Antimicrobial resistance:

soil-landscape conditions across NE England & Scotland

Uni. Strathclyde: Charles W. Knapp (PI), Tatyana Peshkur
Newcastle U.: David W. Graham, Clare McCann, Martin Cooke
James Hutton Institute: Rupert Hough, Eulyn Pagaling, Lisa Avery, Thomas Freitag
Chinese Academy of Sciences - Xiamen: Yong-Guan Zhu, JianQiang Su

Antimicrobial resistance is increasing in nature and threatens the effectiveness of our drug therapies and infection control. However, it remains difficult to distinguish what originates from human activities or what is natural. Therefore, we must extend the scale and depth monitoring efforts to better understand what is driving the increases in resistance traits.

This project utilised two collections of previously characterised soils to compare and contrast distributions of AR genes under widely varying conditions, ranging from urban, agriculture, legacy mining, and pristine rural environments. From the soils, DNA were extracted and quantified for over 230 AR genes in each sample. These soil inventories provided us well-characterised soils and the wealth of information that describes both the soils and the impacts at source locations.

The assay:
High-throughput qPCR (Applied Bioscience OpenArray Platform)[1]

- Nearly 300 AMR genes
- Transposons
- Integrons

Supplemented with:

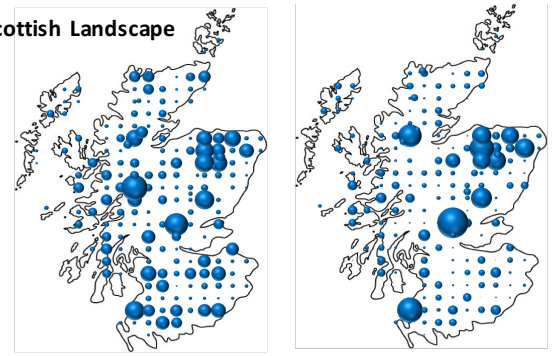
- Metal/ hydrocarbon resistance qPCR assays
- Geochemical and endaphic background data

[1] Zhu et al. (2013) *PNAS* 110: 3435

- Aminoglycosides (37)
- B-lactams (55)
- Multidrug (52)
- Tetracycline (42)
- Other (5)
- Integrase (2)
- am/chlor/fluor-quinolone (9)
- MLSB (48)
- Sulfonamide (7)
- Vancomycin (33)
- Transposon (8)
- 16s-rRNA (1)

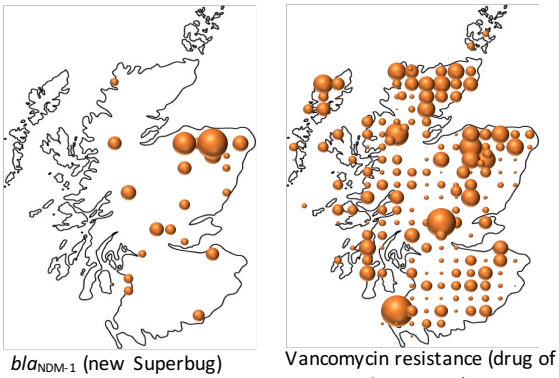
The project generated an astonishing 70,000 AR-related data points (300+ locations x 230 genes), each with extended background information on environmental conditions-creating among the largest geographic representation of AR gene distribution across landscapes ever created, sufficiently detailed to make cross-cutting observations of landscape effects on acquired vs innate AR levels.

#1: Scottish Landscape



Beta-lactamases

Tetracycline resistance



bla$_{NDM-1}$ (new Superbug)

Vancomycin resistance (drug of last resort)

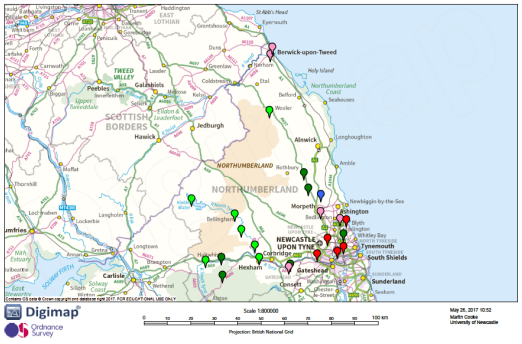
Figure. Example distributions of gene classes found in Scottish soils.[2] We generated detailed profiles of antibiotic resistance traits is Scottish soils that can be compared to geochemical and land-use conditions.

[2] James Hutton Institute (2007-9) The National Soils Inventory of Scotland

#2: Northumberland - Tyne

- 12 urban sites
- 12 rural sites

- Rural – high metals
- Rural – low metals
- Urban – high metals
- Urban – low metals



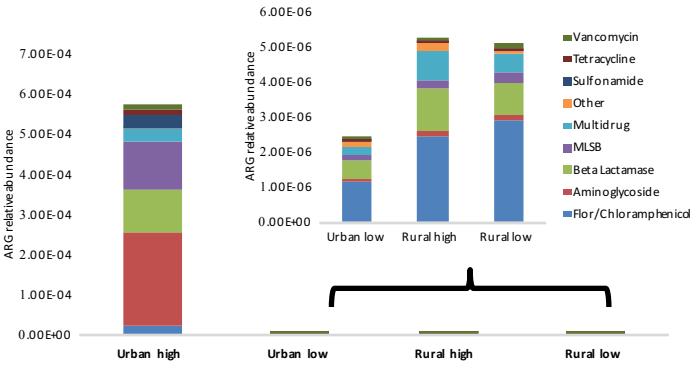


Figure. Distribution of resistance genes in Northumberland & Tyne soils. Soils were collected to represent urban and rural sites with low- and high-levels pollution impacts. Evidence suggest that urban pollution contributes greatly to environmental antimicrobial resistance.