

SELECTION AND CHARACTERIZATION OF NATURAL MICROBIOMES FOR POLYHYDROXYALKANOATES PRODUCTION

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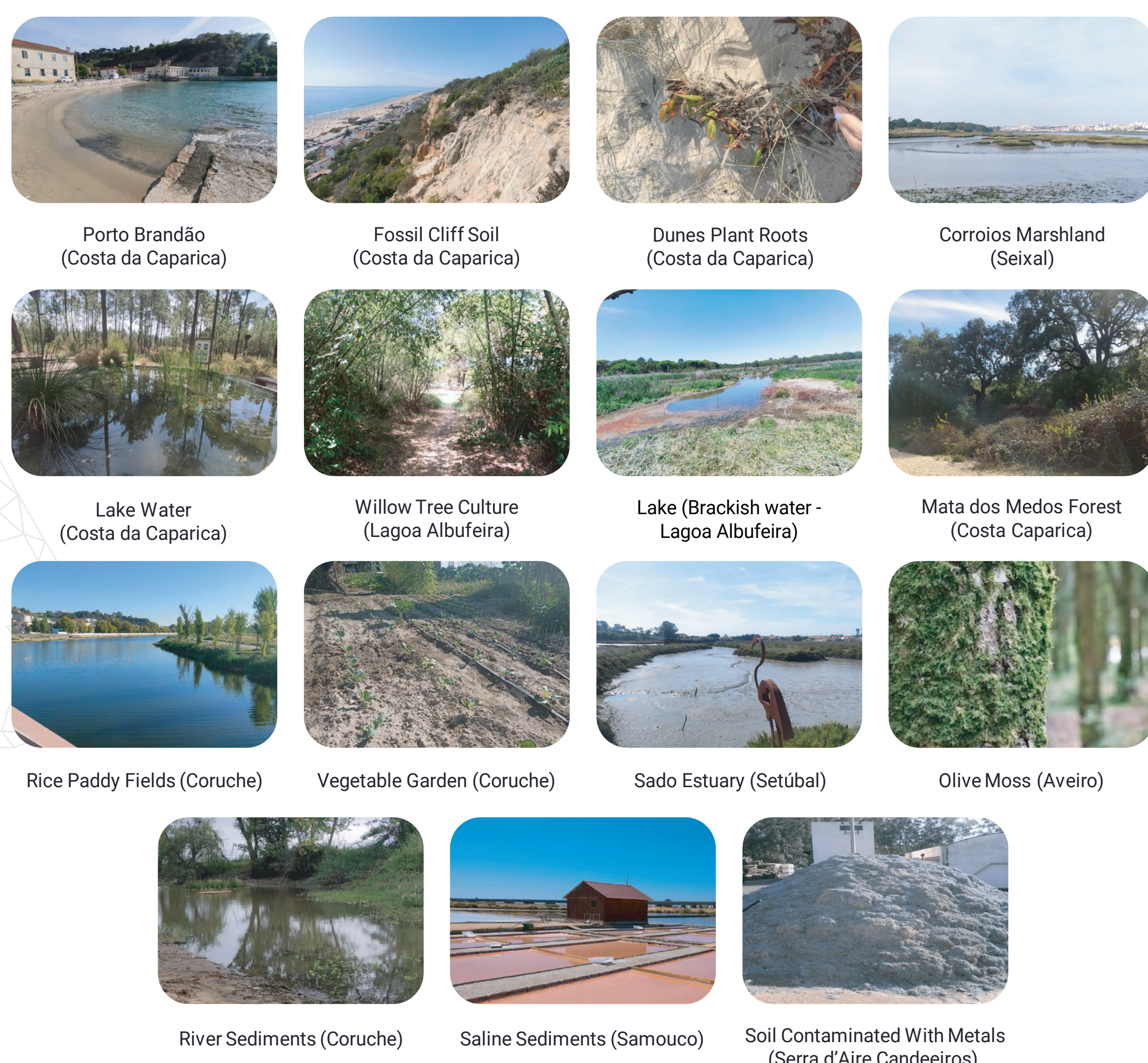
Introduction

In nature, microorganisms thrive within complex ecosystems called microbiomes, where their collective capabilities surpass those of individual populations. Through bacterial communication, involving metabolite exchanges and molecular signalling, microbial consortia achieve a division of labour, enhancing productivity and resilience against environmental fluctuations. Over time, this communal living fosters stability within consortia, making them robust in diverse environmental conditions. Leveraging these attributes, natural microbiomes from various ecosystems can be tailored to produce commercially valuable metabolites, such as biopolymers. Polyhydroxyalkanoates (PHAs), biocompatible and biodegradable polyesters synthesized by select microbial species, offer sustainable alternatives to conventional plastics.

*This proposal studied the evolutionary trajectories of natural microbiomes collected from distinct habitats towards **PHAs-enriched consortia** subjected to specific selective pressure conditions.*

Results

Collection of sediments in different sites of Portugal

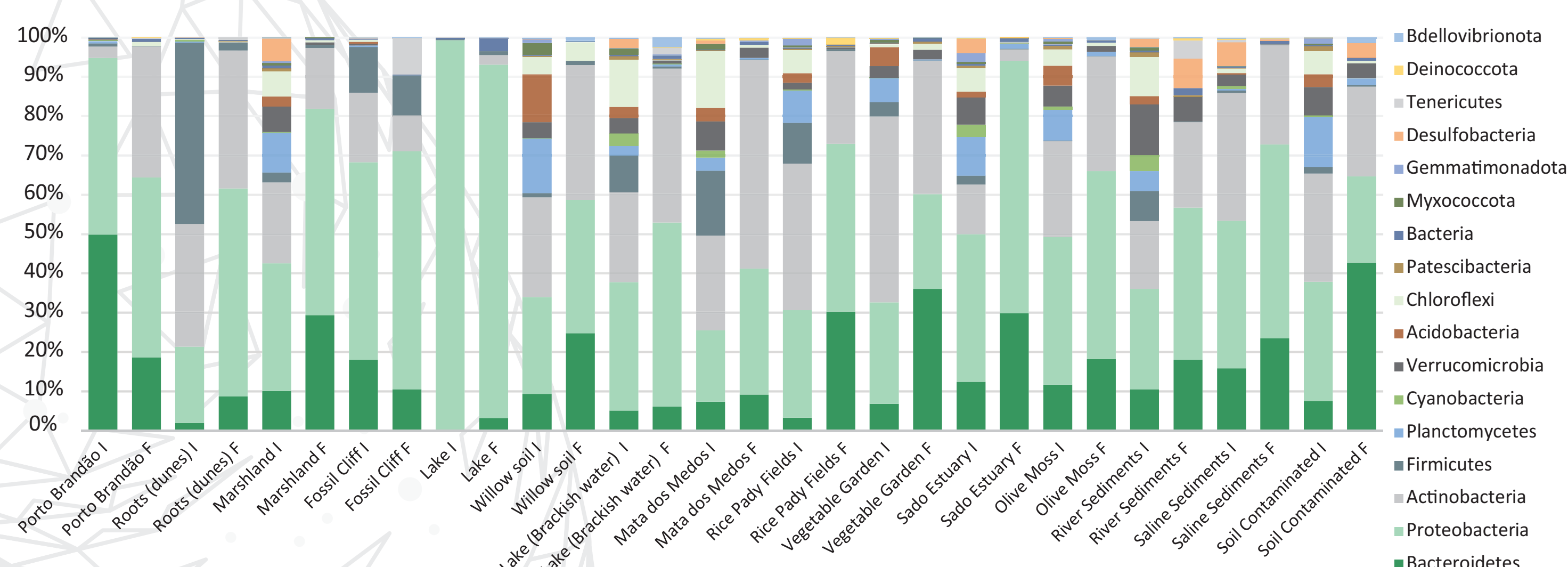


FEAST AND FAMINE STRATEGY
2 hydraulic retention times
20°C
pH7

Quantification of PHA by different microbiomes (Gas chromatography)

MICROBIOME	VSS (g/L)	mgPHA/gVSS
Porto Brandão	6.60 ± 0.00	23.13 ± 0.00
Dunes Plant Roots	6.20 ± 0.00	125.88 ± 0.00
Corroios Marshland	4.50 ± 0.00	116.47 ± 3.46
Fossil Cliff Soil	10.40 ± 0.60	5.07 ± 0.45
Lake Water	9.60 ± 0.20	45.79 ± 0.52
Willow Tree Soil	12.60 ± 0.00	2.18 ± 0.10
Lake (brackish water)	12.75 ± 0.15	16.57 ± 0.49
Mata dos Metos	11.00 ± 0.00	43.35 ± 0.00
Rice Paddy Fields	11.35 ± 0.55	3.50 ± 0.35
Vegetable Garden	11.65 ± 1.45	77.43 ± 3.87
Sado Estuary	13.10 ± 0.00	30.56 ± 3.81
Olive Moss	10.15 ± 0.35	95.44 ± 0.00
River Sediments	8.10 ± 0.70	19.17 ± 0.00
Saline Sediments	11.75 ± 0.25	0.00 ± 0.00
Soil Contaminated	9.00 ± 0.60	4.06 ± 0.04

Genetic characterization of microbiomes



Conclusions

- Microbiomes with diverse physical, chemical and genetic characteristics were collected and subject to the same selective pressure.
- The microbiomes yielding higher amount of PHA were found in Dunes Plant Roots, Marshland, Vegetable Garden and Olive Moss.
- All of the 15 microbiomes evolve into PHA-accumulating organisms - Proteobacteria and Actinobacteria.
- Oceanimonas*, *Halomonas*, *Corynebacterium*, *Alcaligenes*, *Acinetobacter*, *Paracoccus* and *Pararhodobacter* are the most abundant genera after 2 HRT of cultivation.