

Distribution of pathogens and antibiotic resistance genes in the vadose zone of soil-aquifer treatment (SAT) system.

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Background:

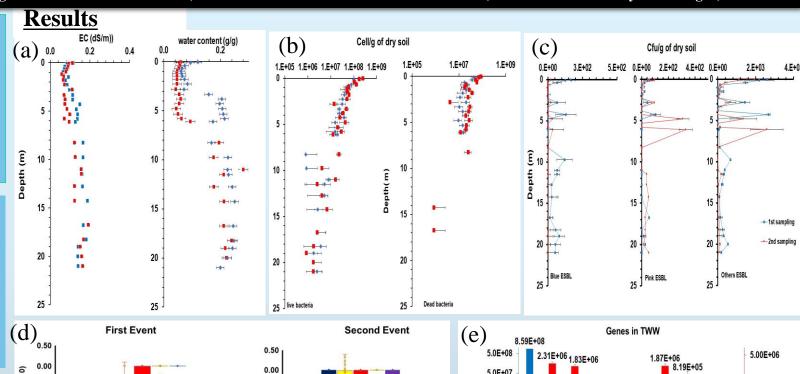
- ➤ Soil Aquifer Treatment (SAT) System.
- > Relies on Percolation and adsorption.
- > Deep layer pathogens viability not really explored.
- ➤ Hypothesis: Pathogens' distribution in the soil profile of the SAT will be mainly governed by the water quality of the recharged Treated Wastewater (TWW) and flooding and drainage/drying cycles of the infiltration basin.

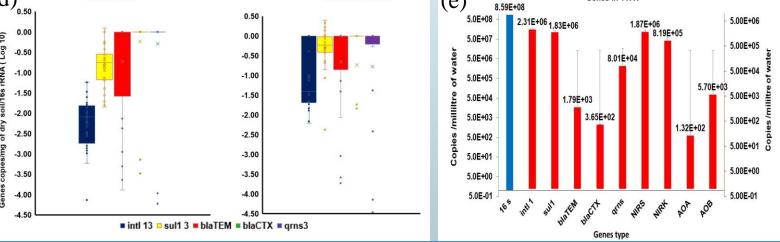
Methodology:

- ➤ Soil profile sampling (20 m) of TWW infiltration basin at the end of flooding and after 3 days of drainage/drying
- ➤ Live/Dead Count. Fluorescence Microscopic
- ➤ Viable Plate count. for total, E.coli and ESBL
- ➤ Enzyme Activity FDA Hydrolysis and spectrophotometer
- ➤ DNA extraction and Quantitative PCR

Conclusions:

- 1. A high prevalence of *Klebsiella sp. and E. coli*, followed by other bacteria, was observed among ESBL isolates.
- 2. High concentration of pathogens in the topsoil layers and a gradual decline with depth.
- 3. Dominating *intl1* in TWW and *Sul1* in soil samples, gene implying on anthropogenic pollution.





Figures: (a) EC and water content, (B) Plate viable bacterial count, (c) live/Dead bacteria, (d) genes in soil, and (e) genes in TWW.