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Soil biological quality and biodiversity at the margins of rice fields: insights from QBS-ar and eDNA metabarcoding

Agricultural intensification and landscape homogenization have driven a widespread decline in agroecosystem biodiversity. Rice field margins serve as surrogate habitats for non-wetland edaphic species. However, conventional agricultural practices can degrade these margins, and the relative beneficial effect of organic management remains poorly understood.

We combined the Arthropod-based Biological Soil Quality Index (QBS-ar), which assesses soil biological quality through the analysis of microarthropod communities and their morphological adaptations to hypogean life, with an environmental DNA (eDNA) approach to characterise soil metazoan communities. This integrated approach was used to evaluate the effects of paddy fields management on soil biodiversity of field margins. We hypothesised that different management practices inside the ground of paddy fields impose different levels of pressure on soil biodiversity even in rice field margins.

We studied a lowland agroecosystem located in the provinces of Vercelli and Novara (NW Italy). A total of 108 soil samples were collected in two monitoring seasons (spring and summer) across two crop systems (organic and conventional) and a natural habitat located in three distinct areas. Within each system, two field margins belonging to three different rice paddies were sampled. In the natural control habitat, we selected six points on the margin of three ponds. The QBS-ar was determined for each soil core. For eDNA, libraries construction involved the amplification of 313 bp region of the metazoan COI gene and subsequent bioinformatic analysis inferring ASVs using the DADA2 R package and a tailored reference database.

Both methods revealed that invertebrate communities of the margins did not differ significantly between organic and conventional crop systems, contrary to known in-field patterns. However, both agricultural systems differed significantly from natural habitats. The eDNA provided a higher taxonomic resolution, identifying indicator species sensitive to management effects. These findings suggest that field margins in both rice systems suffer from similar disturbances, overriding the potential benefits of organic cultivation. Integrating morphological indices like QBS-ar with high-resolution eDNA metabarcoding offers a robust framework for agroecosystem biomonitoring, highlighting the important role of natural wetlands as biodiversity reservoirs.