Prospecting for pathogens in national soil monitoring programme

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Soils provide a habitat for untold numbers of potentially harmful microbial species. Many of these plant and animal pathogens pass through the soil as part of their life cycle while others live in soil and opportunistically infect other organisms. Understanding the dynamics of human and agricultural diseases in soil is of major importance to policy-makers. However, many pathogens can also exist in soil at low levels without causing a major disease outbreak. This fact is often overlooked from policy perspectives, which commonly focus on mitigating the effects of disease outbreaks once they have begun. Yet by identifying pathogens directly from soils, policy can be strengthened to better identify at-risk areas or further limit exposure to pathogens. Here, we harness data generated through the Glastir Monitoring and Evaluation Programme (GMEP) to identify DNA traces of pathogens directly from the soil. Briefly, DNA was extracted from 437 soil samples collected in late spring and early autumn of 2013 and 2014, amplified using two-step PCR, and sequenced using Illumina Mi-Seq technology. For each sample, primers amplifying 16S, ITS1, and 18S regions were applied to create OTU tables for prokaryotes, fungi, and microbial eukaryotes respectively using VSEARCH pipelines. Preliminary results show that pathogenic bacteria including Salmonella, Escherichia coli, several species of Clostdridium, and Legionella as well as several species of both Aspergillus and Phytophthera, and many Apicomplexan and helminth parasites including Plasmodium and root-knot nematodes. Further analysis will identify habitat characteristics favoured by these pathogens and identify potential hotspots for which targeted policies and interventions can be developed. This work highlights a dynamic application of a national-scale dataset and provides a footing for interdisciplinary work between soil science, microbial ecology, epidemiology, and policy.