

In the format provided by the authors and unedited.

Important contribution of macroalgae to oceanic carbon sequestration

Alejandra Ortega ¹, Nathan R. Gerald ¹, Intikhab Alam ², Allan A. Kamau ², Silvia G. Acinas³, Ramiro Logares ³, Josep M. Gasol ^{3,4}, Ramon Massana ³, Dorte Krause-Jensen ^{5,6} and Carlos M. Duarte ^{1,2*}

¹Red Sea Research Center, King Abdullah University of Science and Technology, Thuwal, Saudi Arabia. ²Computational Bioscience Research Center, King Abdullah University of Science and Technology, Thuwal, Saudi Arabia. ³Institut de Ciències del Mar, CSIC, Barcelona, Spain. ⁴Centre for Marine Ecosystem Research, Edith Cowan University, Western Australia, Australia. ⁵Arctic Research Centre, Department of Bioscience, Aarhus University, Aarhus, Denmark. ⁶Department of Bioscience, Aarhus University, Silkeborg, Denmark. *e-mail: carlos.duarte@kaust.edu.sa

Supplementary Information for:

Important contribution of macroalgae to oceanic carbon sequestration

Alejandra Ortega¹, Nathan R. Geraldi¹, Intikhab Alam², Allan A. Kamau², Silvia G. Acinas³,
Ramiro Logares³, Josep M. Gasol^{3,4}, Ramon Massana³, Dorte Krause-Jensen⁵ and Carlos M.
Duarte^{1,2}

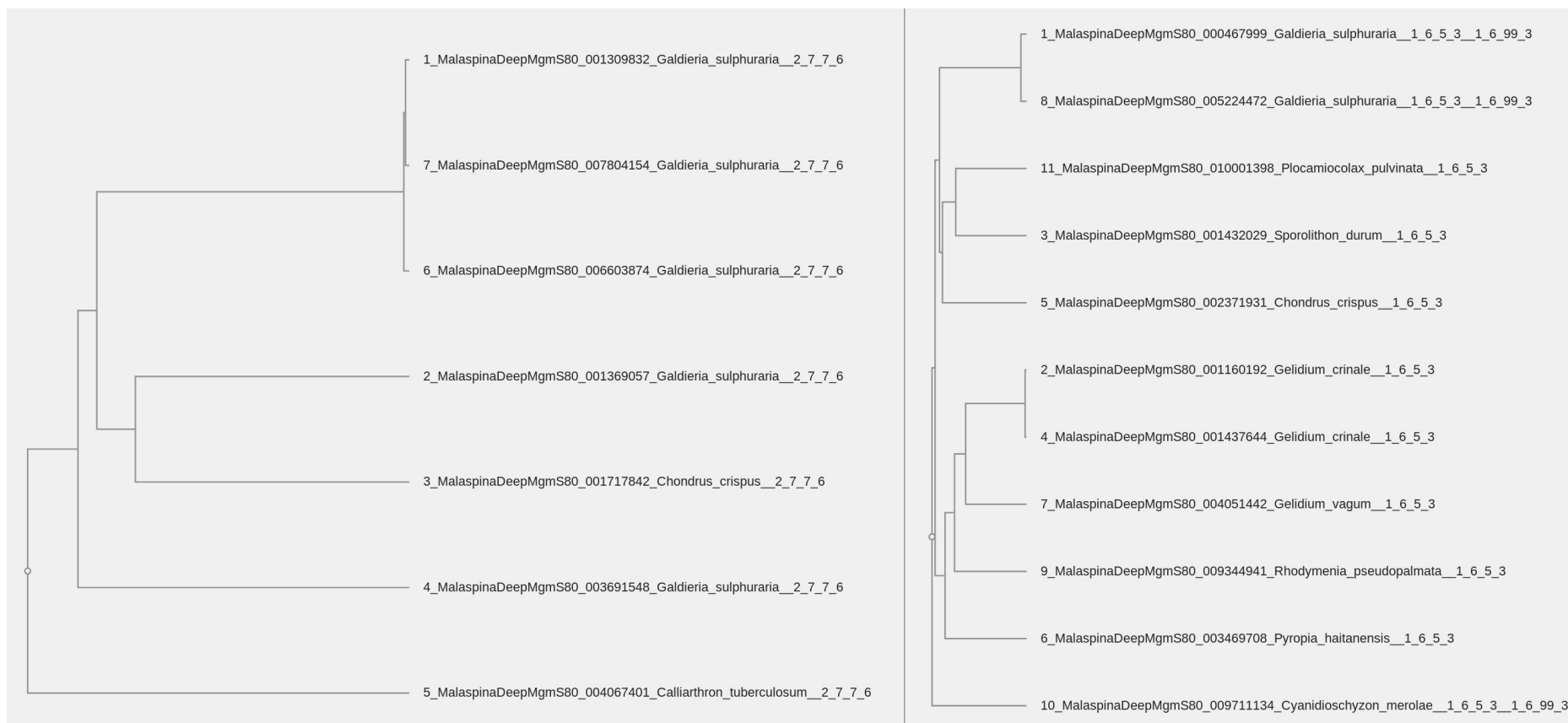
¹ Red Sea Research Center (RSRC), King Abdullah University of Science and Technology (KAUST), Thuwal, Saudi Arabia

² Computational Bioscience Research Center (CBRC), King Abdullah University of Science and Technology (KAUST), Thuwal, Saudi Arabia

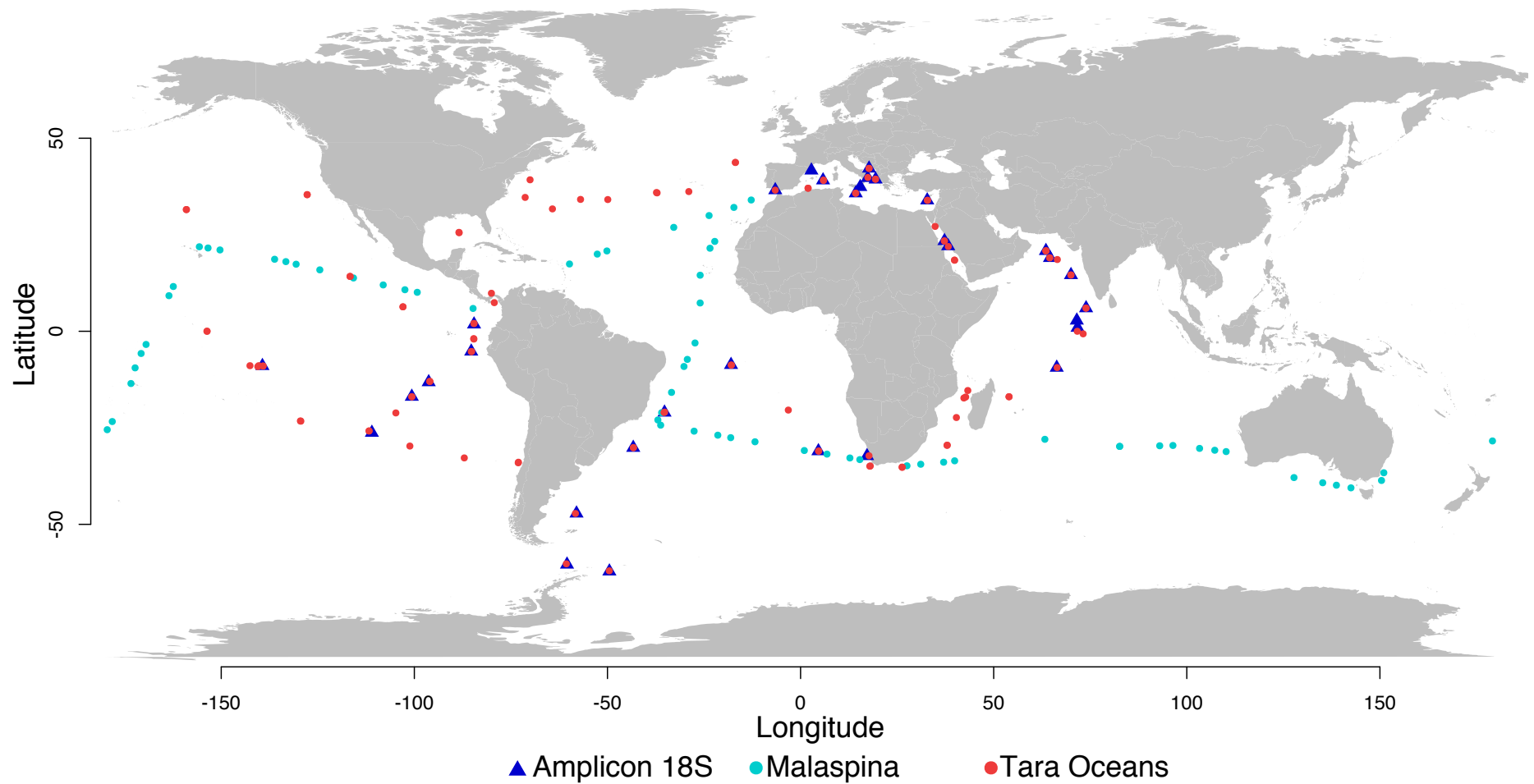
³ Institut de Ciències del Mar, CSIC, Barcelona, Spain

⁴ Centre for Marine Ecosystem Research, Edith Cowan University, Joondalup, Australia

⁵ Department of Bioscience, and Arctic Research Centre, Aarhus University, Denmark



Supplementary Figure 1 | Phylogeny of Rhodophyta SCG from Malaspina dataset. Numbers after species indicates enzyme ID.



Supplementary Figure 2 | Geographical location of sampling points per dataset. Malaspina and Tara Oceans (circles) are metagenomic data. 18S rDNA metabarcodes (triangles) were collected during the Tara Oceans expeditions.

Supplementary Table 1 | Macroalgal diversity indices by oceanic region (mean $\pm$ SD): IO Indian Ocean, MS Mediterranean Sea; NAO, SAO North and South Atlantic Ocean; NPO, SPO North and South Pacific Ocean; RS Red Sea; and SO Southern Ocean. Relative abundance of DNA sequences is in reads per million (RPM), standardized by number of samples per basin. The South Atlantic Ocean was the most diverse region (high abundance and equitability, low dominance), while the Red Sea was the least diverse region. Estimated order richness using the CHAO 2 estimator was in agreement with observed richness: 17 orders.

Index	IO	MS	NAO	NPO	RS	SAO	SO	SPO
Order n	14	9	15	16	6	15	11	14
DNA (RPM)	7.8	7.7	12.7	10.1	9.7	15.1	14.2	15.9
Dominance D	0.2($\pm$ 0.01)	0.4($\pm$ 0.01)	0.2($\pm$ 0.01)	0.2($\pm$ 0.01)	0.6($\pm$ 0.02)	0.2($\pm$ 0.01)	0.2($\pm$ 0.01)	0.3($\pm$ 0.01)
Shannon Diversity (H)	1.8($\pm$ 0.03)	1.4($\pm$ 0.03)	1.9($\pm$ 0.02)	1.8($\pm$ 0.03)	0.8($\pm$ 0.03)	2.1($\pm$ 0.02)	1.8($\pm$ 0.02)	1.6($\pm$ 0.02)
Pielou Equitability (J)	0.7($\pm$ 0.01)	0.6($\pm$ 0.01)	0.7($\pm$ 0.01)	0.7($\pm$ 0.01)	0.5($\pm$ 0.02)	0.8($\pm$ 0.01)	0.8($\pm$ 0.01)	0.6($\pm$ 0.01)

Supplementary Table 2 | One-Way PERMANOVA based on Bray-Curtis similarity, comparing SCG macroalgal DNA assemblage among oceanic regions. Bonferroni corrections of *p* values are shown in the upper right triangle of the matrix; significant differences are shown in bold. F values are shown in the lower left triangle. IO Indian Ocean, MS Mediterranean Sea; NAO, SAO North and South Atlantic Ocean; NPO, SPO North and South Pacific Ocean; RS Red Sea; and SO Southern Ocean.

	IO	MS	NAO	NPO	RS	SAO	SO	SPO
IO		0.0056	0.0028	0.0028	0.6132	0.0028	0.0028	0.0028
MS	4.04		0.224	0.0896	0.5488	0.0028	0.7896	0.0028
NAO	7.767	2.838		0.7448	0.224	0.014	0.0952	0.0364
NPO	5.254	3.405	2.527		1	0.1288	0.0196	0.798
RS	2.163	2.507	2.999	1.755		0.8708	0.1372	0.0924
SAO	4.828	4.339	3.87	2.834	2.007		0.0028	0.0056
SO	6.963	2.383	3.554	4.611	3.136	5.853		0.0028
SPO	11.77	7.7	4.03	2.415	3.403	4.528	7.044	

Supplementary Table 3 | Macroalgae diversity indices (mean $\pm$ SD) by depth, using the Malaspina single-copy protein-encoding gene (SCG) dataset. Relative abundance of DNA sequences is in reads per million (RPM), standardized by number of samples per depth. The highest diversity (high abundance and equitability, low dominance) was found in the epipelagic zone (0-200 m), while the mesopelagic zone (200-1,000 m) was the least diverse depth zone.

Index	Epipelagic	Mesopelagic		Bathypelagic		
	<200 m	<500 m	<1,000 m	<2,000 m	<3,000 m	<4,000 m
Order n	11	12	9	5	6	6
DNA (RPM)	13.5	11	7.7	5.1	5	3.9
Dominance D	0.2($\pm$ 0.01)	0.6($\pm$ 0.02)	0.6($\pm$ 0.02)	0.5($\pm$ 0.02)	0.4($\pm$ 0.02)	0.4($\pm$ 0.01)
Shannon Diversity (H)	1.8($\pm$ 0.02)	1.0($\pm$ 0.04)	1.0($\pm$ 0.04)	1.0($\pm$ 0.04)	1.2($\pm$ 0.04)	1.1($\pm$ 0.04)
Pielou Equitability (J)	0.8($\pm$ 0.01)	0.4($\pm$ 0.02)	0.4($\pm$ 0.02)	0.6($\pm$ 0.02)	0.7($\pm$ 0.02)	0.6($\pm$ 0.02)

Supplementary Table 4 | Number of unique genes per macroalgae order available in the reference gene catalogue of both Malaspina and Tara Oceans expeditions.

Lineage	Order	Unique genes
Chlorophyta	Prasiolales	82
Chlorophyta	Ulvaes	40
Phaeophyta	Ectocarpales	12,815
Phaeophyta	Fragilariales	99
Phaeophyta	Fucales	74
Phaeophyta	Laminariales	69
Rhodophyta	Balliales	1
Rhodophyta	Bangiales	434
Rhodophyta	Batrachospermales	18
Rhodophyta	Bonnemaisoniales	21
Rhodophyta	Ceramiales	230
Rhodophyta	Corallinales	83
Rhodophyta	Cyanidiales	3,510
Rhodophyta	Gelidiales	91
Rhodophyta	Gigartinales	1972
Rhodophyta	Gracilariales	111
Rhodophyta	Halymeniales	33
Rhodophyta	Hapalidiales	3
Rhodophyta	Nemaliales	282
Rhodophyta	Palmariales	39
Rhodophyta	Plocamiales	25
Rhodophyta	Porphyridiales	80
Rhodophyta	Rhodymeniales	47
Rhodophyta	Stylonematales	53
Total		20,212