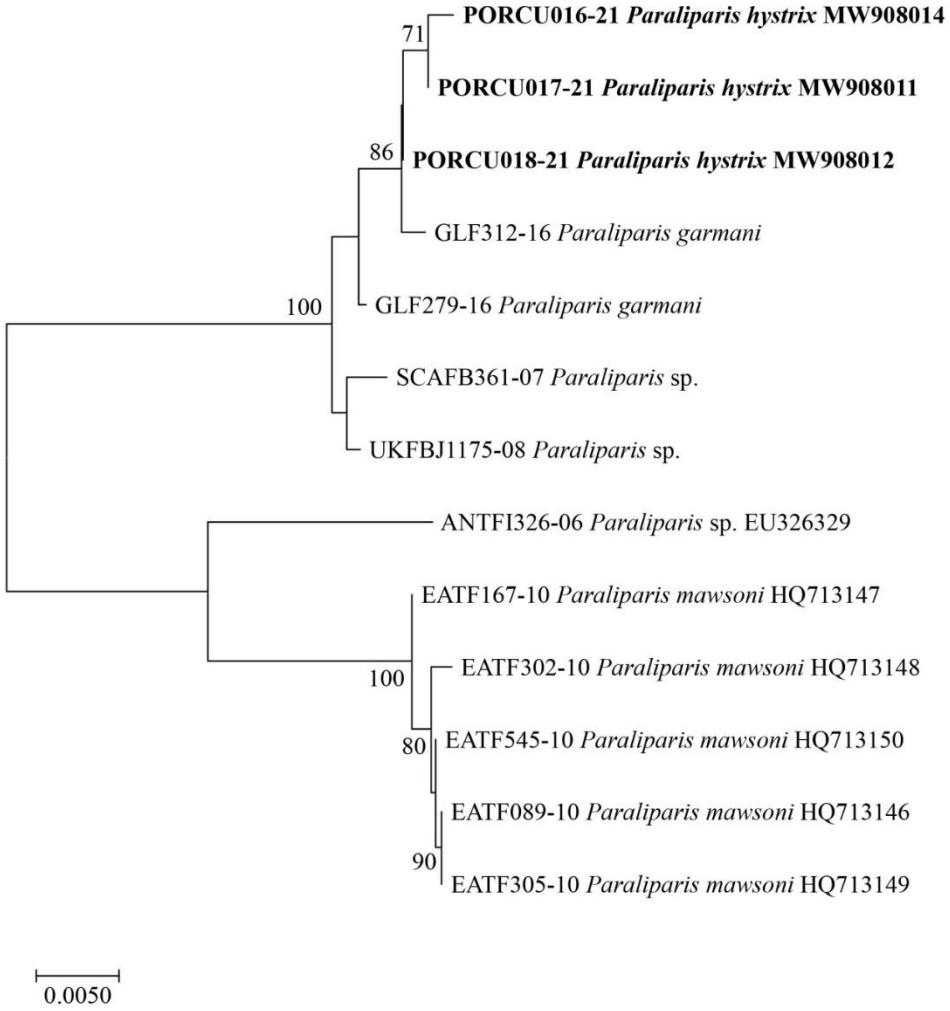
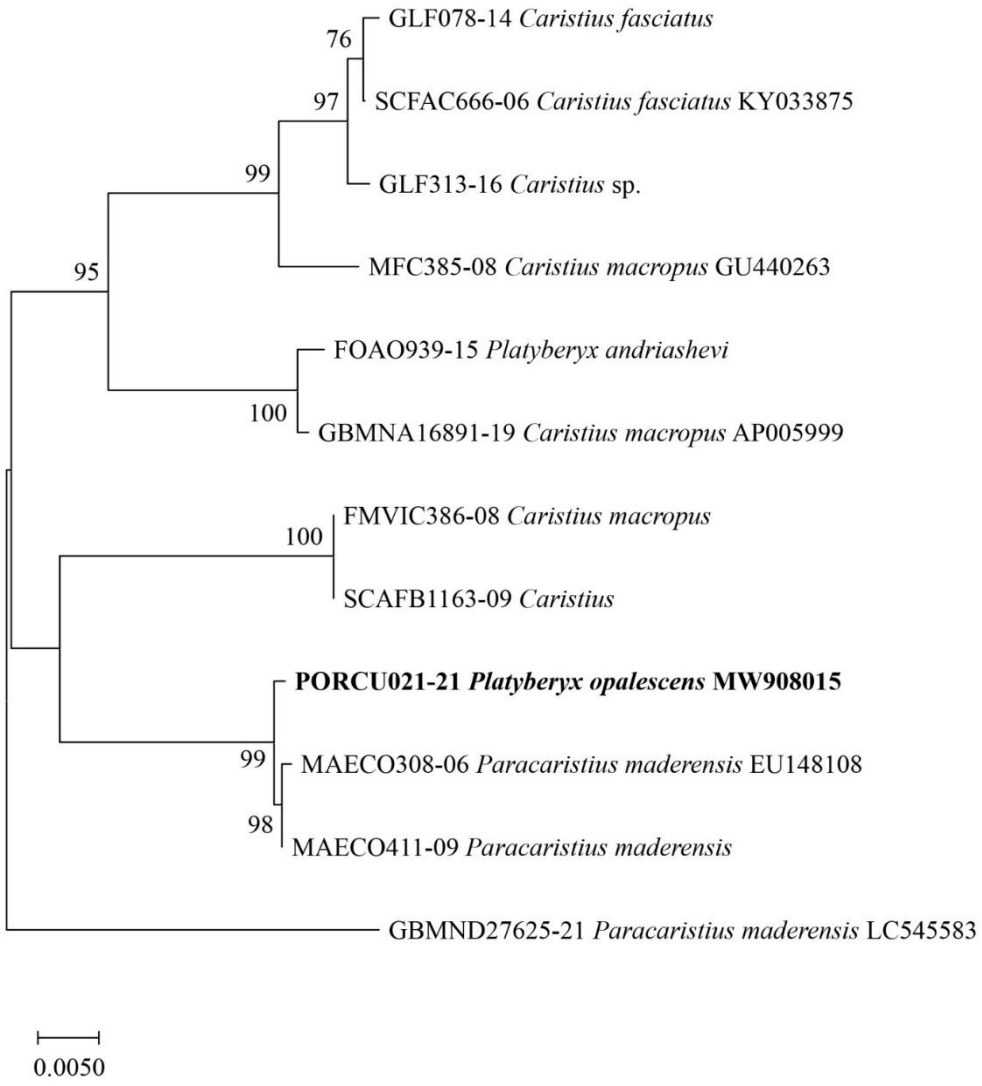
Journal of
Marine Science and Engineering

MDPI

Supplementary



(A)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SCAFB1163-09 *Caristius*
PORCU021-21 *Platyberyx opalescens* MW908015
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MAECO308-06 *Paracaristius maderensis* EU148108
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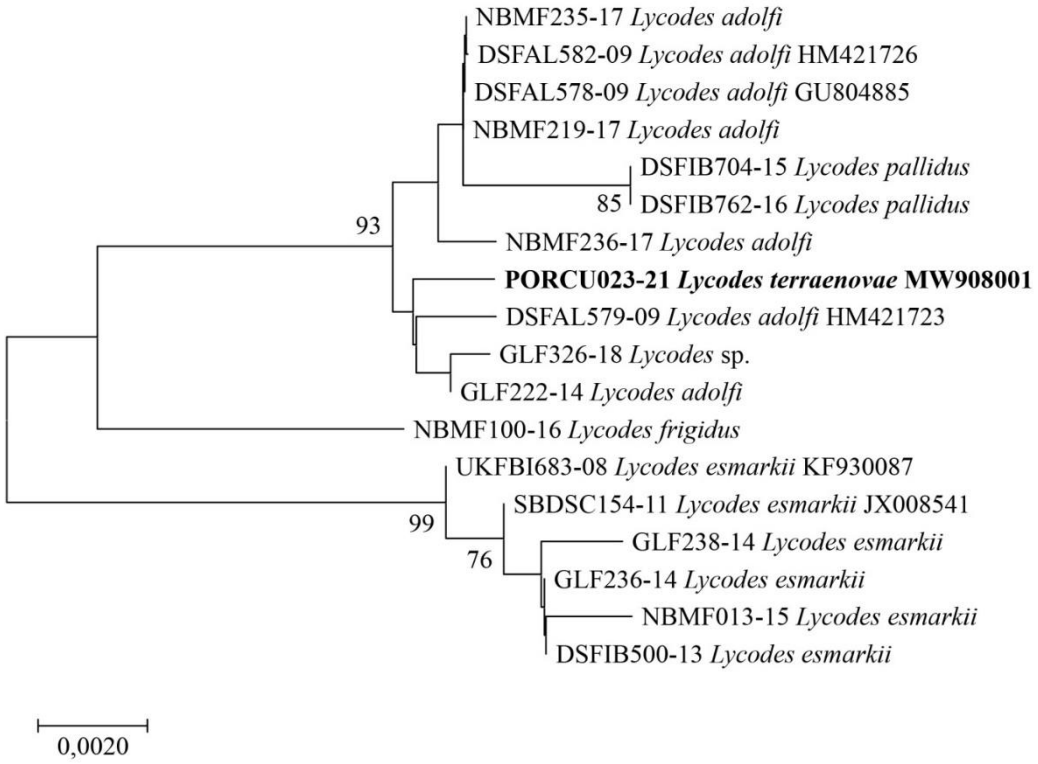
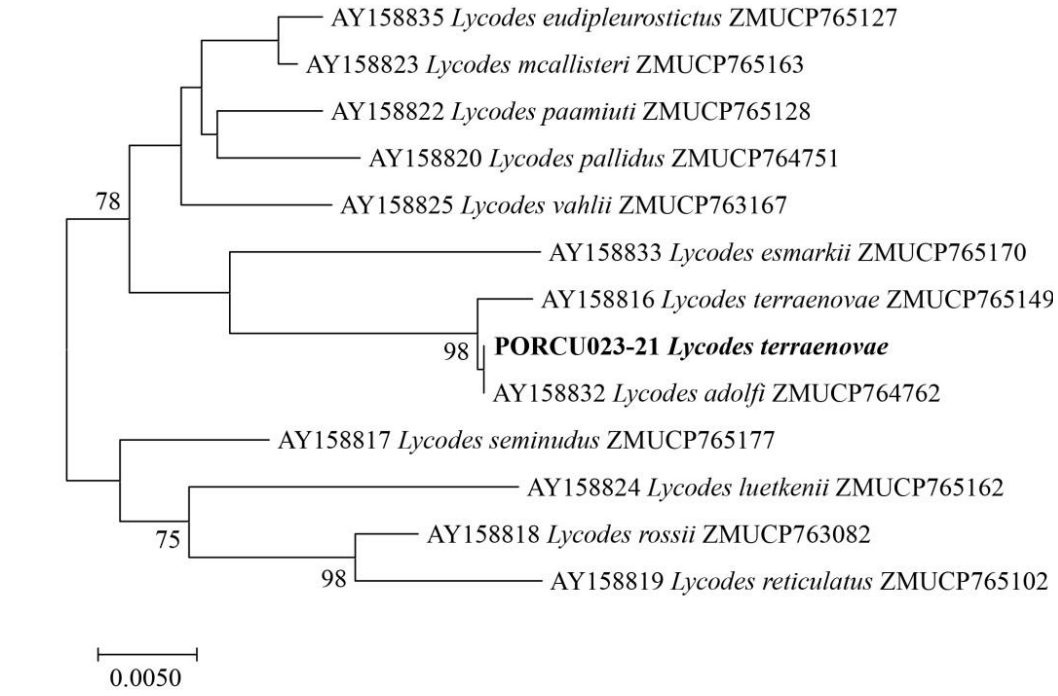
0.0050

(B)

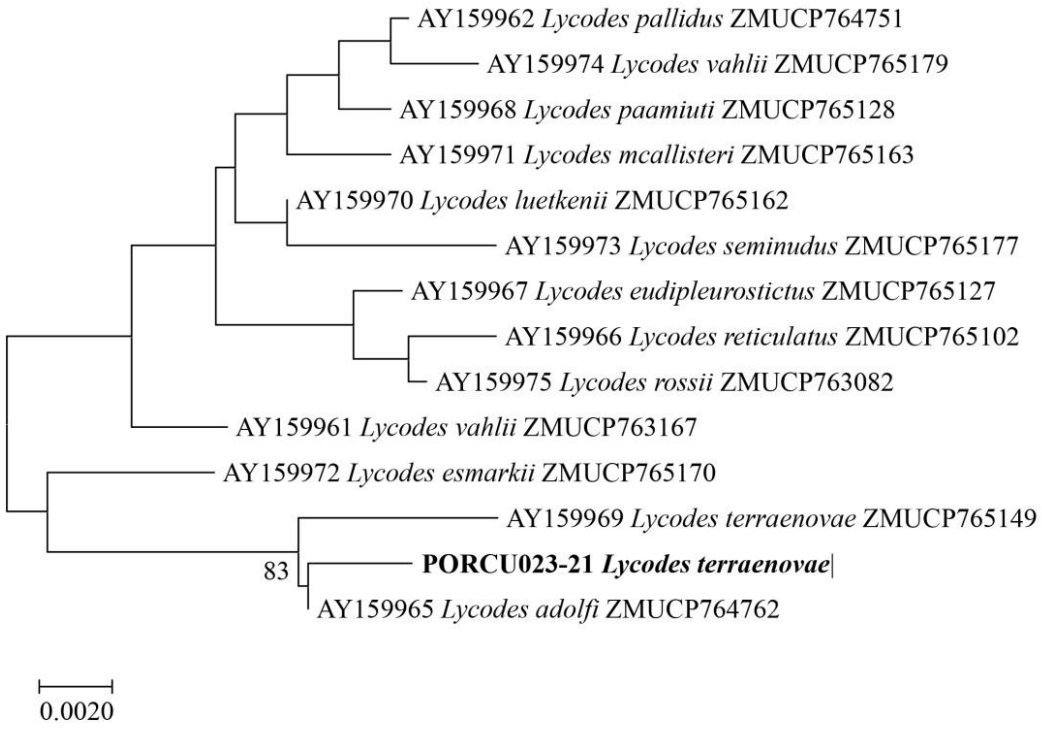


(C)

Figure S1. Neighbour-Joining trees based on p-distances, including COI-5P sequences of the 14 deep-sea species captured at Porcupine Bank. The percentage of replica trees in which the associated taxa clustered together in the bootstrap test (2000 replicates) are shown next to the branches when values are higher than 70%. The trees are drawn to scale, with branch lengths in the same units as those of the genetic distances used to infer the cladograms. Differences among sequences were computed as p-distances and are in the units of the number of base differences per site. All ambiguous positions were removed for each sequence pair (pairwise deletion option). There were a total of 652 positions in each final dataset. The analyses were conducted in MEGA X. Annotations are also included for each tree regarding the location where the specimens were collected. The species names shown in the cladograms are those that were associated with the sequences downloaded from BOLD. (A) *Paraliparis hystrix*; (B) *Platyberyx opalescens*; (C) *Lycodes terraenovae*.



(A)



(B)

Figure S2. Neighbor-Joining trees of *Lycodes terraenovae* mitochondrial Cyt b (A) and 12S rDNA (B) nucleotide sequences based on p-distances. The percentage of replica trees in which the associated taxa clustered together in the bootstrap test (2000 replicates) are shown next to the branches when

values are higher than 70%. The trees are drawn to scale, with branch lengths in the same units as those of the genetic distances used to infer the cladograms. Differences among sequences were computed as p-distances and are in the units of the number of base differences per site. All ambiguous positions were removed for each sequence pair (pairwise deletion option). The analyses were conducted in MEGA X.

Table S1. COI barcodes of specimens captured at Porcupine Bank generated in this research.

Taxon	Museum ID (MHNUSC)	BOLD Process ID	GenBank Acc. No.
Antimora rostrata	25184	PORCU010-21	MW907994
Bathypterois dubius	25182	PORCU008-21	MW907995
Borostomias antarcticus	25180-1	PORCU003-21	MW907998
Borostomias antarcticus	25180-2	PORCU004-21	MW907996
Borostomias antarcticus	25180-3	PORCU005-21	MW907999
Borostomias antarcticus	25180-4	PORCU006-21	MW907997
Evermannella balbo	25183	PORCU009-21	MW908000
Howella atlantica	25190	PORCU022-21	MW908001
Lycodes terraenovae	25191	PORCU023-21	MW908002
Lyconus brachycolus	25186-1	PORCU014-21	MW908003
Lyconus brachycolus	25186-2	PORCU015-21	MW908004
Melanonus zugmayeri	25185-1	PORCU011-21	MW908005
Melanonus zugmayeri	25185-2	PORCU012-21	MW908007
Melanonus zugmayeri	25185-3	PORCU013-21	MW908006
Neocyttus helgae	25188	PORCU020-21	MW908008
Nessorhamphus ingolfianus	25179-1	PORCU001-21	MW908009
Nessorhamphus ingolfianus	25179-2	PORCU002-21	MW908010
Paraliparis hystrix	25187-1	PORCU016-21	MW908014
Paraliparis hystrix	25187-2	PORCU017-21	MW908011
Paraliparis hystrix	25187-3	PORCU018-21	MW908012
Paraliparis hystrix	25187-4	PORCU019-21	MW908013
Platyberyx opalescens	25189	PORCU021-21	MW908015
Pseudoscopelus altipinnis	25192-1	PORCU024-21	MW908016
Pseudoscopelus altipinnis	25192-2	PORCU025-21	MW908017
Scopelosaurus lepidus	25181	PORCU007-21	MW908018