

VALORIZATION AND BIOREMEDIATION OF AGRO-INDUSTRIAL WASTEWATER THROUGH ADVANCED BIOTECHNOLOGICAL PROCESSES

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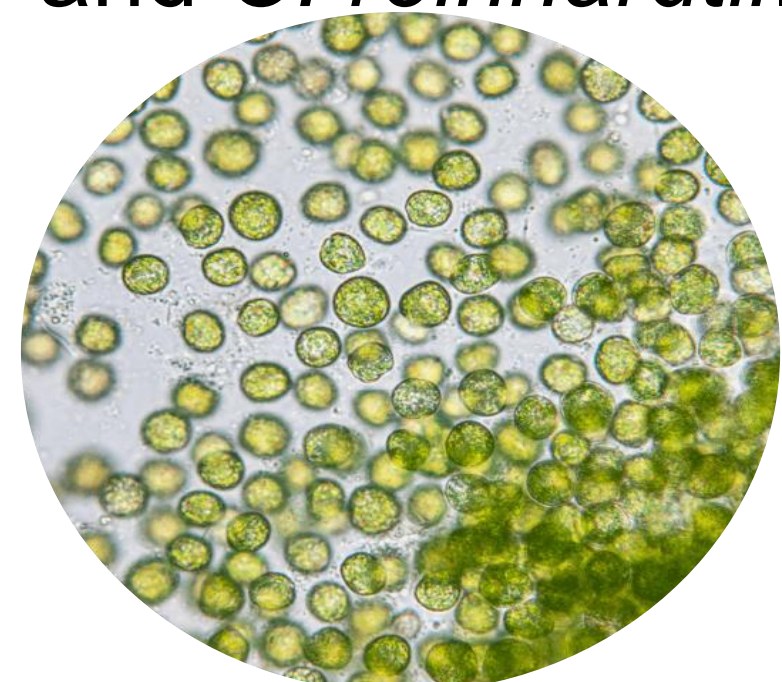
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INTRODUCTION

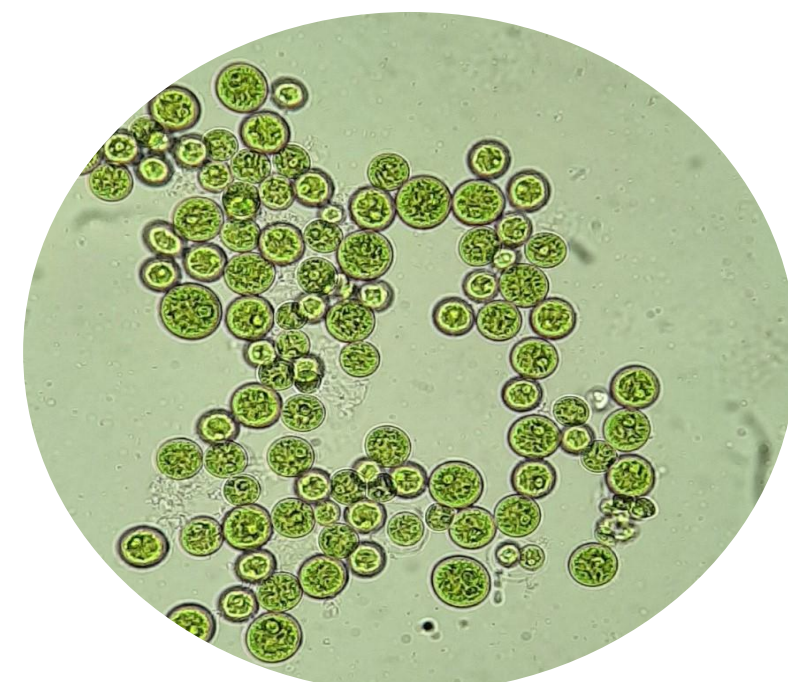
One of the most significant global challenges is the limited availability of water. To overcome this problem, untreated wastewater is used [1]. Pollution from phosphates, nitrates, and organic contaminants threatens human health and the integrity of ecosystems; however, conventional treatment methods are often costly and prone to the production of secondary pollutants [2]. In recent years, scientific research has conducted significant studies on bioremediation, identifying the use of microalgae, photosynthetic eukaryotic unicellular organisms, as one of the most promising strategies [3]. Thanks to their ability to metabolize nutrients present in wastewater to produce commercially valuable biomass, microalgae embody the principles of the circular economy, transforming waste into a resource [4]. The success of this process, however, depends on the identification of highly resilient strains capable of processing complex waste matrices [5].

METHODS

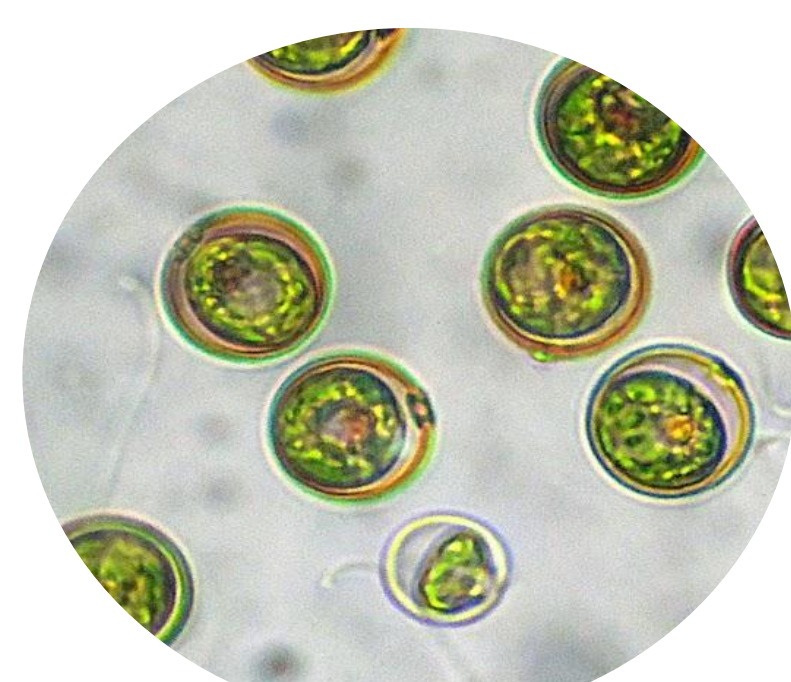
The microalgae strains identified are *C. vulgaris*, *C. reinhardtii*, and *H. pluvialis*. To enhance metabolic efficiency and stress resistance, a somatic hybrid was generated between the C1 strain of *C. vulgaris* and *C. reinhardtii*.



C. vulgaris



H. pluvialis



C. reinhardtii

The experimental phases included:

- ❖ **Selection and Selection Pressure:** Use of wastewater from the processing of tomatoes, lentils, and chickpeas as a growth medium.
- ❖ **Isolation:** Plating on solid medium to identify adapted colonies and subsequent steps to obtain pure lines.
- ❖ **Mutant Screening:** Selection of three mutants for each type of wastewater.
- ❖ **Growth Monitoring:** Evaluation of cell density at predetermined intervals to define growth curves.
- ❖ **Molecular Analysis:** Extraction of high-quality DNA and RNA for subsequent genetic and transcriptomic profiling.

REFERENCES

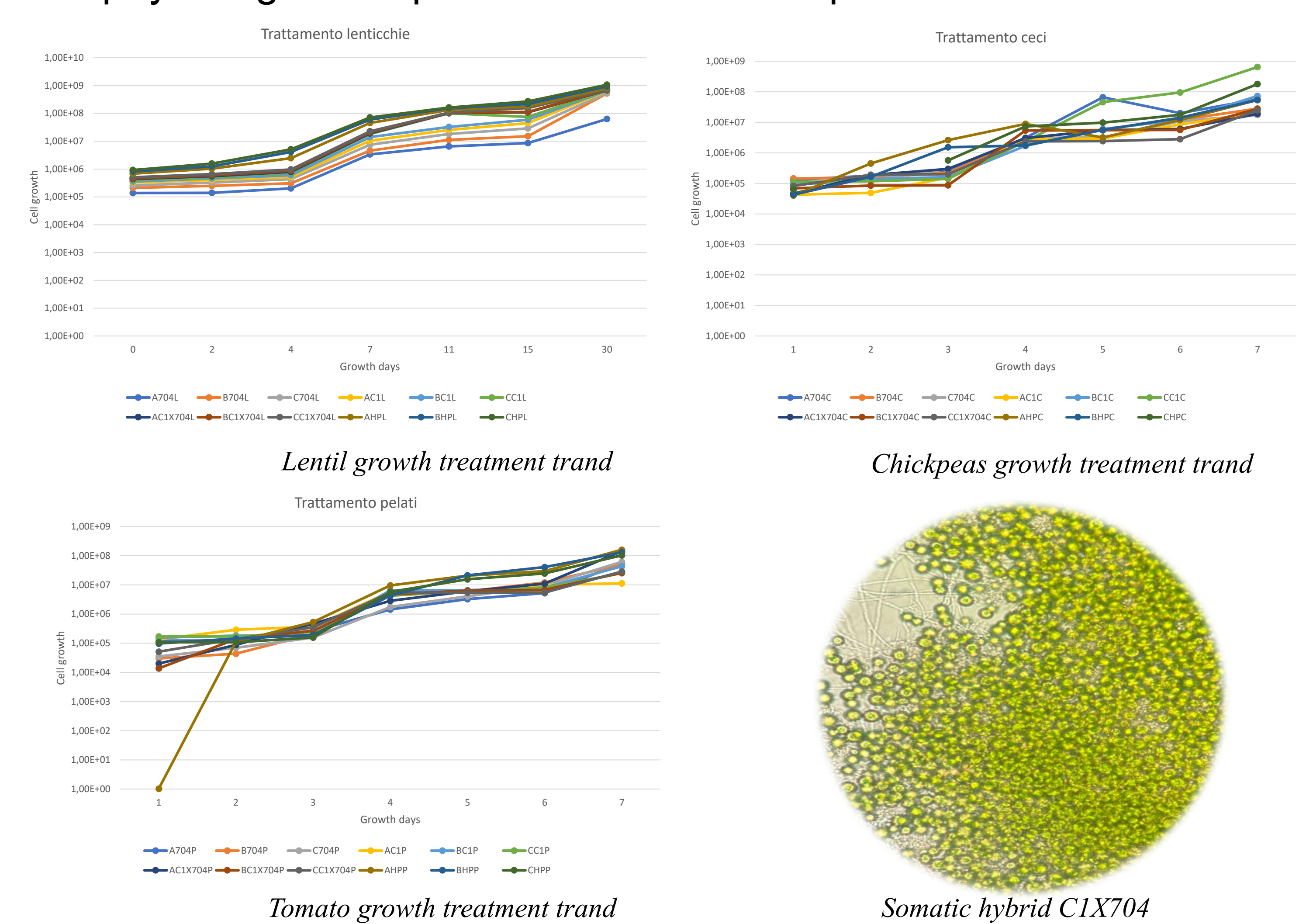
- [1] A. D. M. Satya *et al.*, *Environ. Res.*, **vol. 218**, September 2022, 114948, (2023). [2] C. M. Bellido-Pedraza, M. J. Torres, and A. Llamas, *Cells*, **vol. 13**, (2024). [3] S. S. Ali and L. H. S. Hassan, *Arch Microbiol*, **vol. 343**, (2024). [4] P. Wu, Z. Zhang, Y. Luo, Y. Bai, and J. Fan, *BITE*, **vol. 350**. 126930, (2022). [5] V. Mariyappan, C. Yu, W. Wu, and J. Chang, *Bioresour. Technol.*, **vol. 393**, November 2023, 130134, (2024).

ACKNOWLEDGEMENTS



RESULTS

The mutants exhibit a higher growth rate and greater tolerance to wastewater-induced stresses, demonstrating a superior metabolic and physiological response to the selective pressure exerted.



Furthermore, the mutants clearly demonstrate a greater ability to utilise the nutrients present in the wastewater. The optimisation of DNA and RNA extraction protocols has yielded valid genetic material that is ideal for furthering genomic and transcriptomic studies

CONCLUSIONS

The collected data indicate that the selected mutants exhibit superior performance compared to wild-type strains. Specifically, the mutants exhibited:

Higher growth rates and greater tolerance to biotic and abiotic stresses inherent in wastewater.

Optimized metabolic efficiency in nutrient uptake, confirming excellent adaptation to the agro-industrial matrices tested.

Optimized extraction protocols ensured genomic material suitable for advanced analyses. These data lay the foundation for future correlation studies between genetic distance, phytoremediation efficiency, and bioactive compound yield. In conclusion, These preliminary results lay the groundwork for the development of an integrated system combining wastewater treatment, resource recovery, and sustainable biomass production, opening up promising prospects for various applications in the biotechnology sector.



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