

Representative Works — Annex

Up to five selected outputs & justifications

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Justifications

1. Living on a volcano's edge: genetic isolation of an extremophile terrestrial metazoan (2014)

Heredity 112(2):132-142. DOI: [10.1038/hdy.2013.84](https://doi.org/10.1038/hdy.2013.84)

Authors: Cunha, L.; Montiel, R.; Novo, M.; Orozco-Terwengel, P.; Rodrigues, A.; Morgan, A.J.; Kille, P.

This article investigates **genetic isolation and adaptation of an extremophile metazoan in volcanic environments**, applying population genetic markers and comparative analyses at mitochondrial and nuclear genome levels.

I contributed to **genotyping, dataset curation, and statistical inference in R**, building expertise in **genetics of adaptation to extreme environments and population structure analysis**.

2. Amazonian earthworm biodiversity is heavily impacted by ancient and recent human disturbance (2023)

Science of The Total Environment 895:165087. DOI: [10.1016/j.scitotenv.2023.165087](https://doi.org/10.1016/j.scitotenv.2023.165087)

Authors: Conrado, A.C.; Demetrio, W.C.; Stanton, D.W.; Bartz, M.L.; James, S.W.; Santos, A.; da Silva, E.; et al. and Cunha, L.

This large international collaboration demonstrates how **human land-use history drives biodiversity patterns in Amazonian earthworms**, integrating DNA barcoding, ecological surveys, and advanced statistical models.

My role included leading the **field and lab work** but also contributing to **bioinformatic processing of sequence data and ecological genetics analysis**, emphasizing skills in **biodiversity genomics and large-scale data integration**.

3. Identifying conserved polychaete molecular markers of metal exposure (2021)

Comparative Biochemistry and Physiology Part C: Toxicology & Pharmacology 240:108913. DOI: [10.1016/j.cbpc.2020.108913](https://doi.org/10.1016/j.cbpc.2020.108913)

Authors: Etxabe, A.G.; Pini, J.M.; Short, S.; Cunha, L.; Kille, P.; Watson, G.J.

This work identifies **transcriptome-derived biomarkers of metal exposure in polychaetes**, using RNA-Seq analysis of *Alitta virens*. Comparative bioinformatics highlighted conserved molecular responses across taxa.

I contributed to the **analysis of RNA-Seq data, marker validation, and interpretation of functional pathways**, strengthening expertise in **environmental transcriptomics and stress genomics**.

4. Coping with extremes: How Epigenetic and Molecular Adaptations Enable Earthworms to Thrive in Volcanic Soils (Preprint, 2025)

bioRxiv. DOI: [10.1101/2025.07.24.666578](https://doi.org/10.1101/2025.07.24.666578)

Authors: Rimington, O.; Novo, M.; Hodson, M.E.; Camarinho, R.; Viveiros, F.; Silva, C.; Arruda, H.; Rodrigues, A.S.; Bruford, M.; Short, S.; Morgan, A.J.; Spurgeon, D.; Kille, P.; Cunha, L.

This preprint explores **epigenetic and molecular adaptations of earthworms in volcanic soils**, integrating genome-wide methylation profiling and transcriptomic analyses.

I was responsible for **integrating sequencing pipelines and population epigenomic analysis**, reflecting skills in **epigenetics, stress adaptation, and reproducible workflows** highly relevant to the Genetics & Genomics focus of the UA call:contentReferenceoaicite:0.

5. A large set of microsatellites for the highly invasive earthworm *Amyntas corticis* (2017)

Applied Soil Ecology 119:152-155. DOI: [10.1016/j.apsoil.2017.05.029](https://doi.org/10.1016/j.apsoil.2017.05.029)

Authors: Cunha, L.; Thornber, A.; Kille, P.; Morgan, A.; Novo, M.

This publication describes the development of **SSR markers from low-coverage genomes** to study invasive *Amyntas corticis*. Markers were validated and proposed for monitoring invasion dynamics and population structure.

I led the **design and validation of SSR panels, PCR protocols, and downstream analysis**, consolidating expertise in **molecular marker development and applied population genetics**.