

Soil pH, land use and soil classification account for changes in prokaryotic communities at a broad geographic scale

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Agricultural land has typically been managed based on visible plant life. However, it is known that microbes are key to many processes sustaining the soil environment, necessitating studies of the impact of differential land uses on belowground communities. We surveyed prokaryotic communities from soils representing four geographic regions on the South Island of New Zealand to assess the relationships between land use, edaphic factors and fertilizer amendments and prokaryotic community structure at a multi-region scale. Over the course of a year, we took 864 samples from 24 sites that had been treated with two fertilization methods (lime flour and soft rock phosphate). These sites are under three different uses (dairy, sheep and beef and high country) and contain a large range of pHs (5.1-6.3). 16S profiles showed that prokaryotic community diversity (Shannon) and structure (Detrended Correspondence Analysis) across the South Island varied significantly with pH ($p < 0.001$), and distinct low country/high country communities were observed ($p < 0.001$). On a regional scale, soil order correlated most significantly with prokaryotic community structure ($p < 0.001$). Fertilization had no impact on communities at any spatial scale. However, some communities shifted significantly in accordance with season ($p < 0.001$). These results suggest that edaphic factors may best predict changes in soil prokaryotic communities, and that it is important to examine biogeography at multiple resolutions in order to reveal fine-scale patterns of distribution.