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Distribution Of The Aquaponics Microbiome And Their Division Of Labor

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Distribution Of The Aquaponics Microbiome And Their Division Of Labor

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Background

Farming practices have always been labor intensive and required a great deal of resources including space, nutrients, heavy equipment, and a great deal care. Aquaponics seeks to ameliorate this by delegating the majority of tasks to microbes and plants, which regulate minerals, nutrients, and toxins in a circulated system.

Hypothesis

- Microbial distribution will correlate directly with their intended chambers as result of continuous successful plant growth.
- NO_2 , NH_3 , and NH_4 compositions will vary greatly tank by tank with significant fluctuations after the microbial farming chamber and the water table.

Methods

•16Sr RNA Analysis:

Water samples were taken across 5 sites (Fig 1) at 8 inches from the surface of each sample site. DNA from each samples were extracted, washed, and cleaned for PCR DNA amplification of the 16s rRNA gene. Amplified DNA was modified into the pGEM-T vectors and introduced into live *E.coli* cells. Successful transformation is indicated via color change of colonial growth by the x-gal indicator (Fig 3) located on the pGEM-T plasmid. Successful colonies (8 per site) were sequenced and the greatest two 16s rRNA matches in the BLAST database were recorded (Fig 4)

•Nitrate-Nitrite-Ammonia Analysis:

Water samples were taken at across 5 sites (Fig 1) 8 inches from the surface and analyzed for nitrate, nitrite, and ammonia via IPA color indicator water test kits. Concentrations (ppm) of the chemical compounds were analyzed with a spectrophotometer and absorbances were compared with known standards.

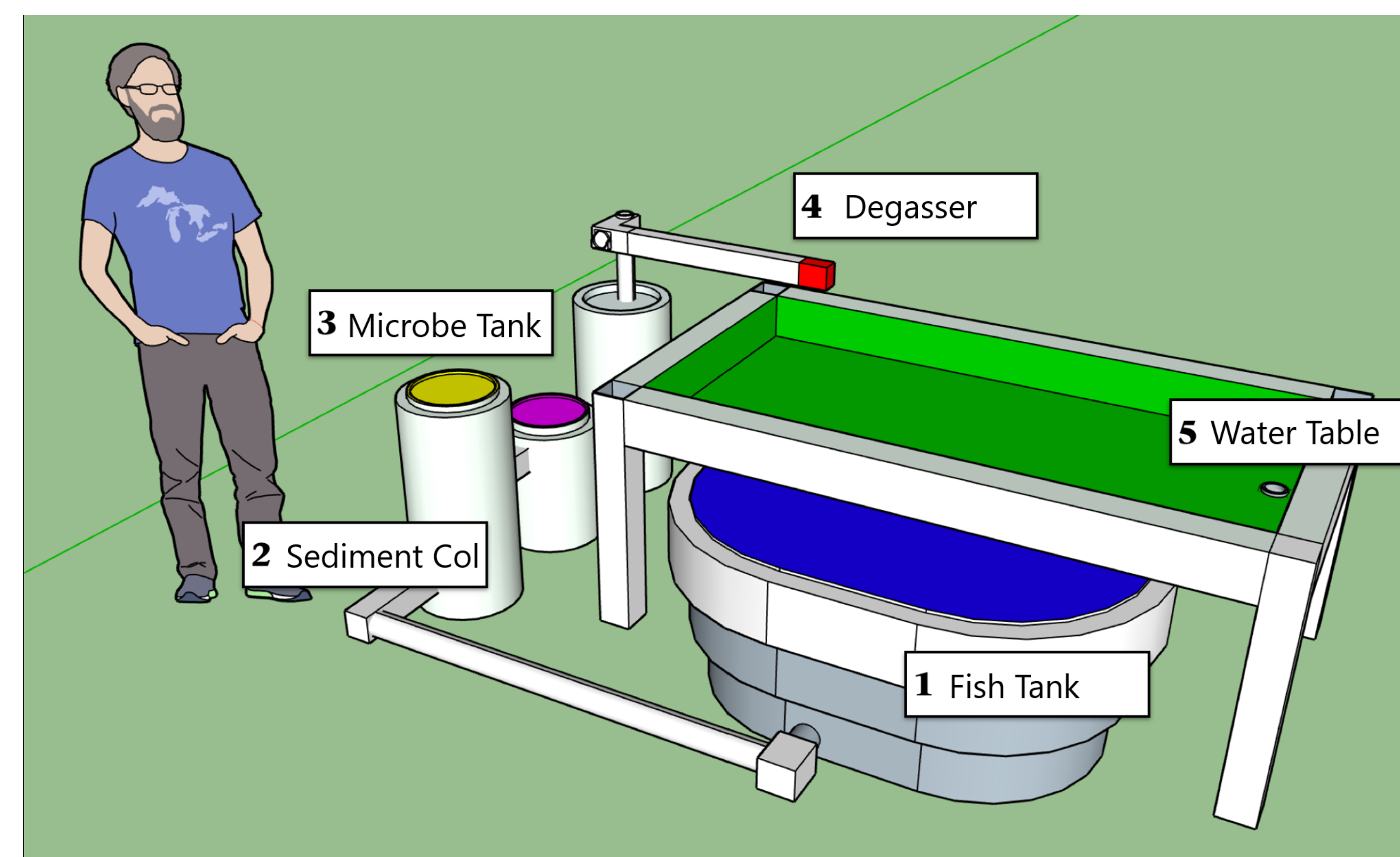


Figure 1. 3D rendering of Gorham aquaponics table of study with experimental site locations and their intended function and color (1-5). Man for scale.

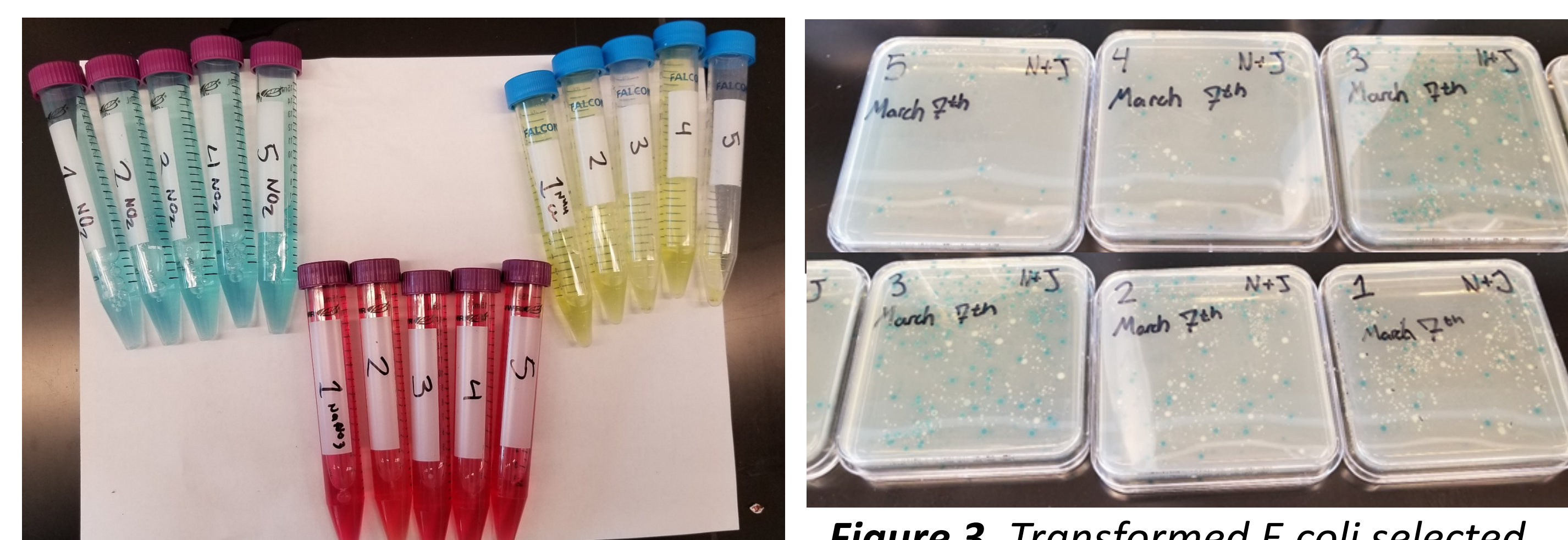


Figure 2. Nitrate(left), Nitrite(middle), and Ammonia (right) concentrations measured using IPA color indicator test kit.

Figure 3. Transformed *E.coli* selected for successful plasmid introduction via X-gal color indicator. Colonies white in color indicate success, blue indicates failure.

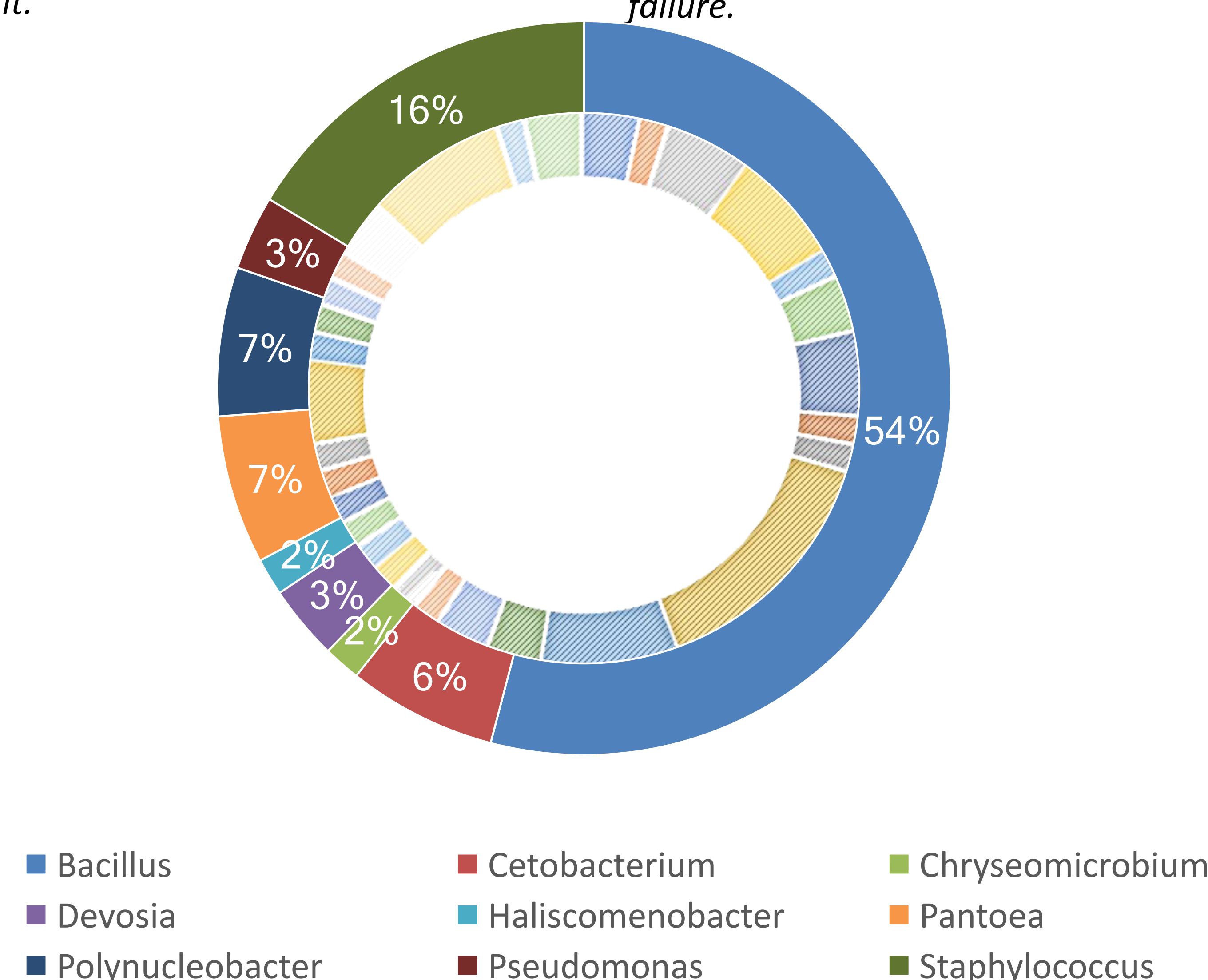


Figure 4. Microbial distribution of genus (solid outer ring) and species (patterned inner ring) observed using 16SrRNA sequencing of 8 samples per sites 1-4. Species list legend not publish for brevity.

Results

16S rRNA Analysis:

- No participants within the nitrogen cycle were observed to be present.
- Site 5 was not sequenced as no successful transformation events had occurred. Time did not permit retrials.
- The frequently observed bacteria was *Bacillus* with significant variety at the species level (Fig 4).
- All 16s rRNA results achieved a BLAST match of 95% or greater at the genus level. No results were taken below 90%.

Nitrate-Nitrite-Ammonia Analysis:

- NO_2 , NH_3 , and NH_4 concentrations differed immeasurably between the sites.
- Average PPM concentrations; NO_2 :1ppm, NH_3 :75ppm, and NH_4 <1ppm

Conclusions

16S rRNA Analysis:

- Lack of bacteria participating in the nitrogen cycle is likely due to sample acquisition methodology. Our methodology only observes microbes suspended in the water. Microbes attached to a biofilm or firmly fixed to a surface is likely to be responsibly for nutrient cycling.

Nitrate-Nitrite-Ammonia Analysis:

- The even distribution of nitrogen formations throughout each stage of the system is likely indicative of a high flow system or total water volume far exceeding the total nutrients contained within the system.

Acknowledgements

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References

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