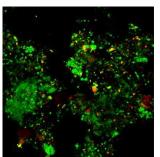
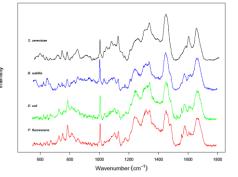
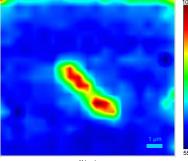
WHO, HOW AND WHERE? MICROBIAL ECOLOGY USING RAMAN SPECTROSCOPY

DR DANIEL READ CENTRE FOR ECOLOGY & HYDROLOGY, WALLINGFORD









"Progress in science depends on new techniques, new discoveries and new ideas, probably in that order". — Sydney Brenner







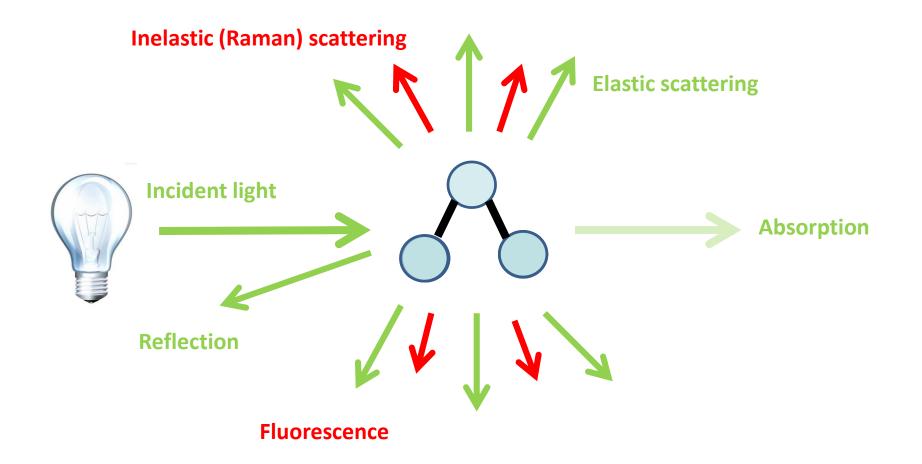


Outline

- A short intro to spectroscopy
- Raman spectroscopy
- Microbiological applications of Raman
 - Phenotyping Who?
 - Microbial function How?
 - Mapping with Raman Where?

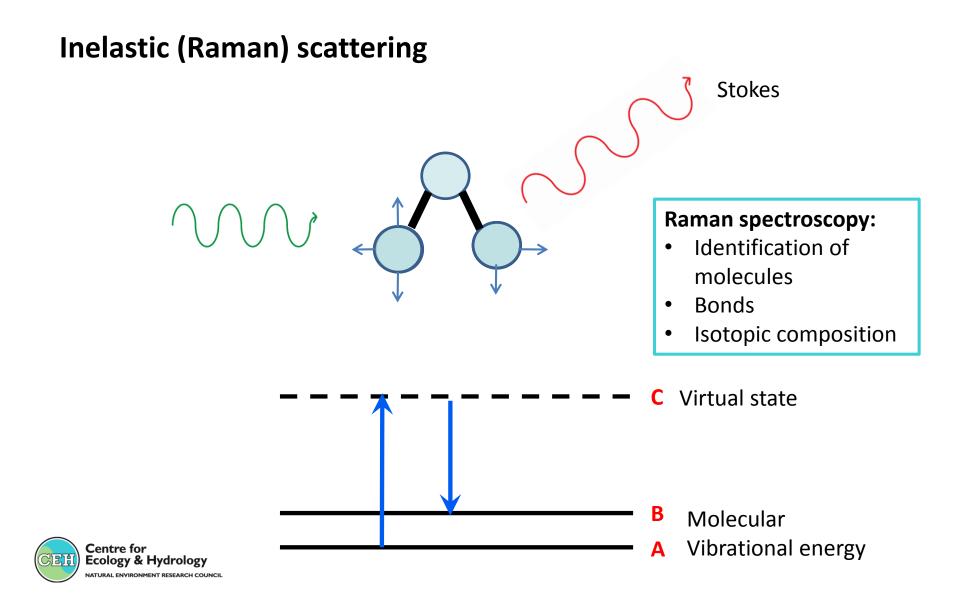


Spectroscopy



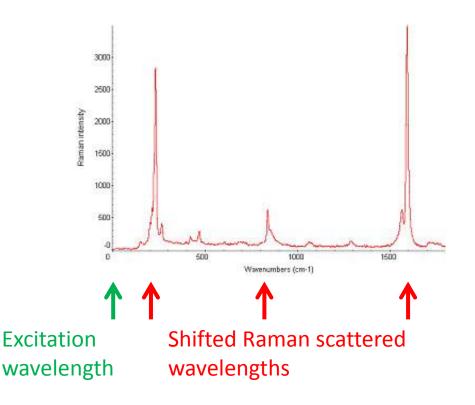


Scattering of light



Raman data

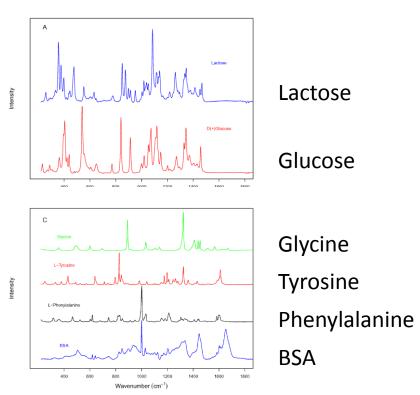
Data is presented relative to the excitation wavelength



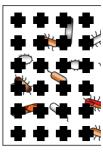


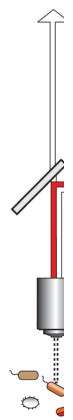
•Characteristic spectroscopic patterns results in a "fingerprint" for molecules

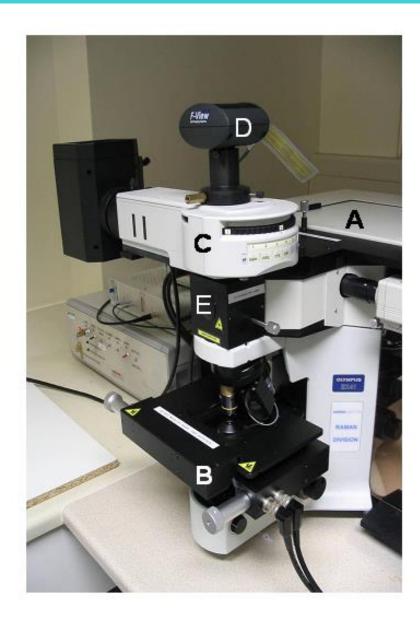
•Can be used to identify and characterise molecules of elements and compounds



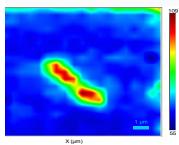
The Raman microspectrometer

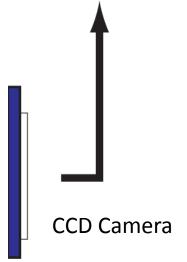




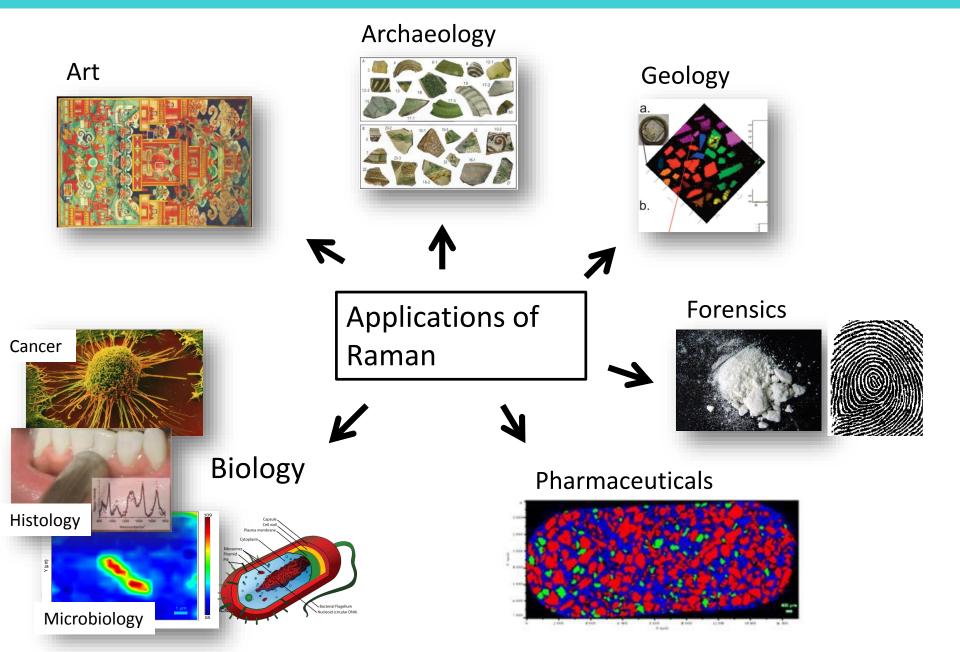


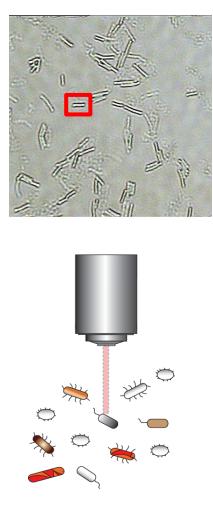
~300 spectra





Raman applications:



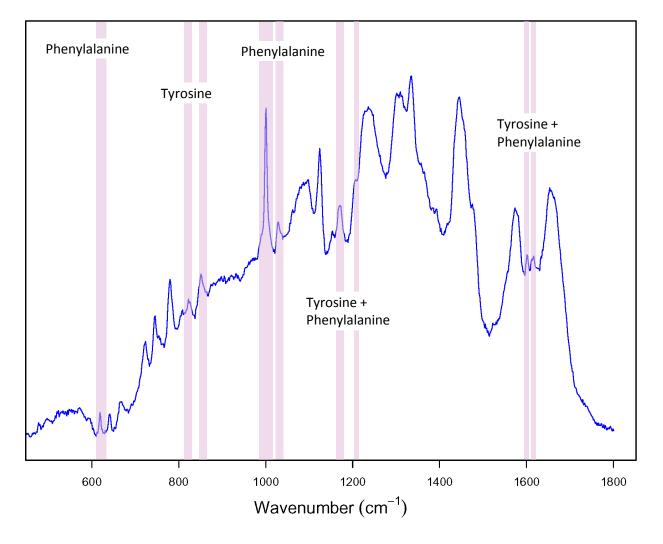


Centre for

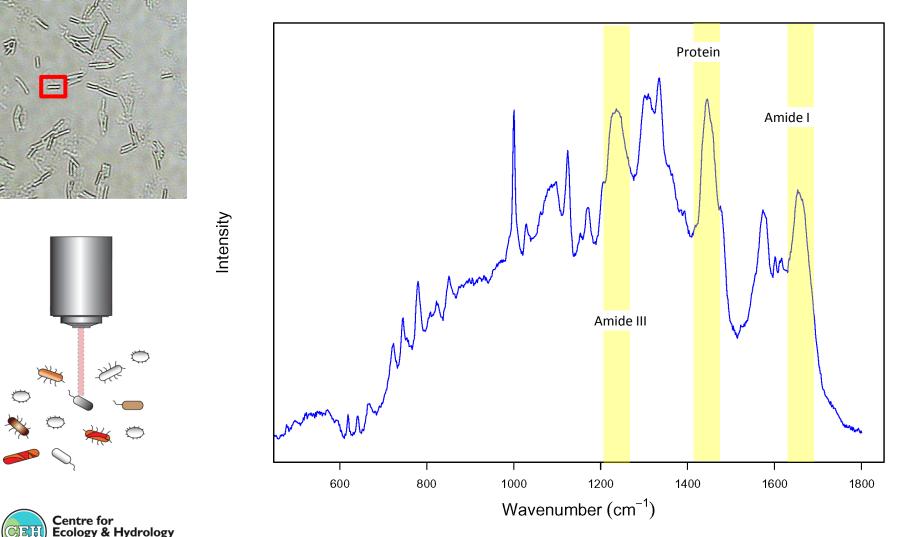
Ecology & Hydrology

Intensity

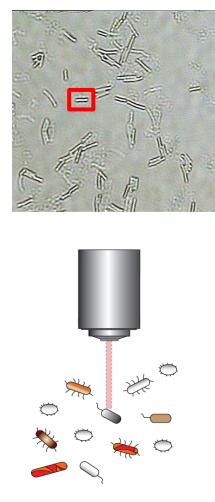
Amino acids



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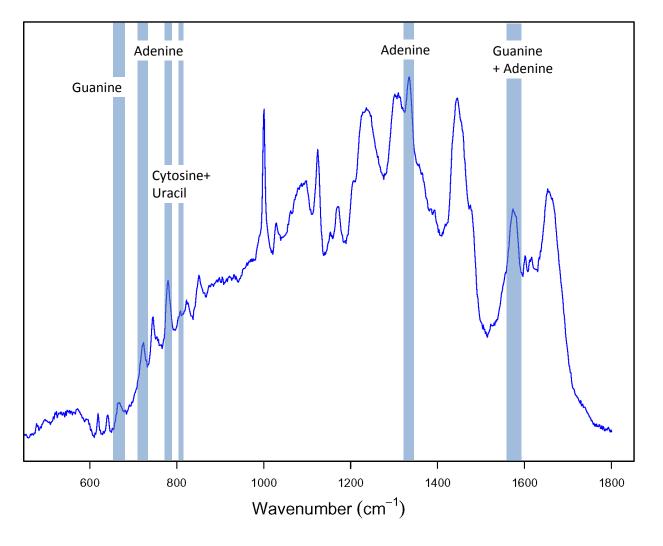


Proteins



Intensity

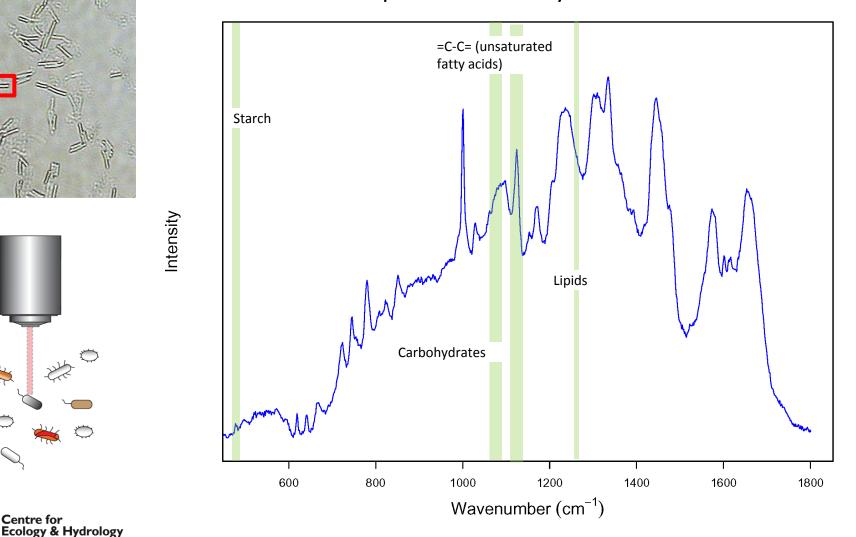
Nucleic acids



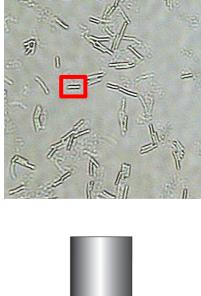
CETTI Centre for Ecology & Hydrology Natural Environment research council

59

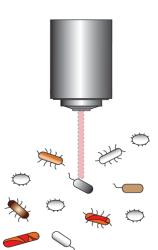
NATURAL ENVIRONMENT RESEARCH COUNCIL



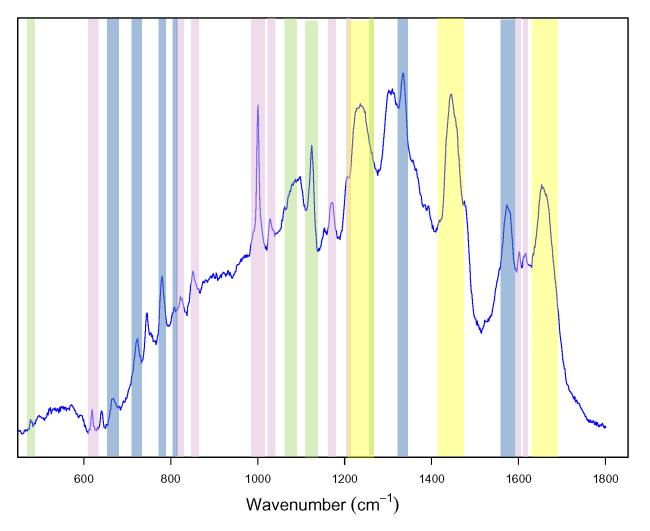
Lipids and carbohydrates



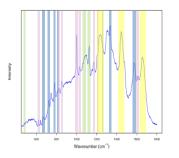
Intensity



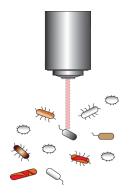




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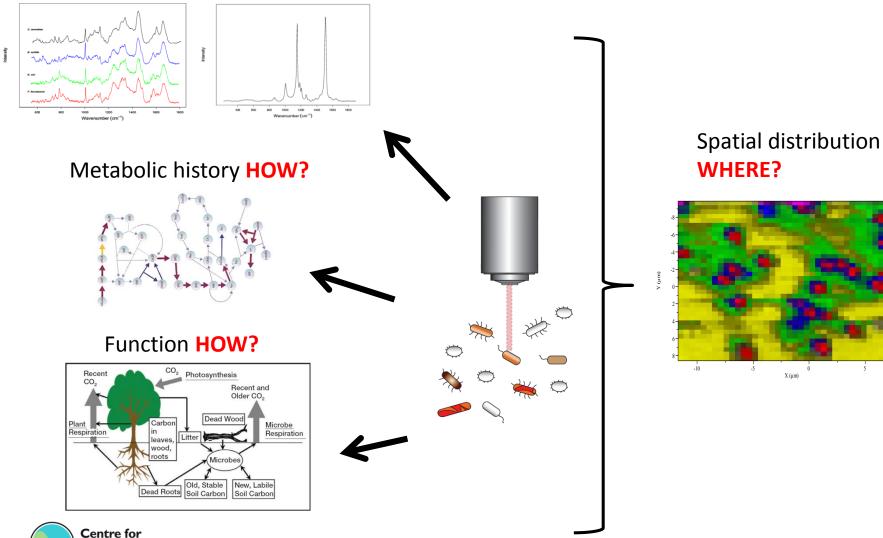
Raman phenotyping or fingerprinting

- Fast (~30s per sample)
- No sample prep
- Cheap to run (after initial outlay)
- Quantitative (peak height)
- Diverse range of data in single assay
- Non-contact and non-destructive
- Single-cell analysis (sampling down to 1 µm dia)
 - \circ $\$ microbiology at the level of the individual



Raman applications: Microbial Ecology

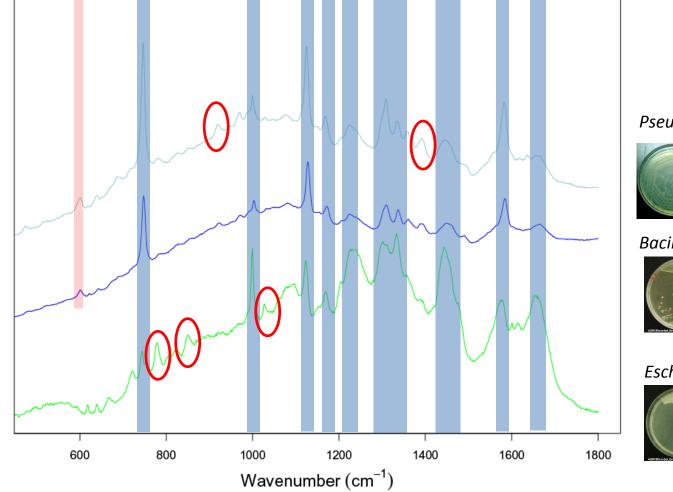
Phenotype WHO?





Who?: Raman Phenotyping

Intensity



Pseudomonas fluorescens



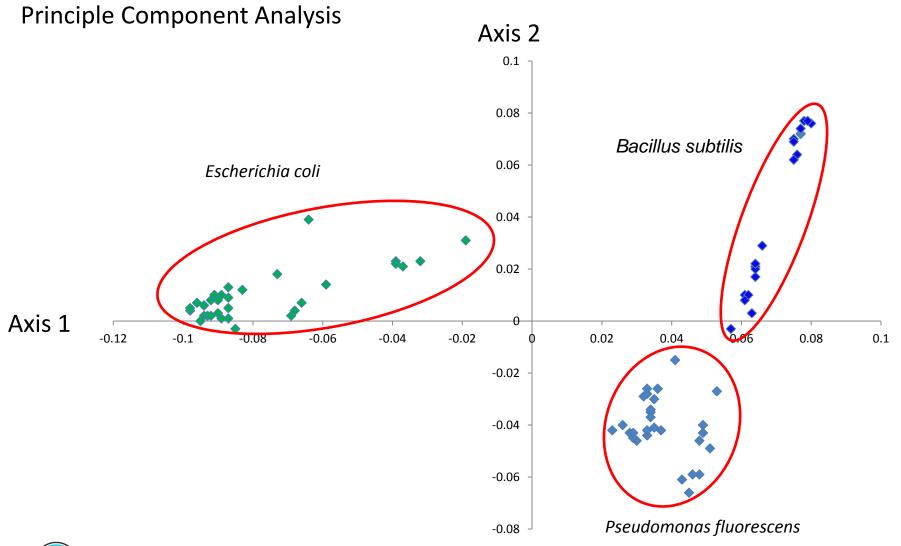
Bacillus subtilis



Escherichia coli

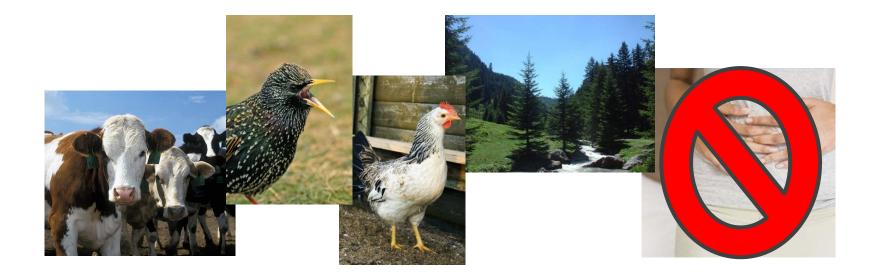


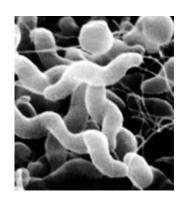
Who?: Raman Phenotyping

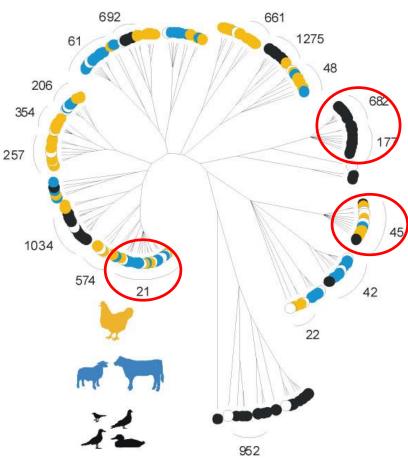




- Campylobacter jejuni and C. coli campylobacteriosis
- Accounts for estimated 2.5 million cases (US) and 1,340,000 (UK) each year
- x13 the number of cases caused by Salmonella, *E. coli*, and *Listeria* combined
- Estimated annual economic burden is £500 million in the UK
- Ability to colonize multiple hosts is a key feature of the ecology of Campylobacter







Multilocus Sequence Typing (MLST)

Single host lineages MLST 682 and 177 found only in wild birds

Multi-host lineages

MLST 45 and 21 found in chickens, cattle, wild birds and in clinical samples

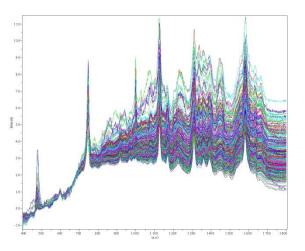
We wished to test whether:

- 1. Campylobacter phenotype is related to genotype (Species, clonal complex and clade)
- Phenotype is related to species of host organism it was isolated from, *independent* of MLST (genetic) classification

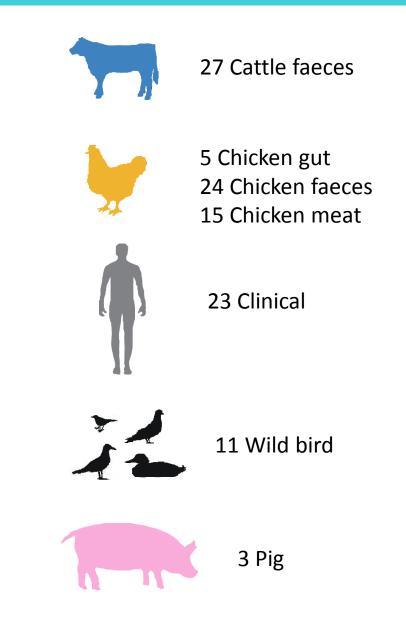


Sheppard, S.K., Maiden, M.C.J., Falush, D. (2009). Population Genetics of *Campylobacter*. In: Bacterial Population Genetics in Infectious Disease. Eds. Robinson, A.D., Falush, D., Feil, E.J. John Wiley & Sons, New Jersey. Pages 181-194.

- Strains used in this study
 - 108 Strains of Campylobacter (cultured and analysed in triplicate)
 - 2 species *C. jejuni* (85) and *C. coli* (23)
 - 66 Multilocus Sequence Types
 - 1,620 Raman spectra







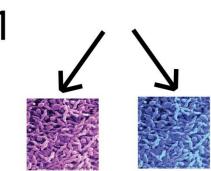
Neural network analysis – supervised statistical classification (Dr Dan Woodcock - Systems Biology Centre, University of Warwick)

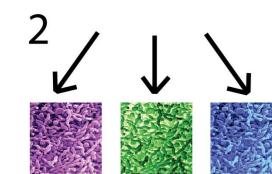
Identifies informative peaks and nonlinear relationships between the wavelengths
Distinguish which inputs provide the most information in separating the classes
Discards least informative peak until peak set with most discriminatory powers is left

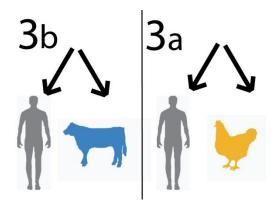
The two species, *C. jejuni* and *C. coli*

Clades 1, & 2 and 3 in C. coli

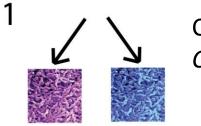
C. jejuni ST21 and ST45a) human vs. cattleb) human vs. chicken





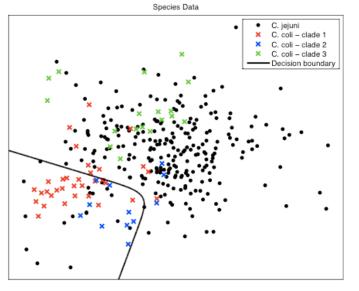




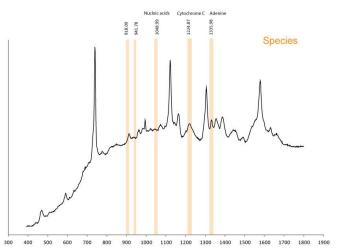


Comparison of *C. jejuni* and *C. coli*

89% classification success

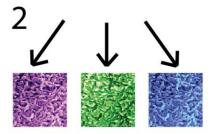


Peaks used in model



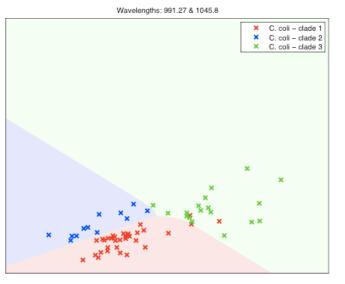
Phenotypic signature associated with nucleic acids, cytochrome *c*, and adenine (a nucleobase)

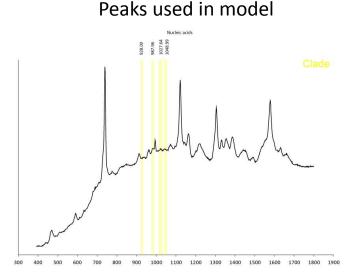




Campylobacter coli – Clade 1, 2, and 3 separation

79% classification success



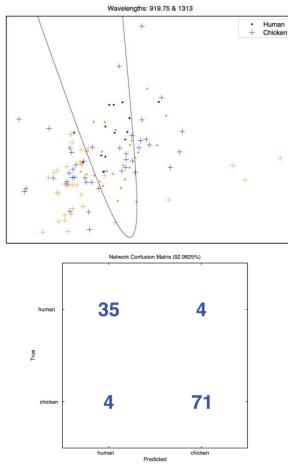


Phenotypic signature associated with phenylalanine and nucleic acids

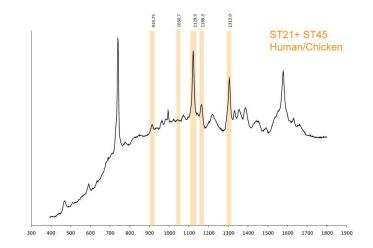


C. jejuni ST45 and ST21 human and chicken

93% classification success





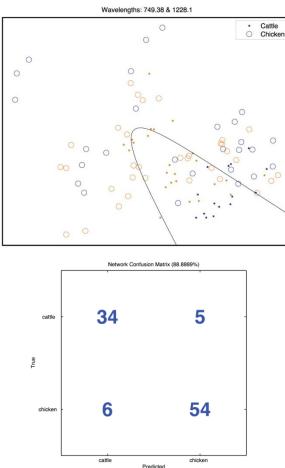


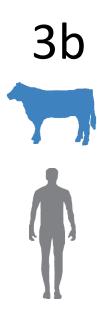
Phenotypic signature associated with cytochrome *c*, nucleic acids and one as yet unidentified peak

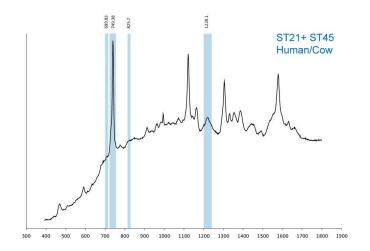


C. jejuni ST45 and ST21 human and cow

89% classification success







Phenotypic signature associated with cytochrome *c*, and two as yet unidentified peaks



Links between phenotype and genotype comparatively weak in *Campylobacter* sp. (compared to other studies)
Why Clade 3 *C. Coli* phenotypically more similar to *C. Jejuni*?

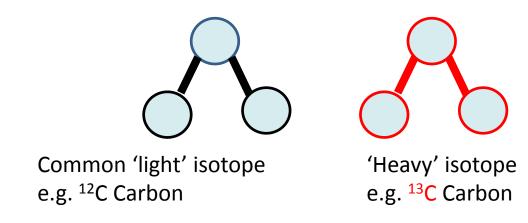
•Link between phenotype and host association proved to be stronger

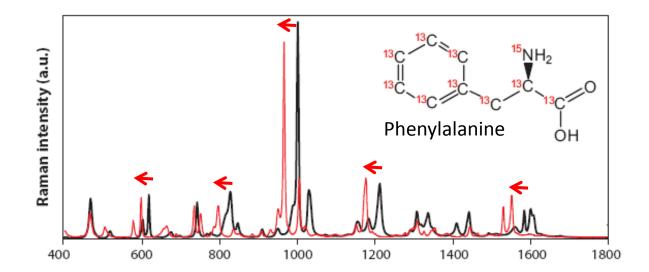
 Possibly due to limitations of MLST technique (only 7 housekeeping genes)

•Campylobacter possibly not a good study organism!



How?: Microbial function

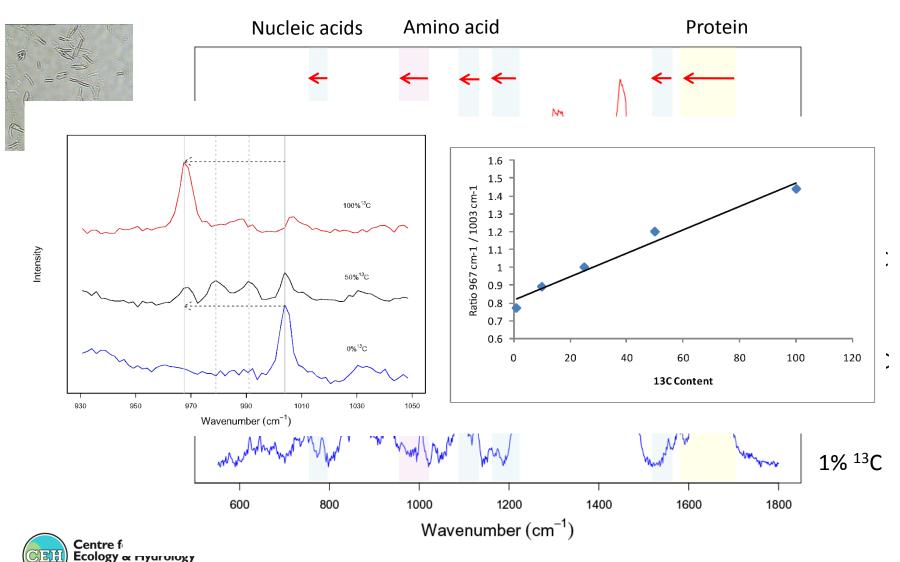






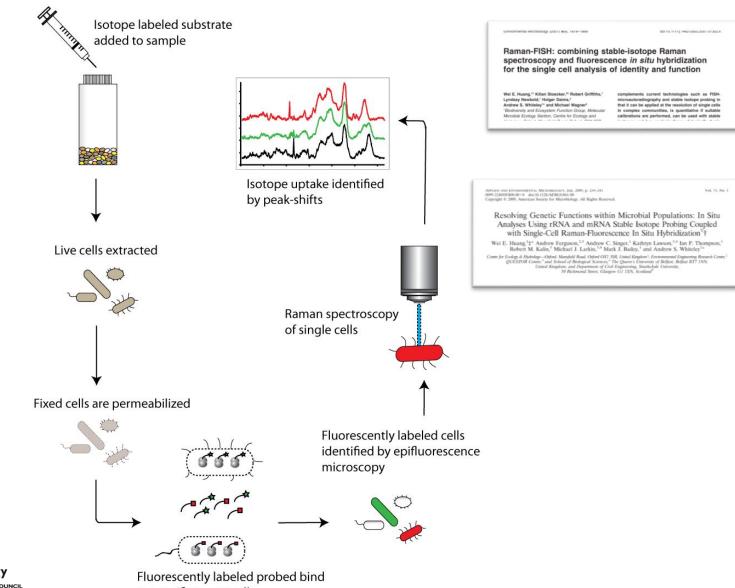
How?: Microbial function

Escherichia coli



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How?: Microbial function (Raman-FISH)



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to specific target cells

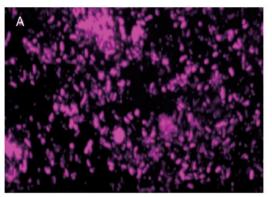
How?: Microbial function (Raman-FISH)

SEquenced REactive BARrier (SEREBAR)

- •Former manufactured gas plant (FMGP) in the United Kingdom
- •Groundwater polluted with Polycyclic Aromatic Hydrocarbons (PAHs) including Naphthalene

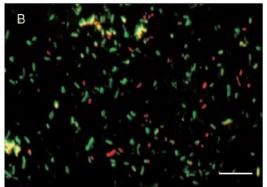


- •RNA Stable Isotope Probing using ¹³C labelled Naphthalene in microcosms
- •Identified *Pseudomonas* sp. and *Acidovorax* sp. as main naphthalene degraders
- •Acidovorax sp. unculturable
- •Raman-FISH approach

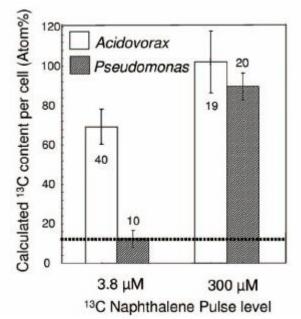


EUB338 (general bacteria)





Acidovorax sp. **Red** Pseudomonas sp. **Green**



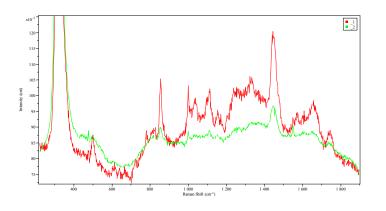
Huang, W. E., Stoecker, K., Griffiths, R., Newbold, L., Daims, H., Whiteley, A. S., & Wagner, M. (2007). Raman-FISH: combining stable-isotope Raman spectroscopy and fluorescence in situ hybridization for the single cell analysis of identity and function. *Environmental Microbiology*, 9(8), 1878-1889

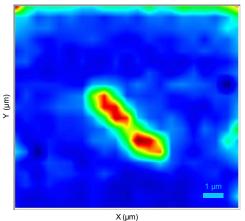
Where?: Raman mapping



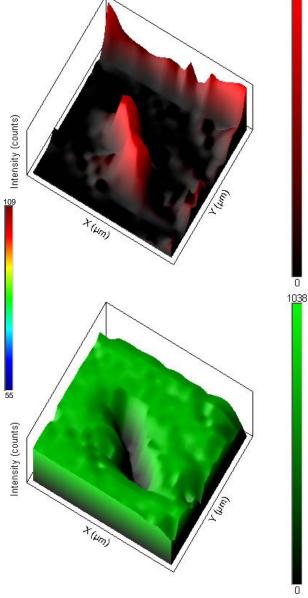
Single Escherichia coli

- Mapped over 20x20 grid
- 0.5µm between each point
- ~400 spectra





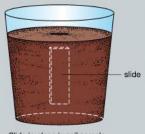
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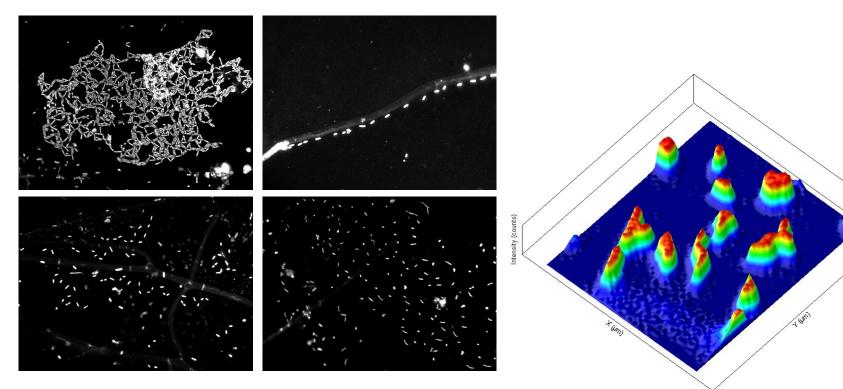
1038

Where?: Raman mapping

DIRECT MICROSCOPIC AND BACTERIOLOGICAL EXAMINATION OF THE SOIL GIACOMO ROSSI ASSISTED BY S. RICCARDO, G. GESUË, M. STANGANELLI, AND TSU KAO WANG Royal Higher Agricultural Institute, Portici, Italy Received for publication May 29, 1935

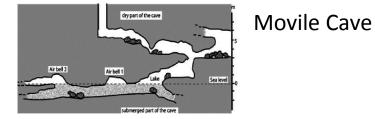


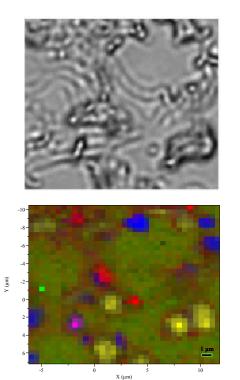
Slide in place in soil sample



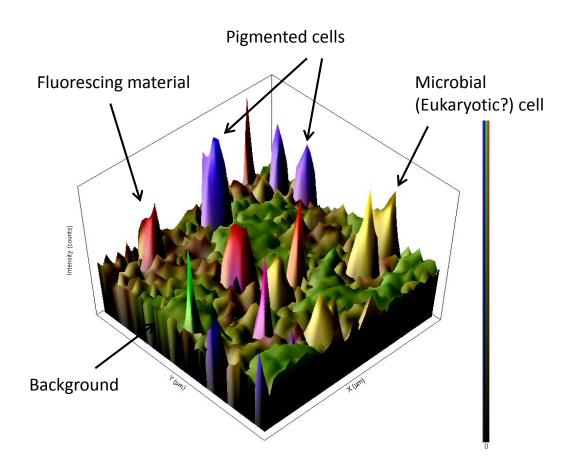


Where?: Raman mapping









Acknowledgements: Dr Wei Huang (University of Sheffield) Prof Andrew Whiteley (CEH Wallingford) Dr Sam Sheppard (University of Oxford) Dr Dan Woodcock (University of Warwick) Mr Simon Fitzgerald (Horiba Scientific) Molecular Microbial Ecology Group (CEH Wallingford)

THANK YOU

Any Questions?...

