

# Species-specific Cd-detoxification mechanisms in lumbricid earthworms Eisenia andrei, Eisenia fetida and their hybrids

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### 1 Species-specific Cd-detoxification mechanisms in lumbricid earthworms *Eisenia andrei*,

### 2 *E. fetida* and their hybrids

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#### 23 Abstract:

24 Hermaphroditic lumbricid Eisenia sp. earthworms are ubiquitous and highly resistant to a variety of environmental stressors, including heavy metals. Among the progeny of laboratory 25 26 mated inter-specific pairs of *Eisenia fetida* (*Ea*) and *Eisenia andrei* (*Ef*) there are fertile *Ha* hybrids derived from Ea ova fertilized by Ef spermatozoa and very rare sterile Hf hybrids 27 from Ef ova fertilized by Ea spermatozoa. The aim of the first part of the experiment was to 28 29 compare the life traits and whole body accumulation of cadmium in adult earthworms from 30 genetically defined Ea, Ef and their hybrids (Ha) exposed for four weeks to commercial soil 31 either unpolluted (control) or cadmium-spiked leading to moderate (M) or high (H) soil pollution (M=425 and H=835 mg kg<sup>-1</sup> dry soil weight). Such exposure impaired cocoon 32 production but not affected earthworm viability despite the massive Cd bioaccumulation in 33 the whole earthworm bodies reaching at M and H groups 316-454, 203-338, 114-253, and 34 377-309 mg kg<sup>-1</sup> dry body weights of *Ea*, *Ef1*, *Ef2*, and *Ha*, respectively, surprisingly reaching 35 36 maximum accumulation quantities in hybrids. The second part of the experiment aimed to 37 investigate cadmium-related defense mechanisms at transcriptomic level in coelomocytes 38 non-invasively extruded from coelomic cavities of the new sets of Ea, Ef, Ha, and Hf earthworms exposed to Cd in microcosms for 0 days (control), 2 days, and 7 days (M=425 mg 39 kg<sup>-1</sup>). Expression level of stress-induced *Cd-metallothionein (mt)* and *superoxide dismutase* 40 41 (sod) were gradually up-regulated, while the immune-connected lysenin (lys) was rapidly down-regulated; the expression of glutathione S-transferase (gst) and phytochelatin synthase 42 (pcs) remained unaffected. Mt and sod gene up-regulation and lys gene down-regulation were 43 44 especially pronounced in Ea-derived hybrids. In sum, capacity of cadmium bioaccumulation 45 and detoxification mechanisms is more efficient in interspecific hybrids than in the pure Ea 46 and Ef species.

47 Keywords: *Eisenia* sp.; hybrids; cadmium; Gene expression; detoxification; Bioaccumulation

48

#### 1. Introduction

49 Cadmium (Cd) contamination of soils is a ubiquitous environmental problem that has resulted 50 from uncontrolled industrialization, unsustainable urbanization, and intensive agricultural practices (Khan et al., 2017). The dispersion of cadmium in the environment had been 51 52 increasing in the past few decades all over the world. As an example, currently, Cd contamination can be found as a direct result of most industrial activities such as, mining, 53 54 smelting, transport, burning of fossil fuels, wastewater irrigation systems, and as a by-product of synthetic phosphate fertilizers (Grobelak et al., 2019). Being a toxic element, Cd is a high 55 56 threat to soil quality, food safety, and human health (Shahid et al., 2016). To date, numerous studies have investigated the toxic impact of Cd in plants and animals, including humans. 57 58 Research focused on human exposure to cadmium shows that Cd induces several types of 59 cancers, neurotoxic effects as well as kidney damage, bone demineralization, and the disruptions of the immune system (Buha et al., 2019). Overall, industrial activities involved in 60 61 a large scale dispersal of heavy metals to the environment are associated with genotoxic and 62 carcinogenic hazards, which creates a crucial challenge for regulatory authorities (Eom et al., 2017). Improvements in the technologies of contaminant detection and quantification in 63 64 environmental samples are essential (Mahajan and Kaushal, 2018). Nevertheless, novel 65 approaches that could take into account not only chemical hazards but its biological and ecological effects are currently needed for accurate safety evaluation (Khan et al., 2017). 66

Earthworms, living in close contact with soil, are constantly confronted with different
pollutants, among the others high cadmium concentrations (Wang et al., 2019). Moreover,
they are a crucial part of soil fauna, which helps to maintain soil structure and organic matter
cycling via soil ingestion and excretion, making them key regulators of soil processes. Hence,
earthworms are widely used as model organisms for the evaluation of the hazardous effects of
different terrestrial toxicants (Yu et al., 2019).

Compared to other lumbricid species, composting earthworms from *Eisenia* genus are very 73 resistant to most pollutants, including heavy metal contamination. Nevertheless, most of the 74 early studies are focused on the *Eisenia* sp., not taking into account the distinction between E. 75 76 fetida and E. andrei (Rombke et al., 2016, Suleiman et al., 2017). Proper distinction of the red earthworm E. and rei and striped E. fetida on basis of morphological criteria is sometimes 77 unequivocal, thus shall be connected with species delimitation by the species-specific DNA 78 79 sequences of the mitochondrial and/or nuclear genes. Such molecular markers revealed a 80 clear distinction between Ea and Ef species, and at least two distinct mitochondrial lineages of the latter, described as Ef1 and Ef2 (e.g. Pérez-Losada et al. 2005; Otomo et al. 2008; Rombke 81 82 et al. 2016). Combined analysis of sequences of the haploid mitochondrial genes (of the maternal origin) and diploid nuclear genes of maternal-paternal origin made possible to find 83 out hybrids between laboratory-mated (Ea+Efl) or (Ea+Efl) pairs (Plytycz et al. 2018a,b; 84 85 2020; Podolak et al. 2020).

Among the progeny of hermaphroditic Ea+Ef pairs appeared both specimens of the pure Ea86 87 or Ef species (derived by self-fertilization) and hybrids derived from Ea ova fertilized by Ef 88 spermatozoa (called here Ha), but non Hf hybrids from Ef ova fertilized by Ea spermatozoa. These later appeared only among progeny of *Ha* hybrids mated with *Ef* pure species but were 89 very rare and sterile. The *Ha* hybrids were relatively common and fertile, giving offspring 90 91 with Ea species consisting off second (and then third) generations of Ha hybrids and pure Ea 92 specimens (Plytycz et al. 2018a,b; Podolak et al. 2020), but fertility of hybrids was gradually 93 diminished in the subsequent generations (Plytycz et al. 2020). The question arose whether hybrids are more sensitive to stressing factors than specimens of the pure parental species? 94

Our previous laboratory studies on effects of cadmium were performed on *E. fetida* (Brulle et al. 2008, Bernard et al. 2010) and more recently on *E. andrei* (Homa et al. 2015; Takacs et al. 2016, Rorat et al. 2017). We have documented that exposure of *E. andrei* earthworms to soil

98 spiked with high concentration of cadmium chloride (500 mg kg<sup>-1</sup> air-dried soil), caused 99 massive cadmium bioaccumulation in earthworm bodies without lethal effects; it caused 100 inhibition of maturation of juveniles, inhibition of cocoon production by adults without 101 adverse effects on regenerative processes (Takacs et al. 2016). Cadmium exposure even 102 enhanced regeneration of amputated posterior segments that corresponded with induction of 103 expression of metallothionein gene of this species (Rorat et al. 2017).

104 In our previous studies, the mechanisms of detoxification of Cd were investigated on 105 transcriptomic level and some genes were identified as involved or potentially involved in 106 those processes, namely, metallothionein (*mt*), glutathione S-transferase (gst), lysenin (lys), 107 superoxide dismutase (sod), phytochelatin synthase (pcs) (Brulle et al. 2008, Bernard et al. 108 2010, Homa et al. 2015). Among the others, it has been shown that the protective mechanisms 109 were mainly based on a strong induction of a gene coding the cadmium metallothionein (*mt2*) 110 in earthworms (Homa et al. 2015, Engelmann et al., 2016). The implication of the other genes 111 mentioned before is not fully elucidated. Even if the two Eisenia species are very resistant to 112 stressors and show similar responses overall, we noted specificities, in particular at the 113 molecular level, which we decided to investigate in this work.

114 Therefore, it was reasonable to compare effects of cadmium exposure on *E. andrei*, two 115 distinct lineages of *E. fetida* (*Ef1* and *Ef2*) and on hybrids appearing among progeny of Ea+Ef116 pairs mated in the laboratory settings (Plytycz et al. 2018a,b, 2020; Podolak et al. 2020). For 117 this, the accumulation of Cd and the level of expression of genes directly or indirectly 118 involved in the response to Cd were measured in pure species and their hybrids investigated at 119 the same laboratory conditions.

120 The main goal of the first part of our experiments was to compare the life traits and the 121 capacity of cadmium accumulation in whole bodies of adult earthworms from genetically 122 defined *Ea*, *Ef1*, *Ef2* and their hybrids (*Ha*). Earthworms were exposed for four weeks to 123 commercial soil either unpolluted (control) or moderately or higly spiked with cadmium 124 chloride at the same concentrations as that used during our previous studies (Takacs et al. 125 2016; Rorat et al. 2017). The second part aimed for gaining insight into cadmium-related 126 defense mechanisms at transcriptomic level in coelomocytes extruded from a new set of *Ea*, 127 *Ef1*, *Ef2*, and *Ha/Hf* earthworms exposed for 0 days (control), 2 days or 7 days to moderately 128 Cd-polluted soil in mesocosms. Overall, the upregulation of *mt* and *sod* genes and down-129 regulation of *lys* genes were more pronounced in hybrids than in parental species.

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#### 2. Materials and methods

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#### 2.1. Earthworms

132 Adult composting E. andrei (Ea) and E. fetida (Ef) earthworms deriving from laboratory 133 stocks at the University in Lille (France) were cultured for a decade in the laboratory of the 134 Institute of Zoology and Biomedical Research of the Jagiellonian University (Krakow, 135 Poland), and in parallel for last four years in the laboratories of Rzeszow University (Poland). 136 Earthworms were cultured in boxes with commercial soil at room temperature and fed ad 137 *libitum* on boiled/dried tea, nettle and dandelion leaves. For several years some of them were 138 used for studies on progeny of laboratory-paired genotyped virgin specimens giving in 139 offspring specimens of *E. andrei* (*Ea*), two mitochondrial lineages of *E. fetida* (*Ef1* and *Ef2*) 140 species, and interspecific hybrids (H) derived either from Ea ova (Ha) or E1/Ef2 ova (Hf), 141 each of them individually delimited by species-specific sequences of the mitochondrial COI 142 gene and diploid nuclear 28S rRNA gene (Plytycz et al. 2018a; 2020; Podolak et al. 2020).

Some of these genetically delimited adult (clitellate) specimens were used for experiments performed in the same laboratory conditions (Plytycz et al. 2020; Podolak et al. 2020). One group of earthworms (54 individuals) was used for the measurement of cadmium accumulation in the whole earthworm bodies, the second group (50 individuals) served as asource of coelomocytes for the measurement of the expression of stress-related genes.

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### 2.2. Soil preparation

The air-dried commercial soil (PPUH BIOVITA, Tenczynek, Poland organic soil, 51.7%organic matter, pH=6.11) was spiked either with water (control) or with cadmium chloride (CHEMPUR, Piekary Slaskie, Polska), 500 mg kg<sup>-1</sup>, as described previously (Takacs et al. 2016; Rorat et al. 2017). Control and Cd-polluted soils were kept separately or mixed 1:1, giving samples of unpolluted control soil, and those with high (425 ± 45.66 mg kg<sup>-1</sup>) or very high (835 ± 35.712 mg kg<sup>-1</sup>) cadmium concentration.

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### 2.3. Experimental design

*Experiment 1 Cd accumulation in earthworms*: In total 54 earthworms were exposed either to unpolluted control soil or to soil with high cadmium concentration during 4 weeks in mesocosms. Briefly, four individuals from each group of species: *Ea*, *Ef1*, *Ef2* and *Ha* were placed in the plastic boxes (of 9 cm diameter) with perforated lids. At the end of the exposure period, the earthworms were depurated overnight in boxes with wet lignin substrate (Paso-Trading, Polska), and then sacrified by freezing and prepared for the metal accumulation analysis.

*Experiment 2: Gene expression in Cd-exposed earthworms:* In total 50 individuals were used as a source of coelomocytes, i.e. the immune cells present in earthworm coelomic cavity, noninvasively retrieved from coelomic cavity by a mild elctric shock as described in 2.4.3.1. E. *andrei, E. fetida*, and their *Ea*-derived (*Ha*) and *Ef*-derived hybrids (*Hf*) were exposed for 2 and 7 days to highly polluted soil in mesocosms (boxes with with perforated lids, 9 cm diameter). The level of gene expression of glutathione S-transferase (*gst*), lysenin (*lys*), 169 metallothionein (*mt*), superoxide dismutase (*sod*) and phytochelatin synthase (*pcs*) was 170 assessed in extruded coelomocytes, and related to the expression of two stable house-keeping 171 genes – actin (*act*) and ribo13 (*r13*).

172 **2.4.** Analyses

173 2.4

### 2.4.1 Earthworm genotyping

Supravitally amputated tail tips of numerically coded adult earthworms were used for DNA
extraction and genetic analysis using oligonucleotide primers amplifying species-specific
variants of mitochondrial COI genes and nuclear 28S rRNA genes, as described earlier
(Plytycz et al. 2018a,b; 2020; Podolak et al. 2020).

As previously established, mitochondrial species-specific sequences of the COI gene were called either 'a' or 'f'/'f2' for *Ea* and *Ef1/Ef2*, respectively, while the diploid species-specific nuclear markers of the 28S rRNA gene were called either 'A' or 'F' for *Ea* and *Ef*, respectively. In a results, the investigated specimens were genotyped either as pure species, *Ea* (*aAA*), *Ef1* (*fFF*), *Ef2* (*f2FF*), or inter-specific hybrids, either *Ea*-derived *aAF*, *Ef*-derived fFA with the two first letters (*aA-*, *fF-*, *f2F*) representing ova-derived genes, i.e. maternity, and the last letter (*A* or *F*) representing spermatozoa-derived genes, i.e. paternity.

185 **2.4.2**.

#### 2.4.2. Cadmium content

Cadmium content in soil and in whole earthworm bodies was measured by slightly modified methods used in our previous studies (Takacs et al. 2016; Rorat et al. 2017). Soil samples were dried at 105°C for 24 h and then divided into subsamples about 0.5 g of dry soil mass of each. Cadmium concentration in soil was determined after half open wet digestion in a quartz glass with 10 mL of mixture of concentrated HNO<sub>3</sub> (69.0-70.0% to trace metal analysis, Baker Instra-Analyzed) and HClO<sub>4</sub> (70% a.r, Chem-Lab) (7:1 v/v), using hot plates. 192 Cadmium concentrations were measured by atomic absorption spectrometry (AAS) with a 193 flame and atomic absorption spectrometry with a graphite furnace nebulizer (Perkin-Elmer) to 194 achieve the desired method sensitivity. Accuracy was verified by analyzing four blanks and 195 three replicates of standard certified material (Loamy Sand 10 CRM033-50G) with the 196 samples.

197 Prior to the analysis of cadmium concentration in whole earthworm bodies, earthworms were 198 kept for 2 days on wet filter papers to remove their gut content, frozen, and then dried in 199 vacuum drier in 70°C for 24 h to achieve constant dry mass. For determination of cadmium 200 concentration in earthworm bodies, the wet digestion method was applied but to reach the 201 required ratio 1: 20 only 4 mL of concentrated HNO<sub>3</sub> (69.0-70.0% to trace metal analysis, 202 Baker Instra-Analyzed) were used. Cadmium concentrations in earthworm bodies were 203 measured by atomic absorption spectrometry methods with four blanks and three replicates of 204 standard certified material (Bovine Liver SRM 1577c) with the sample in digestion.

The cadmium concentrations were calculated on a dry mass of each sample of soil or earthworms and are presented in mg kg<sup>-1</sup> ( $\mu$ g g<sup>-1</sup>).

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## 2.4.3. Gene expression analysis

### 209 2.4.3.1. Extrusion of coelomocytes extrusion via electrostimulation

After 24 h depuration on wet lignin (Paso-Trading, Poland), earthworms were placed
individually on petri dishes and stimulated for 30 s with a 4.5 V electric current to expel
coelomic fluid with suspended coelomocytes through the dorsal pores (Homa et al. 2015;
Rorat et al. 2017). Pellets of coelomocyte samples were resuspended in 2 mL of TriReagent
(Molecular Research Center Inc., USA) for RNA extraction.

215 2.4.3.2. Extraction of RNA and reverse transcription

Expression of five target and two house-keeping genes (HKG) was performed on the total 216 217 RNA extracted from coelomocytes by TRI Reagent® (Molecular Research Center, USA), 218 according to manufacturer's instructions. Overall, coelomocytes' pellets from each sample were suspended in 2 mL of Tri Reagent and 1 mL was later used for each extraction. Samples 219 220 were then treated with DNase I, RNase-free (1 U/µL) (Thermo Fisher Scientific, USA) 221 according to manufacturer's instructions. The quantity and quality of isolated RNA were 222 analyzed spectrophotometrically using spectrometer with a LVis nano plate (SPECTROstar 223 Nano, BMG LABTECH, USA, LVis Plate, BMG LABTECH, USA). RNA integrity was 224 confirmed on 2% agarose gel stained with ethidium bromide (Ethidium Bromide Solution (10 mg mL<sup>-1</sup>), Thermo Scientific, USA). The amount of isolated RNA allowed us to perform the 225 226 reverse transcription of 1.5µg cDNA using QIAGEN OMNISCRIPT RT KIT (QIAGEN, 227 Germany), according to manufacturer instructions. cDNA samples were then stored in -20°C 228 until further analyses.

### 229 2.4.3.3. Real-time qPCR amplification.

The mRNA levels of chosen genes were determined by real-time quantitative PCR after 230 231 reverse transcription. For qPCR, Agilent Mx3000P QPCR System (Agilent Technologies, 232 USA) with 2X Takyon for SYBR Assay - No ROXqPCR Kits for SYBR Assay (Eurogentec, Belgium) were used, and reactions were performed on 96-well qPCR plates (Eppendorf 233 twin.tec® PCR Plates, Eppendorf AG, Germany). All qPCR reactions were performed as 234 235 follows: 95°C 5 min and 40 cycles at 95°C 30 s, 55°C 30 s, and 72°C 60 s. After 40 cycles, the last step of the program consisted of 72°C for 5 min. The Eisenia sp. specific primes were 236 237 used for actin (act), ribosomal protein S13 (r13), metallothionein (mt), glutathione Stransferase (gst), phytochelatin synthase (pcs), lysenin (lys) and superoxide dismutase (sod) 238 (Brulle et al., 2008, Homa et al. 2015) after the validation of their compatibility with hybrids. 239 240 The selected primers are presented in Table 1. Expression levels were determined as the

number of cycles needed for the amplification to reach a threshold fixed in the exponential
phase of PCR reaction (Ct). Levels of expression and amplification effectiveness of target
genes were compared to the expression of two constitutively expressed and validated housekeeping genes. qPCR efficiency of each target gene was calculated according to the method
previously described (Chaâbene et al., 2017). Overall, the relative expression level was
calculated according to the following formula:

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 $R = 2^{\Delta Ct(target gens) - \Delta Ct(reference gens)}$ 

249 Table 1. qPCR primer sequences

Forward primer 5'-3'	Reverse primer 5'-3'	Amplicon	Accession
		size (bp)	number
5'CGCACGGTTTTAGTTTCT3'	5'CCATGCGAGTCTCGAAG3'	148	MG076964
5'CCATCCATCGTCCACAG 3'	5'GCATGTGTGAGTCCTAATTT3'	147	EY893028.1
5'AAAGTGAGTGCTTGCC3'	5'ACTGATGACAGAGTTCCG3'	120	KP770991.1
5'TGGAAGTGGAGGTTTCCTTG3'	5'TGAGGTGGCCAAGTCTTTTC3'	161	EY892760.1
5'TCATGGTCCTGAACACG3'	5' CACAAGTTGCCGAAACTC 3'	154	KP770990.1
5'CGGCAACAAACGTCTAC3'	5'GTGAAATACAGGCAGAAGC 3'	163	MG076962.1
5'GGTGCTCACTTCAACCCATT3'	5'AAGATCGTCCACCAGCTCAT3'	167	DQ286712.1
	5'CGCACGGTTTTAGTTTCT3' 5'CCATCCATCGTCCACAG 3' 5'AAAGTGAGTGCTTGCC3' 5'TGGAAGTGGAGGTTTCCTTG3' 5'TCATGGTCCTGAACACG3' 5'CGGCAACAAACGTCTAC3'	5'CGCACGGTTTTAGTTTCT3'5'CCATGCGAGTCTCGAAG3'5'CCATCCATCGTCCACAG 3'5'GCATGTGTGAGTCCTAATTT3'5'AAAGTGAGTGCTTGCC3'5'ACTGATGACAGAGTTCCG3'5'TGGAAGTGGAGGTTTCCTTG3'5'TGAGGTGGCCAAGTCTTTC3'5'TCATGGTCCTGAACACG3'5'CACAAGTTGCCGAAACTC 3'5'CGGCAACAAACGTCTAC3'5'GTGAAATACAGGCAGAAGC 3'	size (bp)5'CGCACGGTTTTAGTTTCT3'5'CCATGCGAGTCTCGAAG3'1485'CCATCCATCGTCCACAG3'5'GCATGTGTGAGTCCTAATTT3'1475'AAAGTGAGTGCTTGCC3'5'ACTGATGACAGAGTTCCG3'1205'TGGAAGTGGAGGTTTCCTTG3'5'TGAGGTGGCCAAGTCTTTTC3'1615'TCATGGTCCTGAACACG3'5'CACAAGTTGCCGAAACTC 3'1545'CGGCAACAAACGTCTAC3'5'GTGAAATACAGGCAGAAGCC 3'163

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#### 251 **2.5. Data analysis**

HKG stability was quantified using two software's: BestKeeper and NormFinder. All results
are expressed as means ± standard deviation, n=3-6. Descriptive statistics and statistical
analyses were produced using the OriginPro 2015 software and Statistica. Different letters
"a", "b" "c", "d" on top of bars indicate statistically significant differences according to the 1
one-way analysis of variance.

**3. Results** 

### 258 **3.1. Genetic species delimitation**

259 Cytoplasme-rich ova with plenty mitochondria are fertilized by spermatozoa with very scarce 260 cytoplasm and a few mitochondria. DNA barcoding based on specific sequences of 261 mitochondrial haploid COI gene shows three distinct branches; 'a' for *Ea* or 'f'/'f2' for two

mitochondrial lineages of Ef, namely Ef1 and Ef2 (Plytycz et al. 2020). Species-specific 262 maternal-paternal diploid nuclear sequences of 28S rRNA gene, are either 'AA' (for Ea) or 263 264 'FF' for Ef or 'AF' for interspecific hybrids. Fertilization of 'aA' ovum by 'A' spermatozoon gives aAA zygote of the pure Ea species, while 'aA' ovum fertilized by 'F' spermatozoon 265 266 gives Ea-derived aAF hybrid. The 'fF' or 'f2F' ova fertilized by 'A' spermatoza give fFA or f2FA hybrids, respectively (Figure 1). All sequences are deposited in GenBank under the 267 following accession numbers: MT646836-MT646899 and MT649303-MT649399. All the 268 269 earthworms survived the experiment but cadmium exposure inhibited cocoon production 270 almost completely (data not shown).

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### **3.2. Cadmium content in soil and in whole earthworm bodies**

The cadmium concentration in the commercial unpolluted soil was very low (L;  $0.11 \pm 0.,107$ mg kg<sup>-1</sup>); in soil spiked with cadmium chloride was very high (H;  $835 \pm 35.712$  mg kg<sup>-1</sup> dry weight) and intermediate in 1:1 mixture of these soil samples (M;  $425 \pm 45.66$  mg kg<sup>-1</sup>dry weight) (Table 2). Cadmium concentrations in earthworms living in unpolluted soil were low (0.69 -1.12 mg kg<sup>-1</sup>) and did not differ significantly between *Ea*, *Ef1*, *Ef2*, and *Ha* groups of earthworms.

278 Cadmium concentrations in whole bodies of earthworms kept in soil with M or H cadmium pollution were overlapping (113.79 - 376.73 and 252.68 - 454.18 mg kg<sup>-1</sup>, respectively), with 279 lowest accumulation capacity in *Ef2* earthworms (113.79 and 252.68 mg kg<sup>-1</sup> in M and H soil, 280 281 respectively), but these values were not significantly different from those in the second lineage of the Ef species, i.e. Ef1 (203.43 and 337.66 respectively). The whole body Cd 282 bioaccumulation in *Ea* reached 316.43 mg kg<sup>-1</sup> in the M soil and was significantly higher in 283 the *Ea* from the H soil (454.19 mg kg<sup>-1</sup>). Cadmium bioaccumulation was most efficient in the 284 Ha hybrids reaching plateau already in the M soil, as the values at M and H soil were similar 285  $(376.73 \text{ and } 309.246 \text{ mg kg}^{-1}, \text{ respectively}).$ 286

Table 2. Concentration of Cd in soil and earthworms' bodies after 4-week exposure in unpolluted (L), intermediate (M) or very high (H) soil. Results shown as means  $\pm$  SD, n=3 - 6. Mean concentrations in earthworm bodies not sharing the same small letters (in columns) or capital letters (in rows) are statistically significantly different according to ANOVA with post hoc Tukey's test.

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Groups		Cd concentration in soil and earthworm bodies [mg kg <sup>-1</sup> ]			
		L	М	Н	
Soil		$0.11 \pm 0.107$	$425 \pm 45.66$	835 ± 35.712	
	Ea	$1.09 \pm 0.38$ aA	316.43 ± 33.09 bB	454.19 ± 37.58 bC	
orms	Efl	$0.76 \pm 0.26$ aA	$203.43 \pm 82.7$ abB	337.66 ± 115.12 abB	
Earthworms	Ef2	0.69 ± 0.15 aA	113.79 ± 28.16 aB	252.68 ± 62.59 aC	
E -	На	$1.12 \pm 0.10$ aA	376.73 ± 136.99 bB	309.23 ± 59.50 abB	

#### 293

### **3.3. Gene expression in earthworms**

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### **3.3.1. Reference genes**

For determination of the stability of chosen housekeeping genes, the NormFinder and
BestKeeper software were used. Overall, the expression of both chosen reference genes was
stable across all experimental conditions and species (Appendix 1).

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### **3.3.2.** Expression of *gst* and *pcs* genes

The expression level of *pcs* and *gst* was undetectable in coelomocytes of *E. andrei* in both clean and Cd-contaminated soil. However, a negligible expression of those genes was observed for *Ef1*, *Ef3* and *Ha* exposed to soil contaminated by cadmium (Figures 2A and 2B).

#### 303 **3.3.3** Expression of *mt*, *sod*, and *lys* genes

Only two rare *Ef*-drived hybrids (*Hf\**) were used for analysis of *mt*, *sod*, and *lys* expression. In
unpolluted soil (i.e. on day 0 of cadmium exposure), the expression of *mt* and *sod* was very
low while it was relatively in a case of *lys*. In each instance, it was similar to the expression of
these genes in other specimens from unpolluted soil, i.e. on day 0 of cadmium exposure (Fig.
3, right columns of rows A, B, and C).

In all tested organisms, a significant induction of the expression of *mt* and *sod* was observed
after exposure to cadmium (Figure 4, rows A and B), while expression of *lys* was drastically
diminished (Fig. 3, row C).

### 312 3.3.3.1 Expression of *mt*

The expression rate of metallothionein was negligible in earthworms exposed to clean, uncontaminated soil. In coelomocytes of *Ef1*, *Ef2* and *Ha*, the expression of *mt* was significantly (p < 0.05) induced after already two days of exposure, and in *Ef1* and *Ha* continued to increase further until the 7-day timepoint. However, in coelomocytes of *E*. *andrei*, the induction of *mt* expression occurred later than for other earthworms, and was significant only after 7 days post exposure (Figure 3, row A, left column). At each time point the interspecies differences were statistically insignificant (Fig. 3, row A, right column).

**320 3.3.3.2** Expression of *sod* 

Similar results were observed for the expression rate of *sod* (Figure 3, row B). Once again, the expression rate for all organisms living in clean soil was almost undetectable while the exposure to cadmium caused a significant increase in *sod* expression. However, two days post-exposure, the expression rate of *sod* in *E. andrei* was still almost no detectable, whereas for all other organisms was already significantly (p < 0.05) induced. At day 7 day after cadmium exposure, expression of *sod* significantly increased versus day 2 in *Ea*, *Ef*2, and *Ha*  327 (Fig. 3, row B, left column). The interspecies differences were insignificant on day 0 and day
328 2, while on day 7 was significantly higher in *Ha* than in *Ea*, *Ef1*, and *Ef2* (Fig. 3, row B, right
329 column).

**3.3.3.3** Expression of *lys* 

The expression of lysenin gene was highly influenced by exposure to different soil conditions across all tested organisms. In all cases, its expression was at its highest in coelomocytes of earthworms exposed to clean soil and the Cd contamination caused a severe and significant (p < 0.05) downregulation of that expression (Fig. 3, row C). Moreover, for *Ef2* and *Ha*, the downregulation was significant for both, 2 and 7 day post exposure, whereas for Ea and Ef1 it was downregulated by 2 days post-exposure, and then the expression rate stabilized and stayed at the same level without further downregulation (Figure 3, row C, left column). Interspecies comparisons revealed the lack of statistically significant differences in day zero and day 2 after cadmium exposure while on day 7 lys expression differed significantly between species, being the highest in Ef1, and then in Ea, Ef2 and Ha (Fig. 3, row C, right part).

350

#### 4. Discussion

351 Adult specimens of hermaphroditic lumbricid earthworms E. andrei and E. fetida, the latter with two distinct lineages *Ef1* and *Ef2*, and interspecific Ha hybrids developed from *Ea* ova 352 353 fertilized by Ef spermatozoa were fully viable during four week exposure to cadmiumpolluted soil (425  $\pm$  45.66 mg kg<sup>-1</sup> or 835  $\pm$  35.712 mg kg<sup>-1</sup>) despite a high cadmium 354 355 accumulation in the whole earthworm bodies. Bioaccumulation was dose-dependent, similar 356 in *Ef1/Ef2* lineages of Ef, and lower than that in *Ea*. In contrast, Ea-derived hybrids reached 357 plateau of Cd-accumulation capacity already at lower cadmium concentration in soil. 358 Hypothetically, all investigated specimens from genus Eisenia are able to survive in Cd-359 contaminated environments due to adapting the same or similar detoxification mechanisms to 360 those described previously at transcriptomic level in representatives of *E. andrei* and *E. fetida* 361 (Homa et al. 2015, Rorat et al. 2017), while data concerning hybrids were vastly unexplored. 362 Therefore comparative studies on the expression of genes involved in Cd detoxification were imperative. Second part of previous investigations revealed that the expression of stress-363 related genes upon exposure to Cd-polluted soil at  $425 \pm 45.66 \text{ mg kg}^{-1}$  was either up-364 regulated (*mt* and *sod*), down-regulated (*lys*) or unchanged (*gst* and *psc*). 365

366

### 367 *Expression of genes for metallothionein and phytochelatin synthase*

In a study by Brulle et al. (2008) performed on *E. fetida*, the induction pattern of genes encoding phytochelatin synthase was significantly increased in earthworms exposed to a low concentration of cadmium (8 mg kg<sup>-1</sup>). However, in higher concentrations, no difference was noticed between Cd-exposed earthworms and earthworms not exposed to any contamination, which suggests that *pcs* expression is only induced during low exposure to cadmium. Similarly to our study, expression of metallothionein was highly up-regulated after Cd exposure, and in the mentioned Brulle et al. (2008) study, it was also shown to be dose-

dependent in high Cd concentrations. Such relation between different responses of the 375 expression of *pcs* and *mt* genes is of interest when considering their role in metal 376 377 detoxification in animals. In low concentrations of Cd, the expression of pcs was shown to be 378 significant and responsible for metal chelation in worm cells (probably via the synthesis of 379 Phytochelatins (PCs) although the presence of PCs has not been demonstrated), whereas such 380 induction was only noticed at a small exposure level. This is on the contrary to the effects of 381 high concentrations of Cd, where similarly to our study, *pcs* expression patterns did not show 382 any change of their level over control animals, whereas the expression rate of mt was 383 substantially upregulated. In another study, focused on Caenorhabditis elegans, the 384 toxicogenomic analysis after exposure to cadmium also showed no effect on the expression of 385 pcs-1 gene (Cui et al., 2007). Moreover, a recent transcriptomic study on the same species: C. 386 elegans, found similar results - after exposure of nematods to cadmium (300µM) and zinc 387 (500µM), the expression change of pcs-1 was determined via qPCR followed by normalization by the invariant ribosomal *rla-1*. The results showed, that the *pcs* response to 388 389 Zn and Cd contamination was at best negligible, and the change in comparison to control 390 animals was not significant (p < 0.05) (Essig et al., 2016). By combining these studies, we can 391 see that phytochelatins and metallothioneins possibly act together to protect the cells against 392 Cd. Phytochelatins have more of an immediate role at lower concentrations and 393 metallothioneins coming later with higher induction. In addition, a comparison between the 394 chosen gene expression profiles in earthworms exposed or unexposed to Cd showed up-395 regulation of two genes for all tested earthworms after Cd exposure - metallothionein and 396 superoxide dismutase as well as down-regulation of lysenin. Such alterations between the 397 expressions of those genes suggest that earthworms can oppose and reduce the toxic effects of 398 Cd through several different pathways. Moreover, in the presented study, we noticed that the 399 mt overexpression due to Cd exposure occurs not only in E. fetida but also in E. andrei and

hybrids between those species, which suggest, that this biomarker is suitable for both species. 400 401 However, results suggest that E. andrei (aAA) activate its detoxification mechanisms slower 402 than E. fetida (fFF) and their hybrids (aAF). Moreover, fast up regulation of expression of mt 403 genes in hybrids suggests, that they obtained the nuclear allele responsible for a fast reaction 404 from E. fetida, which showed similar tendencies, and not from E. andrei. In addition, such 405 results could indicate that perhaps, *Ef* earthworms possess another detoxification mechanism 406 or a specific regulation mechanism that is responsible for faster *mt* expression in comparison 407 to *Ea*. Thus, by cloning of the genes coding *mt* in both species and studying of the regulation 408 of the gene is needed to broaden our understanding of such response to metal exposure.

409 Similar to our study, the induction of overexpression of the *mt* gene was recently shown in *E*. 410 andrei earthworms after exposure to copper, which is a widely used fungicide, especially in 411 organic farming (Mincarelli et al., 2019). Moreover, an induction of *mt* expression was also 412 noticed in other earthworms including Dendrobaena octaedra and Lumbricus rubellus 413 exposed to Cu (Mustonen et al., 2014, Höckner et al., 2015). The population of Dendrobaena 414 octaedra exposed to Cu-Ni contaminated soil was shown to have higher mt expression levels 415 in comparison to earthworms not exposed to metals. What is even more interesting, during 416 artificial exposure experiment, exposure affected the *mt* expression, but only in the 417 earthworms collected from the clean, unpolluted soil, showing that there is a delay in the *mt* 418 response of earthworms which were not exposed to metals in the past. On the contrary, 419 earthworms collected from the Cu-Ni smelting site showed not only higher but also constant 420 levels of mt expression (Mustonen et al., 2014). Such results reflect on the role of the mt 421 expression and the homeostasis of several metals and protection against oxidant damage.

422

#### 423 Superoxide dismutase and Glutathione S-transferase

424 Glutathione S-transferase (GST) is an enzyme known to take part in the metabolism of 425 lipophilic organic contaminants and in cellular protection against oxidative stress. A study by 426 Mkhinini et al. (2019) showed an induction of gst expression after the exposure of E. andrei 427 to treated wastewater (TWW) containing several trace metals. However, such effects were 428 observed in earthworms exposed to TWW for more than 20 days. Our study showed no effect 429 of cadmium exposure to the expression of this gene in a 7-day period, which could suggest 430 that the *gst* mechanism is induced after prolonged, chronic exposure to heavy metals, but it is 431 not an immediate response to the presence of contamination. In another study, the antioxidant 432 gene expression of E. fetida was explored after worm exposure to various concentrations of 433 hexabromocyclododecane. The results showed a significant up-regulation of the sod gene but 434 no significant differences in the expression rate of *gst*, which further suggests its involvement 435 in protection against the oxidative damage occurs during a prolonged period of time (Shi et 436 al., 2018). Moreover, a recent study of Maity et al. (2018) focused on the oxidative stress 437 response of E. fetida and Eityphoeus waltoni exposed to Cd, the overexpression of the gst 438 gene increased significantly post-exposure and was dose-dependent. However, in E. fetida, 439 after 2 days post-exposure, the expression of gst remained the same as in control animals, 440 which also suggest its late-onset. In a transcriptomic study by Chai et al. (2019), focused on 441 cadmium toxicity in E. fetida, a significant up-regulation od sod genes was also observed in 442 earthworms exposed to 10, 30, 60 mg/kg of  $Cd^{2+}$  in dry soil, respectively.

443

444 Lysenin

Lysenin is a protein involved in immunity processes produced by coelomocytes and
chloragocytes (Munguira et al., 2017). The presence of lysenin and lysenin-related proteins
was documented in *E. andrei* and *E. fetida* and their putative hybrids (Swiderska et al. 2016).
In the present study, the expression rate of *lys* gene was significantly down-regulated post Cd

449 exposure in all tested animals (*Ea*, *Ef*, *Ha*). A similar decrease in *lys* expression was noticed 450 by Rorat et al. (2017) in E. andrei and Brulle et al. (2011) in E. fetida. However, the 451 mechanisms behind such response are still unknown. In a study by Wang et al. (2010) the 452 expression of lys was also shown to diminish after earthworms were exposed to E. coli. 453 Besides, Wu et al. (2013), discovered that lysenin-related protein was significantly up-454 regulated post-exposure to PAH phenanthrene. Hence, lysenin expression in earthworms can 455 have a complex response to exposure to different contaminants. Overall, the results imply the 456 existence of a complex regulatory network that needs to be further explored in future studies.

457

#### 458 Hybrids response to environmental stressors

459 We have shown previously that Eisenia andrei (Ea) and E. fetida (Ef) of French provenance 460 are capable of hybridization, as viable offspring appeared among progeny of laboratory-mated 461 inter-specific Ea+Ef pairs. Recently we have shown that hybridization is not unique for 462 French Ea/Ef earthworms, but is shared by laboratory-mated earthworms from French, 463 Hungarian, and Polish laboratory cultures (Podolak et al. 2020; Plytycz et al. 2020), but 464 fertility of hybrids is gradually diminished in the subsequent generations (Plytycz et al. 2020). 465 Inter-specific hybrids were detected in natural populations of *Ea* and *Ef* from Scandinavia 466 (Martinsson and Erseus, 2018) thus further data on hybridization in natural environment, even 467 such highly polluted, including compost heaps, are expected.

Both *E. andrei* and *E. fetida* earthworms as well as their hybrids are perfect cadmium bioaccumulators and can survive in heavily contaminated soil due to efficient protective mechanisms. *Mt* and *sod* upregulation and *lys* down-regulation are especially pronounced in hybrids. Therefore we shall exclude such a possibility that the improper functioning of investigated stress-related genes is the main factor responsible for gradual impairment of hybrid fertility in the subsequent generations (Plytycz et al. 2020). 474 Interestingly, similar to our results, recent research on several species of plants indicated that 475 hybrids can outperform their parental species after exposure do different stressors (both biotic 476 and abiotic). As an example, a couple of types of poplar hybrids had been shown to better 477 adapt to suboptimal temperatures and demonstrate superior growth, particularly under the less 478 favorable, suboptimal temperature conditions (Guet et al., 2015). Overall, the interspecific 479 hybridization has recently become of-interest to forest geneticists for tree improvement by 480 assessing the possible feasibility of transferring desirable traits such as higher resistance to 481 contamination, droughts, or diseases, among species (Juranović-Cindrić et al., 2018). Apart 482 from trees, another study showed a variation between Cd uptake in maize hybrids, which can 483 be used for phytoremediation of Cd-contaminated soil as well as for the selection and 484 breeding of new, Cd-tolerant genotypes of maize (Akhtar et al., 2016, Wang et al., 2015). 485 Similar tendencies had been observed for the accumulation of Cr in sunflower hybrids, which 486 is currently used in the selection and breeding of Cr-tolerant genotypes of sunflowers (Farid et 487 al., 2017). However, the molecular basis of such differential accumulation and the differences 488 in the genetic makeup of both hybrids and parent species are scarcely researched and need to 489 be further investigated in both, plants and earthworms exposed to contamination (Wang et al., 490 2015, Naeem et al., 2016, Juranović-Cindrić et al., 2018).

491

#### 492 **5.** Conclusions

The insights gained in the presented study have improved our understanding of metal resistance of *E. fetida*, *E. andrei* and their hybrids. The results indicate that all of them are very efficient cadmium bio-accumulators with similar mechanisms of Cd detoxication. Consistently, upregulation of *mt* and *sod* expression was fastest in hybrids, slower in *Ef* and slowest in *Ea*. Hypothetically *Ef* and *Ea* differ in their mechanisms controlling expression of

- 498 stress-related genes and immunity-connected genes thus further studies of these genes and499 their interactions in hybrids are necessary.
- 500
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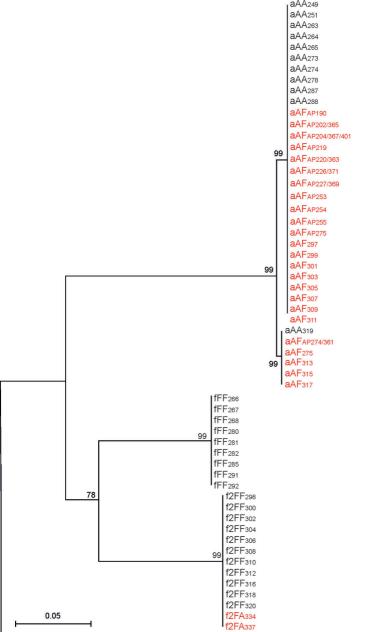
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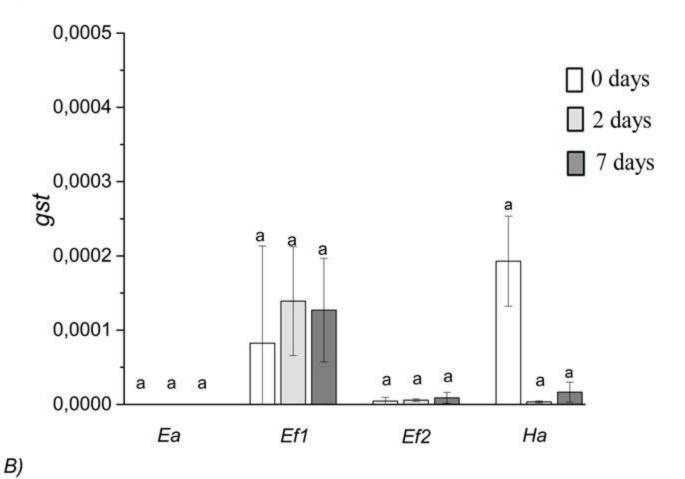
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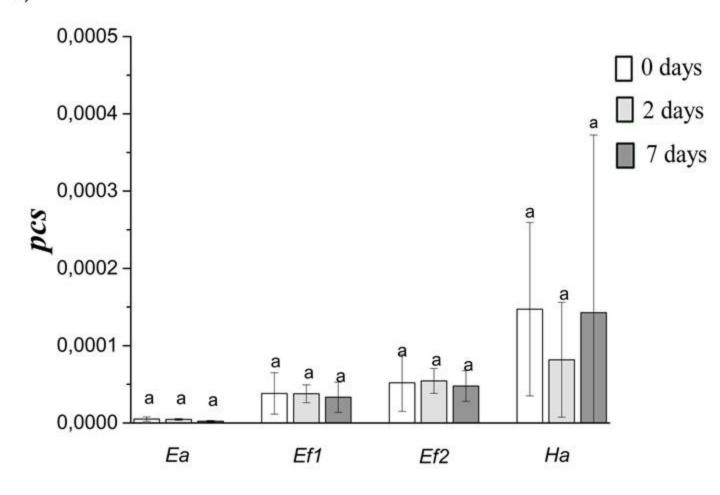
### 663 Figure Captions

Figure 1. Maximum-likelihood phylogram for the species-specific sequences 'a' or 'f'/'f2' of the mitochondrial COI gene, with additional information on the 'A' or 'F' nuclear sequences of 28S rRNA nuclear gene of the same individuals with the same code, showing the pure aAA (*Ea*) and fFF/f2FF (*Ef1/Ef2*) species and their aAF or f2FA hybrids.

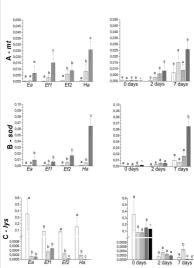
- 668 Figure 2. Relative expression level of *gst* (A) and *pcs* (B) in coelomocytes of groups of
- earthworms exposed to cadmium polluted soil concentration for 0 days (control), 2 days, or 7
- 670 days: Effects of time of exposure. Different letters "a", "b" "c", "d" on top of bars indicate
- 671 statistically significant differences according to the Kruskal–Wallis one-way analysis of
- 672 variance (p<0.05).
- 673 Figure 3. Relative expression level of *mt* (row A), *sod* (row B) and *lys* (row C) in
- 674 coelomocytes of groups of earthworms exposed to cadmium polluted soil concentration for 0
- days (control), 2 days, or 7 days; Left column effects of time of exposure; right column
- 676 interspecies comparisons between *Ea*, *Ef1*, *Ef2*, and *Ha* earthworms at particular time points.
- 677 Results shown as means  $\pm$  SD, n=6; *Hf*\* mean from two specimens only. Different letters
- 678 "a", "b" "c", "d" on top of bars indicate statistically significant differences according to the
- 679 Kruskal–Wallis one-way analysis of variance (p < 0.05).
- 680
- 681
- 682







Relative expression level



0 days 2 days 7 days

Es Ett Ett Ha

