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DNA BARCODING REVEALS A SINGLE GENETIC LINEAGE OF THE PEREGRINE EARTHWORM *LUMBRICUS RUBELLUS* (ANNELIDA, LUMBRICIDAE) IN THE NORTHEASTERN PALEARCTIC

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Lumbricus rubellus, a peregrine earthworm, is believed to trace its origins to Western Europe, from where it has dispersed across the temperate regions of the Northern Hemisphere. It exhibits significant genetic variation, with at least eight recognized cryptic genetic lineages in Europe. This study aimed to assess whether populations from the Northeastern Palearctic possess genetic diversity comparable to that of Western Europe. Our findings revealed that only a single genetic lineage (2/A) colonized the vast territories from Belarus to Kamchatka. All studied populations contained closely related haplotypes, with no evident geographic subdivisions. Consequently, only a small fraction of the *L. rubellus* genetic pool was found outside Western Europe. This limited distribution may be attributed to the 2/A lineage's adaptation to local conditions or its enhanced dispersal capabilities. Alternatively, phylogeographic factors might play a role, suggesting that the ancestral region of this lineage was situated along suitable dispersal corridors.

Keywords: peregrine, *Lumbricus rubellus*, phylogeography, mitochondrial DNA, *cox1*, COI
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