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# Does eco-intensive agriculture improve the resilience of N-cycling related ecosystem services to climatic stresses through modifications of soil microbial community traits and diversity ?

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## Abstract

Conventional agriculture (CA) relies heavily on human inputs and often disregards soil biodiversity and its associated functions. Ecological intensification (EI) has been proposed as an approach to integrate ecological processes into management strategies to enhance ecosystem services (ES). With extreme events becoming more intense and frequent with climate change, the ability to maintain ES under extreme weather is crucial for agroecosystems. Plant and microbial responses to climate events vary between species depending on their functional traits, with fungal dominated microbial communities and conservative plants being expected to be more resistant. The insurance hypothesis claims that higher species diversity insures ecosystems against declines in functioning when facing perturbations. By promoting diversity and selecting for conservative plants and soil fungal communities, we make the hypothesis that EI has a better ability to maintain ES under climatic stresses. Our study aimed to test this hypothesis, comparing responses to climatic stresses (9 months under Drought, Flood or Intermittent rain regimes and 3 months of recovery) of EI versus CA in three land use systems across Europe (arable cropping, grasslands, agroforestry)

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using common incubations of terrestrial model ecosystems. We focused our investigation on N-cycle related ES (plant N provisioning, soil N retention) and indicators: microbial properties (PLFA, enzymatic activities and functional gene abundances and diversity) and soil N pools. Our preliminary results partially support our hypothesis with few beneficial effects of country specific EI management. Furthermore, we observed negative correlation between metallopeptidase gene diversity and leucine aminopeptidase resistance undermining the insurance (biodiversity-stability) hypothesis. Plant and microbial community traits were found to have strong links with N cycling ES level and stability, supporting the interest of trait based approach to understand general drivers of ES in a global change context.