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Marked Inter- and Intraspecific Duckweed Diversity Enables Selection of More Suitable Genotypes for the Valorization of Raw Dairy-wastewater

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Effluents generated by the dairy sector constitute a nutrient-rich matrix with a significant environmental impact. Conventional treatments are generally energy-intensive and based on biological oxidation, leading to nutrient dissipation and secondary waste products. Phytoremediation emerges as a sustainable strategy for nutrient recovery and biomass production within a circular economy framework. Duckweeds are particularly attractive for these applications, and their nutritional properties open perspectives as feed supplements. Their remarkable biodiversity, characterized by extensive genetic variability, polyploidization and hybridization, translates into adaptability to heterogeneous aquatic environments. Such diversity likely corresponds to a wide spectrum of functional traits suitable to phytoremediation systems. This work explores the diversity of autochthonous (EU) duckweed clonal accessions sourced from the IBBA collection, representative of multiple taxonomic levels, including species from different genera, genotypes within the same species, allopolyploids and their parental species. Tested accessions were evaluated for their growth performance on dairy wastewater. Microbial community dynamics were also investigated in order to explore the contribution of cooperative plant-microbe interactions. Specific harsh growth conditions favoured certain species and clones over others, revealing large inter- and intraspecific variability. Two accessions emerged as the best-performing: *Lemna minor* (#5500) and its natural allotriploid *Lemna × mediterranea* (#LER0021). Further characterization of their physiological and biochemical traits, e.g. pigment and protein content, oxidative stress markers as well as nutrient depletion efficiency, revealed two distinctive eco-physiological strategies.

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References

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