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## Soil microbial diversity and ecosystem functioning assessment across Europe

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The global area of cultivated land has increased considerably over the past five decades. Despite the many ecosystem services provided by soil, at large-scale, it is still poorly understood whether land-use intensification influences soil life and the services that rely upon it. Here we used an extensive soil metabarcoding database, derived from the European Union's (EU) Land Use/Cover Area frame statistical Survey (LUCAS), to assess how vegetation (land) cover, biogeographic factors (i.e., climate) and soil properties influence the structure and potential functions of bacterial and fungal communities at a continental scale. We selected 715 LUCAS sampling locations, classified according to an increasing land-use intensification: from woodland (less disturbed), to grassland, and cropland (more disturbed). We found that croplands and grasslands had a higher microbial richness than woodlands. We observed that bacteria and fungi were not driven by the same environmental variables. While soil properties (e.g. pH, C:N ratio, potassium, phosphorus and carbonate contents) drove bacterial community composition, vegetation cover was the main driver for the fungal community. We found that vegetation cover, biogeographic factors and soil properties differently determined the distribution of main functional groups; for example, cropland soils with a higher pH and a lower C:N ratio hosted more nitrogen fixing bacteria whereas woodlands were dominated by ectomycorrhizal fungi, especially in non-compacted clay soils, with lower C:N ratio and potassium content. We observed that increasing aridity may inhibit functions beneficial for the plant communities (i.e. bacterial chemoheterotrophy and nitrogen fixation, arbuscular mycorrhizal symbiosis) and favour the spread of fungal pathogens. In addition, a high diversity was not always a positive aspect for ecosystem functioning, as for example, croplands were characterized by a higher presence of fungal pathogens. Maps of microbial functional groups for the EU were also generated. In conclusion, our results represent a step forward to a more comprehensive assessment of soil microbial diversity and associated functions across the European Union. Beside possible ecological implications, our findings can contribute to the development of indicators and implementation of soil management policies.

