

Genomic insights for conservation:**Phylogeographic structure and genetic erosion in the Italian White-Clawed Crayfish (*Austropotamobius pallipes* complex)**

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9 LIFE IP Gestire2020, <https://naturachevale.it/en/animals/actions-for-freshwater-crayfish-conservation>

10 <https://www.lifeclaw.eu>

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The white-clawed crayfish (*Austropotamobius pallipes*) has undergone a dramatic decline across the Italian peninsula over the past century, driven by crayfish plague outbreaks associated with non-native species and escalating anthropogenic pressures. The two taxa currently found in Italy, i.e. *A. pallipes* and *Austropotamobius fulcisanus*, were once widespread but now survive as small, highly fragmented populations restricted to isolated freshwater basins.

To provide a comprehensive genomic assessment at the national scale, we sampled 2,550 individuals from 124 populations across eight Italian regions (Lombardy, Liguria, Emilia-Romagna, Friuli-Venezia Giulia, Tuscany, Umbria, Abruzzo, and Basilicata). Sampling was conducted as part of the LIFE CLAW project and was then expanded further under the National Biodiversity Future Centre (NBFC). This substantially increased the geographic coverage across northern, central, and southern Italy.

Mitochondrial (COI) sequencing of 1,965 individuals from 102 populations revealed a pronounced phylogeographic structure, with *A. pallipes* confined to north-western Italy and *A. fulcisanus* occupying the remaining regions. Several haplotypes were identified, including private lineages and locally shared variants, which highlight microgeographic differentiation. Notably, phylogenetic and species delimitation analyses suggested the presence of three well-defined species (namely, *A. pallipes*, *A. fulcisanus* and *Austropotamobius meridionalis*) with evidence indicating that *A.f. orientalis* is a distinct subspecies within the *A. fulcisanus* complex based on genetic differentiation.



Genome-wide ddRAD data (currently under completion) corroborate a strong genetic separation between the three taxa, limited gene flow, and reduced within-population diversity. The emerging pattern of fine-scale structuring closely mirrors hydrographic boundaries, emphasizing the role of drainage systems in shaping evolutionary trajectories.

By integrating extensive sampling with mitochondrial and genome-wide markers, this study provides the most comprehensive overview of genomic diversity within the Italian white-clawed crayfish complex to date. These results establish a robust genetic framework to guide evidence-based conservation, management, and restoration strategies across Mediterranean freshwater ecosystems.