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# How can we use faecal source tracking as a tool to evaluate potential backup water resources?

Recent arid summers in Sweden has emphasised the need for a higher redundancy in drinking water production. One solution may be a completely new backup water resource.

## CONCLUSIONS

- Even though the presence of several potential source of fecal contamination a very limited level of contamination was detected.
- Fecal contamination from sewage and wild birds were detected.
- The source tracking results agreed with the levels of faecal indicator bacteria.
- A combination of indicator analysis and faecal source tracking may facilitate the selection of a suitable backup water resource.

## AIM

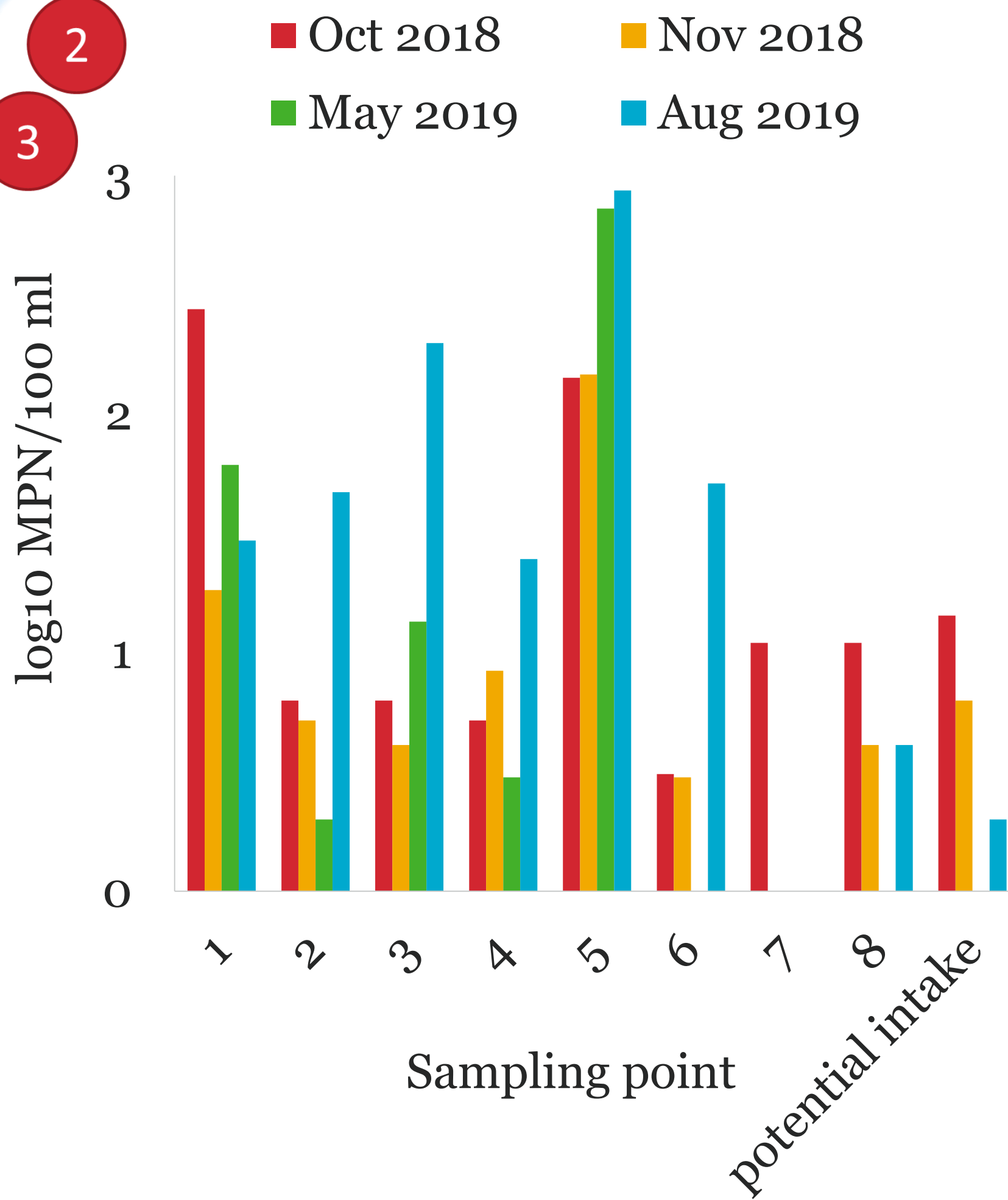
To investigate the water quality in a possible backup water resource and to evaluate the use of faecal source tracking as a tool for investigating the potential impact from effluents, agriculture and wildlife.

## RESULTS

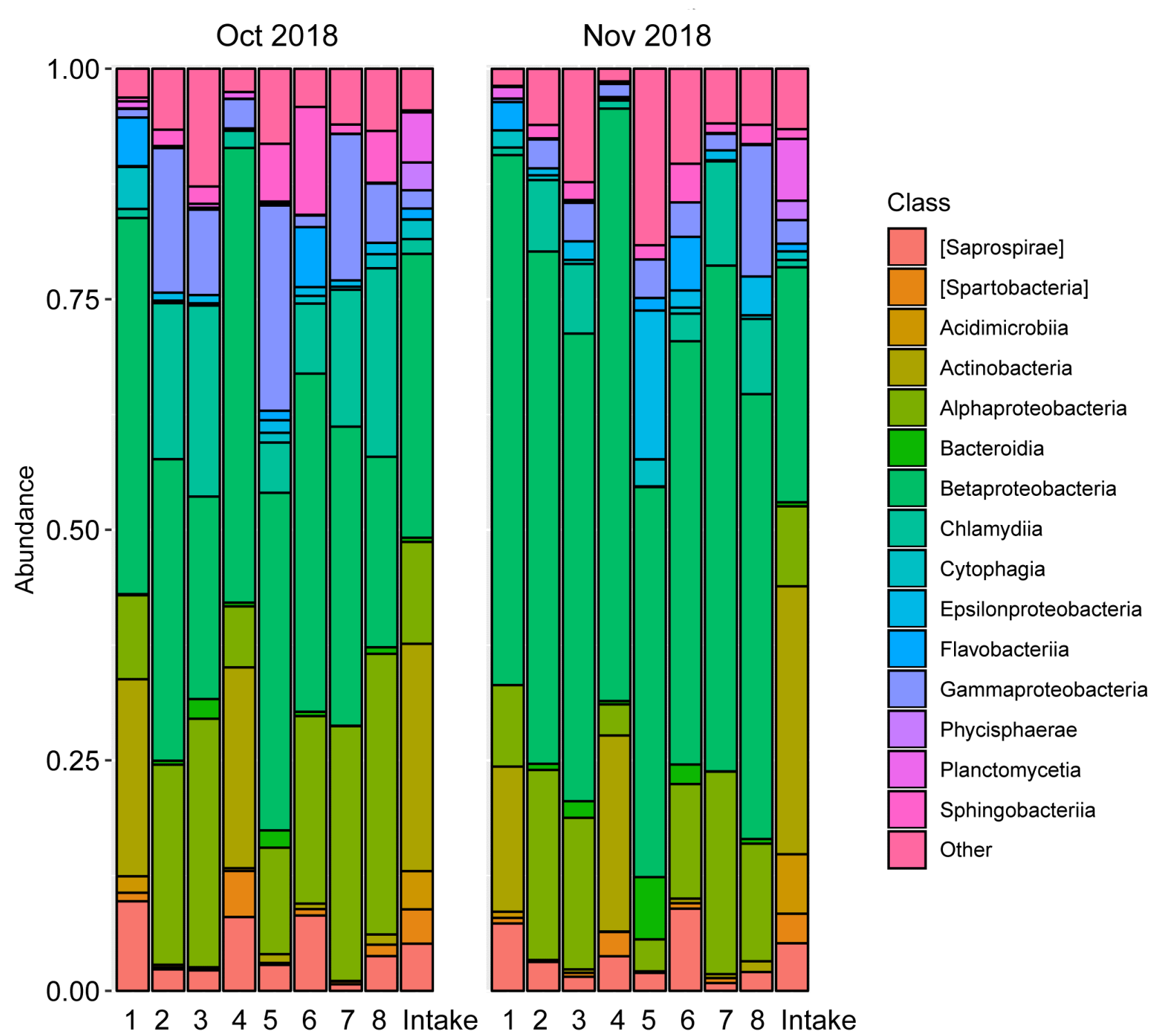
- Indicator analysis shows a relatively low level of contamination.
- In general, indicator analyses shows a slightly higher level of contamination in August and a lower in May.
- Sampling point 5 consistently showed relatively high indicator levels.
- Faecal pollution in sampling point 5 is ascribed to sewage and wild birds.
- The potential raw-water intake remains relatively unaffected and no faecal sources was detected.



*E. coli* levels



Taxonomic composition\*



\* Samples collected during 2019 remains to be analysed

Faecal source-tracking sampling point 5 \*

| Source        | Proportion |          |
|---------------|------------|----------|
|               | Okt 2018   | Nov 2018 |
| Calf          | n.d.       | n.d.     |
| Cow           | n.d.       | n.d.     |
| Dog           | n.d.       | n.d.     |
| Domestic bird | n.d.       | n.d.     |
| Horse         | n.d.       | n.d.     |
| Pig           | n.d.       | n.d.     |
| Sewage        | 0.015      | 0.28     |
| Sheep         | n.d.       | n.d.     |
| Wild bird     | 0.085      | n.d.     |

n.d. source not detected

## STUDY-SETUP

1. Mapping of potential contamination sources in main catchment area based on public records and observation on site.
2. Sample collection from 8 inflows and at the potential raw-water intake (located in the northern part of the lake) at four occasions during the period of October 2018 – August 2019.
3. Analyses
  - microbial indicators (total coliforms, *E. coli*, *Clostridium perfringens* and *Enterococcus* spp.)
  - selected chemical parameters (not presented)
  - faecal source tracking

**Faecal source-tracking** was performed using a library-dependent amplicon-sequencing technique targeting the V3-V4-region of the 16S rRNA gene. The library is based on 158 samples, including eight animal sources, representing typical contaminating sources of Swedish fresh water. The within-source variation in taxonomic composition of the samples included in the library was much smaller than the between source variation, which enables the use of the library to track contaminating sources in the tested water samples.

