

## Meat Processing Wastewater Valorised through Microalgae Production

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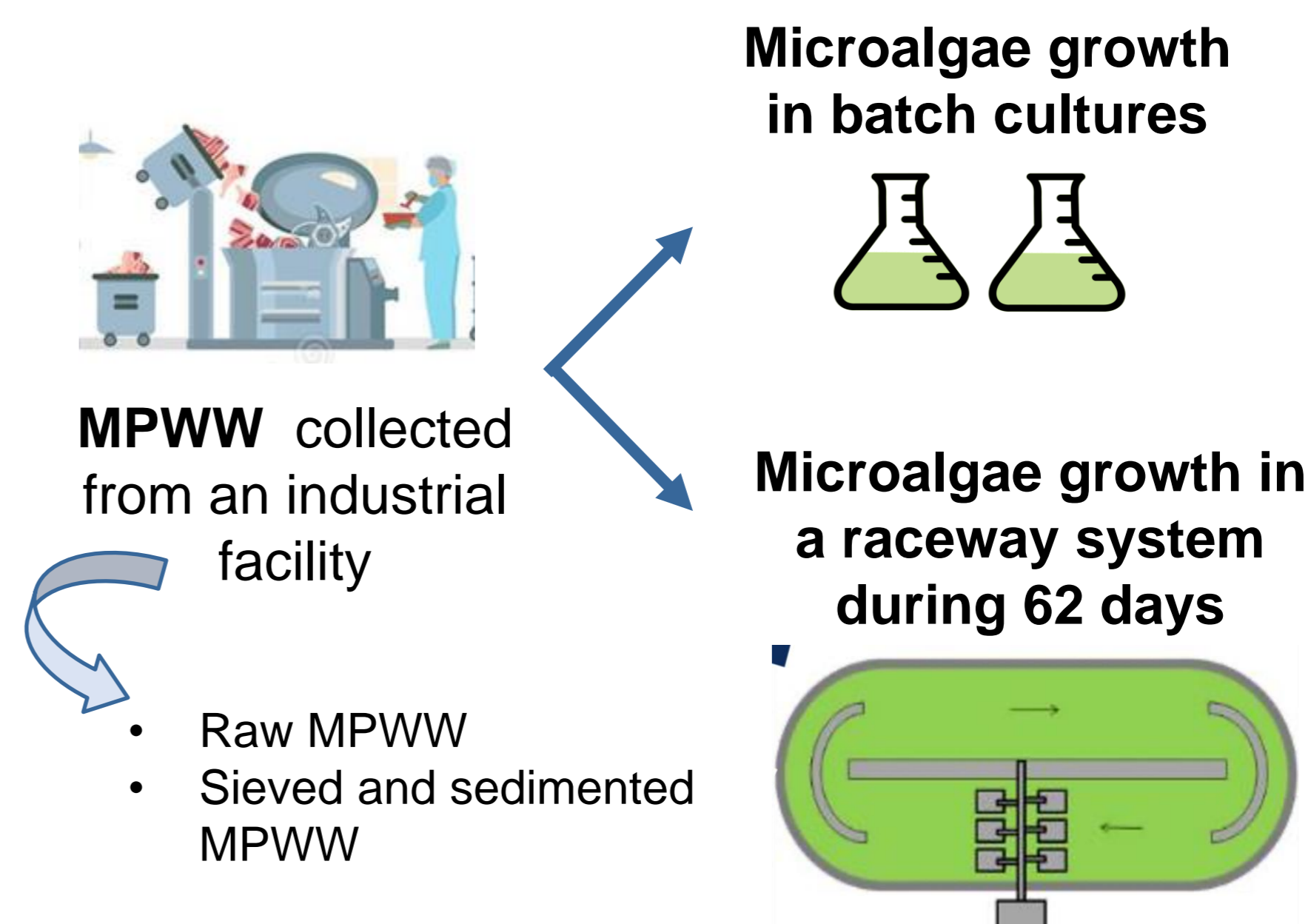
### INTRODUCTION & AIM

The treatment of meat processing wastewater (MPWW) is crucial to mitigating its environmental impact but remains challenging due to its high organic load and elevated nitrogen and solids content.

Microalgae-based processes have been used to treat various types of wastewater, including municipal and industrial sources, offering a sustainable approach that not only cleans wastewater but also produces valuable biomass.

This work aims to evaluate the feasibility and scalability of microalgae-based processes for treating and valorising real MPWW with variable composition in a fed-batch raceway reactor, while exploring the synergistic microbial interactions within the system.

### METHODOLOGY



### RESULTS & DISCUSSION

#### Microalgae growth in batch cultures

	COD removal rate (mg L <sup>-1</sup> day <sup>-1</sup> )	[Maximum pigments] (µg mL <sup>-1</sup> )
Raw WW	828.5±60.5	1.92 ± 0.68 (on day-10)
SS-MPWW	1097.5±22.2	1.96 ± 0.27 (on day-6)

- The use of sieved and sedimented MPWW facilitates COD removal and microalgae growth.

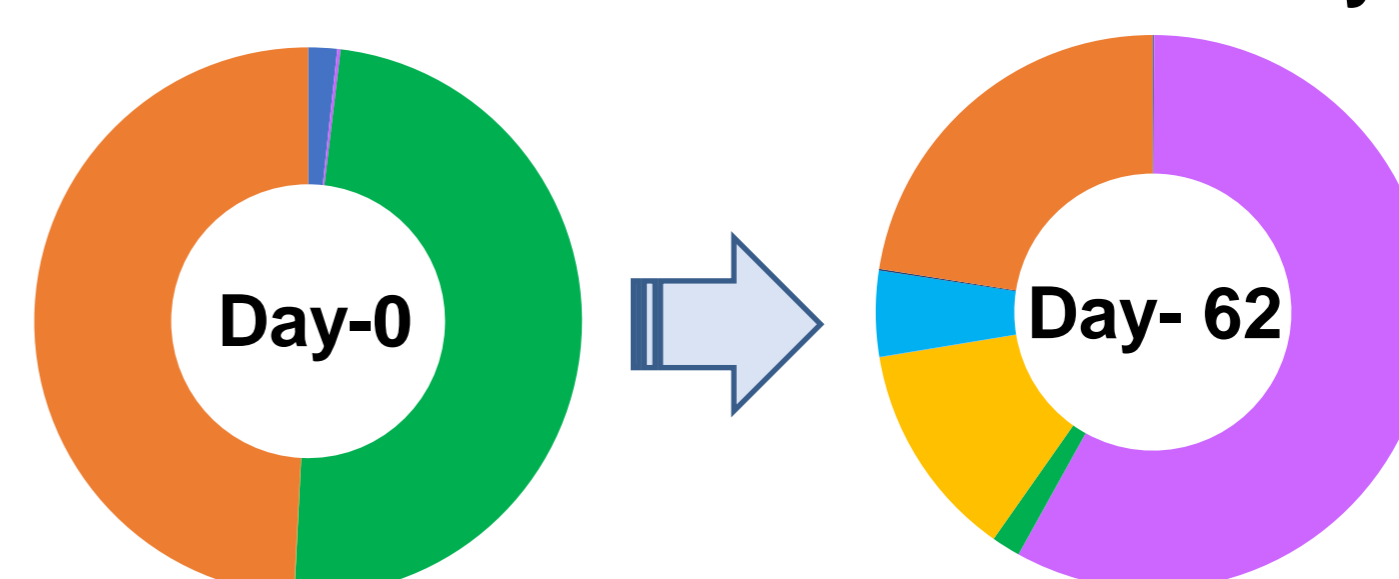
#### Microalgae growth in a raceway under fed-batch mode

Fed-batch cycle	COD <sub>soluble</sub> (mg O <sub>2</sub> L <sup>-1</sup> )	COD removal rate (mg L <sup>-1</sup> day <sup>-1</sup> )	COD removal efficiency (%)	[Total pigments] concentration (µg mL <sup>-1</sup> )
I	6054.1	685.3 ± 6.31	90.6 ± 0.8	0.40
II	6857.1	321.4 ± 0.0	72.2 ± 0.8	1.80
III	5565.2	181.3 ± 7.4	65.2 ± 2.7	1.46
IV	9369.4	806.3 ± 0.0	87.0 ± 0.0	8.49
V	8771.9	351.8 ± 15.3	73.1 ± 3.2	9.00
VI	8301.9	566.0 ± 0.0	76.1 ± 0.0	13.4
VII	7924.5	237.2 ± 15.3	66.7 ± 4.3	17.9

In each fed-batch cycle, SS-MPWW with different composition was added

- Despite variable wastewater composition, COD removal occurred in each fed-batch cycle, albeit at different rates.
- Increase of the photosynthetic pigments' concentrations over operation.

#### Biomass microbiome evolution in the raceway system



- d\_Eukaryota;
- p\_Perclozoa; c\_Heterolobosea\*
- k\_Plantae; p\_Chlorophyta; c\_Trebouxiophyceae
- k\_Fungi; p\_Basidiomycota; c\_Tremellomycetes; o\_Trichosporonales; f\_Trichosporonaceae
- k\_Fungi; p\_Ascomycota; c\_Leotiomycetes; o\_Thelebolales; f\_Thelebolaceae
- k\_Fungi; p\_Ascomycota; c\_Saccharomycetes; o\_Saccharomycetales; f\_Dipodascaceae
- k\_Fungi; p\_Zygomycota; c\_Mucoromycotina incertae sedis; o\_Mucorales; f\_Mucoraceae
- k\_Chromista; p\_Ciliophora; c\_Colpodea; o\_Colpodida; f\_Colpodidae
- k\_Plantae\*\*

The biomass microbiome, initially dominated by microalgae from the *Chlorophyta* and *Ciliophora* phyla, evolved to include other eukaryotic taxa (including yeast and fungi).

### CONCLUSIONS

The microbiome adaptability and its microbial diversity appeared to be a key driver in enhancing biological removal processes in the raceway system.

This work advances microalgae-based processes for treating and valorising MPWW by highlighting microbial ecology's role in system resilience and efficiency and giving insights in process scalability, showcasing its robustness for real-world applications.

### ACKNOWLEDGMENTS

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