From Ecology to Innovation: Unlocking the Biotechnological Potential of Algal–Microbial Interactions in two Azorean macroalgae

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Abstract

Marine macroalgae harbor diverse microbiota that modulate host physiology and mediate nutrient cycling, yet their functional potential remains understudied. Guided by this perspective, the present study investigates microbiomes on the invasive Azorean brown algae *Rugulopteryx okamurae* and *Sargassum* sp. to establish their microbial diversity and metabolic functionality. Community structure was resolved by Illumina MiSeq 16S metabarcoding, whereas functional capacity was profiled through 150 bp paired-end shotgun metagenomes processed with SqueezeMeta and annotated against COG and KEGG. Amino-acid transport and metabolism ranked first (2.6 M reads), supplying nitrogen assimilation and precursors for recombinant proteins and fine chemicals. Energy production and conversion (1.8 M) contained NAD-linked dehydrogenases essential for redox-balanced fermentations, while carbohydrate transport and metabolism (1.65 M) predominantly encoded TRAP and ABC transporter systems involved in the uptake of lignocellulose-derived sugars, consistent with functional requirements for biomass-based biorefinery applications. Inorganic-ion transport and metabolism (1.63 M) supported metal detoxification and recovery; The lipid metabolism category (0.63 M) included pathways directing fatty acid intermediates toward the biosynthesis of biodiesel precursors and polyhydroxyalkanoates (PHAs), highlighting their relevance to microbial biofuel and bioplastic production. Although lower in abundance, cellulose–hemicellulose degradation (53 k), alkane/hydrocarbon degradation (50 k), and PHA/PHB biosynthesis genes (5.9 k) provided routes for fibre hydrolysis, oil-spill remediation and biodegradable polymer production, respectively. Comparative analysis showed Sargassum sp enriched sugar-capture and secondary-metabolite genes, whereas *R. okamurae* favoured hydrocarbon catabolism and bioplastic formation, underscoring host influence on microbiome functionality. Altogether, algal-associated microbiota enable biomass conversion and product biosynthesis, making invasive macroalgae valuable biotechnological resources.

Keywords: Microbiota, Algae microbiome, Macroalgae, metagenomics, microbial diversity, marine biotechnology

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