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Tracking markers of contamination from cowpat runoff

Megan Devane
Environmental Science and Research Ltd. (ESR)

Te Waihora Living Lake Symposium, 9-10 November 2017, Lincoln University




Why are we interested in tracking the markers of faecal contamination from cowpat runoff?

During water quality monitoring, elevated levels of the faecal indicator bacterium, *Escherichia coli*, identify waterways where faecal inputs are occurring.

- ▶ Identification of elevated levels of *E. coli* provides no understanding of the **type of faecal pollution**, and therefore, it is imperative to **confirm the source of faecal pollution** to determine the likely **health risks to the public**.
- ▶ **Faecal source tracking** is important for the identification of sites where mitigation is required to reduce the impacts of faecal contamination.
- ▶ The effects of aged faecal material entering waterways may impact the tools we use to investigate the sources of faecal contamination.


Objective of this research

- ▶ Determine if changes in the bacterial community within the decomposing cowpats undermines the identification of faecal sources in the farm setting




Key messages

- The cowpat environment enhances *Escherichia coli* persistence.
- There are changes in the bacterial community of the cowpat as it decomposes on the field. These changes impact the detection of the markers we use to determine the source of faecal contamination.
- In contrast to *E. coli*, the bacterial groups which target the **faecal source tracking (FST)** markers decrease in abundance as cowpats decompose on the field.
 - When identified in a waterway, the cow specific genetic marker is an indicator of relatively fresh bovine faecal contamination.




Stirring up the cow faecal slurry to make simulated cowpats
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Methods

Investigated the mobilisation of FST markers & *E. coli* from cowpats under two conditions:

- the effects of flood resuspension of cowpats
- and rainfall runoff from cowpats



Rainfall simulator
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Faecal Source Tracking (FST) markers

Genetic markers :
(based on the Polymerase Chain Reaction = PCR)

- ruminant, and cow specific

Microbial indicators

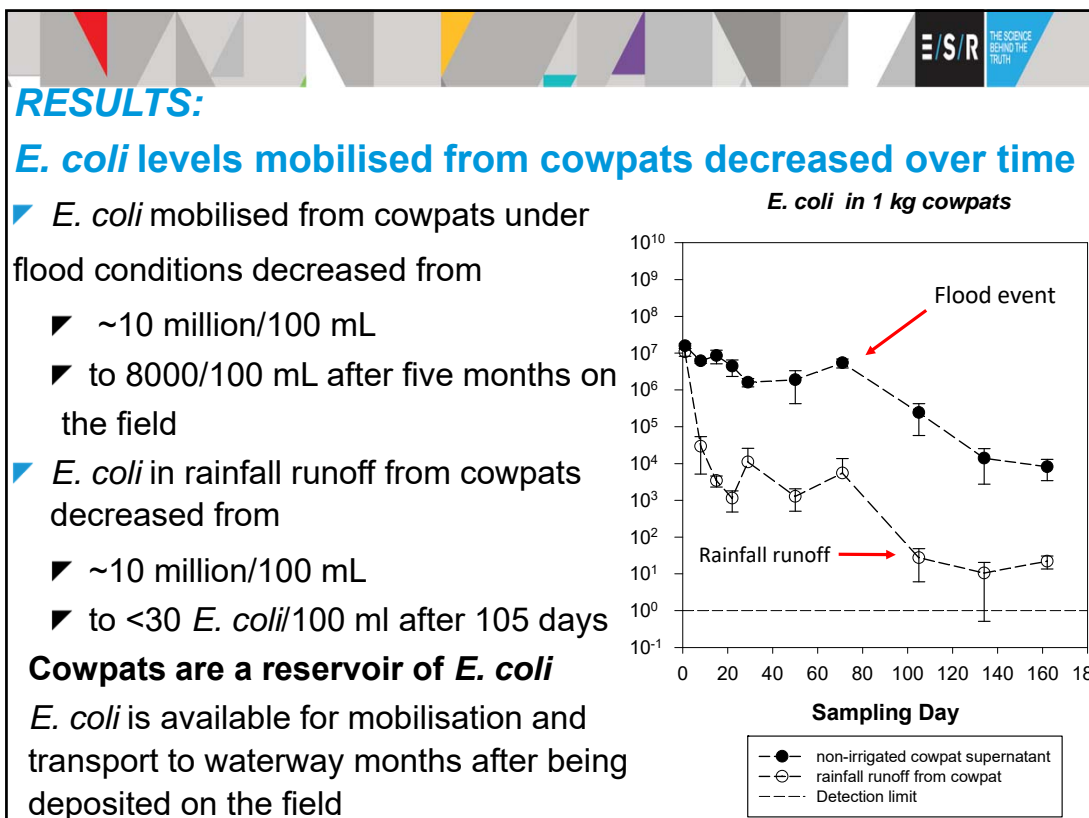
- *Escherichia coli*
- Bacterial community analysis
(sequencing the genetic material (DNA of the bacterium))

Sampling regime

- 10 sampling events over 5½ months
- Weekly for first four weeks, at the six week mark, then monthly

Triplicate samples of cowpat runoff analysed for all assays

Measured temperature and moisture content in the cowpats, and rainfall and sunlight parameters





Genetic faecal source tracking markers

Ruminant marker (cows, sheep, deer, goats)
in flood event : still detected after five months
in rainfall runoff : below detection after 42 days

In comparison,

Cow marker
in flood events: not detected after **Day 50**
in rainfall runoff: not detected after **Day 22**

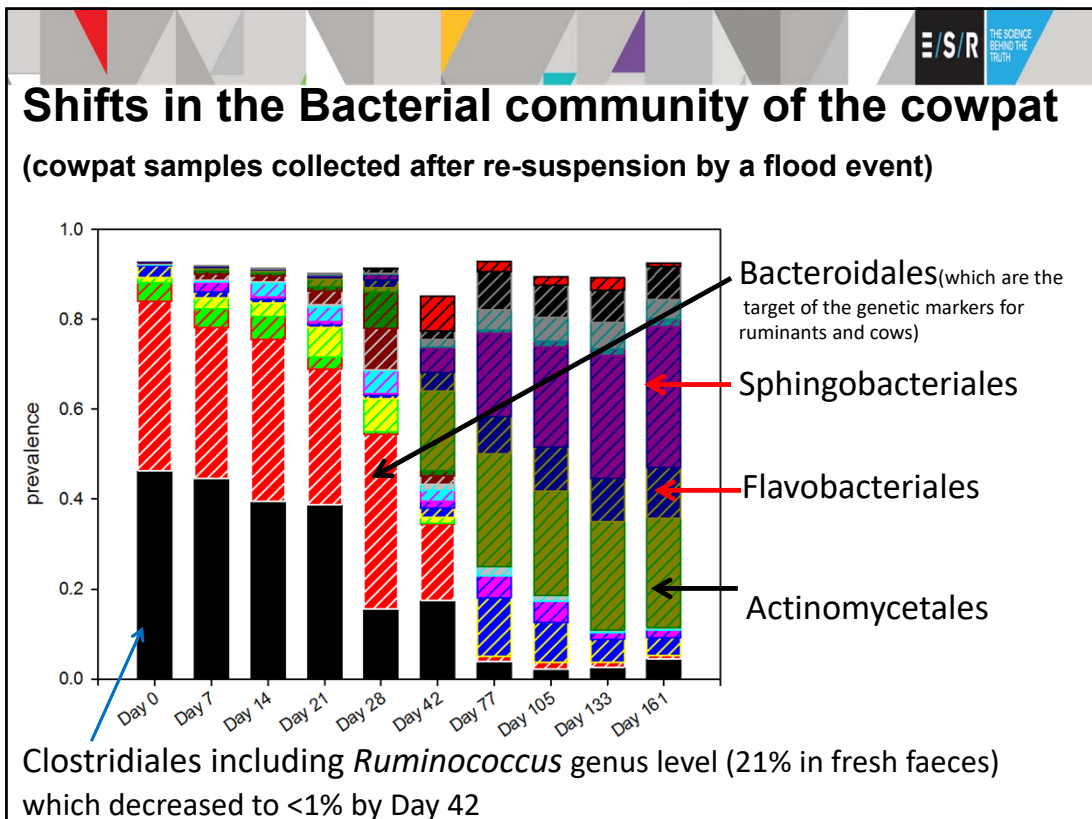
Genetic markers are less persistent in the environment compared with *E. coli*
 Cow specific genetic marker is an indicator of relatively fresh pollution runoff when detected in a waterway

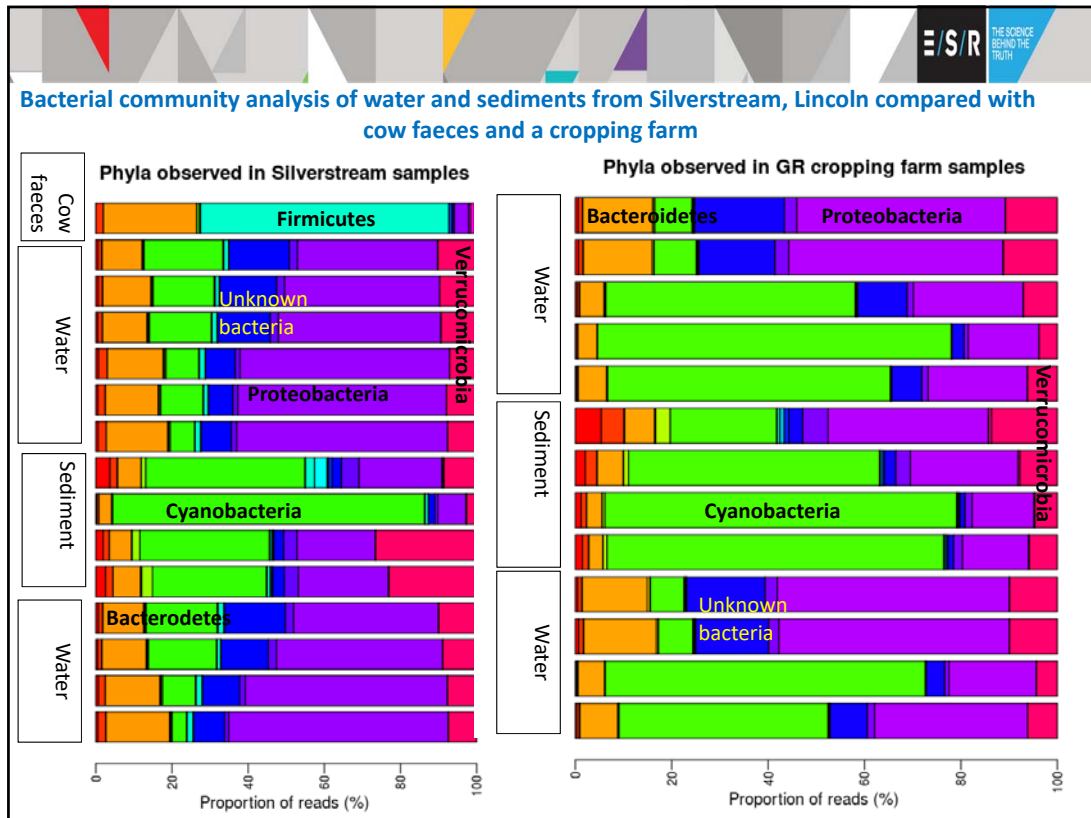


Cowpat after five months on the field

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Implications for this research on tracking the sources of contamination from decomposing cowpats

Informs our work on faecal source tracking and the **stability of the markers** we use to determine sources of faecal inputs.

Contributes to knowledge about:

- the **selection of appropriate FST markers** for monitoring the decline of faecal runoff following remediation efforts to mitigate effluent/faecal inputs.
- the **quantitative assessments by genetic markers**, which enable **monitoring of the reductions in faecal loading** from ruminant pollution once mitigations such as sediment traps have been put in place.
- dairy shed effluent
 The high numbers of FST genetic markers and *E. coli* indicators observed in this study (10^7 - 10^{10} /100 mL⁻¹) in the re-suspensions of fresh faeces (aka the flood event) are reflective of the high concentrations of indicators that could be expected in daily dairy shed effluent.
- the parameters generated for the decline in mobilisation of FST markers and *E. coli* from cowpats over time. These **parameters can be fed into modelling tools** that characterise the faecal microbial contributions from farming: e.g.
 - 1) the burden of *E. coli* and its decay in ageing cowpats
 - 2) the transfer of faecal pollution to water by overland runoff mechanisms.



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- **MBIE: Ministry of Business Innovation and Employment**
- **Waterways Centre for Freshwater Management : Jenny Webster-Brown**
- **Dept. of Conservation and Living Waters**

ESR staff

- **Brent Gilpin, Beth Robson**
- **David Wood, Susan Lin**
- **Phil Abraham, Erin McGill**
- **Margaret MacKenzie, Paula Scholes**



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