  
64 availabilities. Although many terrestrial invertebrates reside in soils containing metal  
65 levels that far exceed effect concentrations for key life-cycle traits (Morgan and  
66 Morgan, 1990; Spurgeon and Hopkin, 1996) and despite being well documented in  
67 plants, evidence for the heritability of adaptive traits and evolution of metal-resistant  
68 ecotypes remain relatively sparse.

69

70 As sites elevated in inorganic pollutants illustrate both spatial and temporal  
71 stochasticity, with geological features alongside ancient and recent industrial activities  
72 providing an array of unique environments to which nature has adapted, cogent data sets  
73 to investigate evolution in action are presented. The Cwmystwyth valley, Wales (UK) is

74 a disused Pb (galena, PbS) mine that is highly heterogeneous in nature comprising of  
75 numerous micro-habitats that relate to soil metal content and pH. In combination with  
76 the acquisition of Pb-adaptive traits in *L. rubellus* ecotypes, a unique model to study  
77 earthworm phylogeography and, more specifically, whether metal contamination-  
78 associated stress and microsite heterogeneity have the potential to alter the genetic  
79 structure of populations through adaptation and speciation is provided. The ancestors of  
80 earthworms now resident at Cwmystwyth would have survived the major glaciations  
81 and climatic instability of the Devensian period in one or more of the sheltered southern  
82 refugia. With the onset of each stadial period and reformation of ice-sheets, retreating  
83 bottlenecked populations would have experienced shrinkage, dissection and extinction,  
84 whereas upon post-glacial expansion undergone adaptation and selection to new  
85 environments (Hewitt, 2000). Repeated climatic oscillations and changes in habitat  
86 range have therefore yielded increased species diversity through several genome  
87 reorganisations, manifested today by the broad environmental conditions and  
88 geographical ranges tolerated by *L. rubellus*. This includes the ability to colonise  
89 heterogeneous and potentially stressful metal-polluted habitats such as are found at  
90 Cwmystwyth.

91

92 Detrimental effects of Pb exposure arise from the ability of Pb to mimic other metals,  
93 primarily Ca (Clarkson, 1993; Warren et al., 1998). Intracellular interactions between  
94 Pb and Ca are well documented, with non-sequestered Pb metal ions shown to interact  
95 and associate with proteins active in the calcium signalling pathway. This shared  
96 chemical affinity between Pb and Ca lead us to hypothesise that the network of  
97 mechanisms evolved to regulate the potentially lethal levels of intracellular free  $\text{Ca}^{2+}$  are

98 somehow implicated in the handling of its non-essential cationic analogue. Ordinarily  
99 the main molecular resistance mechanisms underlying metal tolerance entails either  
100 metal efflux pumps (Callaghan and Denny, 2002) or sequestration by one of three  
101 classes of thiol-rich peptides, namely glutathione, phytochelatin and metallothionein  
102 (Vatamaniuk et al., 2005; Janssens et al., 2007). However, neither of these generic  
103 resistance mechanisms has been found to underpin Pb adaptations in earthworms or any  
104 other organism. Instead, accumulated Pb is sequestered within calcium phosphate-rich  
105 chloragosomes, unique organelles with certain lysosome-like properties that are located  
106 in the chloragogenous tissue (Morgan and Morgan, 1989). It follows that specific  
107 transport mechanisms must reside in vacuolar membranes for the uptake of metals and  
108 accompanying anions, which provide the complexing negatively charged ion needed for  
109 an insoluble precipitate to be formed. With this in mind, this study aimed to provide  
110 insights into the functional mechanisms of Pb management and adaptation in  
111 chronically exposed earthworm populations. This was achieved through global  
112 transcriptomic analyses, targeted single loci experiments and in-situ biochemical  
113 fingerprinting of the main metal sequestering organ of the earthworm. Combined with  
114 characterising the entire site in terms of metal content and pH and, in parallel,  
115 measuring population divergence from whole-genome and mtDNA loci, a sophisticated  
116 means of studying earthworm speciation and evolution to ecological heterogeneity on a  
117 micro-geographic scale is presented.

118

119 Materials and Methods

120

121 Portable XRF and pH mapping of the Cwmystwyth site. A portable XRF (NITON  
122 XLiand, Thermo Scientific Inc) and GPS system (Garmin, Etrex Venture) were used in  
123 order to create a Pb profile the Cwmystwyth valley, with a total of 97 measurements  
124 taken. A series of 71 soil samples were also collected and the pH of each recorded. The  
125 mapping software SURFER<sup>®</sup> was used to convert both the metal and pH data sets into a  
126 series of 3D rendered surface maps, stacked alongside a base-map of the valley.

127

128 Mitochondrial and AFLP genotyping. *Lumbricus rubellus* earthworms were collected  
129 by digging and hand-sorting. The animals were transported back to the laboratory in  
130 their native soil and depurated as described in (Arnold and Hodson, 2007). Genomic  
131 DNA was extracted from C<sub>Pb\*</sub><sup>pH5</sup> (n=27), C<sub>Pb\*</sub><sup>pH4</sup> (n=33), C<sub>Pb\*\*\*</sub><sup>pH7</sup> (n=32) and C<sub>Pb\*</sub><sup>pH6</sup> (n=30)  
132 earthworms using DNAzol reagent (Invitrogen Ltd., Paisley, UK.). DNA was also  
133 isolated from *L. castaneus* and *L. eiseni*. Forward (5'-TAGCTCACTTAGATGCCA)  
134 and reverse (5'-GTATGCGGATTCTAATTGT) *L. rubellus* specific cytochrome  
135 oxidase II (COII) primers were designed from mitochondrial sequences deposited in  
136 LumbriBASE (www.earthworms.org). For each PCR reaction ~100ng DNA template  
137 was amplified using 10pmole/μl forward and reverse primer, 10mM dNTP mix and  
138 5U/μl Taq DNA polymerase buffered with 5X Mg-free Taq PCR amplification buffer  
139 and supplemented with MgCl<sub>2</sub> (1.5mM). The reaction was denatured at 95°C for 10  
140 minutes and then cycled 35 times at 95°C for 30 seconds, 30 seconds at the required  
141 primer annealing temperature and 72° for 1 minute. This was followed by a 10 minute  
142 final extension at 70°C. The amplicon (469bp) was resolved by electrophoresis in 1X  
143 TAE buffer at 120V for approximately 30 minutes in a Pharmacia GNA-100 tank.  
144 Nucleic acid bands were then visualised on a UV gel documentation system. Prior to



145 sequencing PCR clean-ups were performed using Exo-SAP-IT (Amersham Pharmacia,  
146 UK) reagents. Exonuclease 1 (0.25µl) and Shrimp Alkaline Phosphatase (0.5µl) were  
147 mixed with the PCR product (10µl) and incubated at 37°C for 45 minutes followed by  
148 80°C for 15 minutes. DNA was sequenced using ABI PRISM<sup>®</sup> BigDye v3.1 Terminator  
149 Sequencing technology (Applied Biosystems, Foster City, USA) on the ABI PRISM<sup>®</sup>  
150 3100 DNA Sequencer run by the Cardiff University Molecular Biology Support Unit.  
151 Raw sequence traces were confirmed using Finch TV before being imported into Mega  
152 v3.1 (Kumar et al., 2004) for alignment and tree construction. The distance-based  
153 neighbour joining (NJ) algorithm (Saitou and Nei, 1987), using p-distances, was used to  
154 estimate tree topology and calculate branch lengths. Relationships between phylogenetic  
155 haplotypes were determined by maximum parsimony (MP), maximum likelihood (ML)  
156 and Bayesian methods using PAUP v3.1 and MRBAYES respectively (Huelsenbeck  
157 and Crandall, 1997; Huelsenbeck and Ronquist, 2001), MRMODELTEST v2.2  
158 (Nylander, 2004) and the Akaike Information Criterion (AIC) were used to select the  
159 optimum model (HKY+G) of sequence evolution that best fitted the data (base  
160 frequencies of A=0.3638, C=0.2244, G=0.1277, T=0.2842 and T-ratio=3.5050 and  
161 Gamma distribution parameter= 0.2005). Node support for MP and ML analyses was  
162 determined using a non-parametric bootstrap, with 500 and 1000 replicates respectively  
163 (Holmes, 2003). For the analysis 3x10<sup>6</sup> generations were run, with one tree retained  
164 every 300th generation and the first 2500 trees discarded as burn-in. Genetic distances  
165 were calculated using p-distance in Mega and median-joining networks were drawn  
166 using NETWORK and dnap4.  
167

168 AFLP analysis was adapted from (Ajmone-Marsan et al., 1997) with approximately  
169 200ng of genomic DNA extracted from  $C1_{Pb^*}^{pH5}$  (n=24),  $C2_{Pb^*}^{pH4}$  (n=30),  $C3_{Pb^{***}}^{pH7}$  (n=23) and  
170  $C4_{Pb^*}^{pH6}$  (n=18) individuals. Pre-selective EcoR1 (GACTGCGTACCAATTCA) and Taq1  
171 (GACTGCGTACCAATTCC) primers were used and for the selective amplifications  
172 two primer combinations (E32 (5'-GACTGCGTACCAATTCAAC-3')/T32 (5'-  
173 GATGAGTCCTGACCGAAAC-3') and E32/T38 5'-GATGAGTCCTGAC CGAACT-  
174 3') were employed. Reactions were run by the Cardiff University Molecular Biology  
175 Support Unit and analysed on an Applied Biosystems 3130x1 fragment analyser. Bands  
176 between 70 and 325 base pairs (bp) and with a minimum peak height of 70 units were  
177 scored using GeneMapper analysis software. Microsoft Access, Excel and the Excel  
178 macro GenAlEx6 were used to create a cumulative table of all loci from each individual  
179 and transform the data into a binary form. Principal coordinates (PCO) analysis and  
180 phylogenetic tree construction, supported by bootstrap analysis (1000 replicates), was  
181 performed using the neighbour joining algorithm (based upon the Nei's distance) to in  
182 PAUP v4.0b10 to estimate tree topology and calculate branch length. The software  
183 Structure v2.2 was used to delineate clusters of individuals on a multi-locus, genotype  
184 basis using a Bayesian algorithm. The number of inferred populations ran from 1 to 5,  
185 with 8 replicate runs, a burn-in of 75 000 cycles followed by 300 000 for data  
186 collection. L(K), the modal choice criterion, is calculated in Structure and the true  
187 number of populations (K) can be deferred from its maximal value.  $\Delta K$ , the rate of  
188 change in the log probability of data between successive K-values, provides a visual  
189 means to easily identify the number of clusters in a sample of individuals (Evanno et al.,  
190 2005).  
191

192 EST libraries and informatics. Upon sampling  $C3_{Pb^{***}}^{pH7}$  (n=5) earthworms were  
193 immediately immersed and maintained in liquid nitrogen and stored at  $-80^{\circ}C$  until  
194 required. R1 (n=5) earthworms were transported back to the laboratory in their native  
195 soil and individuals exposed to 500, 750, 1250, 1750 and 2250  $mg/kg^{-1}$  Pb in the form  
196 of  $Pb(NO_3)_2$  spiked Kettering loam soil and maintained at a WHC of 75% for three  
197 weeks at  $15^{\circ}C$ . Spiked soil was left to equilibrate for three days prior to earthworm  
198 addition. Following exposure, earthworms were snap-frozen in liquid nitrogen and  
199 stored at  $-80^{\circ}C$ . Earthworm total RNA ( $\sim 1.25mg$ ) was extracted using the TRI-reagent  
200 method (Sigma-Aldrich, UK) and mRNA isolated using an mRNA Purification Kit  
201 (Amersham, UK). cDNA libraries were constructed using the pBluescript® II XR  
202 cDNA Library Construction Kit (Stratagene Europe, Amsterdam, The Netherlands).  
203 PCR was used to screen the libraries and quantify insert size. Each PCR contained  $5\mu l$   
204 neat culture, 10X Triton free PCR Buffer ( $10\mu l$ ),  $MgCl_2$  ( $0.25\mu l$ , 1mM), universal  
205 M13F and M13R primers ( $0.2\mu l$ , 10mM), dATP, dCTP, dTTP, dGTP ( $0.2\mu l$ , 100mM)  
206 and Taq polymerase ( $0.16\mu l$ , 50U/ml) in a  $95\mu l$  reaction. The reaction was denatured at  
207  $95^{\circ}C$  for 10 minutes and then cycled 35 times at  $95^{\circ}C$  for 30 seconds, 30 seconds at the  
208 primer annealing temperature of  $56^{\circ}C$  and  $72^{\circ}$  for 1 minute. This was followed by a 10  
209 minute final extension at  $70^{\circ}C$ . Products were resolved by electrophoresis using E-Gel®  
210 technology (Invitrogen Ltd., Paisley, UK) and associated editing software. High quality  
211 clones were cherry-picked using the MultiPROBE® II HT EX liquid handling system  
212 (PerkinElmer, Bucks., UK) and associated WinPrep® software. The composite plate  
213 products were purified using Montage® Multiscreen PCR $\mu$ 96 cleanup plates by vacuum  
214 filtration and the DNA was resuspended in sterile water ( $30\mu l$ ). Sequencing reactions  
215 were completed by the SBSSS facility at Edinburgh University and sequences named

216 according to the NERC Environmental Genomics scheme to allow for bioinformatics  
217 analysis. The raw trace chromatograms from the sequencing reaction were processed  
218 using trace2dbEST (Sturzenbaum et al., 2003) which contains a base calling component  
219 (phred) and a sequence trimming component (cross\_match). This software produces  
220 good quality EST sequences, formatted for submitting to NCBI dbEST  
221 (<http://www.ncbi.nlm.nih.gov/dbEST>). The EST sequences were clustered using  
222 CLOBB (Sturzenbaum, et al., 2003) to derive a consensus putative gene sequence  
223 contig and then processed by the software package PartiGene (Sturzenbaum, et al.,  
224 2003) (<http://www.nematodes.org/PartiGene>). Cluster information can be retrieved by  
225 LumbriBASE (<http://www.earthworms.org>) through simple text queries, identification  
226 of sequence similarity and library specific searches. The biological process and  
227 molecular function of gene sequences were described by defining their Gene Ontology  
228 (GO) classification using blast2go (<http://www.blast2GO.de>).

229

230 Fourier-transform Infrared Spectroscopy. Soil and adult (fully clitellate) *L. rubellus*

231 earthworms were collected from  $C2_{Pb^*}^{pH4}$  and  $C3_{Pb^{***}}^{pH7}$  and the posterior segments  
232 immediately excised and quench-frozen in liquid nitrogen. The frozen tissue was  
233 transported to the laboratory under liquid nitrogen and stored at -20°C until required.  
234 Tissues were mounted in CryoEmbed and sectioned longitudinally at a nominal  
235 thickness of 50µm in a Bright cryostat. Sections were mounted on Kevley slides and air-  
236 dried overnight in the cold chamber of the cryostat. Infra-red spectra were collected in  
237 transmission mode from station 11.1 at the CLRC Daresbury Synchrotron Radiation  
238 Source. The chloragogenous tissue was visually identified and each section imaged and

239 analysed, with five spectra from five different regions of the tissue (i.e. x25 spectra per  
240 individual earthworm) collected.

241

242 SERCA. Plasmid preparations of individual LumbriBASE clones (Genbank accession  
243 numbers CF416761 and CO048347) were prepared using a Wizard<sup>®</sup> Plus SV Miniprep  
244 kit (Promega Ltd., Southampton, UK). Preparations were sequenced in their entirety by  
245 “walking” along the gene, after each step re-designing a specific reverse primer to  
246 complement the universal M13 forward. Primers were designed using the software  
247 Primer3 (Rozen and Skaletsky, 2000) and Oligo<sup>®</sup> (MBI Inc, USA) and sequencing  
248 performed as described above. These full-length library sequences were used to design  
249 *L. rubellus* specific SERCA primers in order to amplify the gene transcribed in  
250 individuals of each genealogical lineage. Reactions were denatured at 95°C for 10  
251 minutes and then cycled 35 times at 95°C for 30 seconds, 30 seconds at the required  
252 primer annealing temperature and 72° for 1 minute. This was followed by a 10 minute  
253 final extension at 72°C. DNA was sequenced as described above by the Cardiff  
254 University Molecular Biology Support Unit.

255

256 Total RNA was extracted from tail-clips of an adult individual sampled from C3<sup>pH7</sup><sub>Pb\*\*\*</sub> and  
257 C2<sup>pH4</sup><sub>Pb\*</sub> using the Tri-reagent method (Sigma-Aldrich, UK). Complementary DNA  
258 (cDNA) was synthesised from messenger RNA (mRNA) using reverse transcriptase.  
259 Total RNA (7-20µg) was heated at 65°C for 3 minutes and combined with anchored  
260 oligo d(T) (1µl, 100mM) and random hexamers (2µl, 100mM) and incubated at 70°C  
261 for ten minutes. A reaction mix of 5X RT buffer (6µl), DTT (3µl, 0.1M) and dNTP mix  
262 (1.2µl, 10mM) was prepared and added to the RNA mix and incubated at 25°C for two

263 minutes. Superscript (1µl) was added and the reaction incubated at 42°C for 3 hours. A  
264 series of three PCR reactions were optimised and performed in order to obtain the full-  
265 length SERCA sequence of each individual; between sequenced sections of the gene  
266 there was a large overlap to ensure the same SERCA isoform was being amplified in  
267 each instance. PCRs were performed as described above. Reactions that yielded  
268 products >2000bp were modified. For these reactions DNA (~100ng) template was  
269 amplified using 10µM forward and reverse primer, 25mM dNTP mix and 1µl  
270 Herculase® II Fusion DNA Polymerase buffered with 5X Herculase® II PCR reaction  
271 buffer (Stratagene Europe, Amsterdam, The Netherlands). Each reaction was  
272 supplemented with an optimised quantity of MgCl<sub>2</sub> (25mM). The reaction was  
273 denatured at 95°C for 10 minutes and then cycled 35 times at 95°C for 20 seconds, 20  
274 seconds at the required primer annealing temperature and 68° for 4 minutes. This was  
275 followed by a 4 minute final extension at 68°C. Protein sequences were aligned using  
276 bioinformatic software tool Mega v3.1 (Kumar, et al., 2004) and modelled using  
277 SWISS-MODEL ([http://swissmodel.expasy.org//SWISS MODEL.html](http://swissmodel.expasy.org//SWISS_MODEL.html)), Swiss-  
278 PdbViewer and Pymol.

279

280 Total RNA was extracted from nine, previously genotyped (mtDNA) adult individuals

281 sampled from C1<sup>pH5</sup><sub>Pb\*</sub>, C2<sup>pH4</sup><sub>Pb\*</sub>, C3<sup>pH7</sup><sub>Pb\*\*\*</sub> and C4<sup>pH6</sup><sub>Pb\*</sub>. This was followed by cDNA synthesis,

282 as described above. A PCR was designed to enable easy identification by gel

283 electrophoresis of the expressed isoform, with a combination of three primers used in

284 each reaction (F1 5'-CTGGCCGGAATTCGTGTTATC-3', F2 5'-ATACTCTTCG

285 CTGTCTTGCGT-3', R1 5'-CCGCTGGCTCTTCTTCCG-3'). The two forward primers

286 were designed so that each one isolated one of the two isoforms. The resulting products

287 were of different sizes to enable simple identification on an agarose gel following  
288 resolution by electrophoresis.

289

## 290 Results and Discussion

291

292 The ‘field laboratory’: the metalliferous site and its resident earthworms. Mine sites are  
293 notoriously heterogeneous in geochemical nature. Mineral (galena, PbS) extraction from  
294 the Cwmystwyth Mine stopped in 1921. Today, the contaminated surface spoils are  
295 situated on base-poor underlying geology, punctuated by calcareous ‘islands’ around  
296 derelict buildings (Figure 1). In the decades since its abandonment, the spatially  
297 chequered and hostile site has developed micro-habitats colonised by a limited variety  
298 of naturally occurring plants and invertebrates. Thus, it serves as an ideal evolutionary  
299 field laboratory. *L. rubellus* was sampled from four sites across the

300 mine: C1<sup>pH5</sup><sub>Pb\*</sub>, C2<sup>pH4</sup><sub>Pb\*</sub>, C3<sup>pH7</sup><sub>Pb\*\*\*</sub>, and C4<sup>pH6</sup><sub>Pb\*</sub> (the number of asterisks denotes the level of  
301 contamination as classified by the Kelly index (ICRCL 59/83): \* contaminated (1000-  
302 2000ppm), \*\* heavily contaminated (2000-10 000ppm) and \*\*\* unusually heavily  
303 contaminated (>10 000ppm) (Figure 1). Population divergence was measured using  
304 amplified fragment length polymorphism (AFLP) analysis and mitochondrial  
305 cytochrome oxidase II (mtDNA COII) gene sequence data of individuals split between  
306 the four sites. Two distinct lineages, differentiated at both the mitochondrial and nuclear  
307 level, were revealed with a mean inter-lineage mtDNA sequence divergence of  
308 approximately 13%, indicative of a cryptic species complex (Figures 2A and B).

309 Moreover, from the distinct clustering of C3<sup>pH7</sup><sub>Pb\*\*\*</sub> individuals a true genetic archipelago  
310 is inferred that can be related to the calcareous, circum-neutral (pH6.5) and heavily

311 polluted nature of this island in an otherwise acidic, moderately polluted environment.  
312 Such cryptic complexes are typical in taxa that thrive in specialised environments and it  
313 perhaps explains why islands of anthropogenic contamination result in the loss or  
314 “erosion” of genetic diversity. Potential adaptive and sympatric speciation processes  
315 may be occurring, with the concurrent, contaminant-driven acquisition of adaptive gene  
316 complexes in response to the unique nature of the site.

317

318 As phylogenetic population structure is shaped by ongoing processes of genetic drift  
319 and gene flow, combined with past historical events, unravelling the *L. rubellus* species  
320 complex requires inferences on both the structure of the phylogeny and demographic  
321 tendencies. Accurately inferring the population-level dynamics of evolutionary  
322 mechanisms that involve adaptive, and also sympatric, speciation is complex, especially  
323 as the process is not clearly defined and involves both temporal and spatial  
324 stochasticity. The timeline of divergence leading to sustained differentiation is neither  
325 rapid nor definable and, due to the combined effects of gene flow and selection of  
326 adaptively important genes, the genomes of incompletely isolated populations will  
327 contain an assortment of variable and undifferentiated regions (Supporting data).

328 Fluctuations in the global climate have led to major ice ages during the Quaternary  
329 period, with the Pleistocene epoch (1 808 000 to 11 500 before present (BP)) covering  
330 the most recent period of repeated glaciations. Glaciation evidence can be related to the  
331 profile of mtDNA haplotypes in both lineage A and B, the shape of the corresponding  
332 mismatch distributions (Figures 2C and D), and estimated time since population  
333 expansion. Lineage A comprises nine haplotypes that contain two or more individuals.  
334 This, combined with a ragged multimodal mismatch distribution, is suggestive of a



335 stationary population that has undergone multiple introductions and bottleneck episodes  
336 (Harpending, 1994). Additionally, from the parameters Tau and date of growth in  
337 mutational units, expansion is estimated to have occurred approximately 250 000 years  
338 BP (assuming one generation per year) and may have corresponded with a non-glacial  
339 environment such as the Hoxnian interstadial (~250 000 BP) (Brown, 1979) (Figure  
340 2E). In contrast, lineage B consists of three haplotypes that contain two or more  
341 individuals, and displays a unimodal mismatch distribution, and a post-glacial  
342 population expansion time of approximately 17 000 years BP was calculated. This  
343 combined evidence suggests that the population experienced a single burst of growth  
344 and expanded after the height of the last glaciation period (~25 000 BP) with adaptation  
345 or selection occurring in response to the warmer climate experienced towards the end of  
346 the Devensian glaciation and onset of the Windermere interstadial (Brown, 1979;  
347 Harpending, 1994).

348

349 'In-situ' biochemical fingerprinting and EST libraries from Pb-mine and laboratory  
350 exposed naïve worms. These field earthworm populations prodigiously accumulate up  
351 to 1.5% of total body dry mass Pb (Morgan, 2001), with Ca/PO<sub>4</sub>-rich earthworm  
352 chloragocyte cells constituting the main metal sequestering organ (Cotter-Howells et al.,  
353 2005). Fourier transform infrared (FT-IR) microspectroscopy on a high energy  
354 synchrotron source was used to determine the chemical composition of cryo-sectioned  
355 chloragocytes in earthworms belonging to each lineage at the two heavily polluted,  
356 albeit one acidic ( $C_{Pb^*}^{pH4}$ ) and one calcareous ( $C_{Pb^{***}}^{pH7}$ ), mine sites. The chlorogogenous  
357 tissue was found to have a distinctive FTIR spectrum (Supporting data) and site-specific  
358 disparities in the composition of chlorogogenous tissue (in the 1100cm<sup>-3</sup> region of the

359 spectrum) were apparent, which correlated with phosphorous-containing functional  
360 groups (Figure 3A and B). As the earthworm chloragocyte is thought to be involved in  
361 haem biosynthesis (Jamieson and Molyneux, 1981), a conserved pathway that is  
362 inhibited by Pb at several junctures (Warren, et al., 1998), Pb trafficking into and across  
363 earthworm chloragocytes must be tightly regulated in these animals that are  
364 continuously exposed to high concentrations of metal in their native environments and  
365 whose strategy for dealing with it involves intracellular accumulative immobilization.  
366 Indeed, inferences on the mechanisms of adaptive evolution to environmental  
367 heterogeneity require not only abstract genotype- to phenotype associations but more  
368 meaningful molecular genetic interpretations regarding the nature of induced  
369 phenotypic variation. The transcriptomic profile of an organism provides a snapshot of  
370 gene expression to provide information regarding developmental stage, life-history or  
371 responses in relation to particular environmental stressors. EST libraries are also the  
372 substrate for comparative genomic studies, through investigating differential expression  
373 between cDNA populations. Two libraries were constructed from earthworm  
374 populations with contrasting histories of Pb exposure; C3<sup>pH7</sup><sub>Pb\*\*\*</sub> earthworms, chronically  
375 exposed in the field, and earthworms sampled from a clean reference site, R1, acutely  
376 exposed to lead in the form of Pb(NO<sub>3</sub>)<sub>2</sub> under laboratory conditions. In combination  
377 with the plethora of EST cluster information already available in LumbriBASE  
378 ([www.earthworms.org](http://www.earthworms.org)), originating from control (adult, head-enriched), life-stage (late  
379 cocoon, juvenile) and other exposure (Cu, Cd, fluoranthene, atrazine) libraries, a metal  
380 tolerant genotype may be related to phenotype and the functional systems that underlie  
381 lead handling within these earthworm populations defined. Both libraries comprised  
382 high quality sequences with an average length of between 500 and 600 base pairs. This

383 ensured the maximum numbers of sequences were annotated to enable accurate  
384 downstream analysis and interpretation using the software LumbriBASE, Blast2GO and  
385 associated KEGG resource, which generates pathway maps that highlight gene ontology  
386 relationships between annotated sequences. Of interest was the significant number of  
387  $C3_{Pb^{***}}^{pH7}$  gene products (when compared to other libraries) associated with intracellular  
388  $Ca^{2+}$  sensing (Calmodulin, Troponin C) and buffering (Sarcoplasmic calcium binding  
389 protein (SCP), Parvalbumin) (Gao et al., 2006; Ishida and Vogel, 2006). Both sets of  
390 proteins belong to the EF-hand super-family of proteins implicated in calcium binding  
391 and central to the Ca-signalling pathway. These observations indicate that components  
392 of the Ca signalling pathway are central to Pb sequestration within chloragocytes which,  
393 in turn, may be associated with adjustments in the metabolism of their common  
394 complexing  $PO_4^-$  anion. This yields a number of candidate loci that may contribute to a  
395 Pb-tolerance phenotype by modifying molecules involved in the cellular physiology of  
396 an essential cation ( $Ca^{2+}$ ) to accommodate its non-essential cationic mimic ( $Pb^{2+}$ ).

397

398 Sarcoplasmic/ endoplasmic reticulum calcium ATPase (SERCA).

399 Sarcoplasmic/endoplasmic reticulum calcium ATPase (SERCA) is a central transport  
400 carrier protein of the Ca signalling pathway that resides in membranes of intracellular  
401 storage sites for the uptake of excess Ca and, conceivably, Pb (Tsien et al., 1987). Three  
402 isoforms have been described in vertebrates (MacLennan et al., 1985; Campbell et al.,  
403 1991; Vilsen and Andersen, 1992) and one in invertebrates (Palmero and Sastre, 1989;  
404 Escalante and Sastre, 1994; Shi et al., 1998a; b), fungi (Ghislain et al., 1990) and plants  
405 (Wimmers et al., 1992). All isoforms are similar in structure and have a 75-85%  
406 identical amino acid sequence (Toyofuku et al., 1992). Despite the identification of

407 several vertebrate isoforms, *L. rubellus* is the first invertebrate found to harbour  
408 multiple SERCA proteins. Two structurally different forms were identified in  
409 populations, sampled from different field sites, and expression was found to be co-  
410 incident with the mitochondrial lineage marker (COII), even where nuclear  
411 hybridisation was observed (Figure 4A and B). Their structure differed in amino acids  
412 located in the cytosolic nucleotide-binding domain (the flap) of the protein, a region  
413 thought to have a critical role in determining calcium affinity and turnover (Figure 4C).  
414 This observation indicates that not only are the intracellular trans-membrane Ca and Pb  
415 pathways confluent at the molecular (SERCA) level and are associated with adjustments  
416 in the metabolism of their common complexing  $\text{PO}_4^-$  anion, but the entire machinery is  
417 demonstrably genotype-specific (Figure 4C). It is important to point out, however, that  
418 whilst the SERCA molecule is an important connector between the vulnerable cytosol  
419 and the intra-vesicular depository of immobilized Pb, other components of the Ca  
420 pathway warrant study to determine whether they are structurally or functionally  
421 modified.

422

423 Conclusion

424

425 Findings presented here demonstrate that tolerance in earthworms with a protracted  
426 history of Pb exposure is not merely an expression of genetic divergence, rather that  
427 field populations may evolve Pb-adaptation traits by modifying molecular regulators of  
428 Ca physiology. Whilst adaptive changes in enzyme structure are, for good reason, less  
429 probable than changes in the promoters that regulate enzyme expression (Crawford et  
430 al., 1999b; a), they are clearly not molecular traits that can be ignored, as the similarity

431 in the ionic radii of  $\text{Ca}^{2+}$  (1.00Å) and  $\text{Pb}^{2+}$  (1.19Å) (Bridges and Zalups, 2005) may, for  
432 example, facilitate structural mutations. Together, these observations describe a  
433 molecular mechanism for Pb resistance in earthworms that may underpin their  
434 phylogenetic differentiation within fairly discrete microhabitats across the study site.  
435 Furthermore, the concept serves as a paradigm for invertebrates generally because the  
436 ability for incorporating Pb into ‘calcospherites’ is ubiquitous, demonstrating that  
437 evolution innovates by modifying existing structures or pathways.

438

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446

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576

577

578 Figure legends

579

580 Figure 1. Earthworm population structure superimposed on a geochemical map of the  
581 Cwmystwyth Pb mine. Surface maps depicting the pH (B) and Pb (C) levels are  
582 overlaid on a topographical map of the Cwmystwyth valley (D), derived from 71 and  
583 97 independent measurements respectively, and generated using SURFER<sup>®</sup>. The four  
584 earthworm sampling sites are indicated by vertical black guide lines together with the  
585 median joining networks depicting the phylogenetic structure, based upon COII  
586 sequence data, of each population studied (A). The size of each haplotype group within  
587 the network is proportional to the total number of individuals attributed to the genotype.  
588 Mitochondrial lineage A individuals are shown as open circles whilst lineage B are  
589 filled circles.

590

591 Figure 2. Mitochondrial and nuclear analysis of the earthworm, *L. rubellus*, population  
592 structure and corresponding mitochondrial mismatch distributions. Earthworms  
593 collected at four equally specially distributed sites with contrasting geo-chemical

594 properties were analysed for their mitochondrial (panel A) and nuclear (panel B)  
595 genotype. Sites included  $C4_{Pb^*}^{pH6}$  (blue triangles) and  $C1_{Pb^*}^{pH5}$  (purple diamonds), at the  
596 boundary of mine, together with  $C3_{Pb^{***}}^{pH7}$  (grey circles) and  $C2_{Pb^*}^{pH4}$  (red squares).  
597 A. Median-joining network analysis based upon 440 bp sequence of the COII  
598 mitochondrial gene of 119 *L. rubellus* individuals. The size of each haplotype group  
599 within the network is proportion to the total number of individuals attributed to the  
600 genotype whilst the earthworm source is indicated by fill colour. The left and right hand  
601 branches of the network are denoted lineage A & B respectively. B. AFLP multi-locus  
602 profiling principal component analysis showing individuals from the four sample  
603 stations. Those individuals exhibiting mitochondrial lineage B genotype are circled in  
604 red whilst those attributed to lineage A are circled in grey. The clustering of  $C3_{Pb^{***}}^{pH7}$   
605 earthworms distinct from other lineage A earthworms is indicated with a dotted grey  
606 line. Hybrid individuals are shown by a lack of fill colour. C and D. Arlequin simulated  
607 mitochondrial mismatch distributions, using the model of demographic expansion, of  
608 lineage A (C) and lineage B (D) haplotypes respectively. The solid lines are the  
609 observed mismatch distribution and the dotted line shows the distribution simulated  
610 under the expansion model. E. Associated sum of squared deviation (SSD), Raggedness  
611 (Rg) and p-value statistics, based on 1000 data bootstraps.

612

613 Figure 3. Metabolomic fingerprinting of earthworm chloragogenous tissue using Fourier  
614 Transform Infrared spectroscopy. A. The fingerprint region of averaged infra-red  
615 spectra of earthworm chloragogenous tissue collected from  $C3_{Pb^{***}}^{pH7}$  (grey) and  $C2_{Pb^*}^{pH4}$   
616 (red). Individual spectra were processed by the software package OPUS<sup>®</sup>). B. The main

617 difference in  $C3_{Pb^{***}}^{pH7}$  and  $C2_{Pb^*}^{pH4}$  averaged spectra ( $\sim 1080\text{cm}^{-1}$ ), corresponded to  
618 phosphorus-containing functional groups, C. XLSTAT simulated dendrogram  
619 illustrating the clustering of  $C3_{Pb^{***}}^{pH7}$  and  $C2_{Pb^*}^{pH4}$  earthworms according to their infra-red  
620 spectral patterns ( $1096\text{-}1123\text{cm}^{-1}$ )

621

622 Figure 4. Analysis of earthworm SERCA variants. A. phylogenetic analysis of  
623 genotyped individuals, based upon the cytochrome oxidase II (COII) gene, from sites  
624 including the control sites  $C4_{Pb^*}^{pH6}$  (blue triangles) and  $C1_{Pb^*}^{pH5}$  (purple diamonds) at the  
625 boundary of the mine and contaminated sites  $C3_{Pb^{***}}^{pH7}$  (grey circles) and  $C2_{Pb^*}^{pH4}$  (red  
626 squares) alongside *L. castaneus* and *L. eiseni* (white triangles). B. Discriminatory PCR  
627 illustrating the lineage-specific expression of the SERCA variants and C. PyMol  
628 simulated model of SERCA. The conserved calcium binding sites are indicated in  
629 yellow and amino acid differences in the two *L. rubellus* isoforms in red. The  
630 phosphorylation (P) and nucleotide binding (N) domains are shown

631