

NAMR-S-111003 (自行研究報告)

南沙太平島周邊海域環境DNA資訊蒐集研究

(正式報告)

中華民國111年12月

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主辦單位：本院海洋生態及保育研究中心

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「本研究報告絕無侵害他人智慧財產權之情事，如有違背願  
自負民、刑事責任。」

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# 提 要

關鍵詞：環境DNA、太平島、海洋生態監測

## 一、研究緣起

全球氣候變遷下，有限的文獻指出海水暖化引起南沙太平島110年大規模石珊瑚群集衰退與棘冠海星(*Acanthaster planci*)爆發，亟需持續掌握生態系復原情形，然而，太平島因地處偏遠，不易進行海洋生態監測及管理。有鑒於此，本研究規劃蒐集南沙太平島周邊海域環境DNA (environmental DNA, eDNA)資訊，所得資料可作為重大環境變化事件前後之對照基準，探討氣候變遷下不同年間海洋生態的變動，以提供南沙太平島海洋生物多樣性保育及管理之參據。

## 二、研究方法及過程

本研究於110年及111年由海巡署協助南沙太平島周圍海域8測站採集海水，以提取環境DNA資訊進行16S、18S及12S基因片段次世代定序(next generation sequencing, NGS)，分別針對三個生物類群包含(1)海洋菌種、(2)真核生物(eukaryote)及(3)海水魚等進行物種比對，建立生物多樣性指標(diversity index)，並統計分析。

## 三、重要發現

以環境DNA資訊蒐集結果顯示，太平島110年及111年海洋生物組成有年間差異，可能與太平島海域環境改善、珊瑚礁生態系恢復有關，海洋菌種多樣性顯著回升( $P < 0.05$ )，110年(373 amplicons)與111年(200 amplicons)僅約25%相同，原以藍菌(Cyanobacteria)為優勢之菌種減少，物種均勻度(species evenness)增加；真核生物種類增加(110年41門590科，111年46門961科)，原劣化棲地由大型藻類、海綿取代，並有石珊瑚新入添；海水魚類物種數增加(110年34科44屬58種，111年31科50屬81種)，物種組成由沿岸性魚類轉為珊瑚礁及中層魚類，且有101個魚種在過去文獻未曾於南沙發現。

## 四、主要建議事項

本研究建立南沙太平島環境DNA對照基準，並發展運用於偏遠地區環境DNA海洋生態長期監測之流程。短期建議持續蒐集南沙太平島環境DNA生物資訊，以追蹤珊瑚礁生態系恢復之情形，並可應用本研究環境DNA調查流程輔助偏遠地區生態監測。中長程建議持續擴充臺灣海域海洋生物基因資料庫，以提高環境DNA比對正確性。

# Abstract

Keywords : Environmental DNA 、Taiping Island 、Marine ecological monitoring

## I. Purpose

Under global climate change, limited studies reported that seawater warming induced massive degradation of hard coral communities and Crown-of-thorns starfish outbreaks in 2021, Taiping Island in Nansha. Continuing monitoring of ecosystem rehabilitation in this area is urgent. However, Taiping Island is so remote and isolated that the marine ecological monitoring and management remain difficulties. This study aimed to collect environmental DNA information in the waters surrounding Taiping Island in Nansha. The collected data can be served as a baseline for major environmental events, explore shifts of species under climate change across years and provide reference for the conservation of marine biodiversity at Taiping Island in Nansha.

## II. Methods and Procedures

In 2021 and 2022, seawater sampling for eDNA of 8 stations at Taiping Island in Nansha was conducted with the assistance of Coast Guard Administration, Ocean Affairs Council. The eDNA information were sequencing by next generation sequencing (NGS) targeting 16S, 18S, and 12S rDNA genes for three categories, marine bacteria, eukaryotes and marine fishes separately. The eDNA sequences were analyzed including species annotation, diversity indices measurement and statistical analysis.

## III. Results

According to this study, annual difference of marine organism composition at Taiping Island between 2021 and 2022 was found and related to the environment improvement and rehabilitation of coral-reef ecosystem. The marine bacterial diversity significantly increases ( $P < 0.05$ ) and the amplicons between 2021 (373 amplicons) and 2022 (200 amplicons) only 25% is similar. The dominant strain, Cyanobacteria decrease and the species evenness increases. The taxon of eukaryotes increases (590 classes, 41 phyla in 2021; 961 classes, 46 phyla in 2022). The originally degraded habitats were covered by macroalgae and sponges with some new recruitment of hard coral. Marine fish species increase (58 species, 44 genus, 34 classes in 2021; 81 species, 50 genus, 31 classes in 2022). The species composition transformed from coastal fishes to coral-reef and mesopelagic fishes. There are 101 species has not been found in Nansha from the past references.

## IV. Suggestions

This study provides the baseline information of eDNA at Taiping Island, Nansha. Moreover, a protocol of eDNA collection for long-term monitoring of marine ecology in remote areas was demonstrated. For short term, it is recommended to continue

collecting eDNA information at Taiping Island to trace the rehabilitation of coral-reef ecosystem. Besides, utilization of the eDNA survey process to strengthen the marine ecosystem monitoring in the remote areas is also recommended. For mid-long term, continuing expand the genetic database of marine organisms in Taiwan to improve the accuracy of the species annotation of eDNA.

# 第一章 前言

## 第一節 研究緣起與背景

南沙太平島位於熱帶地區，其周邊海域以珊瑚礁生態系為主，過去研究調查曾紀錄珊瑚覆蓋率高達63.6%(陳等, 2020)，依據本院 110 年度西南海域珊瑚礁生態監測調查報告(鄭等, 2021)，110年發生南沙太平島大規模石珊瑚死亡，恐嚴重影響生態系提供棲地及食物來源之功能。

有限的文獻顯示，南沙太平島珊瑚群集衰退的原因與109年海水溫度上升引發珊瑚白化(coral bleaching)以及棘冠海星大爆發有關(張, 2020；鄭等, 2021)，亟需持續掌握生態系復原情形。然而，地處偏遠島嶼通常面臨海洋生態保育監測及管理不易的問題。

近年來許多國家正在研究以環境DNA技術進行生態監測，於現有比對資料庫尚未健全下，已有相當顯著及突破性的成果(DiBattista et al., 2020; Oka et al., 2021)。環境DNA技術具備僅須從環境樣本提取DNA的優點，比起研究船或潛水調查等一般調查方法，可降低人力需求，亦提升在新冠疫情(COVI-19)期間監測偏遠島嶼生態環境之可行性。

## 第二節 研究目的及研究重點

為持續監測110年南沙太平島大規模石珊瑚死亡後生態系變化，本研究依據本院與海洋委員會海巡署(以下簡稱海巡署)南沙海洋研究站合作備忘錄，以海巡署南沙太平島現有資源，包含人力、船艇及物資協運等，就本研究於110至111年度共同合作，蒐集南沙太平島周邊海域環境DNA資訊，由海巡署協助於現地環境DNA海水樣本採集，交由本院分析環境DNA生物資訊，進行物種比對及生物多樣性指標建立，所得資料可作為重大環境變化事件前後之對照基準，探討氣候變遷下不同年間生物種類變化，並測試發展運用於偏遠地區海洋生態長期監測之流程，以提供南沙太平島海洋生物多樣性保育之建議。

## 第三節 研究內容及重要文獻回顧

本研究針對海洋菌種、真核生物及海水魚等三個生物類群進行環境DNA資訊蒐集，以下分述其重要文獻回顧：

### 一、海洋菌種

微生物佔海洋中70%以上的生物量(biomass)，包含細菌及浮游生物等，本研究所指海洋菌種包含古菌域 (domain Archaea)及細菌域 (domain Bacteria)，分析環境樣本的菌種組成研究開始較早，目前生技產業已發展出商業模式，且一般可信的鑑定層級可至屬(genus)或種(species)，因此本研究選定以菌種建立

生物多樣性指標，以利運用於不同年間、不同地點的生物多樣性比較。

## 二、真核生物

真核生物泛指細胞內具有細胞核膜包覆遺傳物質的生物，本研究所指真核生物為真核生物域(domain Eukaryota)，除了古菌及細菌之外的生物皆涵蓋在內，包含浮游生物、藻類、真菌及動植物等，本研究所選用的方法可信鑑定層級至科(family) (DiBattista et al., 2021)，部分序列可鑑定至種，因此可再針對珊瑚及棘冠海星等關注生物進行探討。

## 三、海水魚

海水魚為一般生態調查的主要對象之一，本研究所指海水魚為於海水、半海水水域生活的魚類，包含軟骨魚與硬骨魚，本研究所選用的方法可信鑑定層級可至屬或種(Miya et al., 2015)，由於此方法所比對的MitoFish資料庫(Sato et al., 2018)主要收錄範圍為日本鄰近海域，因此目前仍存在缺乏臺灣周圍海域特定魚類可供比對序列之問題。

## 第四節 預期目標

- 一、蒐集南沙太平島周邊海域環境DNA資訊。
- 二、了解南沙太平島生物多樣性現況。
- 三、比較南沙太平島不同年間環境DNA生物種類變化。
- 四、比較環境DNA及一般調查方法生物種類數量及差異。

## 第二章 材料與方法

### 第一節 樣本採集及 DNA 萃取

本計畫於南沙太平島 8 個測站進行水樣採集，採水瓶須事先以市售漂白水清洗，並以當地海水充分潤洗後裝海水至 1 公升，每測站採集 3 瓶 1 公升水樣，採集日期為 110 年 6 月 29 日、111 年 6 月 3 日，所得水樣立即冷凍保存，送至本院水質實驗室進行水樣過濾。將 1 公升水樣以 0.2  $\mu\text{m}$  孔徑濾紙過濾，再以 DNA 管柱法萃取濾紙上的環境 DNA。

表 1、南沙太平島採樣測站

測站編號	測站名稱	測站座標	
		經度	緯度
TP01	太平島西北測站	E114°21'73.4"	N10°22'90.0"
TP02	太平島東北測站	E114°22'02.9"	N10°22'96.9"
TP03	太平島正東測站	E114°22'53.6"	N10°22'82.1"
TP04	太平島東南測站	E114°22'29.2"	N10°22'55.9"
TP05	太平島西南測站	E114°22'06.2"	N10°22'39.7"
TP06	太平島正西測站	E114°22'06.2"	N10°22'45.9"
TP07	太平島西南方淺水	E114°21'08.3"	N10°22'23.0"
TP08	中洲礁	E114°24'18.5"	N10°23'08.7"

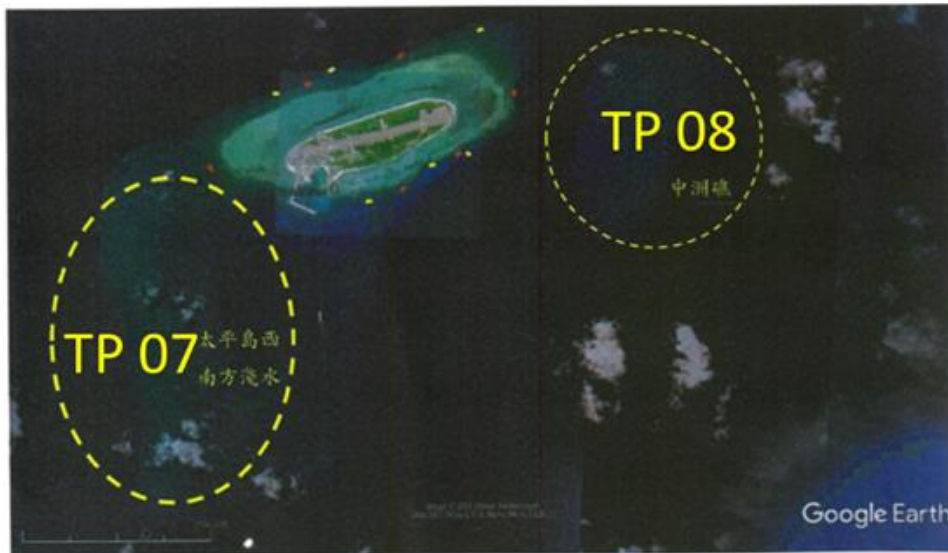


圖 1、南沙太平島採樣測站地理位置圖



圖 2、海巡署協助於南沙太平島中洲礁採集海水樣本

## 第二節 目標基因片段擴增及定序

環境DNA粗萃物分別以生物科技公司微生物總基因體分析商業套組 (Genomics BioSci & Tech Co.) 針對菌種16S rRNA V3-V4變異區、已發表之通用引子(universal primer) 針對真核生物18S rRNA (DiBattista et al., 2021) 以及已發表之MiFish-U 通用引子針對海水魚12S rRNA (Miya et al., 2015)，進行聚合酶連鎖反應 (polymerase chain reaction, PCR)，剪取與擴增目標基因片段，再使用 Illumina MiSeq平臺進行次世代定序(next generation sequencing, NGS)，讀長為2 x 300 bp，每樣本數據量約10萬條序列，準確度Q30須達70%，取得總基因序列資料。由於次世代定序為專門知識有關之服務，定序工作以勞務採購由基龍米克斯生物科技有限公司(Genomics BioSci & Tech Co.)通過TAF ISO17025 國際標準認證之高速核酸定序實驗室分工完成。

### 第三節 物種比對

每樣站所獲的環境DNA序列之總基因序列資料以DADA2 (v1.22)演算模型(Callahan et. al., 2016) 校正產生擴增子序列變異(amplicon sequence variants, ASV)，以QIIME2 Naive-Bayes classifier (v2021.8) 軟體(Caporaso et al., 2010) 搭配現有基因資料庫進行物種比對，菌種使用SILVA 138資料庫(序列相似度99%)(Quast et al., 2013; Yilmaz et al., 2014)，真核生物則BLASTn資料庫(National Center for Biotechnology Information, 2022)；海水魚則使用MitoFish資料庫(Sato et al., 2018)，並針對序列相似度較低者至BLASTn資料庫比對，比對標準以E值(E-value)、比對長度及比對相似度為標準，以得到環境DNA中生物種類清單。

為了解大規模石珊瑚死亡前後海洋生物種類之變化，本研究將回顧過去太平島珊瑚礁生態系調查之文獻，與本院110、111年蒐集之環境DNA資訊比較，討論不同調查方法獲得之生物種類數量及差異。

### 第四節 資料分析

本研究以蒐集之南沙太平島周邊海域環境DNA資訊，依三種生物類別分別建立以不同年間各測站數值化之生物多樣性指標(如： $\alpha$ 歧異度、 $\beta$ 歧異度)。

菌種之資料分析， $\alpha$ 歧異度包含物種豐富度(species richness)計算實際觀察到的物種數目(observed species)、Chao1指數，物種均勻度計算Shannon、Simpson指數； $\beta$ 歧異度包含以UniFrac distance矩陣進行群歸分析(UPGMA)，並以Bray-Curtis similarity進行空間排序分析(principal coordinate analysis, PCoA、non-metric multi-dimensional scaling, nMDS)；以Analysis of similarities (ANOSIM)統計分析檢測不同年間菌種組成差異顯著性；最後以linear discriminant analysis effect size (LEfSe)鑑定造成不同年間差異的菌種類群，並以Tax4Fun預測分析菌落功能。

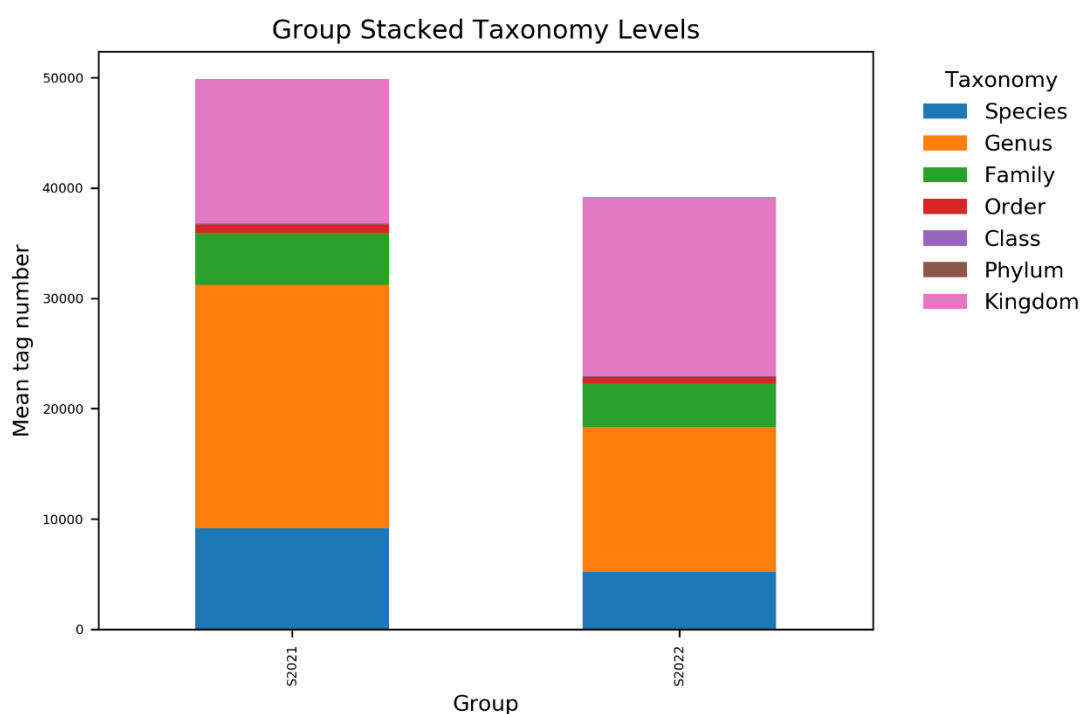
真核生物及海水魚之資料分析，不同地點及年間組成結果以PRIMER軟體(v5)進行群歸分析(CLUSTER)及空間排序分析(multi-dimensional scaling, MDS)，另計數真核生物各生物門下科層級(family level)數進行比較討論。

### 第三章 研究結果與討論

總樣本48件分別進行3種目標基因片段次世代定序，檢出率皆為100%，平均數據量皆達10萬條序列以上(124,446 - 623,971條)。

#### 第一節 海洋菌種

依據分析結果，海洋菌種16S基因序列比對多數可以到屬的層級(圖O、附錄一)，由於太平島西南方淺水測站及中洲礁測站(TP07、TP08)與其他測站菌種組成較為不同，因此在探討不同年間之差異，以6個太平島周圍測站(TP01至TP06)為主。



圖O、太平島110與111年16S基因序列比對不同分類階層序列量

#### 一、生物種類分析

本研究發現之菌種中110年(373 amplicons)與111年(200 amplicons)僅約25%相同(圖3)，且不同年間優勢菌種組成及比例不同(圖4)，110年菌種以藍菌門(Cyanophyta)下的Cyanobiaceae科為優勢，111年則以變形菌門(Proteobacteria)下SAR11 clade (Clade I)為優勢。110年太平島西南測站(TP05) 優勢菌種為變形菌門下紅桿菌科(Rhodobacteraceae) (圖5)，與其他測站明顯不同。

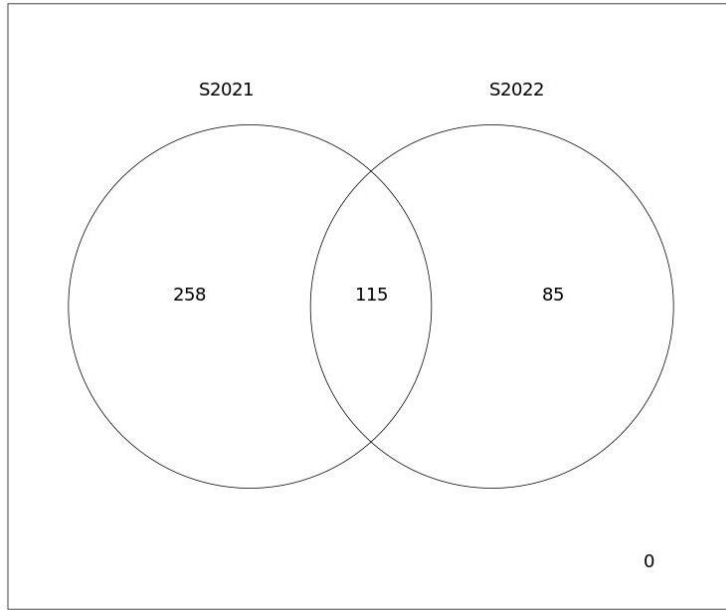


圖 3、110 與 111 年太平島海洋菌種文氏圖(Venn diagram)

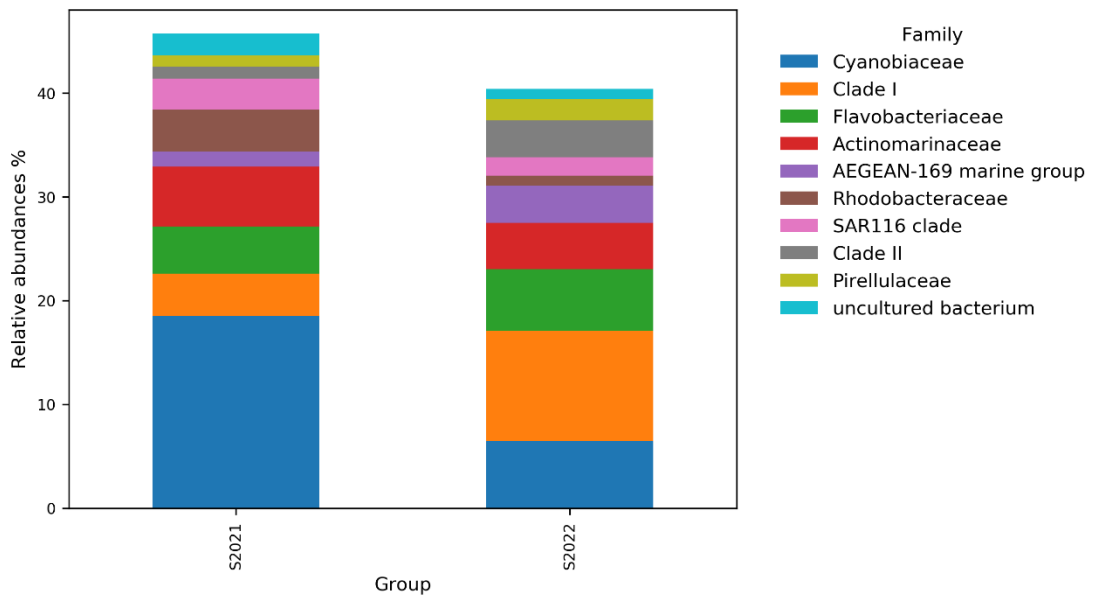


圖 4、110 與 111 年太平島科層級物種豐富度前十的海洋菌種

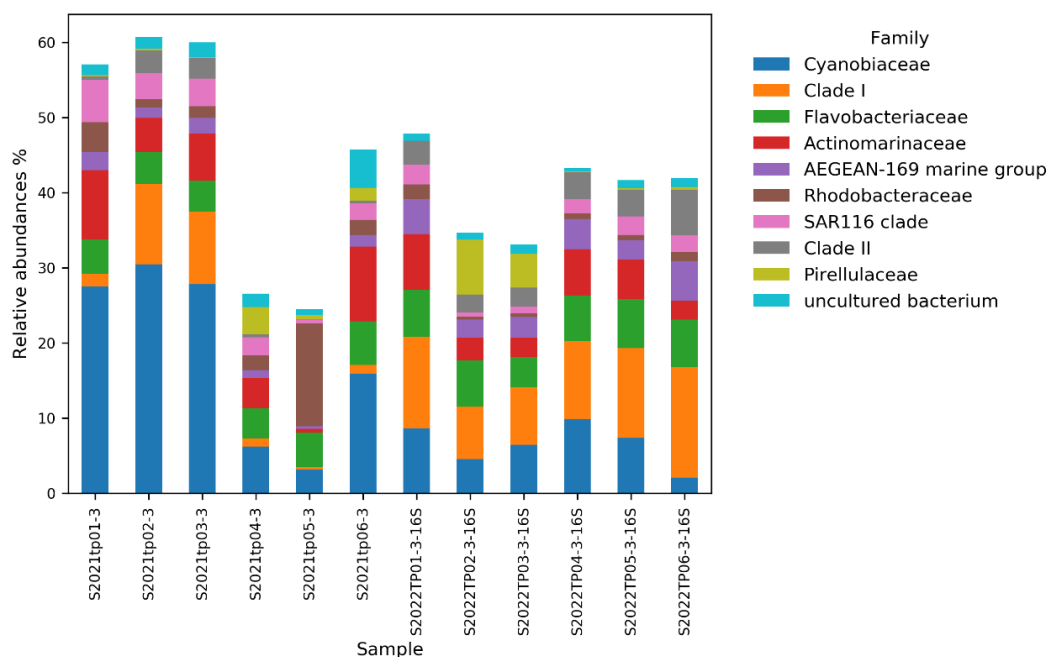


圖 5、110 與 111 年太平島不同測站科層級物種豐富度前十的海洋菌種

## 二、生物多樣性指標建立

### (一) $\alpha$ 歧異度

太平島110與111年海洋菌種 $\alpha$ 歧異度指標(表2、圖6)，由實際觀察到的物種數目，以太平島正東測站(TP03) 110年最低(185 amplicons)、111年最高(281 amplicons)，顯示此測站的物種豐富度第二年大幅增加，由Chao1也有類似的結果，並顯示111年整體物種豐富度高於110年；由Shannon、Simpson指數計算物種均勻度結果，以110年太平島西南測站(TP05)最高(7.73)，整體而言仍以111年物種均勻度高於110年，顯示111年太平島海洋菌種多樣性相對較高。

表 2、110 與 111 年太平島海洋菌種 $\alpha$ 歧異度指標

Station	Observed species		Shannon		Simpson		Chao1	
	110年	111年	110年	111年	110年	111年	110年	111年
TP01	212	255	5.64	6.05	0.95	0.97	212.33	328.93
TP02	220	238	5.71	6.43	0.95	0.98	220.00	298.00
TP03	185	329	5.71	6.66	0.95	0.98	185.00	363.50
TP04	281	208	6.90	5.66	0.97	0.96	281.00	239.00
TP05	297	250	7.73	6.36	0.99	0.98	297.00	275.07
TP06	299	291	6.64	6.68	0.97	0.98	299.00	399.10

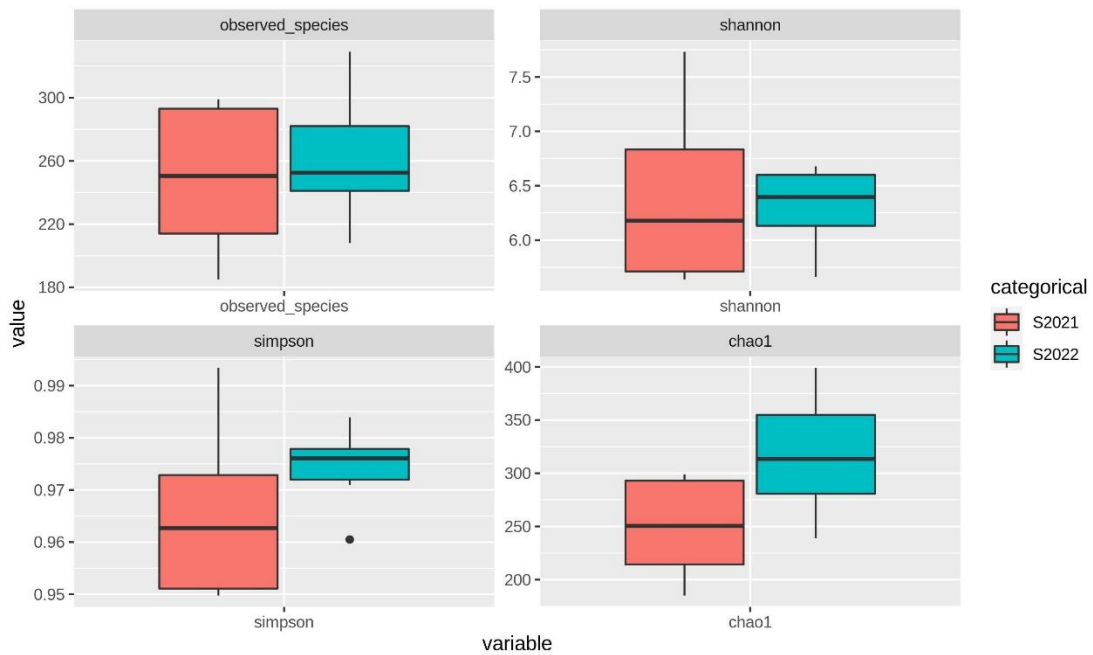


圖 6、110 與 111 年太平島海洋菌種 $\alpha$ 歧異度指標直方圖

## (二) $\beta$ 歧異度

為比較太平島110與111年不同測站及不同年間海洋菌種差異，進行 $\beta$ 歧異度分析，由UPGMA(圖7)顯示，除了太平島東南測站(TP04)之外，110與111年不同年間海洋菌種組成不同，並由PCoA分析(圖8)，可見110年太平島西南測站(TP05)海洋菌種組成與其他測站最具差異，於nMDS分析(圖9)也有類似的結果。

進一步進行ANOSIM統計分析檢測，結果為不同年間有顯著差異( $R=0.270$ ,  $p<0.05$ )，而測站間無顯著差異( $p>0.05$ )。以LEfSe分析之進化分支圖(圖10)顯示造成年間差異的菌種，主要為110年變形菌門(Pseudomonadota)下的彎曲菌目(Campylobacteriales)、浮黴菌門(Planctomycetota)下的Phycisphaerae科，以及111年擬桿菌門(Bacteroidota)下的黃桿菌科(Flavobacteriaceae)及圓桿菌科(Cyclobacteriaceae)等。

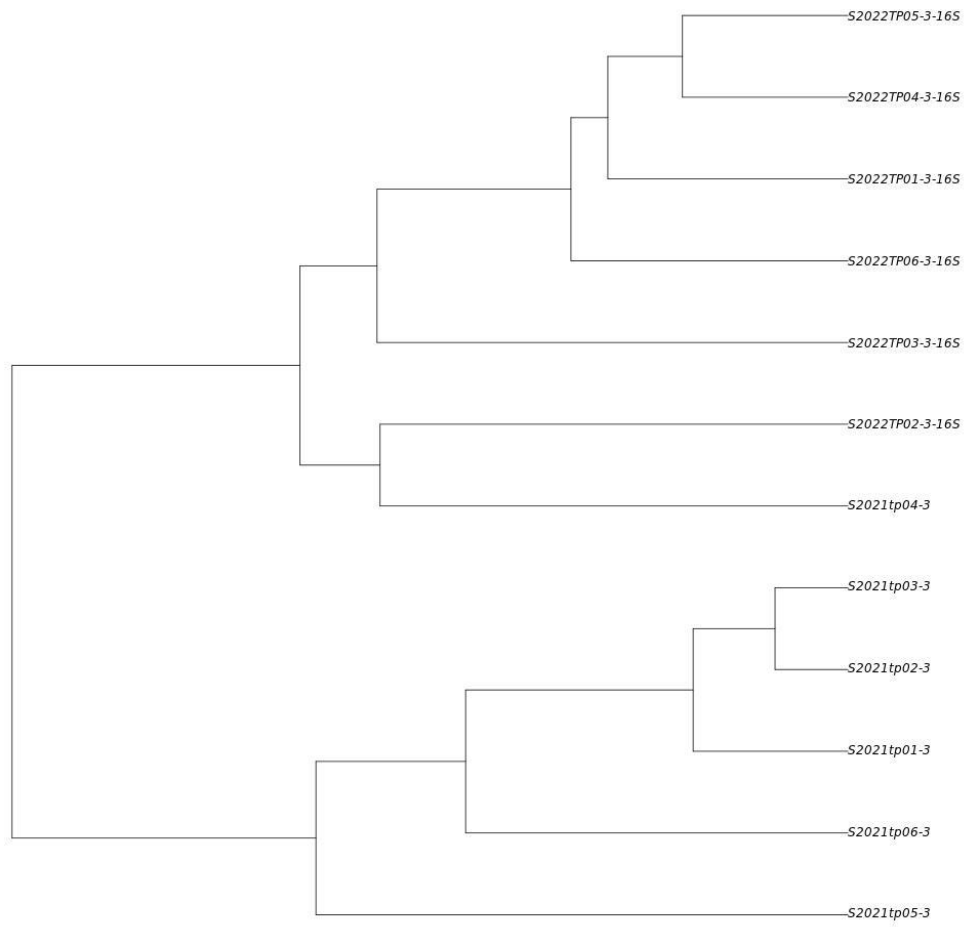


圖 7、110 與 111 年太平島海洋菌種 $\beta$ 歧異度指標演化樹圖(UPGMA)

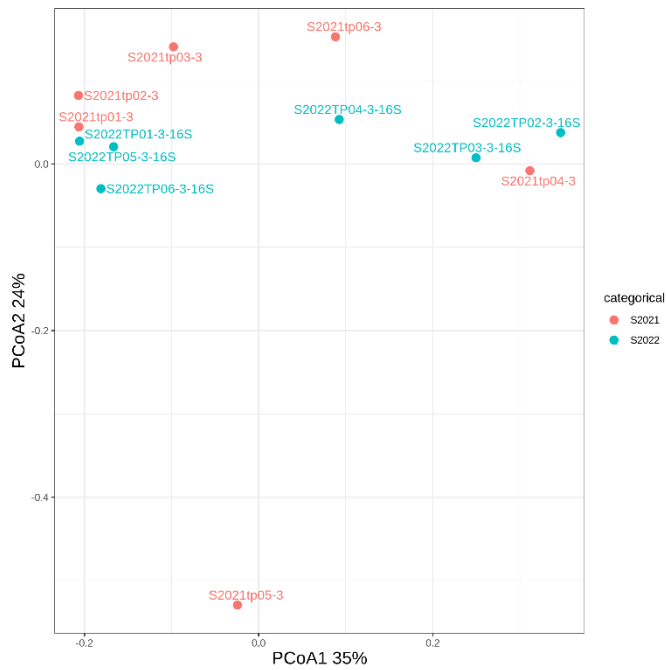


圖 8、110 與 111 年太平島海洋菌種β歧異度指標主座標分析圖(PCoA)

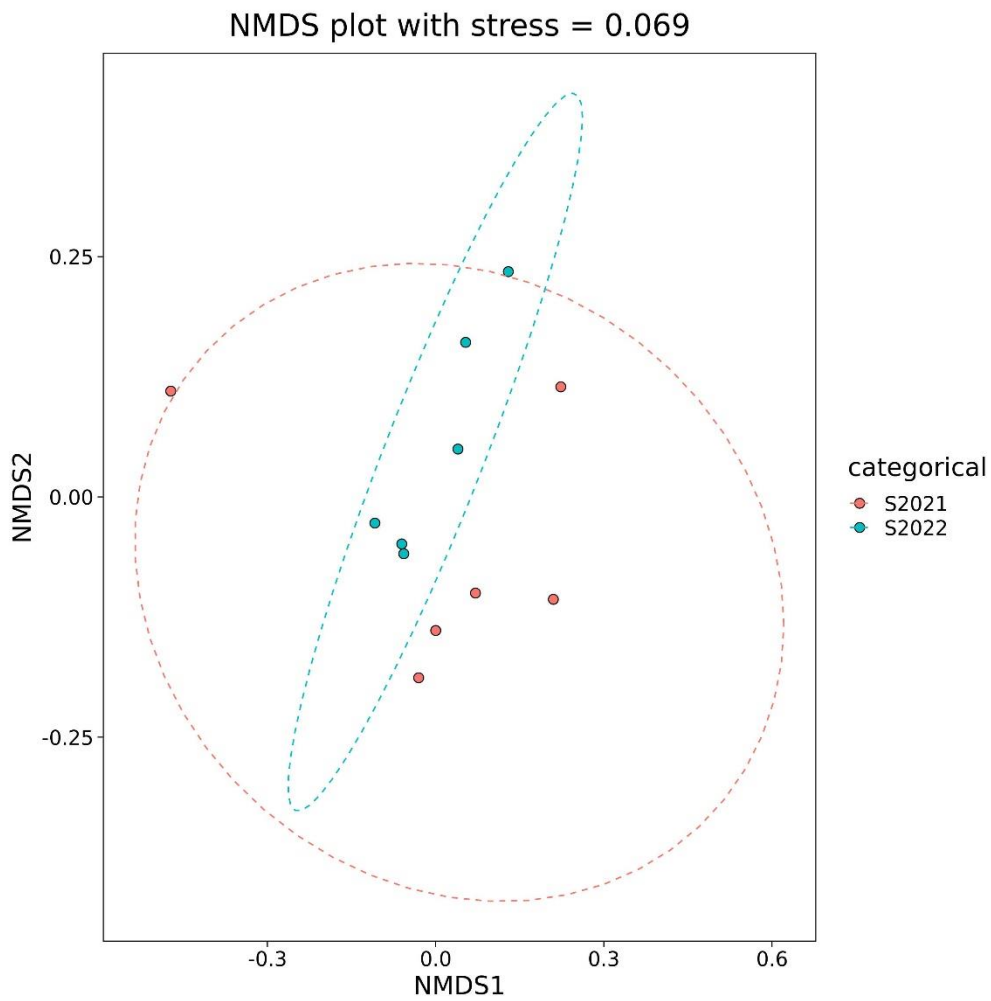


圖 9、110 與 111 年太平島海洋菌種β歧異度指標空間排序分析圖(nMDS)

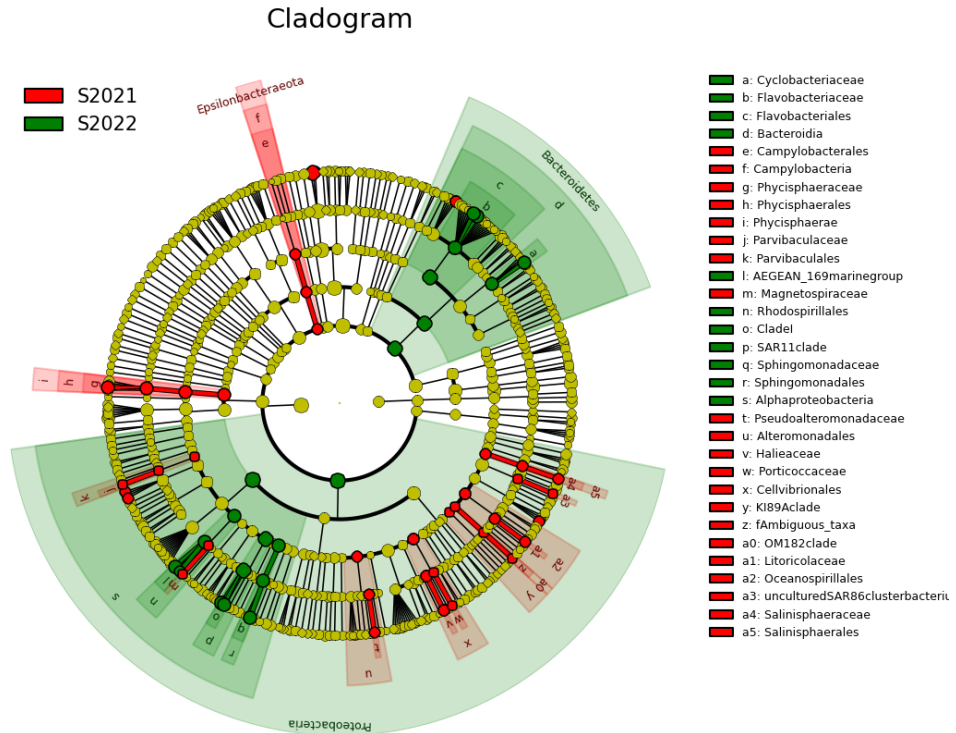


圖 10、110 與 111 年太平島海洋菌種 16S rDNA LEfSe 進化分支圖(紅色為 110 年，綠色為 111 年)

### (三) 菌落功能預測分析

為評估菌落的基因功能及可能的生物代謝途徑，以KEGG PATHWAY資料庫，進行Tax4Fun菌落功能預測分析(圖11)，110年的菌種之功能預測與外源物生物分解及代謝相關功能之菌落相對豐度較高，111年則以與碳、能量代謝相關之菌落相對豐度較高。

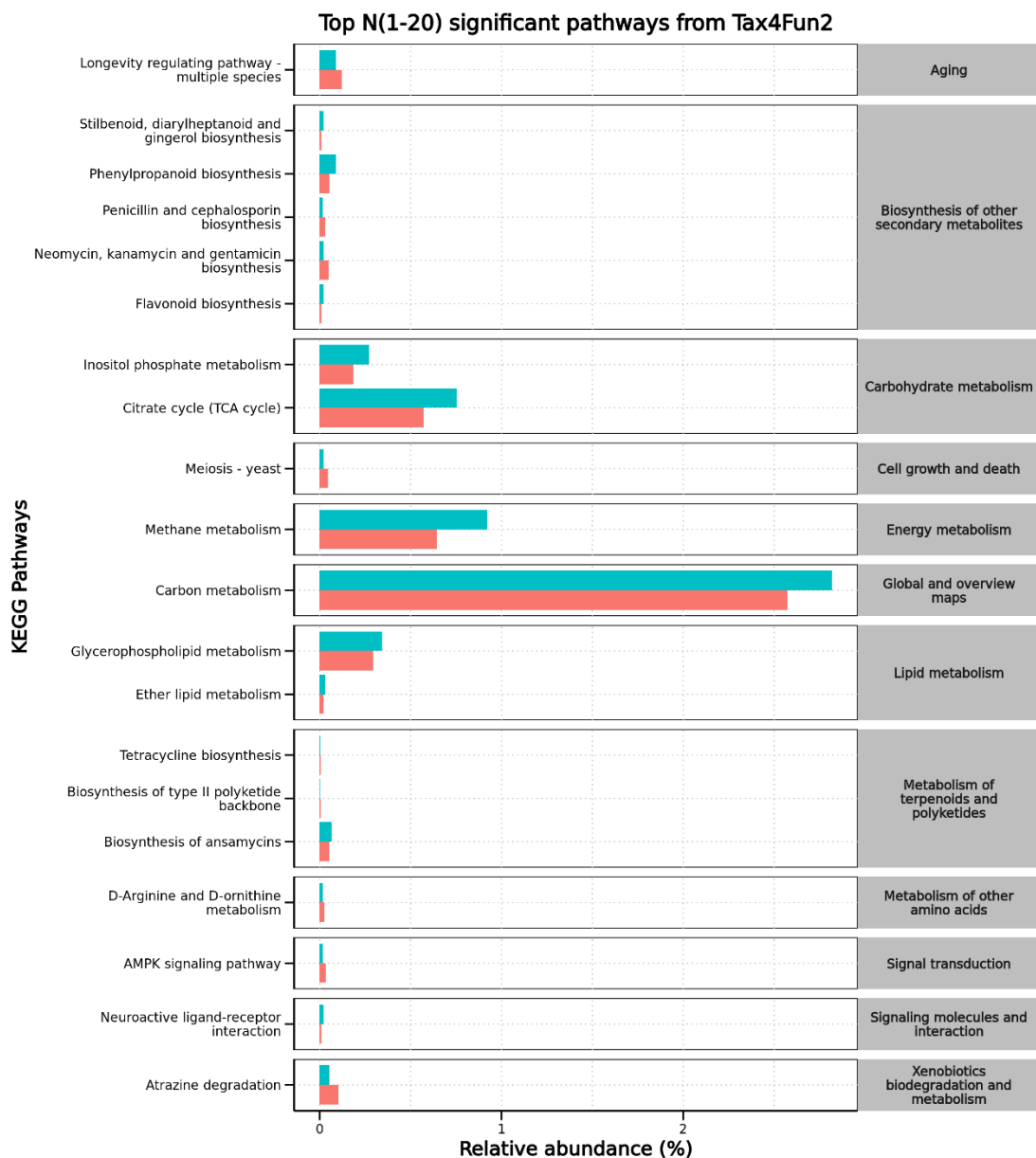


圖 11、110 與 111 年太平島海洋菌種 Tax4Fun 菌落功能預測分析圖

## 第二節 真核生物

真核生物18S基因片段NGS之檢出率為100%，以下以8測站、3重複水樣中取其中之1進行真核生物種類分析。

### 一、生物種類分析

以環境DNA 18S片段次世代定序結果，本研究總計發現48門1,204科(表3、附錄二)，110年發現41門590科，111年則發現46門961科，由圖12與圖13可見太平島110與111年不同測站科層集物種豐富度前十的真核生物組成變化，刺絲胞

動物門(Cnidaria)111年科層級數高於110年(分別為72、11科)，其中珊瑚綱(Anthozoa)、水螅綱(Hydrozoa)之物種數皆有增加之情形，將於後方段落進一步探討石珊瑚等關注海洋生物；海綿動物門(Porifera)111年科層級數高於110年(分別為62、21科)，其中鈣質海綿綱(Calcarea)、尋常海綿綱(Demospongiae)之物種數皆有增加之情形，推測在部分珊瑚死亡的原棲地可能被海綿取代；擔子菌門(Basidiomycota)則於110年高於111年(分別為45、24科)，推測有陸源淡水注入影響而帶來擔子菌孢子。

從110與111年太平島不同測站海洋真核生物CLUSTER分析(圖14)顯示，不同年間的生物組成可獨立分群，以MDS分析(圖15)也有類似的結果。

以18S基因序列進行南沙太平島周邊八個測站的環境DNA，發現很多不同類型之海洋真核生物(如附錄三)，因大部分真核生物很難以肉眼觀察，除非個別針對不同的真核生物類群採取不同採樣方法進行採集並在顯微鏡下觀察外，很難發現這些生物的存在。這時以環境DNA分析進行各類群真核生物的分析就成為非常有效率的分析方法，但同樣得考慮核酸引子的通用性及可供比對序列的變異性。

表 3、110 與 111 年太平島環境 DNA 海洋真核生物總科層級數

	110年	111年
TP01	289	530
TP02	304	300
TP03	261	339
TP04	265	486
TP05	233	511
TP06	232	403
TP07	274	372
TP08	241	337
當年度	590	961
總計	1,204	

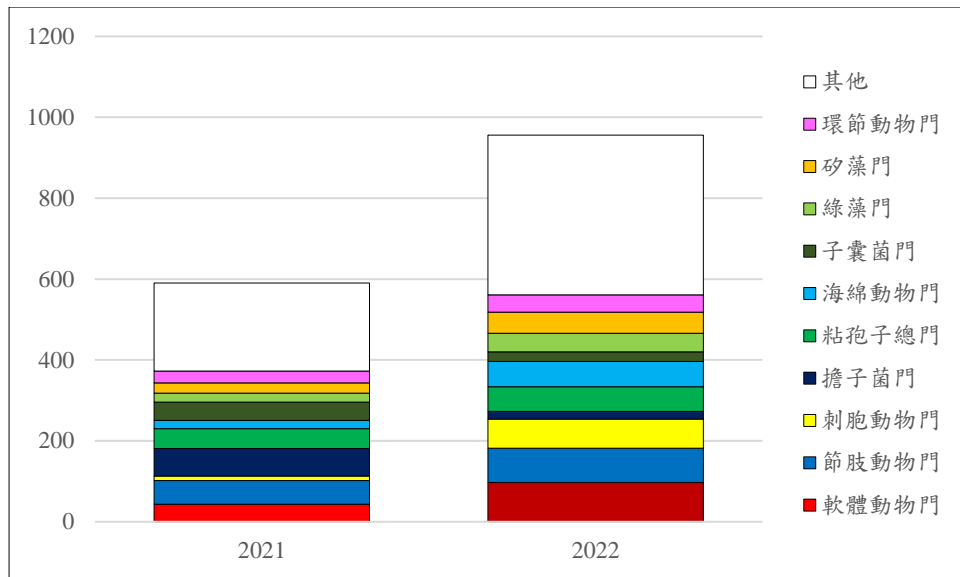


圖 12、110 與 111 年太平島科層級物種豐富度前十的真核生物

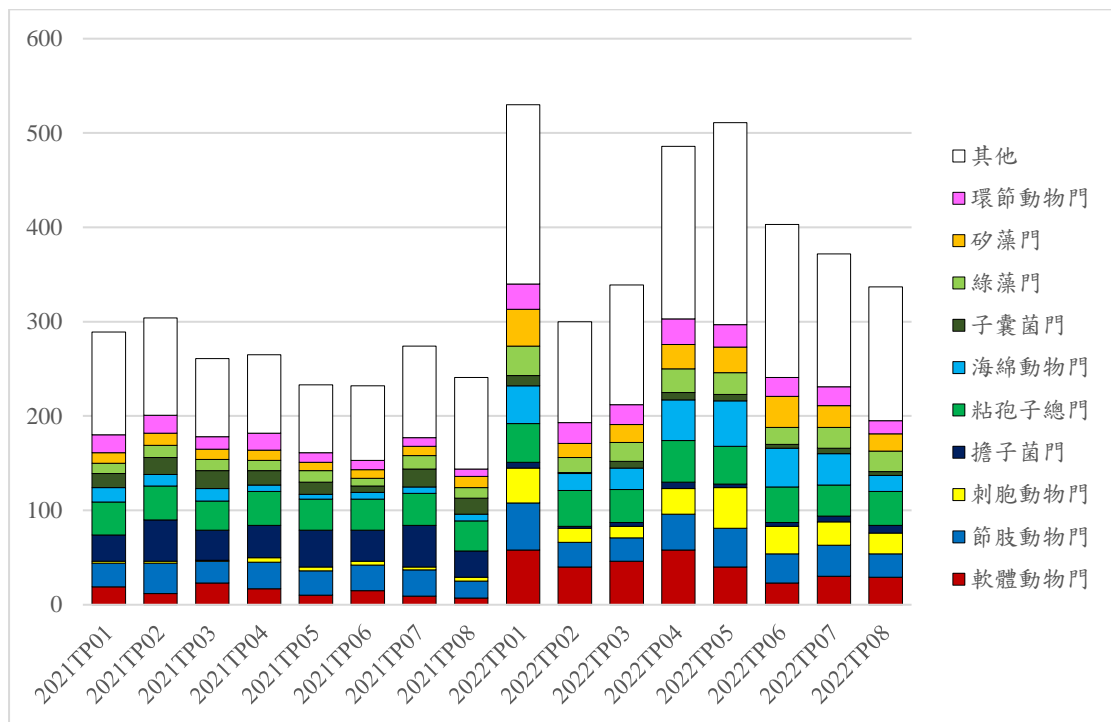


圖 13、110 與 111 年太平島不同測站科層級物種豐富度前十的海洋真核生物

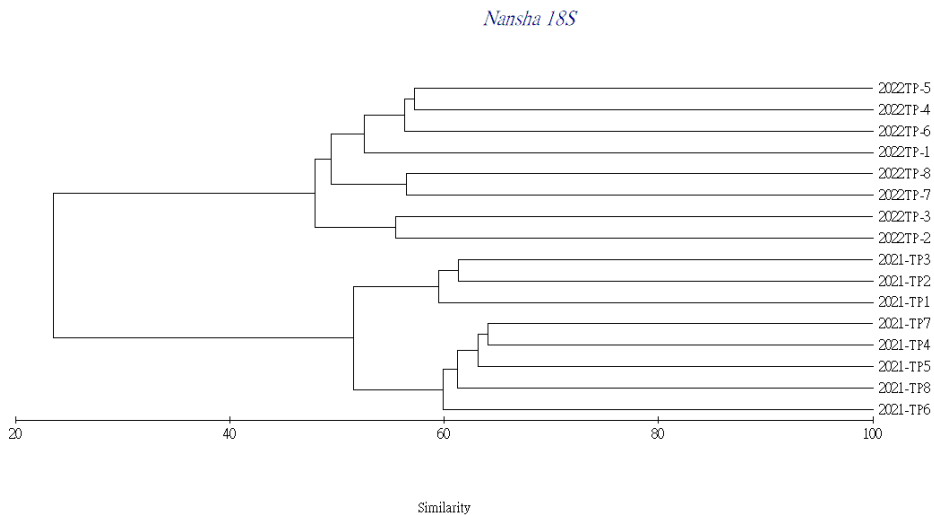


圖 14、110 與 111 年太平島不同測站海洋真核生物群歸分析(CLUSTER)

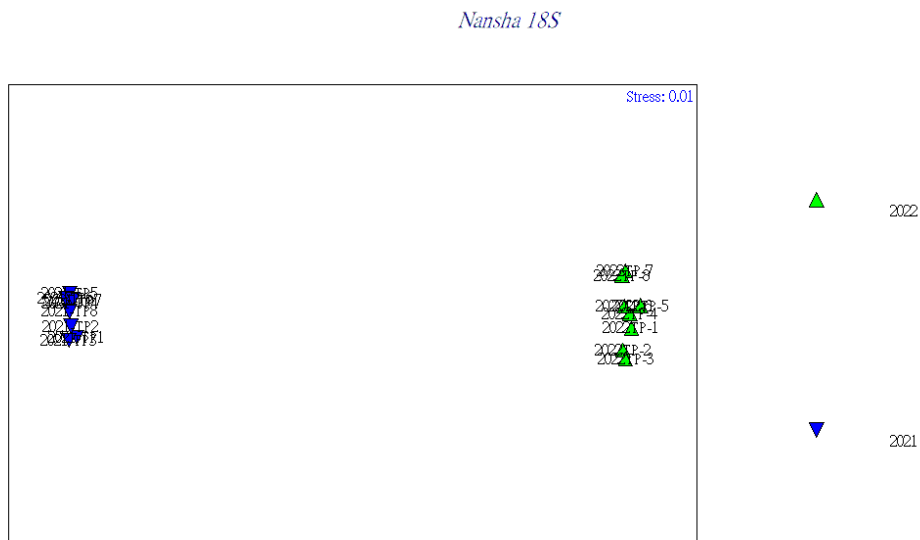


圖 15、110 與 111 年太平島不同測站海洋真核生物空間排序分析(MDS)

## 二、關注之海洋真核生物

本研究關注之海洋真核生物包含石珊瑚、棘冠海星及大型藻類等海洋生物。石珊瑚方面，以環境DNA 18S片段次世代定序結果，本研究總計發現13科32種，110年僅發現2科(微孔珊瑚科、葵珊瑚科)2種，111年發現13科31種，其中不同測站間石珊瑚科層級數量(圖16)，以太平島西北測站(TP01)及太平島西南測站(TP05)最高，離太平島較遠的西南方淺水(TP07)及中洲礁(TP08)的石珊瑚科層級數量則相對較少。值得注意的是，本研究期間棘冠海星DNA序列於110年太平島東北測站(TP02)及太平島正東測站(TP03)有出現，而111年各測站則皆無。大型藻類方面，本研究總計發現3門38科93種，紅藻門(Rhodophyta) 19科56種，綠藻門(Chlorophyta) 11科24種，淡色藻門(Ochrophyta) 8科13種；不同年間大型藻類種類大幅增加，110年僅發現7科9種，111年發現38科92種。

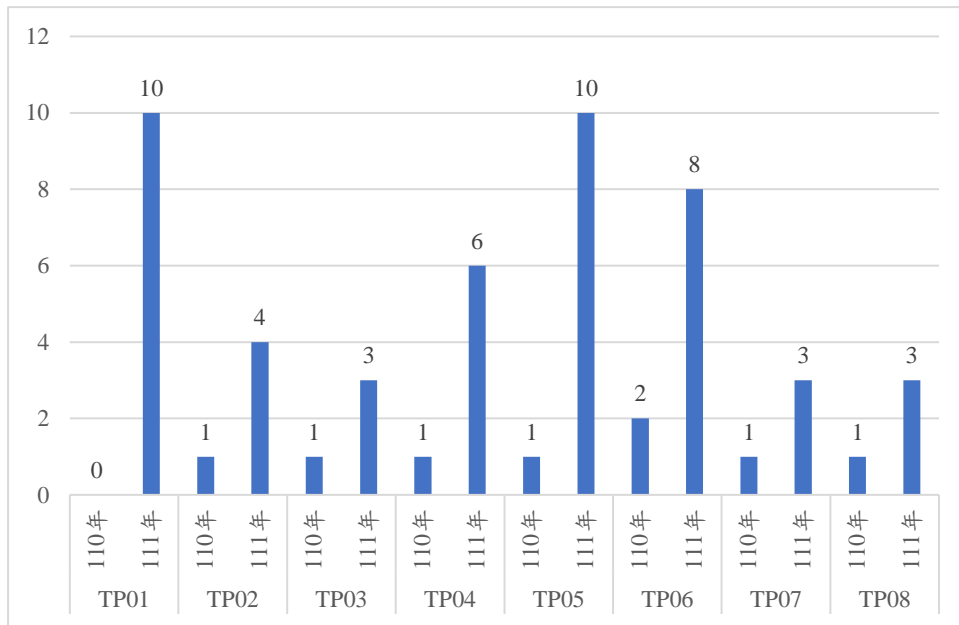


圖 16、110 與 111 年太平島不同測站石珊瑚科層級數量

### 第三節 海水魚類

以12S基因序列進行南沙太平島周邊八個測站的環境DNA結果發現，在110年和111年的調查中，魚類組成的差異性相當大。110年總計發現了34科44屬58種(13種未知)，除了一些大型海水硬骨魚、軟骨魚及少數珊瑚礁魚類外，出現了一些陸源性及沿岸性的魚類；111年總計發現了31科50屬81種(3種未知)，除了一些大型海水硬骨魚及軟骨魚外，主要以珊瑚礁魚類為主及一些中層水域之燈籠科魚類。相關調查結果如附錄四所示。在兩年間所發現的133種魚類當中有32種是過去曾經在南沙太平島有發現過的物種，另外101種在臺灣魚類資料庫的紀載中並無在南沙被發現過，可能的原因在於南沙地處偏遠，過去對南沙的調查並不多。

以PRIMER進行CLUSTER分析結果(圖17)，顯示110年和111年間的相似度只有21%，110年地點間的相似度高達70%，肇因於物種種類少且各地點間均質性較高；111年地點間的相似度比較低，肇因於魚種多樣性較高且分布均質性較低。MDS分析(圖18)同樣顯示110年和111年分群明顯，110年地點間分布較集中；111年地點間分布較分散。

大型軟骨魚類是過去在南沙太平島較不易發現的類群，由環境DNA的分析結果顯示，在110年大眼長尾鯊(*Alopias superciliosus*)、大青鯊(*Prionace glauca*)及長臂鯖鯊(*Isurus paucus*)在南沙太平島周遭海域出現；111年的調查除了同樣出現大眼長尾鯊(*A. superciliosus*)外，多了淺海狐鯊(*Alopias pelagicus*)、鮫鯊(*Galeocerdo cuvier*)及尖吻鯖鯊(*Isurus oxyrinchus*)等大型軟骨魚類(圖19)。

110年出現的沿岸性魚類包括烏魚(*Mugil cephalus*)隱蔽種NWP2及NWP3，此兩種烏魚隱蔽種過去在中南半島也有發現過，其直接或透過遺傳物質間接傳送到南沙群島的機會大，特別是在颱風過後大量陸源性遺傳物質沖刷下海，包括一些淡水魚類或食用性及養殖性魚種(*Reinogobius gigas*, *Oreochromis niloticus*)等。

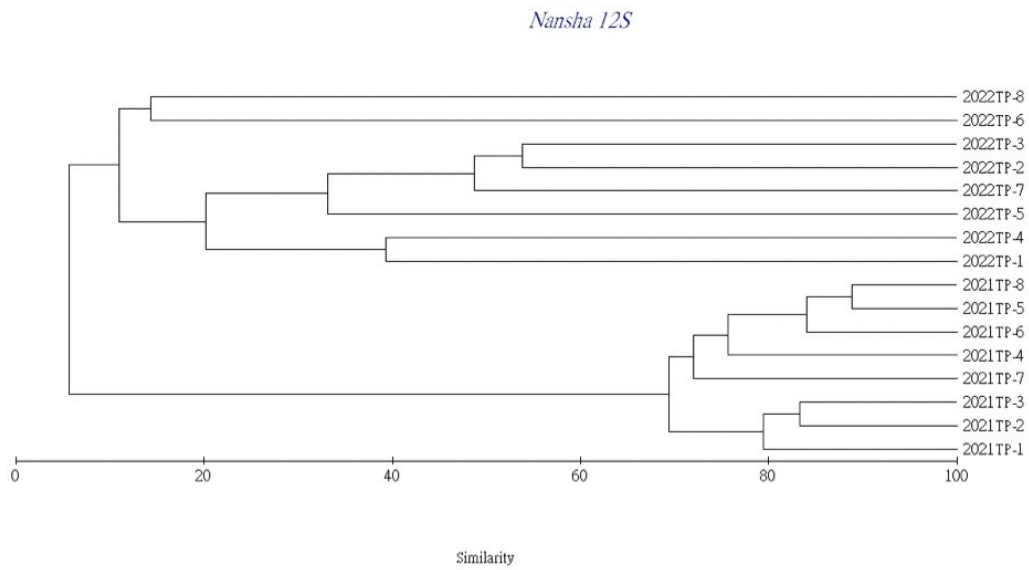


圖 17、110 與 111 年太平島不同測站海水魚類群歸分析(CLUSTER)

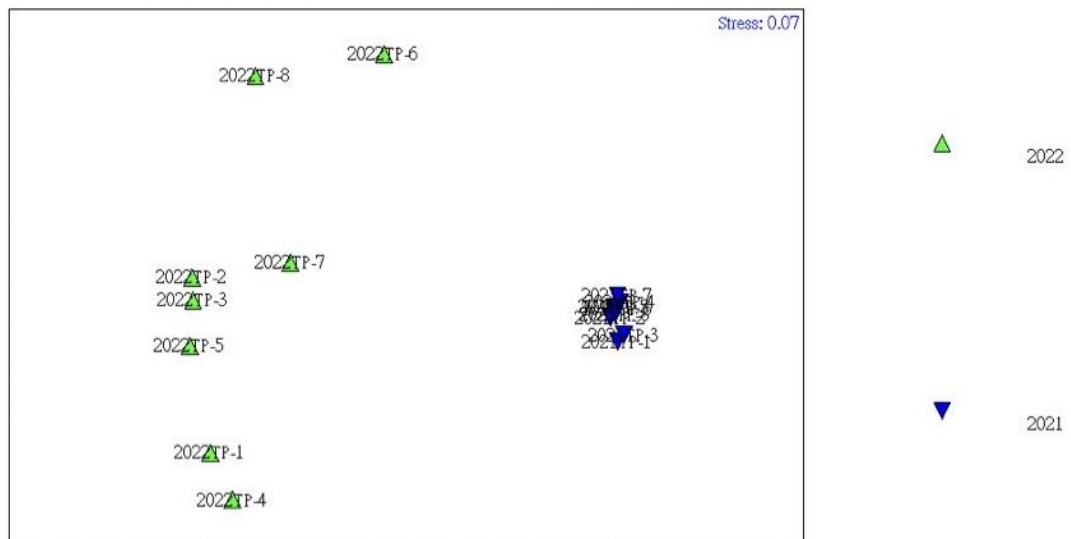


圖 18、110 與 111 年太平島不同測站海水魚類空間排序分析(MDS)

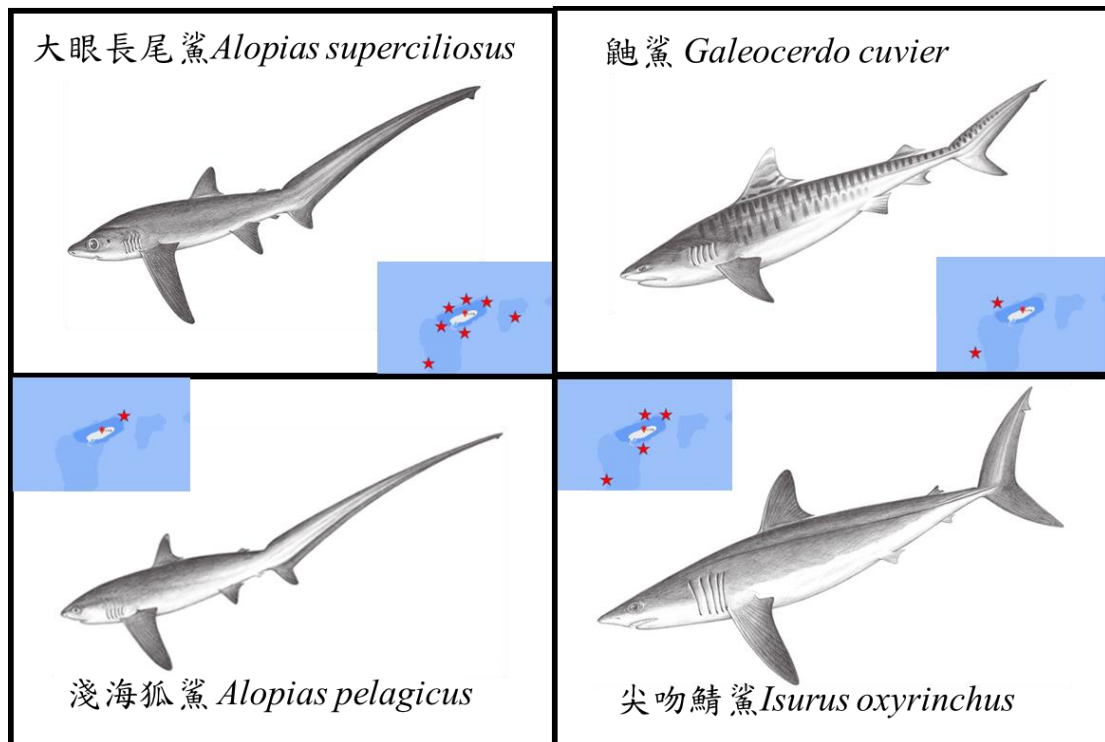


圖 19、111 年太平島軟骨魚類種類及分布測站(圖片來源：臺灣魚類資料庫)

#### 第四節 討論

依據本院110年西南海域珊瑚礁生態監測調查報告(鄭等, 2021)，110年太平島珊瑚大量死亡時，於7至10公尺水深處毛叢狀海藻覆蓋率超過70%，推測可能為鞘絲藻屬(*Lyngbya* sp.)之藍菌，為本研究110年海洋菌種優勢物種。依據海保署111年南沙太平島周邊海域棘冠海星與珊瑚礁生態監測報告初步結果(鄭等, 2022)，棘冠海星密度降低，大型藻類覆蓋率增加，並有珊瑚入添的情形。

綜合本研究結果，110年至111年間海洋菌種、真核生物及海水魚類等組成皆有明顯差異，並以真核生物數據，可推測111年太平島棘冠海星數量的減少，在部分珊瑚死亡的原棲地可能被大型藻類或海綿所取代，使得藻類覆蓋率可能增加，而石珊瑚也有新添入之情形，可推測珊瑚礁生態系應有恢復之趨勢，而110年太平島西南測站(TP05)與其他測站的生物組成較為不同，推測與鄰近碼頭及人口聚集處等人為干擾有關。本研究展現了以環境DNA技術輔助偏遠島嶼的珊瑚礁生態監測之潛力。

## 第四章 研究發現與建議

### 一、研究主要發現

以環境 DNA 資訊蒐集結果顯示，太平島 110 年及 111 年之海洋菌種、真核生物及海水魚類等海洋生物組成有年間差異，可能與太平島海域環境改善、珊瑚礁生態系恢復有關，說明如下：

- (一)海洋菌種(16S)：菌種多樣性回升，原以藍菌為優勢之菌種減少，物種均勻度增加。
- (二)真核生物(18S)：真核生物種類增加，原劣化棲地由大型藻類、海綿取代，並有石珊瑚新入添。
- (三)海水魚類(12S)：魚種數增加，物種組成由沿岸性魚類轉為珊瑚礁及中層魚類。

### 二、環境 DNA 研究建議

- (一)建立南沙太平島環境 DNA 對照基準：持續蒐集南沙太平島環境 DNA 生物資訊，增加採樣頻率，以了解珊瑚礁生態系恢復之情形。
- (二)應用環境 DNA 技術輔助偏遠地區生態監測：本研究採樣方法人力及成本低、步驟簡單、檢出率高，可運用於偏遠地區海洋生態長期監測，作為與一般調查方法之參照資料。
- (三)臺灣海域海洋生物基因資料庫之擴充：研究調查中發現有些基因序列無法比對到相似的物種，顯示可供比對的環境 DNA 基因庫還是有很大的擴增空間，應積極建立可供臺灣比對的海洋生物基因庫。

## 第五章 結 論

環境 DNA 是調查海洋生物的一種分子生物學方法，具有效率高等特性，特別是針對稀少、不容易觀察到的生物，也可以減少採樣造成的生物傷亡，但須建立在核酸引子的有效性及比對基因庫的多樣性及正確性，未來須有更多研究以突破此限制。

## 謝 誌

感謝海洋委員會海巡署東南沙分署及艦隊分署於 110 至 111 年協助本研究南沙太平島海水樣本採集、保存及運送；感謝海洋委員會海洋保育署提供 111 年珊瑚礁生態監測報告資訊；感謝國立中山大學海洋生物科技暨資源學系劉商隱副教授於研究期間惠予寶貴意見。



## 附 錄

附錄一、以 16S 基因序列發現之南沙太平島環境 DNA 海洋菌種屬層級名錄

genus	110年						111年					
	TP01	TP02	TP03	TP04	TP05	TP06	TP01	TP02	TP03	TP04	TP05	TP06
Archaea;Euryarchaeota;Thermoplasmata;Marine.Group.II;__;_	0	0	0	0	0	0.002055675	0	0	0.00143575	0	0.003914	0.003175023
Archaea;Euryarchaeota;Thermoplasmata;Marine.Group.II;marine.metagenome;marine.metagenome	0	0	0	0	0	0.006680942	0	0.008758087	0	0	0.005916092	0
Archaea;Euryarchaeota;Thermoplasmata;Marine.Group.II;uncultured.archaeon;uncultured.archaeon	0	0	0	0	0	0	0	0	0	0	0.00299412	0.004663315
Archaea;Euryarchaeota;Thermoplasmata;Marine.Group.II;unidentified.archaeon;unidentified.archaeon	0	0	0	0	0	0.00137045	0	0	0	0	0	0.002215902
Bacteria;__;__;__;__	0.245354501	0.261364357	0.254496241	0.361334157	0.231168104	0.183925767	0.346023238	0.326258482	0.441455397	0.390192443	0.393961257	0.377133219
Bacteria;Acidobacteria;Blastocatellia;(Subgroup.4);11-24;__;_	0	0	0	0	0.004305576	0	0	0	0	0	0	0
Bacteria;Actinobacteria;Acidimicrobiia;Actinomarinales;Actinomarinales;Candidatus.Actinomarina	0.091962836	0.045394028	0.062756892	0.039800803	0.004878764	0.09958601	0.073992076	0.029824838	0.025767937	0.061473052	0.052252805	0.025400185
Bacteria;Actinobacteria;Acidimicrobiia;Microtrichales;Microtrichaceae;Sva0996.marine.group	0.000796801	0.000301148	0	0	0	0.002255532	0.001148583	0.003432223	0	0	0.000541106	0.002414341
Bacteria;Actinobacteria;Actinobacteria;Corynebacteriales;Corynebacteriaceae;__	0	0	0	0.002586473	0	0	0	0	0	0	0	0
Bacteria;Actinobacteria;Actinobacteria;Corynebacteriales;Corynebacteriaceae;Corynebacterium.1	0	0	0	0	0.004265586	0	0	0	0	0	0	0
Bacteria;Actinobacteria;Actinobacteria;Corynebacteriales;Corynebacteriaceae;Lawsonella	0	0	0	0	0.002599342	0	0	0.000631214	0	0	0	0
Bacteria;Actinobacteria;Actinobacteria;Corynebacteriales;Mycobacteriaceae;Mycobacterium	0	0	0	0.003049722	0.0030259	0	0	0	0.002569237	0	0	0
Bacteria;Actinobacteria;Actinobacteria;Frankiales;Sporichthyaceae;hgI.clade	0	0	0	0	0.006878258	0	0	0	0	0	0	0

genus	110年						111年					
	TP01	TP02	TP03	TP04	TP05	TP06	TP01	TP02	TP03	TP04	TP05	TP06
Bacteria;Actinobacteria;Actinobacteria;Micrococcales;Intrasporangiaceae;	0	0	0	0	0	0.000856531	0	0	0	0	0	0
Bacteria;Actinobacteria;Actinobacteria;Micrococcales;Microbacteriaceae;	0	0	0	0	0.002639331	0	0	0	0	0	0	0
Bacteria;Actinobacteria;Actinobacteria;Micrococcales;Microbacteriaceae;Aurantimicrobium	0	0	0	0	0.003599088	0	0	0	0	0	0	0
Bacteria;Actinobacteria;Actinobacteria;Micrococcales;Microbacteriaceae;Candidatus.Aquiluna	0	0	0	0	0.005291993	0	0	0	0	0	0	0
Bacteria;Actinobacteria;Actinobacteria;Micrococcales;Microbacteriaceae;Leifsonia	0	0	0	0.004092032	0	0	0	0	0	0	0	0
Bacteria;Actinobacteria;Actinobacteria;Micrococcales;Microbacteriaceae;MWH-Ta3	0	0	0	0	0.003945667	0	0	0	0	0	0	0
Bacteria;Actinobacteria;Actinobacteria;Micrococcales;Micrococaceae;Rothia	0	0	0	0	0.001919514	0	0	0	0	0	0	0
Bacteria;Actinobacteria;Actinobacteria;PeM15;Ambiguous_taxa;Ambiguous_taxa	0	0	0	0	0.007558085	0	0	0	0	0	0	0
Bacteria;Actinobacteria;Actinobacteria;Propionibacteriales;Propionibacteriaceae;Cutibacterium	0	0	0	0	0.002532692	0	0	0	0	0	0	0
Bacteria;Bacteroidetes;Bacteroidia;Bacteroidales; ;	0	0.000110949	0	0.000733477	0	0.001227695	0	0	0.001133487	0	0	0
Bacteria;Bacteroidetes;Bacteroidia;Bacteroidales;Bacteroidaceae;Bacteroides	0	0	0	0	0.001532945	0	0	0	0	0	0	0
Bacteria;Bacteroidetes;Bacteroidia;Bacteroidales;Bacteroidales_RF16_group;unculturedbacterium	0	0	0	0	0	0	0	0	0.001020138	0	0	0
Bacteria;Bacteroidetes;Bacteroidia;Bacteroidales;Marinifilaceae;Marinifilum	0	0	0	0.001852996	0	0.000599572	0	0	0	0	0	0
Bacteria;Bacteroidetes;Bacteroidia;Bacteroidales;Marinifilaceae;uncultured	0	0	0	0	0	0	0	0	0	0	0	0.000115756
Bacteria;Bacteroidetes;Bacteroidia;Bacteroidales;Muribaculaceae;unculturedbacterium	0	0	0	0.000579061	0	0	0	0	0	0	0	0

genus	110年						111年					
	TP01	TP02	TP03	TP04	TP05	TP06	TP01	TP02	TP03	TP04	TP05	TP06
Bacteria;Bacteroidetes;Bacteroidia;Bacteroidales;Porphyromonadaceae;Porphyromonas	0	0	0	0	0.002132793	0	0	0	0	0	0	0
Bacteria;Bacteroidetes;Bacteroidia;Bacteroidales;Rikenellaceae;Alistipes	0	0	0	0.001466955	0	0.000456817	0	0	0.001133487	0	0	0
Bacteria;Bacteroidetes;Bacteroidia;Bacteroidales;Tannerellaceae;Macellibacteroides	0	0	0	0	0	0.001598858	0.000532676	0	0.001246836	0	0	0.000148829
Bacteria;Bacteroidetes;Bacteroidia;Bacteroidales;Tannerellaceae;uncultured	0	0	0	0	0	0	0	0.001814739	0	0	0	0
Bacteria;Bacteroidetes;Bacteroidia;Chitinophagales;Saprospiraceae;	0	0	0	0.00084929	0	0.00137045	0	0	0	0	0	0
Bacteria;Bacteroidetes;Bacteroidia;Chitinophagales;Saprospiraceae;Phaeodactylibacter	0	0	0	0.001389747	0	0	0	0	0	0	0	0
Bacteria;Bacteroidetes;Bacteroidia;Chitinophagales;Saprospiraceae;uncultured	0	0.000380397	0	0.001158122	0	0.002683797	0.000382861	0.002011993	0	0	0	0.000463024
Bacteria;Bacteroidetes;Bacteroidia;Chitinophagales;uncultured;uncultured.Bacteroidetes.bacterium	0	0	0	0	0	0.000599572	0	0	0	0	0	0
Bacteria;Bacteroidetes;Bacteroidia;Cytophagales;Amoebophila ceae;Candidatus.Amoebophilus	0	0	0	0.001466955	0	0	0	0	0	0	0	0
Bacteria;Bacteroidetes;Bacteroidia;Cytophagales;Amoebophila ceae;uncultured	0	0	0	0.000579061	0	0	0	0.000710115	0.001738013	0	0	0
Bacteria;Bacteroidetes;Bacteroidia;Cytophagales;Cyclobacteriaceae;Algoriphagus	0	0	0	0	0.003932337	0	0	0	0	0	0	0
Bacteria;Bacteroidetes;Bacteroidia;Cytophagales;Cyclobacteriaceae;Marinoscillum	4.51E-05	0.000412097	0.000441103	0.0018916	0.000813127	0.002912206	0.006675101	0.004260691	0.004571731	0.00783198	0.009830093	0.020290382
Bacteria;Bacteroidetes;Bacteroidia;Cytophagales;Cyclobacteriaceae;Persicobacter	6.01E-05	0	0	0.002740889	0	0	0	0	0	0	0	0
Bacteria;Bacteroidetes;Bacteroidia;Cytophagales;Cyclobacteriaceae;Reichenbachiella	0	0	0	0	0	0.001513205	0	0	0	0	0	0
Bacteria;Bacteroidetes;Bacteroidia;Cytophagales;Cyclobacteriaceae;uncultured	0	0	0	0	0	0.001256246	0	0	0	0	0	0

genus	110年						111年					
	TP01	TP02	TP03	TP04	TP05	TP06	TP01	TP02	TP03	TP04	TP05	TP06
Bacteria;Bacteroidetes;Bacteroidia;Cytophagales;Flammeovirgaceae;Flammeovirga	0	0	0	0.000463249	0	0.000485368	0	0	0	0	0	0
Bacteria;Bacteroidetes;Bacteroidia;Cytophagales;Flammeovirgaceae;Flexithrix	0	0	0	0.000617665	0	0	0	0	0	0	0	0
Bacteria;Bacteroidetes;Bacteroidia;Cytophagales;Spirosomaceae;Emticicia	0	0	0	0	0.005078713	0	0	0	0	0	0	0
Bacteria;Bacteroidetes;Bacteroidia;Cytophagales;Spirosomaceae;Pseudarcicella	0	0	0	0	0.001812874	0	0	0	0	0	0	0
Bacteria;Bacteroidetes;Bacteroidia;Flavobacteriales;Crocinitomacaceae;Crocinitomix	0	0	0	0	0	0.000456817	0	0	0	0	0	0
Bacteria;Bacteroidetes;Bacteroidia;Flavobacteriales;Crocinitomacaceae;Fluviicola	6.01E-05	0	0	0	0.006598328	0	0	0	0	0.00028859	0.000297658	
Bacteria;Bacteroidetes;Bacteroidia;Flavobacteriales;Crocinitomacaceae;uncultured	0	0	0	0	0.006651648	0	0	0	0	0	0	0
Bacteria;Bacteroidetes;Bacteroidia;Flavobacteriales;Cryomorphaceae;	0	0	0	0	0	0.000199857	0	0	0	0	0	0
Bacteria;Bacteroidetes;Bacteroidia;Flavobacteriales;Cryomorphaceae;uncultured	0.006449576	0.002963926	0.002205514	0.001312539	0.023287434	0.004282655	0.010487066	0	0.002682586	0.014513139	0.003823816	0.001587512
Bacteria;Bacteroidetes;Bacteroidia;Flavobacteriales;Flavobacteriaceae;	0	0.000237748	0	0.001158122	0.00309255	0.000428266	0	0	0.000755658	0.000607378	0	0
Bacteria;Bacteroidetes;Bacteroidia;Flavobacteriales;Flavobacteriaceae;Algitalia	0	0	0	0	0	0	0.00029963	0	0	0	0	0
Bacteria;Bacteroidetes;Bacteroidia;Flavobacteriales;Flavobacteriaceae;Aquibacter	0	0	0.000340852	0	0	0	0	0	0	0	0	0
Bacteria;Bacteroidetes;Bacteroidia;Flavobacteriales;Flavobacteriaceae;Aurantivirga	0	0	0	0	0	0	0	0	0	0.001374592	0	0
Bacteria;Bacteroidetes;Bacteroidia;Flavobacteriales;Flavobacteriaceae;Aureicoccus	0	3.17E-05	0	0	0	0	0	0	0	0.000799182	0	0
Bacteria;Bacteroidetes;Bacteroidia;Flavobacteriales;Flavobacteriaceae;Capnocytophaga	0	0	0	0.001003706	0	0	0	0	0.001284619	0	0	0

genus	110年						111年					
	TP01	TP02	TP03	TP04	TP05	TP06	TP01	TP02	TP03	TP04	TP05	TP06
Bacteria;Bacteroidetes;Bacteroidia;Flavobacteriales;Flavobacteriaceae;Dokdonia	0	0	0	0	0	0.000256959	0	0	0	0	0	0
Bacteria;Bacteroidetes;Bacteroidia;Flavobacteriales;Flavobacteriaceae;Flavobacterium	0	0	0	0	0.008744451	0	0	0	0	0	0	0
Bacteria;Bacteroidetes;Bacteroidia;Flavobacteriales;Flavobacteriaceae;Formosa	0.000255578	0	0	0	0	0	0	0	0	0	0	0
Bacteria;Bacteroidetes;Bacteroidia;Flavobacteriales;Flavobacteriaceae;Lutibacter	0	0	0	0	0.004758794	0	0	0	0	0	0	0
Bacteria;Bacteroidetes;Bacteroidia;Flavobacteriales;Flavobacteriaceae;Marixanthomonas	0	0	0.000180451	0	0	0.001570307	0	0	0	0	0	0
Bacteria;Bacteroidetes;Bacteroidia;Flavobacteriales;Flavobacteriaceae;NS2b.marine.group	0.013365205	0.015453623	0.013112782	0.011233786	0.014423013	0.020099929	0.024286713	0.028207354	0.015831035	0.023623809	0.033728942	0.030675354
Bacteria;Bacteroidetes;Bacteroidia;Flavobacteriales;Flavobacteriaceae;NS4.marine.group	0.022505863	0.02074748	0.020932331	0.020691785	0.004625495	0.025210564	0.020840963	0.017831782	0.012959535	0.014097564	0.01825331	0.020224236
Bacteria;Bacteroidetes;Bacteroidia;Flavobacteriales;Flavobacteriaceae;NS5.marine.group	0.009366168	0.006197299	0.006496241	0.004092032	0	0.008936474	0.014815061	0.013492189	0.007745494	0.01566396	0.013563724	0.01063302
Bacteria;Bacteroidetes;Bacteroidia;Flavobacteriales;Flavobacteriaceae;Pseudofulvibacter	0	0	0	0	0	0.000999286	0	0	0	0	0	0
Bacteria;Bacteroidetes;Bacteroidia;Flavobacteriales;Flavobacteriaceae;Psychroflexus	0	0	0	0	0	0	0	0.001222976	0	0	0	0
Bacteria;Bacteroidetes;Bacteroidia;Flavobacteriales;Flavobacteriaceae;Seonamhaeicola	0	0	0	0	0	0.000599572	0	0	0	0	0	0
Bacteria;Bacteroidetes;Bacteroidia;Flavobacteriales;Flavobacteriaceae;Tenacibaculum	0	0	0	0	0	0	0	0	0	0	0	0.001339463
Bacteria;Bacteroidetes;Bacteroidia;Flavobacteriales;Flavobacteriaceae;uncultured	0.000796801	0	0	0.000694873	0.010117437	0	0.001431568	0	0.000982355	0.004827057	0	0
Bacteria;Bacteroidetes;Bacteroidia;Flavobacteriales;Flavobacteriaceae;Wenyinzhuangia	0	0	0	0	0	0	0	0.001183525	0	0	0	0
Bacteria;Bacteroidetes;Bacteroidia;Flavobacteriales;Flavobacteriaceae;Winogradskyella	0	0	0	0.001737183	0	0	0.001331691	0	0.000491178	0	0	0

genus	110年						111年					
	TP01	TP02	TP03	TP04	TP05	TP06	TP01	TP02	TP03	TP04	TP05	TP06
Bacteria;Bacteroidetes;Bacteroidia;Flavobacteriales;NS7.marine.group;	0.002179927	0.002710328	0.002566416	0.003899012	0.000426559	0.00662384	0.002729966	0.005799274	0	0.002045905	0.004346885	0.003786877
Bacteria;Bacteroidetes;Bacteroidia;Flavobacteriales;NS9.marine.group;	0.00491611	0.005816902	0.00479198	0.005481779	0.004652155	0.008137045	0	0.002761559	0	0	0	0.001141024
Bacteria;Bacteroidetes;Bacteroidia;Flavobacteriales;NS9.marine.group;Ambiguous taxa	0.007877804	0.012616497	0.004270677	0.003281347	0	0.016017131	0	0	0	0	0	0
Bacteria;Bacteroidetes;Bacteroidia;Flavobacteriales;NS9.marine.group;hydrothermal.vent.meta genome	0	0.000507196	0	0	0	0	0	0	0	0	0	0
Bacteria;Bacteroidetes;Bacteroidia;Flavobacteriales;NS9.marine.group;uncultured Flavobacteriales.bacterium	0.003307475	0.003169974	0.001303258	0	0.00603847	0.006138473	0.002213936	0.005207511	0	0.005050828	0	0
Bacteria;Bacteroidetes;Bacteroidia;Flavobacteriales;NS9.marine.group;uncultured Flavobacteria.bacterium	0.001082446	0.001077791	0.000822055	0	0	0.001970021	0.001231814	0.005168061	0	0.000927051	0.000829696	0.000611853
Bacteria;Bacteroidetes;Bacteroidia;Flavobacteriales;NS9.marine.group;uncultured.marine.bacterium	0	0.000142649	0.000200501	0	0	0.000571021	0.000565969	0.00185419	0	0	0.000559143	0.000545707
Bacteria;Bacteroidetes;Bacteroidia;Flavobacteriales;Weeksellaceae;Bergevella	0	0	0	0	0.00306589	0	0	0	0	0	0	0
Bacteria;Bacteroidetes;Rhodothermia;Balneolales;Balneolaceae;Balneola	0	0.000237748	0	0	0	0.001084939	0	0	0	0	0	0
Bacteria;Bacteroidetes;Rhodothermia;Balneolales;Balneolaceae;uncultured	0	0	0.000822055	0	0	0.001827266	0	0	0	0	0	0
Bacteria;Chlamydiae;Chlamydiae;Chlamydiales;	0	0	0	0	0	0.000314061	0	0	0	0	0	0
Bacteria;Chlamydiae;Chlamydiae;Chlamydiales;Simkaniaceae;Candidatus Fritschea	0	0	0	0	0	0	0	0.002011993	0	0	0	0
Bacteria;Chlamydiae;Chlamydiae;Chlamydiales;Simkaniaceae;Simkania	0	0	0	0.002470661	0	0	0	0	0	0	0	0
Bacteria;Chlamydiae;Chlamydiae;Chlamydiales;Simkaniaceae;uncultured	0	0	0	0.001273935	0	0	0	0	0	0	0	0

genus	110年						111年					
	TP01	TP02	TP03	TP04	TP05	TP06	TP01	TP02	TP03	TP04	TP05	TP06
Bacteria;Chloroflexi;Anaerolineae;Caldilineales;Caldilineaceae;uncultured	0	0	0	0.00123533	0	0	0	0	0	0	0	0
Bacteria;Chloroflexi;Chloroflexia;Chloroflexales;Roseiflexaceae;uncultured	0	0	0	0	0.00607846	0	0	0	0	0	0	0
Bacteria;Chloroflexi;Dehalococcoidia;SAR202.clade;metagenome;metagenome	0	0	0	0.000501853	0	0	0	0	0	0	0	0
Bacteria;Cyanobacteria;Melainabacteria;Caenarcaniphilales;uncultured.bacterium;uncultured.bacterium	0	0	0	0	0	0	0	0	0.000793441	0	0	0
Bacteria;Cyanobacteria;Melainabacteria;Caenarcaniphilales;uncultured.cyanobacterium;uncultured.cyanobacterium	0	0	0	0	0	0	0	0	0.000982355	0	0	0
Bacteria;Cyanobacteria;Melainabacteria;Gastranaerophilales;uncultured.bacterium;uncultured.bacterium	0	0	0	0.001968808	0	0	0	0.001656935	0	0	0	0
Bacteria;Cyanobacteria;Melainabacteria;Gastranaerophilales;uncultured.organism;uncultured.organism	0	0	0	0	0	0	0	0	0.000528961	0	0	0
Bacteria;Cyanobacteria;Melainabacteria;Obscuribacterales;uncultured.bacterium.mle1-12;uncultured.bacterium.mle1-12	0	0	0	0	0	0	0	0	0.001662448	0	0	0
Bacteria;Cyanobacteria;Melainabacteria;Vampirovibrionales;uncultured.bacterium;uncultured.bacterium	0	0	0	0	0	0	0	0	0.001020138	0	0	0
Bacteria;Cyanobacteria;Melainabacteria;Vampirovibrionales;uncultured.cyanobacterium;uncultured.cyanobacterium	0	0	0	0	0	0	0	0	0.000793441	0	0	0
Bacteria;Cyanobacteria;Oxyphotobacteria; ; ;	0	0	0	0.003590179	0	0	0	0.000789017	0	0	0	0
Bacteria;Cyanobacteria;Oxyphotobacteria;Nostocales;Microcystaceae;Crocospaera.WH.0003.(UCYN-B)	0	0	0	0.001196726	0	0	0	0	0	0	0	0
Bacteria;Cyanobacteria;Oxyphotobacteria;Nostocales;Microcystaceae;SU2.symbiont_group	0	0	0	0.003242742	0	0	0	0	0	0	0	0

genus	110年						111年					
	TP01	TP02	TP03	TP04	TP05	TP06	TP01	TP02	TP03	TP04	TP05	TP06
Bacteria;Cyanobacteria;Oxyphotobacteria;Nostocales;Microcystaceae;Synechocystis.CCALA.700	0	0	0.000180451	0.001312539	0	0.001227695	0	0	0.002153625	0	0	0
Bacteria;Cyanobacteria;Oxyphotobacteria;Nostocales;Nostocaceae;Richelia.HH01	0	0	0	0.002818098	0	0	0	0	0	0	0	0
Bacteria;Cyanobacteria;Oxyphotobacteria;Nostocales;Nostocaceae;Rivularia.PCC-7116	0	0	0	0	0	0	0	0.00047341	0	0	0	0
Bacteria;Cyanobacteria;Oxyphotobacteria;Nostocales;Nostocales.Incertae.Sedis;Hormoscilla.SI04.45	0	0	0	0.010345893	0	0	0	0	0	0	0	0
Bacteria;Cyanobacteria;Oxyphotobacteria;Nostocales;Phormidiaceae;Planktothrix.NIVA-CYA.15	0	0	0	0.000733477	0.010477346	0	0	0	0	0	0	0
Bacteria;Cyanobacteria;Oxyphotobacteria;Nostocales;Phormidiaceae;Trichodesmium.IMS101	0	0	0	0	0	0	0	0	0	0	0	0.001339463
Bacteria;Cyanobacteria;Oxyphotobacteria;Nostocales;Xenococcaceae;uncultured	0	0	0	0	0	0	0	0.001025722	0	0	0	0
Bacteria;Cyanobacteria;Oxyphotobacteria;Synechococcales;Cyanobiaceae;Cyanobium.PCC-6307	0	0.001109491	0	0.004323657	0.002052813	0.001855817	0	0	0	0	0	0
Bacteria;Cyanobacteria;Oxyphotobacteria;Synechococcales;Cyanobiaceae;Prochlorococcus.MIT9313	0.152700102	0.183668294	0.172631579	0.021656887	0.01835535	0.055189151	0.007607284	0	0	0	0.009036471	0.004084535
Bacteria;Cyanobacteria;Oxyphotobacteria;Synechococcales;Cyanobiaceae;Synechococcus.CC9902	0.122361537	0.119809168	0.10554386	0.03636504	0.011170503	0.101870093	0.078686287	0.045526274	0.064457626	0.099066556	0.064337506	0.016437359
Bacteria;Dadabacteria;Dadabacteriia;Dadabacteriales;marine.metagenome.marine.metagenome	0.001488364	0.001489888	0.001984962	0.001544163	0	0.002655246	0.001065353	0	0	0.00070328	0.001064175	0.001422146
Bacteria;Deinococcus-Thermus;Deinococci;Deinococcales;Deinococcaceae;Deinococcus	0	0	0	0.001003706	0.007838014	0.000571021	0	0	0	0	0	0

genus	110年						111年					
	TP01	TP02	TP03	TP04	TP05	TP06	TP01	TP02	TP03	TP04	TP05	TP06
Bacteria;Deinococcus-Thermus;Deinococci;Thermale s;Thermaceae;Thermus	0	0	0	0	0.002705981	0	0	0	0	0	0	0
Bacteria;Epsilonbacteraeota;Ca mpylobacteria;Campylobactera les;Arcobacteraceae;Arcobacte r	0	0	0	0.000231624	0.004825444	0.000942184	0	0	0	0	0	0
Bacteria;Epsilonbacteraeota;Ca mpylobacteria;Campylobactera les;Sulfurospirillaceae;Sulfuros pirillum	0	0	0	0.000887894	0.004305576	0	0	0	0	0	0	0
Bacteria;Epsilonbacteraeota;Ca mpylobacteria;Campylobactera les;Thiovulaceae;	0	0	0	0	0	0	0	0	0.000604526	0	0	0
Bacteria;Epsilonbacteraeota;Ca mpylobacteria;Campylobactera les;Thiovulaceae;Thiovulum	0	6.34E-05	0	0	0	0	0	0	0	0	0	0
Bacteria;Firmicutes;Bacilli;Bac illales;Alicyclobacillaceae;Alic yclobacillus	0	0	0	0	0.004278916	0	0	0	0	0	0	0
Bacteria;Firmicutes;Bacilli;Bac illales;Bacillaceae;Aeribacillus	0	0	0	0	0.002372732	0.000770878	0	0	0	0	0	0
Bacteria;Firmicutes;Bacilli;Bac illales;Bacillaceae;Anaerobacill us	0	0	0	0	0	0	0	0.002919362	0	0	0	0
Bacteria;Firmicutes;Bacilli;Bac illales;Bacillaceae;Anoxybacill us	0	0	0	0	0.012396859	0	0	0	0	0	0	0
Bacteria;Firmicutes;Bacilli;Bac illales;Bacillaceae;Bacillus	0	0	0	0.01107937	0.014183074	0	0	0	0	0	0	0
Bacteria;Firmicutes;Bacilli;Bac illales;Bacillaceae;Geobacillus	0	0	0	0	0.001612925	0	0	0	0	0	0	0
Bacteria;Firmicutes;Bacilli;Bac illales;Staphylococcaceae;Stap hylcococcus	0	0	0	0	0.003385809	0	0	0	0	0	0	0
Bacteria;Firmicutes;Bacilli;Lac tobacillales;Enterococcaceae;E nterococcus	0	0	0	0	0	0	0	0	0.002984849	0	0	0
Bacteria;Firmicutes;Bacilli;Lac tobacillales;Streptococcaceae;S treptococcus	0	0	0	0.00123533	0	0	0	0	0	0	0	0
Bacteria;Firmicutes;Clostridia; Clostridiales;Caldicoprobactera ceae;Caldicoprobacter	0	0	0	0	0	0	0	0	0.000680092	0	0	0
Bacteria;Firmicutes;Clostridia; Clostridiales;Clostridiaceae.1_	0	0	0	0	0.007278156	0	0	0	0	0	0	0

genus	110年						111年					
	TP01	TP02	TP03	TP04	TP05	TP06	TP01	TP02	TP03	TP04	TP05	TP06
Bacteria;Firmicutes;Clostridia; Clostridiales;Clostridiaceae.1; Clostridium_sensu_stricto.1	0	0	0	0.004323657	0	0.000942184	0	0.001933091	0.001095704	0	0	0
Bacteria;Firmicutes;Clostridia; Clostridiales;Clostridiaceae.1;uncultured	0	0.000174349	0	0.009226374	0	0.000513919	0	0	0.005402955	0	0	0
Bacteria;Firmicutes;Clostridia; Clostridiales;Lachnospiraceae;	0	0	0	0	0.002599342	0	0	0	0	0	0	0
Bacteria;Firmicutes;Clostridia; Clostridiales;Lachnospiraceae; Cellulosilyticum	0	0	0	0.001389747	0	0	0	0	0	0	0	0
Bacteria;Firmicutes;Clostridia; Clostridiales;Lachnospiraceae; Epulopiscium	0	0	0	0.002200432	0	0	0	0	0	0	0	0
Bacteria;Firmicutes;Clostridia; Clostridiales;Lachnospiraceae; Lachnospiraceae.UCG-004	0	0	0	0	0	0	0	0	0.000415612	0	0	0
Bacteria;Firmicutes;Clostridia; Clostridiales;Lachnospiraceae; uncultured	0	0	0	0.002547869	0.004798784	0	0	0	0	0	0	0
Bacteria;Firmicutes;Clostridia; Clostridiales;Lachnospiraceae; Vallitalea	0	0	0	0	0	0	0	0	0.000528961	0	0	0
Bacteria;Firmicutes;Clostridia; Clostridiales;Peptostreptococcaeae;Romboutsia	0	0	0	0.007605003	0.012010291	0	0	0	0	0	0	0
Bacteria;Firmicutes;Clostridia; Clostridiales;Peptostreptococcaeae;Terrisporobacter	0	0	0	0	0	0	0	0.003550576	0	0	0	0
Bacteria;Firmicutes;Clostridia; Clostridiales;Ruminococcaeae; Anaerotruncus	0	0	0	0	0	0	0	0	0	0	7.21E-05	0
Bacteria;Firmicutes;Clostridia; Thermoanaerobacterales;Family.III;Caldicellulosiruptor	0	0	0	0.005134342	0.00918434	0.001627409	0	0	0	0	0	0
Bacteria;Firmicutes;Clostridia; Thermoanaerobacterales;Family.III;Thermoanaerobacterium	0	0	0	0.002702285	0	0	0	0	0	0	0	0
Bacteria;Firmicutes;Erysipelotrichia;Erysipelotrichales;Erysipelotrichaceae;Erysipelatoclostridium	0	0	0	0	0	0	0	0	0.003098198	0	0	0
Bacteria;Firmicutes;Erysipelotrichia;Erysipelotrichales;Erysipelotrichaceae;Erysipelothrix	0	0	0	0	0	0	0	0.001775288	0.002380323	0	0	0

genus	110年						111年					
	TP01	TP02	TP03	TP04	TP05	TP06	TP01	TP02	TP03	TP04	TP05	TP06
Bacteria;Firmicutes;Erysipelotrichia;Erysipelotrichales;Erysipelotrichaceae;Turicibacter	0	0	0	0.000810686	0	0	0	0	0	0	0	0
Bacteria;Fusobacteria;Fusobacteriia;Fusobacteriales;Fusobacteriaceae;Cetobacterium	0	0	0	0.001158122	0	0.000114204	0	0.002011993	0	0	0	0
Bacteria;Gemmatimonadetes;S0134.terrestrial_group;unculturedGemmatimonadetes.bacterium;unculturedGemmatimonadetes.bacterium;unculturedGemmatimonadetes.bacterium	0	0	0	0	0.005531932	0	0	0	0	0	0	0
Bacteria;Kiritimatiellaeota;Kiritimatiellae;Kiritimatiellales;Kiritimatiellaceae;R76-B128	0	0	0	0	0	0.001427552	0.000116523	0.003432223	0	0	0	0
Bacteria;Lentisphaerae;Lentisphaeria;Lentisphaerales;Lentisphaeraeae;Lentisphaera	0	0	0	0	0	0	0	0	0.002493671	0	0	0
Bacteria;Lentisphaerae;Lentisphaeria;Victivallales;unculturedbacterium;unculturedbacterium	0	0	0	0	0	0.001456103	0	0	0	0	0	0
Bacteria;Lentisphaerae;Oligosphaeria;P.palmC41;	0	0	0	0	0	0	0	0	0.001209053	0	0	0
Bacteria;Lentisphaerae;Oligosphaeria;P.palmC41;unculturedbacterium;unculturedbacterium	0	0	0	0.002316245	0	0	0	0	0.004873994	0	0	0
Bacteria;Marinimicrobia(SAR406.clade);	0	0	0.000882206	0	0	0	0	0.001893641	0	0	0.001064175	0.003753803
Bacteria;Marinimicrobia(SAR406.clade);Ambiguous_taxa;Ambiguous_taxa;Ambiguous_taxa	0.001443262	0	0.002345865	0.002586473	0	0.006423983	0.006209009	0.008797538	0	0	0.00207424	0.004812144
Bacteria;Marinimicrobia(SAR406.clade);marine.metagenome;marine.metagenome;marine.metagenome;marine.metagenome	0.000285646	0	0	0	0	0	0	0	0	0	0	0
Bacteria;Marinimicrobia(SAR406.clade);unidentified.marine.bacterioplankton;unidentified.marine.bacterioplankton;unidentified.marine.bacterioplankton;unidentified.marine.bacterioplankton	0	0	0	0	0	0	0	0.002682657	0.000680092	0	0	0

genus	110年						111年					
	TP01	TP02	TP03	TP04	TP05	TP06	TP01	TP02	TP03	TP04	TP05	TP06
Bacteria;Omnitrophicaeota;Omnitrophia;Omnitrophales;Omnitrophaceae;Candidatus.Omnitrophus	0	0	0	0.00104231	0	0	0	0	0.000302263	0	0	0
Bacteria;Omnitrophicaeota;Omnitrophia;uncultured.bacterium;uncultured.bacterium;uncultured.bacterium	0	0	0	0	0	0.000885082	0	0	0	0	0	0
Bacteria;Patescibacteria;Gracilibacteria;Candidatus.Peregrinibacteria;uncultured.bacterium;uncultured.bacterium	0	0	0	0	0	0.00054247	0	0	0	0	0	0
Bacteria;Patescibacteria;Gracilibacteria;Candidatus.Peribacteria;uncultured.bacterium;uncultured.bacterium	0	0	0	0	0.002532692	0	0	0	0	0	0	0
Bacteria;Patescibacteria;Gracilibacteria;uncultured.bacterium;uncultured.bacterium;uncultured.bacterium	0	0	0	0	0	0	0	0	0.000642309	0	0	0
Bacteria;Patescibacteria;Microgenomatia;Candidatus.Levybacteria;uncultured.soil.bacterium;uncultured.soil.bacterium	0	0	0	0	0.000199949	0	0	0	0	0	0	0
Bacteria;Patescibacteria;Parcubacteria; ;	0	0	0	0	0	0	0	0	0.000982355	0	0	0
Bacteria;Patescibacteria;Parcubacteria;Candidatus.Kaiserbacteria;uncultured.bacterium;uncultured.bacterium	0	0	0	0	0	0	0	0	0.000831224	9.59E-05	0	0
Bacteria;Patescibacteria;Parcubacteria;Candidatus.Kaiserbacteria;uncultured.organism;uncultured.organism	0	0	0	0	0	0	0	0	0	0.002429512	0	0
Bacteria;Patescibacteria;Saccharimonadia;Saccharimonadales;Saccharimonadaceae;uncultured.bacterium	0	0	0	0	0	0.001027837	0	0	0	0	0	0
Bacteria;Patescibacteria;Saccharimonadia;Saccharimonadales;uncultured.bacterium;uncultured.bacterium	0	0	0	0	0	0	0	0	0.001473533	0	0	0
Bacteria;Planctomycetes;BD7-11;metagenome;metagenome.m etagenome	0	0	0	0	0	0	0	0	0.000680092	0	0	0

genus	110年						111年					
	TP01	TP02	TP03	TP04	TP05	TP06	TP01	TP02	TP03	TP04	TP05	TP06
Bacteria;Planctomycetes;OM190;Ambiguous_taxa;Ambiguous_taxa;Ambiguous_taxa	0	0.000348697	0	0	0	0	0	0	0	0	0	0
Bacteria;Planctomycetes;OM190;unculturedPlanctomycetaceae.bacterium;unculturedPlanctomycetaceae.bacterium;unculturedPlanctomycetaceae.bacterium	0	0	0	0	0	0	0	0.000631214	0	0	0	0
Bacteria;Planctomycetes;Phycisphaerae;mls1-8	0	0	0	0	0	0	0	0	0.000453395	0	0	0
Bacteria;Planctomycetes;Phycisphaerae;Phycisphaerales;Phycisphaeraceae;CL500-3	0	0	0	0.003705991	0	0.00385439	0	0	0	0	0	0
Bacteria;Planctomycetes;Phycisphaerae;Phycisphaerales;Phycisphaeraceae;Phycisphaera	0	0	0	0	0	0	9.99E-05	0	0	0	0	0
Bacteria;Planctomycetes;Phycisphaerae;Phycisphaerales;Phycisphaeraceae;SM1A02	0	0	0	0	0	0	0	0.000907369	0	0	0	0
Bacteria;Planctomycetes;Phycisphaerae;Phycisphaerales;Phycisphaeraceae;uncultured	0	0	0	0	0	0	0	0	0.002040277	0	0	0
Bacteria;Planctomycetes;Phycisphaerae;Phycisphaerales;Phycisphaeraceae;Urania-1B-19_marine_sediment_group	0.004705635	0.009034426	0.004471178	0.01316399	0.000826457	0.029835832	0.001015414	0	0	0.000639345	0	0.000711073
Bacteria;Planctomycetes;Planctomycetacia;Gemmatales;Gemmataceae;Fimbrigliobus	0	0	0	0	0	0.000742327	0	0	0	0	0	0
Bacteria;Planctomycetes;Planctomycetacia;Pirellulales;Pirellulaceae;Blastopirellula	0	0.000253598	0	0.002046016	0	0.004225553	0	0.004931356	0.004118336	0	0	0
Bacteria;Planctomycetes;Planctomycetacia;Pirellulales;Pirellulaceae;Bythopirellula	0	0	0	0	0	0.001827266	0	0	0	0	0	0
Bacteria;Planctomycetes;Planctomycetacia;Pirellulales;Pirellulaceae;Pir4_lineage	0	0	0	0.003165534	0.002199443	0.001227695	0	0	0.00117127	0	0	0
Bacteria;Planctomycetes;Planctomycetacia;Pirellulales;Pirellulaceae;Pirellula	0.000676529	0.000919292	0	0.016522545	0.000386569	0.004054247	0	0.005325864	0.000642309	0	0	0.001653658
Bacteria;Planctomycetes;Planctomycetacia;Pirellulales;Pirellulaceae;Rhodopirellula	0	0	0	0.002123224	0	0	0	0	0.001209053	0	0	0

genus	110年						111年					
	TP01	TP02	TP03	TP04	TP05	TP06	TP01	TP02	TP03	TP04	TP05	TP06
Bacteria;Planctomycetes;Planctomycetacia;Pirellulales;Pirellulaceae;Rubripirellula	0	0	0	0.000540457	0	0.001170592	0	0.009665457	0	0	0	0
Bacteria;Planctomycetes;Planctomycetacia;Pirellulales;Pirellulaceae;uncultured	0.000887005	0.001157041	0.000902256	0.01192866	0.00299924	0.004511064	0	0.052982484	0.037178373	0.001310658	0.001767613	0.002248975
Bacteria;Planctomycetes;Planctomycetacia;Planctomycetales;_	0	0	0	0	0	0.000742327	0	0	0	0	0	0
Bacteria;Planctomycetes;Planctomycetacia;Planctomycetales;Gimesiaceae;uncultured	0	0	0	0	0	0	0	0	0.002229191	0	0	0
Bacteria;Planctomycetes;Planctomycetacia;Planctomycetales;Rubinisphaeraceae;Rubinisphaera	0	0	0	0	0	0.001170592	0	0	0	0	0	0
Bacteria;Planctomycetes;Planctomycetacia;Planctomycetales;Rubinisphaeraceae;uncultured	0	0	0	0.001003706	0	0	0	0.00560202	0.000982355	0	0	0
Bacteria;Proteobacteria;_	0	0	0	0.000463249	0	0	0	0	0	0	0	0
Bacteria;Proteobacteria;Alphaproteobacteria;_	0	0	0	0.003705991	0	0	0	0.000907369	0.000793441	0	0	0
Bacteria;Proteobacteria;Alphaproteobacteria;Acetobacterales;Acetobacteraceae;Acidiphilium	0	0	0	0	0	0	0	0	0.002984849	0	0	0
Bacteria;Proteobacteria;Alphaproteobacteria;Caulobacterales;Caulobacteraceae;Brevundimonas	0	0	0	0.000926498	0	0	0	0	0.001775796	0	0	0
Bacteria;Proteobacteria;Alphaproteobacteria;Caulobacterales;Hyphomonadaceae;Henriciella	0	0	0.000501253	0	0	0	0	0	0	0	0	0
Bacteria;Proteobacteria;Alphaproteobacteria;Caulobacterales;Parvularculaceae;uncultured	0	0	0	0.001505559	0	0	0	0	0	0	0	0
Bacteria;Proteobacteria;Alphaproteobacteria;Holo sporales;Holosporaceae;uncultured	0	0	0	0.006524089	0	0	0	0	0	0	0	0
Bacteria;Proteobacteria;Alphaproteobacteria;Holo sporales;Holosporaceae;uncultured. bacterium	0	0	0	0	0	0	0	0	0.001926928	0	0	0
Bacteria;Proteobacteria;Alphaproteobacteria;Micavibrionales;Micavibrionaceae;uncultured	0	0	0.000561404	0.002663681	0	0	0	0	0	0	0	0

genus	110年						111年					
	TP01	TP02	TP03	TP04	TP05	TP06	TP01	TP02	TP03	TP04	TP05	TP06
Bacteria;Proteobacteria;Alphaproteobacteria;Micavibrionales;uncultured;uncultured.bacterium	0	0	0	0	0	0	0	0.000828468	0	0	0	0
Bacteria;Proteobacteria;Alphaproteobacteria;Parvibaculales;OCS116.clade;	0.000511155	0.000570595	0.000661654	0	0	0.00082798	0	0	0	0	0	0
Bacteria;Proteobacteria;Alphaproteobacteria;Parvibaculales;Parvibaculaceae;uncultured	0.001037344	0	0.000781955	0.000270229	0	0.000685225	0	0	0	0	0	0
Bacteria;Proteobacteria;Alphaproteobacteria;Parvibaculales;PS1.clade;	0.001307956	0.00122044	0.001343358	0	0	0.003454675	0	0.00280101	0	0	0	0.001488292
Bacteria;Proteobacteria;Alphaproteobacteria;Parvibaculales;PS1.clade;Ambiguous taxa	0.001428228	0	0	0	0	0.002284083	0	0	0	0	0	0
Bacteria;Proteobacteria;Alphaproteobacteria;Puniceispirillales;SAR116.clade;	0.044094654	0.024678248	0.027849624	0.017217418	0.002892601	0.012562455	0.024037021	0.002485403	0.00638531	0.016974618	0.018992821	0.020207699
Bacteria;Proteobacteria;Alphaproteobacteria;Puniceispirillales;SAR116.clade;alpha.proteobacterium.SCGC.AAA015.N04	0.002585844	0.004422114	0.003769424	0.005674799	0	0.002683797	0	0	0	0	0	0
Bacteria;Proteobacteria;Alphaproteobacteria;Puniceispirillales;SAR116.clade;Ambiguous taxa	0.003938902	0.002377481	0.00318797	0.001312539	0.000399899	0.005110635	0.002313813	0	0.002266974	0.001694265	0.002164424	0.002298584
Bacteria;Proteobacteria;Alphaproteobacteria;Puniceispirillales;SAR116.clade;uncultured;Oceanibaculum.sp.	0.003187203	0.001695936	0	0	0.001692904	0	0	0.003195518	0	0	0.002741604	0
Bacteria;Proteobacteria;Alphaproteobacteria;Puniceispirillales;SAR116.clade;unidentified.marine.bacterioplankton	0.002901558	0.001886135	0.00166416	0	0	0.001399001	0	0	0	0	0.000829696	0
Bacteria;Proteobacteria;Alphaproteobacteria;Rhizobiales;Beijerinckiaceae;Methylobacterium	0	0	0.000481203	0	0.008371213	0	0	0	0	0	0	0
Bacteria;Proteobacteria;Alphaproteobacteria;Rhizobiales;Hyphomicrobiaceae;Filomicrobium	0	0	0	0	0	0.001027837	0	0	0	0	0	0
Bacteria;Proteobacteria;Alphaproteobacteria;Rhizobiales;Methyloiligellaceae;uncultured	0	0	0	0.002007412	0	0	0	0	0	0	0	0
Bacteria;Proteobacteria;Alphaproteobacteria;Rhizobiales;Pleomorphomonadaceae;uncultured	0	0	0	0	0.003679068	0	0	0	0	0	0	0

genus	110年						111年					
	TP01	TP02	TP03	TP04	TP05	TP06	TP01	TP02	TP03	TP04	TP05	TP06
Bacteria;Proteobacteria;Alphaproteobacteria;Rhizobiales;Rhizobiaceae;	0	0	0	0	0	0.00028551	0	0	0	0	0	0
Bacteria;Proteobacteria;Alphaproteobacteria;Rhizobiales;Rhizobiaceae;Allorhizobium-Neorhizobium-Pararhizobium-Rhizobium	0	0	0	0	0.001133046	0	0	0	0	0	0	0
Bacteria;Proteobacteria;Alphaproteobacteria;Rhizobiales;Rhizobiaceae;Phyllobacterium	0	0	0	0.004130636	0.010144097	0	0	0	0	0	0	0
Bacteria;Proteobacteria;Alphaproteobacteria;Rhizobiales;Rhizobiales.Incertae.Sedis;uncultured	0	0	0	0	0.014169744	0	0	0	0	0	0	0
Bacteria;Proteobacteria;Alphaproteobacteria;Rhizobiales;Stappiaceae;Labrenzia	0	0	0	0.00312693	0	0	0	0	0	0	0	0
Bacteria;Proteobacteria;Alphaproteobacteria;Rhizobiales;Stappiaceae;Pseudovibrio	0	0	0	0.007527795	0	0	0	0	0	0	0	0
Bacteria;Proteobacteria;Alphaproteobacteria;Rhizobiales;Xanthobacteraceae;Bradyrhizobium	0	0	0	0	0	0	0	0.004970806	0	0	0	0
Bacteria;Proteobacteria;Alphaproteobacteria;Rhodobacterales;Rhodobacteraceae;	0.005697877	0.00366132	0.005192982	0	0.035017795	0.00633833	0.004261411	0	0	0	0	0.002100146
Bacteria;Proteobacteria;Alphaproteobacteria;Rhodobacterales;Rhodobacteraceae;HIMB11	0.023558242	0.001838585	0.003067669	0.004400865	0.027006492	0	0.004927256	0	0.002833717	0.007256569	0	0
Bacteria;Proteobacteria;Alphaproteobacteria;Rhodobacterales;Rhodobacteraceae;Nautella	0.001713873	0.001093641	0	0	0	0	0	0	0	0	0	0
Bacteria;Proteobacteria;Alphaproteobacteria;Rhodobacterales;Rhodobacteraceae;Paracoccus	0	0	0	0.004671093	0.005598582	0	0	0	0	0	0	0
Bacteria;Proteobacteria;Alphaproteobacteria;Rhodobacterales;Rhodobacteraceae;Rhodobacter	0	0	0	0	0.000573188	0	0	0	0	0	0	0
Bacteria;Proteobacteria;Alphaproteobacteria;Rhodobacterales;Rhodobacteraceae;Rhodovulum	0	0	0	0	0.005918501	0	0	0	0	0	0	0
Bacteria;Proteobacteria;Alphaproteobacteria;Rhodobacterales;Rhodobacteraceae;Roseicyclus	0	0	0	0	0.002332742	0	0	0	0	0	0	0

genus	110年						111年					
	TP01	TP02	TP03	TP04	TP05	TP06	TP01	TP02	TP03	TP04	TP05	TP06
Bacteria;Proteobacteria;Alphaproteobacteria;Rhodobacterales;Rhodobacteraceae;Roseivivax	0	0	0	0.001621371	0	0.008793719	0	0	0	0	0	0
Bacteria;Proteobacteria;Alphaproteobacteria;Rhodobacterales;Rhodobacteraceae;Ruegeria	0	0	0	0	0.001919514	0.002084226	0	0	0	0	0	0
Bacteria;Proteobacteria;Alphaproteobacteria;Rhodobacterales;Rhodobacteraceae;Salinhabitans	0	0	0	0.002007412	0.034817846	0	0	0	0	0	0	0
Bacteria;Proteobacteria;Alphaproteobacteria;Rhodobacterales;Rhodobacteraceae;Tropicimonas	0	0	0	0	0.017662192	0	0	0	0	0	0	0
Bacteria;Proteobacteria;Alphaproteobacteria;Rhodobacterales;Rhodobacteraceae;uncultured	0.008629503	0.004231915	0.007057644	0.006987338	0	0.003340471	0.010620235	0.004181789	0.002191408	0	0.007250821	0.009558143
Bacteria;Proteobacteria;Alphaproteobacteria;Rhodobacterales;Rhodobacteraceae;Youngimonas	0	0	0	0	0.005785201	0	0	0	0	0	0	0
Bacteria;Proteobacteria;Alphaproteobacteria;Rhodospirillales;AEGEAN-169.marine.group;__	0.005607673	0.005373106	0.005533835	0.004439469	0.001839534	0.003169165	0.007474115	0.004970806	0.008765633	0.006489355	0	0.009310094
Bacteria;Proteobacteria;Alphaproteobacteria;Rhodospirillales;AEGEAN-169.marine.group;Ambiguous_taxa	0.013861327	0.007132442	0.010987469	0.003319951	0.001799544	0.004025696	0.035356394	0.017161117	0.014773114	0.032191036	0.016413549	0.040498082
Bacteria;Proteobacteria;Alphaproteobacteria;Rhodospirillales;AEGEAN-169.marine.group;uncultured.alpha.proteobacterium	0	0	0	0	0	0.001227695	0	0	0	0	0	0
Bacteria;Proteobacteria;Alphaproteobacteria;Rhodospirillales;AEGEAN-169.marine.group;uncultured.marine.bacterium	0.002706116	0	0.003087719	0.002740889	0	0.005110635	0	0	0.001549099	0	0.006367014	0
Bacteria;Proteobacteria;Alphaproteobacteria;Rhodospirillales;AEGEAN-169.marine.group;unidentified.marine.bacterioplankton	0.001608636	0.001347239	0.001423559	0	0	0.00165596	0.003412458	0.001814739	0.002455888	0.001694265	0.002723567	0.002761609

genus	110年						111年					
	TP01	TP02	TP03	TP04	TP05	TP06	TP01	TP02	TP03	TP04	TP05	TP06
Bacteria;Proteobacteria;Alphaproteobacteria;Rhodospirillales;Magnetospiraceae;uncultured	0.000511155	0.000174349	0.000461153	0.001119518	0	0.000513919	0	0	0	0	0	0
Bacteria;Proteobacteria;Alphaproteobacteria;Rhodospirillales;Terasakiellaceae;Terasakiella	0	0	0	0	0	0.000685225	0	0	0	0	0	0
Bacteria;Proteobacteria;Alphaproteobacteria;Rhodovibrionales;Kiloniellaceae;Kiloniella	0.0015485	0	0	0	0	0	0	0	0	0	0	0
Bacteria;Proteobacteria;Alphaproteobacteria;Rhodovibrionales;Kiloniellaceae;uncultured	0	0	0	0	0	0.000571021	0	0	0	0	0	0
Bacteria;Proteobacteria;Alphaproteobacteria;Rickettsiales;AB1;uncultured.alpha.proteobacterium	0	0	0	0.001080914	0	0	0	0	0	0	0	0
Bacteria;Proteobacteria;Alphaproteobacteria;Rickettsiales;Midichloriaceae;MD3-55	0	0	0	0.014592341	0	0.000713776	0	0.010178318	0	0	0	3.31E-05
Bacteria;Proteobacteria;Alphaproteobacteria;Rickettsiales;Rickettsiaceae;Candidatus.Megaira	0	0	0	0.001158122	0	0	0	0	0	0	0	0
Bacteria;Proteobacteria;Alphaproteobacteria;Rickettsiales;Rickettsiaceae;Candidatus.Trichorickettsia	0	0	0	0	0.004185606	0	0	0	0	0	0	0
Bacteria;Proteobacteria;Alphaproteobacteria;Rickettsiales;Rickettsiaceae;uncultured	0	0	0	0.000772082	0	0	0	0	0	0	0	0
Bacteria;Proteobacteria;Alphaproteobacteria;Rickettsiales;S25-593;	0.012102351	0.007576238	0.009403509	0.003744595	0	0.006538187	0.007124546	0.005049708	0	0.003132792	0.004797807	0.003753803
Bacteria;Proteobacteria;Alphaproteobacteria;Rickettsiales;S25-593;metagenome	0.000962175	0.00122044	0	0	0	0	0	0	0	0	0	0
Bacteria;Proteobacteria;Alphaproteobacteria;Rickettsiales;S25-593;uncultured.marine.bacterium	0.000405917	0.000412097	0	0.000965102	0	0	0	0	0	0	0	0
Bacteria;Proteobacteria;Alphaproteobacteria;SAR11.clade;Clade.I;	0.002886524	0.015738921	0.019067669	0	0	0	0.013150448	0.015464731	0.017493482	0.018189374	0.015367411	0.016751554
Bacteria;Proteobacteria;Alphaproteobacteria;SAR11.clade;Clade.Ia	0.009531541	0.065095416	0.055137845	0.010384497	0.001932844	0.007394718	0.077304658	0.04110778	0.044508256	0.062240266	0.075448216	0.091281916

genus	110年						111年					
	TP01	TP02	TP03	TP04	TP05	TP06	TP01	TP02	TP03	TP04	TP05	TP06
Bacteria;Proteobacteria;Alphaproteobacteria;SAR11.clade;Clade.I;Clade.Ib	0.004089242	0.025740189	0.022215539	0	0.001306336	0.004197002	0.030995106	0.013058229	0.014281936	0.022760693	0.028985246	0.039373594
Bacteria;Proteobacteria;Alphaproteobacteria;SAR11.clade;Clade.I;uncultured	0	0	0	0	0	0	0	0	0.00026448	0	0	0
Bacteria;Proteobacteria;Alphaproteobacteria;SAR11.clade;Clade.II;	0.004419989	0.02810182	0.027989975	0.003937616	0.000799797	0.003483226	0.031477844	0.023670507	0.025692372	0.035707436	0.035604776	0.059035587
Bacteria;Proteobacteria;Alphaproteobacteria;SAR11.clade;Clade.II;unidentified.marine.bacterioplankton	0	0.001981234	0	0	0	0	0	0	0	0	0	0.001637121
Bacteria;Proteobacteria;Alphaproteobacteria;SAR11.clade;Clade.III;	0	0	0	0	0	0	0	0	0.001624665	0	0.001442949	0
Bacteria;Proteobacteria;Alphaproteobacteria;SAR11.clade;Clade.III;Ambiguous taxa	0	0.000285298	0.000781955	0	0	0	0.001265106	0	0	0.00070328	0	0.001752877
Bacteria;Proteobacteria;Alphaproteobacteria;SAR11.clade;Clade.IV;	0.004615431	0.003296773	0.00485213	0.006948734	0	0.005538901	0.002863135	0	0	0.00210984	0.003066267	0.004828681
Bacteria;Proteobacteria;Alphaproteobacteria;Sneathiellales;Sneathiellaceae;Ferrovibrio	0	0	0	0	0.004092297	0	0	0	0	0	0	0
Bacteria;Proteobacteria;Alphaproteobacteria;Sphingomonadales;Sphingomonadaceae;	0	0	0	0	0.008144603	0	0	0	0	0	0	0
Bacteria;Proteobacteria;Alphaproteobacteria;Sphingomonadales;Sphingomonadaceae;Erythrobacter	0	0	0	0	0.001399645	0.000456817	0	0	0	0	0	0
Bacteria;Proteobacteria;Alphaproteobacteria;Sphingomonadales;Sphingomonadaceae;Novosphingobium	0	0	0	0	0.001253016	0	0	0	0	0	0	0
Bacteria;Proteobacteria;Alphaproteobacteria;Sphingomonadales;Sphingomonadaceae;Sphingomonas	0	0	0	0	0.003905677	0	0.00198089	0.094366419	0.038009597	0.003164759	0.004960139	0.001190634
Bacteria;Proteobacteria;Alphaproteobacteria;Thalassobaculales;Nisaeaceae;OM75.clade	0.003773528	0.001711786	0.00156391	0	0	0	0	0	0	0	0	0
Bacteria;Proteobacteria;Alphaproteobacteria;Thalassobaculales;uncultured;Ambiguous taxa	0.000691563	0	0	0	0	0	0	0	0	0	0	0

genus	110年						111年					
	TP01	TP02	TP03	TP04	TP05	TP06	TP01	TP02	TP03	TP04	TP05	TP06
Bacteria;Proteobacteria;Alpha proteobacteria;uncultured;uncultured.marine.bacterium;uncultured.marine.bacterium	0.001864213	0.001569137	0.000561404	0.001775788	0	0.002169879	0.001298399	0	0	0	0	0.000777219
Bacteria;Proteobacteria;Alpha proteobacteria;uncultured;unidentified.marine.bacterioplankton;unidentified.marine.bacterioplankton	0.001758975	0	0.001343358	0.001582767	0.000319919	0.003140614	0.00366215	0	0.000415612	0.004763123	0.002741604	0
Bacteria;Proteobacteria;Deltaproteobacteria;Bdellovibrionales;Bacteriovoraceae;Halobacteriovorax	0	0	0	0	0	0.000599572	0	0	0	0	0	0
Bacteria;Proteobacteria;Deltaproteobacteria;Bdellovibrionales;Bacteriovoraceae;Pereidibacter	0	0	0	0.000965102	0	0	0	0	0.000377829	0	0	0
Bacteria;Proteobacteria;Deltaproteobacteria;Bdellovibrionales;Bacteriovoraceae;uncultured	0.000180408	0	0	0.000887894	0	0	0	0	0	0	0	0
Bacteria;Proteobacteria;Deltaproteobacteria;Bdellovibrionales;Bdellovibrionaceae;Bdellovibrion	0	0	0	0	0	0	0	0	0.000604526	0	0	0
Bacteria;Proteobacteria;Deltaproteobacteria;Bdellovibrionales;Bdellovibrionaceae;OM27.clade	0	0.000126799	0	0.001737183	0	0.005024982	0	0.00138078	0	0	0	0
Bacteria;Proteobacteria;Deltaproteobacteria;Bradymonadales;	0	0	0	0	0	0	0	0	0.000680092	0	0	0
Bacteria;Proteobacteria;Deltaproteobacteria;Bradymonadales;uncultured.marine.bacterium;uncultured.marine.bacterium	0.000165374	0	0	0	0	0.004710921	0	0	0	0	0	0
Bacteria;Proteobacteria;Deltaproteobacteria;Desulfobacteriales;Desulfobacteraceae;Desulfobacter	0	0	0	0.001119518	0	0	0	0	0	0	0	0
Bacteria;Proteobacteria;Deltaproteobacteria;Myxococcales;bacteriap25;	0	0	0	0.001351143	0	0	0	0	0	0	0	0
Bacteria;Proteobacteria;Deltaproteobacteria;NB1-j;	0	0	0	0	0	0.000485368	0	0	0	0	0	0
Bacteria;Proteobacteria;Deltaproteobacteria;Oligoflexales;0319-6G20;uncultured.bacterium	0	0	0	0	0.49	0.000856531	0	0	0	0	0	0

genus	110年						111年					
	TP01	TP02	TP03	TP04	TP05	TP06	TP01	TP02	TP03	TP04	TP05	TP06
Bacteria;Proteobacteria;Deltaproteobacteria;Oligoflexales;Oligoflexaceae;uncultured	0	0	0	0	0	0.000628123	0	0.001301878	0	0	0	0
Bacteria;Proteobacteria;Deltaproteobacteria;PB19; ;	0	0	0	0	0	0.000685225	0	0	0	0	0	0
Bacteria;Proteobacteria;Deltaproteobacteria;PB19;Ambiguous taxa;Ambiguous taxa	0	0	0	0	0	0	0.002169796	0	0	0	0	0
Bacteria;Proteobacteria;Deltaproteobacteria;SAR324.clade(Marine.group.B);Ambiguous_taxa;Ambiguous_taxa	0	0.001442338	0	0.002470661	0.005291993	0.003625981	0	0.001972542	0	0.000799182	0.002543198	0.004531023
Bacteria;Proteobacteria;Deltaproteobacteria;SAR324.clade(Marine.group.B);uncultured.bacterium;uncultured.bacterium	0	0	0	0	0	0.000770878	0	0	0	0	0	0.001653658
Bacteria;Proteobacteria;Deltaproteobacteria;SAR324.clade(Marine.group.B);uncultured.marine.bacterium;uncultured.marine.bacterium	0	0.000538896	0	0	0	0.002027123	0	0	0	0	0	0
Bacteria;Proteobacteria;Gammaproteobacteria; ; ;	0	0	8.02E-05	0.005481779	0	0.004568166	0	0	0	0	0	0
Bacteria;Proteobacteria;Gammaproteobacteria;Aeromonadales;Aeromonadaceae;Aeromonas	0	0	0	0.001814392	0	0	0	0	0	0	0	0
Bacteria;Proteobacteria;Gammaproteobacteria;Alteromonadales;Alteromonadaceae;	0	0	0	0	0	0.001256246	0	0	0	0	0	0
Bacteria;Proteobacteria;Gammaproteobacteria;Alteromonadales;Alteromonadaceae;Aestuariibacter	0	0	0	0	0	0.002084226	0	0	0	0	0	0
Bacteria;Proteobacteria;Gammaproteobacteria;Alteromonadales;Alteromonadaceae;Aliiglaciicola	0	0.000491346	0	0	0	0	0	0	0	0	0	0
Bacteria;Proteobacteria;Gammaproteobacteria;Alteromonadales;Alteromonadaceae;Rheinheimera	0	0	0	0	0.006878258	0	0	0	0	0	0	0
Bacteria;Proteobacteria;Gammaproteobacteria;Alteromonadales;Alteromonadaceae;uncultured	0.000330747	0	0.000882206	0	0	0	0	0.002209247	0	0	0	0
Bacteria;Proteobacteria;Gammaproteobacteria;Alteromonadales;Colwelliaceae;Thalassotalea	0	0	0	0.001930204	0	0	0	0	0	0	0	0

genus	110年						111年					
	TP01	TP02	TP03	TP04	TP05	TP06	TP01	TP02	TP03	TP04	TP05	TP06
Bacteria;Proteobacteria;Gammaproteobacteria;Alteromonadales;Idiomarinaceae;Idiomarina	0	0	0	0	0	0.00111349	0	0	0	0	0	0
Bacteria;Proteobacteria;Gammaproteobacteria;Alteromonadales;Marinobacteraceae;Mairinobacter	0	0	0.002586466	0	0	0	0	0	0	0	0	0
Bacteria;Proteobacteria;Gammaproteobacteria;Alteromonadales;Pseudoalteromonadaceae;Pseudoalteromonas	0.001187684	0.000982692	0	0.002702285	0	0.001541756	0	0	0	0	0	0
Bacteria;Proteobacteria;Gammaproteobacteria;Alteromonadales;Shewanellaceae;Shewanella	0	0	0	0.003590179	0	0	0	0	0.001397967	0	0	0
Bacteria;Proteobacteria;Gammaproteobacteria;Arenicellales;Arenicellaceae;uncultured	0.000135306	0	0	0	0	0.000513919	0	0	0	0	0	0
Bacteria;Proteobacteria;Gammaproteobacteria;Betaproteobacteriales;Burkholderiaceae;_	0	0	0	0	0.023953932	0	0	0	0	0	0	0
Bacteria;Proteobacteria;Gammaproteobacteria;Betaproteobacteriales;Burkholderiaceae;Achromobacter	0	0	0	0	0	0.000485368	0	0	0.001246836	0	0	0
Bacteria;Proteobacteria;Gammaproteobacteria;Betaproteobacteriales;Burkholderiaceae;Burkholderia-Caballeronia-Paraburkholderia	0	0	0	0.001582767	0.001439635	0	0	0	0	0	0	0
Bacteria;Proteobacteria;Gammaproteobacteria;Betaproteobacteriales;Burkholderiaceae;Hydrogenophaga	0	0	0	0	0.009650888	0	0	0	0	0	0	0
Bacteria;Proteobacteria;Gammaproteobacteria;Betaproteobacteriales;Burkholderiaceae;Limnhabitans	0	0	0	0	0.005705221	0	0	0	0	0	0	0
Bacteria;Proteobacteria;Gammaproteobacteria;Betaproteobacteriales;Burkholderiaceae;Massilia	0	0	0	0	0.002732641	0	0	0	0	0	0	0
Bacteria;Proteobacteria;Gammaproteobacteria;Betaproteobacteriales;Burkholderiaceae;MWH-UniP1.aquatic.group	0	0	0.000681704	0.000926498	0.006518349	0	0.001614675	0	0	0.001662298	0.001064175	0.001141024
Bacteria;Proteobacteria;Gammaproteobacteria;Betaproteobacteriales;Burkholderiaceae;Ottowia	0	0	0	0	0.003345819	0	0	0	0	0	0	0

genus	110年						111年					
	TP01	TP02	TP03	TP04	TP05	TP06	TP01	TP02	TP03	TP04	TP05	TP06
Bacteria;Proteobacteria;Gammaproteobacteria;Betaproteobacterales;Burkholderiaceae;Pandoraea	0	0	0	0	0	0	0	0.002130346	0	0	0	0
Bacteria;Proteobacteria;Gammaproteobacteria;Betaproteobacterales;Burkholderiaceae;Pelomonas	0	0	0	0	0	0	0	0.001656935	0	0	0	0
Bacteria;Proteobacteria;Gammaproteobacteria;Betaproteobacterales;Burkholderiaceae;Poly nucleobacter	0	0	0	0	0.005425292	0	0	0	0	0	0	0
Bacteria;Proteobacteria;Gammaproteobacteria;Betaproteobacterales;Burkholderiaceae;Rambliabacter	0	0	0	0	0.002306082	0	0	0	0	0	0	0
Bacteria;Proteobacteria;Gammaproteobacteria;Betaproteobacterales;Burkholderiaceae;Thiomonas	0	0	0	0	0	0	0	0	0.000377829	0	0	0
Bacteria;Proteobacteria;Gammaproteobacteria;Betaproteobacterales;Neisseriaceae;Neisseria	0	0	0	0.001582767	0	0	0	0	0	0	0	0
Bacteria;Proteobacteria;Gammaproteobacteria;Betaproteobacterales;Rhodocyclaceae;C39	0	0	0	0	0.029685813	0	0	0	0	0	0	0
Bacteria;Proteobacteria;Gammaproteobacteria;Betaproteobacterales;Rhodocyclaceae;Dechloromonas	0	0	0	0	0.001466295	0	0	0	0	0	0	0
Bacteria;Proteobacteria;Gammaproteobacteria;Cellvibrionales;	0	0	0	0	0	0.000428266	0	0	0	0	0	0
Bacteria;Proteobacteria;Gammaproteobacteria;Cellvibrionales;Cellvibrionaceae;Marinagarivorans	0	0	0	0	0	0.000628123	0	0	0	0	0	0
Bacteria;Proteobacteria;Gammaproteobacteria;Cellvibrionales;Halieaceae;OM160(NOR5).clade	0.005758013	0.003154124	0.003769424	0.004748301	0.006505019	0.007480371	0.00189766	0.002564305	0	0.002237709	0.001749576	0
Bacteria;Proteobacteria;Gammaproteobacteria;Cellvibrionales;Microbulbiferaceae;Microbulbifer	0	0	0	0.001505559	0	0	0	0	0	0	0	0
Bacteria;Proteobacteria;Gammaproteobacteria;Cellvibrionales;Porticoccaceae;SAR92.clade	0.002014553	0.001632537	0.001363409	0	0	0.001170592	0	0	0	0	0	0



genus	110年						111年					
	TP01	TP02	TP03	TP04	TP05	TP06	TP01	TP02	TP03	TP04	TP05	TP06
Bacteria;Proteobacteria;Gammaproteobacteria;K189A.clade;Ambiguous_taxa;Ambiguous_taxa	0	0.000602295	0.000140351	0	0	0.000770878	0	0	0	0	0	0
Bacteria;Proteobacteria;Gammaproteobacteria;K189A.clade;uncultured_bacterium;uncultured_bacterium	0	0	0	0.000887894	0	0	0	0	0	0	0	0
Bacteria;Proteobacteria;Gammaproteobacteria;K189A.clade;uncultured_deep-sea_bacterium;uncultured_deep-sea_bacterium	0	0	0	0.000887894	0	0	0	0	0	0	0	0
Bacteria;Proteobacteria;Gammaproteobacteria;K189A.clade;uncultured_marine_bacterium;uncultured_marine_bacterium	0.000887005	0	0	0	0	0.000799429	0	0	0	0	0	0
Bacteria;Proteobacteria;Gammaproteobacteria;Oceanospirillales;Alcanivoracaceae;Alcanivorax	0	0.000316997	0	0	0.002599342	0	0	0	0	0	0	0
Bacteria;Proteobacteria;Gammaproteobacteria;Oceanospirillales;Endozoicomonadaceae;Endozoicomonas	0	0	0	0	0	0.000799429	0	0	0	0	0	0
Bacteria;Proteobacteria;Gammaproteobacteria;Oceanospirillales;Halomonadaceae;Halomonas	0.001503398	0.000570595	0.000220551	0.001852996	9.33E-05	0.003711635	0	0.003511125	0.003476027	0	0	0
Bacteria;Proteobacteria;Gammaproteobacteria;Oceanospirillales;Litoricolaceae;Litoricola	0.003096999	0.000396247	0.004952381	0	0.003359149	0.000999286	0.000532676	0	0	0	0.000360737	0
Bacteria;Proteobacteria;Gammaproteobacteria;Oceanospirillales;Oleiphilaceae;Oleiphilus	0	0	0	0	0.000773137	0	0	0	0	0	0	0
Bacteria;Proteobacteria;Gammaproteobacteria;Oceanospirillales;Pseudohongiellaceae;Pseudohongiella	0.001007276	0	0.000661654	0	0.006771618	0.000342612	0	0	0	0	0	0.000644927
Bacteria;Proteobacteria;Gammaproteobacteria;Oceanospirillales;Saccharospirillaceae;Bernella	0	0	0	0	0.002359402	0	0	0	0	0	0	0
Bacteria;Proteobacteria;Gammaproteobacteria;Oceanospirillales;Saccharospirillaceae;Thalassolituus	0	0	0	0	0.010104107	0	0	0	0	0	0	0

genus	110年						111年					
	TP01	TP02	TP03	TP04	TP05	TP06	TP01	TP02	TP03	TP04	TP05	TP06
Bacteria;Proteobacteria;Gammaproteobacteria;OM182.clade;Ambiguous_taxa;Ambiguous_taxa	0.000871971	0.000618145	0.000561404	0	0	0.002683797	0	0	0	0	0	0
Bacteria;Proteobacteria;Gammaproteobacteria;Pseudomonadales;Moraxellaceae;Acinetobacter	0	0	0.000501253	0.002046016	0.014476333	0.000571021	0	0	0	0	0	0
Bacteria;Proteobacteria;Gammaproteobacteria;Pseudomonadales;Moraxellaceae;Alkanindiges	0	0	0	0	0.00311921	0	0	0	0	0	0	0
Bacteria;Proteobacteria;Gammaproteobacteria;Pseudomonadales;Moraxellaceae;Enhydrobacter	0	0	0	0	0.004372226	0.001798715	0	0.001696386	0	0	0	0
Bacteria;Proteobacteria;Gammaproteobacteria;Pseudomonadales;Moraxellaceae;uncultured	0	0	0	0	0	0	0	0	0.005062909	0	0	0
Bacteria;Proteobacteria;Gammaproteobacteria;Pseudomonadales;Pseudomonadaceae;Pseudomonas	0.00287149	0.002044633	0	0	0	0	0	0.00280101	0	0	0	0
Bacteria;Proteobacteria;Gammaproteobacteria;Salinisphaerales;Salinisphaeraceae;Salinisphaera	0	0	0.003649123	0.00123533	0.007358136	0.002169879	0	0	0	0	0	0
Bacteria;Proteobacteria;Gammaproteobacteria;SAR86.clade;_;	0.016642612	0.011063209	0.01437594	0.013009574	0.003772378	0.025124911	0.012051803	0.005483667	0.005176257	0.007000831	0.013455503	0.015676677
Bacteria;Proteobacteria;Gammaproteobacteria;SAR86.clade;Ambiguous_taxa;Ambiguous_taxa	0.00227013	0.002171432	0.003428571	0.002123224	0	0.005281941	0.002030829	0	0	0	0.002236572	0.004696388
Bacteria;Proteobacteria;Gammaproteobacteria;SAR86.clade;metagenome;metagenome	0	0.000950992	0.001804511	0.002895306	0	0.003940043	0.001315045	0	0.00234254	0.003292628	0.004364922	0.004117608
Bacteria;Proteobacteria;Gammaproteobacteria;SAR86.clade;Rhodobacteraceae.bacterium.REDSEA-S29_B10;Rhodobacteraceae.bacterium.REDSEA-S29_B10	0.00022551	0	0	0	0	0.000942184	0	0	0	0	0	0
Bacteria;Proteobacteria;Gammaproteobacteria;SAR86.clade;uncultured.bacterium;uncultured.bacterium	0.014342414	0.014819628	0.019368421	0.012507721	0.001439635	0.045710207	0.009721344	0.006509389	0.003022632	0.004603286	0.010226904	0.009409313

genus	110年						111年					
	TP01	TP02	TP03	TP04	TP05	TP06	TP01	TP02	TP03	TP04	TP05	TP06
Bacteria;Proteobacteria;Gammaproteobacteria;SAR86.clade;uncultured.gammaproteobacterium.HF0070_25G02;uncultured.gammaproteobacterium.HF0070_25G02	0.005532503	0.005198757	0.005994987	0.002818098	0.000519868	0.00910778	0.00387855	0	0	0.002972956	0.006475235	0.015478238
Bacteria;Proteobacteria;Gammaproteobacteria;SAR86.clade;uncultured.SAR86.cluster.bacterium;uncultured.SAR86.cluster.bacterium	0.000661495	0.000491346	0.000340852	0	0	0.001056388	0	0	0	0	0	0
Bacteria;Proteobacteria;Gammaproteobacteria;Thiotrichales;Thiotrichaceae;Thiothrix	0	0	0	0	0	0	0.000133169	0	0	0	0	0
Bacteria;Proteobacteria;Gammaproteobacteria;Thiotrichales;Thiotrichaceae;uncultured	0.001067412	0.00117289	0.001182957	0.00019302	0	0.000799429	0.00146486	0.000867919	0.001813579	0	0.001298654	0.001190634
Bacteria;Proteobacteria;Gammaproteobacteria;Vibrionales;Vibrionaceae;Photobacterium	0	0	0	0.002393453	0	0.002055675	0	0	0	0	0	0
Bacteria;Proteobacteria;Gammaproteobacteria;Vibrionales;Vibrionaceae;uncultured	0	0.000523046	0	0.003937616	0	0	0	0	0	0	0	0
Bacteria;Proteobacteria;Gammaproteobacteria;Vibrionales;Vibrionaceae;Vibrio	0.000616393	0	0.001263158	0.01023008	0	0.004082798	0	0.001301878	0	0.005050828	0	0.000380341
Bacteria;Proteobacteria;Gammaproteobacteria;Xanthomonadales;Xanthomonadaceae;Stenotrophomonas	0	0	0.000942356	0.007566399	0.010490676	0.002626695	0	0.01167745	0.004345033	0	0	0
Bacteria;Verrucomicrobia;Verrucomicrobiae;Arctic97B-4.marine.group.metagenome;metagenome	0	0	0.000240602	0	0	0.000342612	0	0	0	0	0	0.000479561
Bacteria;Verrucomicrobia;Verrucomicrobiae;Opitutales;Punicococcaceae;Cerasicoccus	0	0	0	0.003088326	0	0	0	0	0.000566743	0	0	0
Bacteria;Verrucomicrobia;Verrucomicrobiae;Opitutales;Punicococcaceae;Coraliomargarita	0	0	0	0	0	0.001256246	0	0	0	0	0	0
Bacteria;Verrucomicrobia;Verrucomicrobiae;Opitutales;Punicococcaceae;Lentimonas	0	0.000285298	0	0	0	0	0	0	0	0	0	0
Bacteria;Verrucomicrobia;Verrucomicrobiae;Opitutales;Punicococcaceae;MB11C04.marine.group	0.000721631	0.001521588	0.001062657	0	0	0	0	0.00142023	0	0	0	0

genus	110年						111年					
	TP01	TP02	TP03	TP04	TP05	TP06	TP01	TP02	TP03	TP04	TP05	TP06
Bacteria;Verrucomicrobia;Verrucomicrobiae;uncultured;uncultured.Opitutae.bacterium;uncultured.Opitutae.bacterium	0	0	0	0	0.001213026	0	0	0	0	0	0	0
Bacteria;Verrucomicrobia;Verrucomicrobiae;Verrucomicrobiales;DEV007;	0	0	0	0	0.001666245	0	0	0	0	0	0	0
Bacteria;Verrucomicrobia;Verrucomicrobiae;Verrucomicrobiales;DEV007;Ambiguous_taxa	0	0	0	0	0	0.001912919	0	0	0	0	0	0
Bacteria;Verrucomicrobia;Verrucomicrobiae;Verrucomicrobiales;DEV007;hydrothermal.vent.metagenome	0	0.000665695	0	0	0	0	0	0	0	0	0	0.000413414
Bacteria;Verrucomicrobia;Verrucomicrobiae;Verrucomicrobiales;Rubritaleaceae;Rubritalea	0	0	0	0	0	0.001027837	0.001098645	0	0.001738013	0.00374017	0	0
Unassigned;__;__;__;__	0.065262493	0.033173778	0.041443609	0.070375232	0.04273584	0.074718059	0.093934148	0.074917153	0.095590736	0.101048526	0.0976516	0.08613904

附錄二、以 18S 基因序列發現之南沙太平島環境 DNA 真核生物科層級數

Phylum	中文名	110年	111年	Total	110年								111年							
					TP01	TP02	TP03	TP04	TP05	TP06	TP07	TP08	TP01	TP02	TP03	TP04	TP05	TP06	TP07	TP08
Amoebozoa	變形蟲門	8	4	8	5	3	4	1	0	2	4	4	3	2	1	2	1	3	2	1
Annelida	環節動物門	30	43	51	19	19	13	18	10	10	9	8	27	22	21	27	24	20	20	14
Arthropoda	節肢動物門	59	85	109	25	32	23	28	26	27	28	18	50	26	25	38	41	31	33	25
Ascomycota	子囊菌門	45	24	57	15	18	19	15	13	7	19	17	11	1	7	8	7	4	6	4
Bacillariophyta	矽藻門	25	52	54	11	13	11	11	9	9	10	12	39	15	19	26	27	33	23	18
Basidiomycota	擔子菌門	68	19	72	28	44	32	34	39	33	44	28	6	2	4	7	4	4	6	8
Bigyra	雙環總門	7	7	10	1	3	1	1	0	0	2	3	6	2	3	4	5	4	4	3
Blastocladiomycota	芽枝霉門	1	0	1	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0
Brachiopoda	腕足動物門	1	5	6	0	0	0	1	0	0	0	1	2	0	0	1	2	0	0	0
Bryozoa	外肛動物門	3	8	10	1	0	2	1	0	1	0	0	2	1	0	4	2	0	3	1
Cercozoa	絲足蟲門	12	33	39	5	9	6	6	3	5	4	5	12	2	10	14	21	12	6	11
Chaetognatha	毛顎動物門	0	1	1	0	0	0	0	0	0	0	0	1	1	1	1	1	0	1	1
Chlorophyta	綠藻門	22	46	55	11	13	12	11	12	8	14	11	31	16	20	25	23	18	22	22
Choanozoa	聚胞動物門	1	7	7	1	1	1	1	1	1	0	1	0	2	0	3	5	3	4	5
Chordata	脊索動物門	17	29	36	10	4	4	3	4	3	4	4	11	8	15	10	12	9	9	5
Chytridiomycota	壺菌門	3	6	6	1	2	0	1	0	0	0	1	5	1	0	1	3	0	3	2
Ciliophora	纖毛蟲門	18	39	44	12	13	10	11	8	6	7	10	20	10	15	19	22	13	13	12
Cnidaria	刺胞動物門	11	72	78	2	2	1	5	4	4	3	4	37	15	12	27	43	29	25	22
Cryptomycota	隱真菌門	1	0	1	0	0	0	1	1	0	0	0	0	0	0	0	0	0	0	0
Cryptophyta	隱藻門	5	12	13	1	4	1	2	2	3	4	1	6	2	0	4	6	3	4	6
Ctenophora	櫛板動物門	2	4	5	0	0	0	0	0	2	1	1	2	2	1	1	1	1	2	2
Cycliophora	環口動物門	0	1	1	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0
Echinodermata	棘皮動物門	12	10	18	3	4	8	0	1	4	0	1	2	5	1	7	3	3	2	1
Entoprocta	內肛動物門	1	2	2	1	0	1	0	0	1	0	0	1	0	0	0	1	0	2	0
Euglenozoa	眼蟲門	4	5	6	2	0	3	0	0	0	1	1	1	1	0	2	3	2	2	4

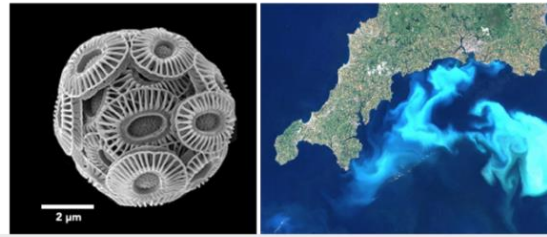
Phylum	中文名	110年	111年	Total	110年								111年							
					TP01	TP02	TP03	TP04	TP05	TP06	TP07	TP08	TP01	TP02	TP03	TP04	TP05	TP06	TP07	TP08
Foraminifera	有孔蟲門	1	1	1	1	1	1	1	0	1	1	1	1	1	1	1	1	0	0	
Gastrotricha	腹毛動物門	2	1	3	1	1	0	1	0	0	1	0	0	0	0	1	0	0	0	
Haptista	定鞭藻門	12	22	23	6	8	5	5	6	4	7	5	11	8	7	15	12	15	12	
Hemichordata	半索動物門	0	2	2	0	0	0	0	0	0	0	0	0	0	1	0	0	0	1	
Mollusca	軟體動物門	43	97	109	19	12	23	17	10	15	9	7	58	40	46	58	40	23	30	
Mucoromycota	毛黴菌門	3	4	5	1	0	0	0	1	0	1	0	0	0	0	2	1	0	0	
Myzozoa	粘孢子總門	49	61	69	35	36	31	36	33	33	34	32	41	38	35	44	40	38	33	
Nematoda	線蟲動物門	3	8	10	2	0	1	2	3	2	2	2	7	4	4	5	7	5	1	
Nemertea	紐形動物門	4	9	12	1	2	1	2	1	2	2	1	3	1	2	1	6	2	2	
Ochrophyta	淡色藻門	9	28	30	4	1	1	2	1	4	3	1	13	4	5	10	14	11	8	
Oomycota	卵菌門	3	8	9	0	1	1	1	1	1	2	1	3	1	0	4	1	2	1	
Percolozoa	透色門	1	1	2	1	1	1	0	0	0	0	1	0	1	1	0	0	0	0	
Phoronida	帚蟲動物門	1	1	1	0	0	0	1	0	1	0	0	1	0	0	1	0	1	0	
Platyhelminthes	扁形動物門	1	6	7	0	0	0	1	0	0	0	0	4	3	4	1	1	1	0	
Porifera	海綿動物門	21	62	63	15	12	13	7	5	7	7	7	40	18	23	43	48	41	33	
Radiozoa	放射蟲門	8	17	20	5	1	2	3	4	4	5	7	11	9	7	8	11	10	9	
Rhodophyta	紅藻門	3	25	26	1	1	0	1	0	0	1	0	5	4	12	10	13	13	10	
Rotifera	輪形動物門	0	1	1	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	
Sipuncula	星蟲動物門	0	4	4	0	0	0	0	0	0	0	0	3	3	4	4	2	3	1	
Streptophyta	鏈型植物門	35	16	43	20	18	10	10	13	11	19	15	4	1	2	2	8	4	1	
Tardigrada	緩步動物門	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	1	0	1	
Xenacoelomorpha	異無腔動物門	0	3	3	0	0	0	0	0	0	0	0	3	2	2	2	2	1	2	
Zoopagomycota	捕蟲黴門	1	3	4	0	0	0	1	0	0	0	0	0	0	0	1	2	0	1	
Others	其他	34	61	66	23	25	19	23	21	21	26	30	47	26	27	41	44	40	34	
總計		591	961	1,204	289	304	261	265	233	232	274	241	530	300	339	486	511	403	372	

附錄三、以 18S 基因序列發現之南沙太平島環境 DNA 不同類型海洋真核生物

赫氏圓石藻 *Emiliania huxleyi* (100%)

18S:

```
GCCAGTAGTCATATGCTTGTCTCAAAGATTAAAGCCATGCATGT
CTAAGTATAAGCGACTATACTGTGAAACTGCGAATGGCTCATT
AAATCAGTTATGGTTTATTTGATGGTACCTTGCTACTTGGATA
ACCGTAGTAATTCTAGAGCTAATACATGCAGGAGTTCCCGAC
TCCGGAGGGATGTATTTATTAGATAAGAAACCAAACCGGTC
TCCGGTTGCGTGTGAGTCATAATACTGCTCGAATCGCACG
GCTCTACGCCGGCGATGGTTCATCAAATTTCTGCCCT
```



Hit Table

Name	e...	Topology	Molecule Ty...	# Sequences	% Pairwise L...	% Identic...	Query start	Query end	Query cover...	Accession	Organism	Max Sequen...	Mi
XM_005792518		linear	DNA	2	100.0%	100.0%	9	301	97.34%	XM_005792518	<i>Emiliania huxleyi</i>	293	29
XM_005789981		linear	DNA	2	100.0%	100.0%	9	301	97.34%	XM_005789981	<i>Emiliania huxleyi</i>	293	29
XM_005786329		linear	DNA	2	100.0%	100.0%	9	301	97.34%	XM_005786329	<i>Emiliania huxleyi</i>	293	29
XM_005783536		linear	DNA	2	100.0%	100.0%	9	301	97.34%	XM_005783536	<i>Emiliania huxleyi</i>	293	29
XM_005783370		linear	DNA	2	100.0%	100.0%	9	301	97.34%	XM_005783370	<i>Emiliania huxleyi</i>	293	29
XM_005770834		linear	DNA	2	100.0%	100.0%	9	301	97.34%	XM_005770834	<i>Emiliania huxleyi</i>	293	29
XM_005769835		linear	DNA	2	100.0%	100.0%	9	301	97.34%	XM_005769835	<i>Emiliania huxleyi</i>	293	29
MG022751		linear	DNA	2	100.0%	100.0%	9	301	97.34%	MG022751	<i>Emiliania huxleyi</i>	293	29
KP404907		linear	DNA	2	100.0%	100.0%	9	301	97.34%	KP404907	Uncultured eukaryote	293	29
KP404687		linear	DNA	2	100.0%	100.0%	9	301	97.34%	KP404687	Uncultured eukaryote	293	29

Selected sequences are only summaries [Download Full Sequence\(s\)](#)

Alignment View Distances Dotplot Text View Download Lineage Info

← → Extract R.C. Translate Add/Edit Annotation (restricted) Allow Editing (restricted) Annotate & Predict Save

Identity

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1. M02662:168:000000000-KLC6K:1:111... GCGT GCT GAGTCATAATAACTGCTCGAA TCGCACGGCTCTACGCCGGCGATGGTTCATCAAATTTCTGCCCT
2. XM_005792518 GCGT GCT GAGTCATAATAACTGCTCGAA TCGCACGGCTCTACGCCGGCGATGGTTCATCAAATTTCTGCCCT
```

Cursor before column 258 (original base 1,159)

Statistics

Nucleotide Statistics:

- Length (mean): 293 bp
- Sequences: 2
- Identical Sites: 293 (100.0%)
- Pairwise Identity: 100.0%

Read Lengths (restricted):

- Mean: -
- Std Dev: -
- Minimum: -
- Maximum: -

Confidence Mean: (restricted)

Expected Errors: (restricted)

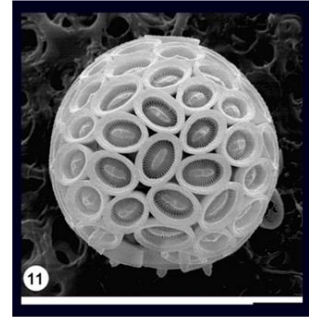
圖片來源：WIKIPEDIA

## 地中海花冠球藻

### *Coronosphaera mediterranea* (100%)

18S:

```
CGCGCCTGCTGCCTTCCTTGGATGTGGTAGCCATTTCTCAGGCTC  
CCTCTCCGGAATCGAACCCCTAATTCTCCGTTACCCGTA AACGCCA  
TGGTAGGCCTCTATCCTACCATCGAAAGCTGATAGGGCAGAAAT  
TTGAATGAACCATCGCCAGCGTAAAGCCGTGCGATTTCGAGCAGT  
TATTATGACTCAGCACGCAACCGGAGACCGGATTGTTTCTTATC  
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Hit Table

Name	Topology	Molecule Ty...	# Sequences	% Pairwise I...	% Identic...	Query start	Query end	Query cover...	Accession	Organism	Max Sequen...	Min Seq
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KF621001	year	DNA	2	99.7%	99.7%	6	301	98.34%	KF621001	Uncultured haptophyte	296	296
KU743783	year	DNA	2	99.3%	99.3%	6	301	98.34%	KU743783	Uncultured eukaryote	296	296
KF422621	year	DNA	2	99.3%	99.3%	6	301	98.34%	KF422621	Syracosphaera pulchra	296	296
AM490987	year	DNA	2	99.3%	99.3%	6	301	98.34%	AM490987	Syracosphaera pulchra	296	296
KF130396	year	DNA	2	99.0%	99.0%	6	301	98.34%	KF130396	Uncultured eukaryote	297	296
MN723153	year	DNA	2	98.6%	98.6%	6	301	98.34%	MN723153	Tisochrysis lutea	296	296
MH298754	year	DNA	2	98.6%	98.6%	6	301	98.34%	MH298754	Isochrysis nuda	296	296
MH182066	year	DNA	2	98.6%	98.6%	6	301	98.34%	MH182066	Isochrysis galbana	296	296
MH166731	year	DNA	2	98.6%	98.6%	6	301	98.34%	MH166731	Isochrysis galbana	296	296

Alignment View

Selected sequences are only summaries. Download Full Sequence(s)

Extract R.C. Translate Add Annotation (restricted) Allow Editing (restricted) Annotate & Predict Save

Statistics

Nucleotide Statistics:

- Length: 296 bp
- Sequences: 1
- Identical Sites: 296 (100.0%)
- Pairwise Identity: 100.0%
- Rough Tm: (restricted)

Read Lengths (restricted):

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- Minimum: - Maximum: -

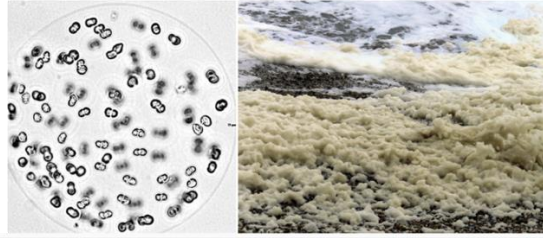
Selected 296 columns from 1 to 296 (296 ungapped bases from 6 to 301).

圖片來源：Andrleit, H., Rogalla, U., & Stäger, S. (2005). Living coccolithophores recorded during the onset of upwelling conditions off Oman in the western Arabian Sea. *Journal of Nannoplankton Research*, 27(1), 1-14.

球形棕囊藻 *Phaeocystis globosa* (100%)

18S:

CCAGTAGTCATATGCTTGCTCAAAGATTAAGCCATGCATGCT  
 TAAGTATAAGCGACTTGTACTGTGAAACTGCGAATGGCTCAT  
 TAAATCAGTTATGGTTCTTTGATGGTACCTTGTACTTGGAT  
 ACCCGTAGTAATTCTAGAGCTAATACATGCAGGAATGCCCGA  
 CTTCCGGAAGGGCTGATTATTAGATAAGAAACCTTCTCGGG  
 TTCGCCGGTTGTGTGCTGAGTCATAATAACTGCTCGAATCG  
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Hit Table	Query Centric View	Distances	Info
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<input type="checkbox"/>	AF182112	DNA	2
<input type="checkbox"/>	AF182113	DNA	2

Name	Molecule Ty...	# Sequences	% Pairwise L...	% Identic...	Query start	Query end	Query cover...	Accession	Organism	Max Sequen...	Min Sequenc...
MZ365004	DNA	2	100.0%	100.0%	9	301	97.34%	MZ365004	Phaeocystis globosa	293	293
MW575291	DNA	2	100.0%	100.0%	9	301	97.34%	MW575291	Phaeocystis globosa	293	293
MW575290	DNA	2	100.0%	100.0%	9	301	97.34%	MW575290	Phaeocystis globosa	293	293
KP404911	DNA	2	100.0%	100.0%	9	301	97.34%	KP404911	Uncultured eukaryote	293	293
KP404690	DNA	2	100.0%	100.0%	9	301	97.34%	KP404690	Uncultured eukaryote	293	293
FJ537335	DNA	2	100.0%	100.0%	9	301	97.34%	FJ537335	Uncultured Phaeocystis	293	293
EF100712	DNA	2	100.0%	100.0%	9	301	97.34%	EF100712	Phaeocystis globosa	293	293
AF182115	DNA	2	100.0%	100.0%	9	301	97.34%	AF182115	Phaeocystis globosa	293	293
AF182112	DNA	2	100.0%	100.0%	9	301	97.34%	AF182112	Phaeocystis globosa	293	293
AF182113	DNA	2	99.8%	99.7%	9	301	97.34%	AF182113	Phaeocystis globosa	293	293

Selected sequences are only summaries [Download Full Sequence\(s\)](#)

Alignment View Distances Dotplot Text View Download Lineage Info

← → Extract R.C. Translate Add/Edit Annotation (restricted) Allow Editing (restricted) Annotate & Predict Save

Identity

1. M02662:168:000000000-KLC6K:1:110... TATGGTTCTTTGATGGTACCTTGTACTTGGATACCCGTAGTAATCTAGAGCTAATACATGCAGGAATGCCCGACTTCGGAAAGGGCTGATTATTAGATAAG

2. MZ365004 TATGGTTCTTTGATGGTACCTTGTACTTGGATACCCGTAGTAATCTAGAGCTAATACATGCAGGAATGCCCGACTTCGGAAAGGGCTGATTATTAGATAAG

Statistics

Nucleotide Statistics:  
 Length (mean): 293 bp  
 Sequences: 2  
 Identical Sites: 293 (100.0%)  
 Pairwise Identity: 100.0%

Read Lengths (restricted):  
 Mean: - Std Dev: -  
 Minimum: - Maximum: -

Confidence Mean (restricted)  
 Expected Errors (restricted)

圖片來源：Karasiewicz, S. (2017). *The phytoplankton community response(s) to global changes and their effect(s) on ecosystem functioning with a special focus on Phaeocystis spp, a harmful algae* (Doctoral dissertation). Université de Lyon, France.

棒筆帽螺 *Creseis clava* (100%)

18S:

GCGCGCCTGCTGCCTTCCTTGGATGTGGTAGCCGTTTCTCATG  
 CTCCTCTCCGGAATCGAACCTGATCCCCGTACCCGTGAC  
 AAACACTGTAGGCATATCACCTACAGTCGACATTTGATAGGG  
 CGGACATTTGAAAAGACGCGTCGCCGACGTAAAGTCATCGGA  
 TCAGCACAAAGTTATCCAGAGTCACCAAAGAGTGCGCCTTCT  
 GACAAGCAGGCAGGCGATTGGTTTTGGGCTAATAAAAGCGC  
 TCTTCCCTTACGGGTCGGAGCTTTGAAGCATGTATTAGCTCT  
 AG



Name	Query Ty...	# Sequences	% Pairwise I...	% Identical Sites	Query start	Query end	Query cover...	Accession	Organism
GU969166		2	100.0%	100.0%	5	301	98.67%	GU969166	Creseis clava
MF049031		2	94.3%	94.3%	5	301	98.67%	MF049031	Creseis virgula
MF049030		2	94.3%	94.3%	5	301	98.67%	MF049030	Creseis virgula
MF049029		2	94.3%	94.3%	5	301	98.67%	MF049029	Creseis clava
DQ279946		2	94.3%	94.3%	5	301	98.67%	DQ279946	Creseis sp.
MW203806		2	93.8%	93.8%	28	301	91.03%	MW203806	Creseis acicula
MW203243		2	93.8%	93.8%	28	301	91.03%	MW203243	Creseis virgula
MW203772		2	93.5%	93.5%	43	301	86.05%	MW203772	Creseis virgula
MH933281		2	89.1%	89.1%	5	301	98.67%	MH933281	Phanerophthalmus cylindricus
KC984289		2	88.7%	88.7%	5	301	98.67%	KC984289	Pontohedyle verrucosa
KC984288		2	88.7%	88.7%	5	301	98.67%	KC984288	Pontohedyle verrucosa
KC984287		2	88.7%	88.7%	5	301	98.67%	KC984287	Pontohedyle verrucosa
AB501328		2	88.6%	88.6%	5	301	98.67%	AB501328	Aplysiopsis minor
MH933333		2	88.4%	88.4%	5	301	98.67%	MH933333	Philine sp.
KX721049		2	88.4%	88.4%	5	301	98.67%	KX721049	Bathyledyle boucheti
DQ923453		2	88.4%	88.4%	5	301	98.67%	DQ923453	Cylichna cylindracea
DQ246443		2	88.4%	88.4%	5	301	98.67%	DQ246443	Phyllaplysia lafonti

Selected sequences are only summaries    Download Full Sequence(s)

Alignment View    Distances    Dotplot    Text View    Download    Lineage    Info

← → Extract R.C. Translate Add/Edit Annotation (restricted) Allow Editing (restricted) Annotate & Predict Save

Identity

1. M02662:168:000000000-KLC6K:1:... GCGCGCCTGCTGCCTTCCTTGGATGTGGTAGCCGTTTCTCATGCTCCCTCTCCGGAATCGAACCTGATCCCCG  
 2. GU969166 GCGCGCCTGCTGCCTTCCTTGGATGTGGTAGCCGTTTCTCATGCTCCCTCTCCGGAATCGAACCTGATCCCCG

General  
 Colors: CGT- Base Call Quality  
 Graphs Options  
 Annotations Options  
 Consensus Options  
 Highlighting Options

Ctrl left click on a sequence position or annotation, or select a region to zoom in. Ctrl-shift left click to zoom out.

圖片來源：Alvaro E. Migotto.(2022, December 31). Pteropod mollusk. Cifonauta image database. Retrieved from <http://cifonauta.cebimar.usp.br/media/6756/>

長尾柱唇海兔 *Stylocheilus longicauda* (100%)

18S:

GGATGTGGTAGCCGTTTCTCATGCTCCCTCTCCGGAATCGAAC  
 CCTGATCCCCGTTACCCGTTACAAACATGGTAGGCATATCAC  
 GTACCATCGACATTTGATAGGGCAGACATTTGAAAAGATGCGT  
 CGCCAGCGCAAAGGCCATGCGATCAGCACAAAGTTATCCAG  
 AGTCACCAATGGGGGACGCCGCCGCCGAAACGGAACGAC  
 GATTGGTTTTGAACTAATAAAAGCGCTCTTCCACGAGGGTC  
 GGAGCTTGATAAGCATGTATTAGCTC



Hit Table

Name	Scale Ty...	# Sequences	% Pairwise I...	% Identical Sites	Query start	Query end	Query cover...	Accession	Organism
DQ237963	.	2	99.7%	99.7%	5	301	98.67%	DQ237963	<i>Stylocheilus longicauda</i>
DQ246443	.	2	99.3%	99.3%	5	301	98.67%	DQ246443	<i>Phyllaplysia lafonti</i>
DQ237962	.	2	99.3%	99.3%	5	301	98.67%	DQ237962	<i>Petalifera petalifera</i>
DQ237960	.	2	99.3%	99.3%	5	301	98.67%	DQ237960	<i>Dolabrifera dolabrifera</i>
AY427503	.	2	98.3%	98.3%	5	301	98.67%	AY427503	<i>Dolabella auricularia</i>
DQ237961	.	2	97.6%	97.6%	5	301	98.67%	DQ237961	<i>Bursatella leachii</i>
MH933239	.	2	96.3%	96.3%	5	301	98.67%	MH933239	<i>Diniatys</i> sp.
EF012192	.	2	96.3%	96.3%	5	301	98.67%	EF012192	<i>Planorbis planorbis</i>
KF709276	.	2	96.3%	96.3%	5	301	98.67%	KF709276	<i>Hedylopsis</i> sp.
EF012185	.	2	96.3%	96.3%	5	301	98.67%	EF012185	<i>Choanomphalus maacki</i>
EF012188	.	2	96.0%	96.0%	5	301	98.67%	EF012188	<i>Kessneria papillosa</i>
KF709297	.	2	96.0%	96.0%	5	301	98.67%	KF709297	<i>Asperspina</i> sp.
KF709296	.	2	96.0%	96.0%	5	301	98.67%	KF709296	<i>Asperspina</i> sp.
KC261493	.	2	96.0%	96.0%	5	301	98.67%	KC261493	<i>Vorticifex</i> sp.
FR797811	.	2	96.0%	96.0%	5	301	98.67%	FR797811	<i>Planorbis corneus</i>
KF709318	.	2	96.0%	96.0%	5	301	98.67%	KF709318	<i>Paraganitus</i> sp.
KF709317	.	2	96.0%	96.0%	5	301	98.67%	KF709317	<i>Paraganitus</i> sp.

Selected sequences are only summaries [Download Full Sequence\(s\)](#)

Alignment View

Identity

1. M02662:168:000000000-KLC6K:1...  
 2. DQ237963

GGCGGCCTGCTGCCTTCCTTGGATGGTAGCCGTTTCTCATGCTCCCTCTCCGGAATCGAACCCGATTCCTCCCG  
 GGCGGCCTGCTGCCTTCCTTGGATGGTAGCCGTTTCTCATGCTCCCTCTCCGGAATCGAACCCGATTCCTCCCG

General  
 Colors: CGT- Base Call Quality  
 Graphs  
 Annotations  
 Consensus  
 Highlighting

圖片來源：2006 CREEF expedition; French Frigate Shoals; Oct. 19, 2006.

方格星蟲 *Sipunculus nudus* (100%)

18S:

TCATATGCTTGTCTCAAAGACTAAGCCATGCATGTCTAAGTACAG  
 GCTTTACAAAGCGAAACCGGAATGGCTCATTAGGTCGGACA  
 TGGTTCCTTAGATCGTACACTCCTACTTGGATAACTGTGGTAATC  
 TAGAGCTAATACATGCGAGCAAGCTCCGACCTCGCGGGAAGAG  
 CGCTTTTATTAGATCAAAACCAATCGGGCCCCGGGTCCGCTCG  
 TTTGGTGA CTCTGGATAACTTTGTGCTGATCGCACGGCCCCGAG  
 CCGCGCAGCTATCTTTCAAG



Name	Molecule Ty...	# Sequences	% Pairwise I...	% Identical Sites	Query start	Query end	Query cover...	Accession	Organism
MW203228	DNA	2	100.0%	100.0%	44	301	85.71%	MW203228	Sipunculus nudus
MN729828	DNA	2	100.0%	100.0%	15	301	95.35%	MN729828	Sipuncula sp.
JN865020	DNA	2	100.0%	100.0%	17	301	94.68%	JN865020	Sipunculus nudus
JN865019	DNA	2	100.0%	100.0%	17	301	94.68%	JN865019	Sipunculus nudus
DQ300007	DNA	2	100.0%	100.0%	17	301	94.68%	DQ300007	Sipunculus nudus
DQ300006	DNA	2	100.0%	100.0%	17	301	94.68%	DQ300006	Sipunculus nudus
DQ300005	DNA	2	100.0%	100.0%	17	301	94.68%	DQ300005	Sipunculus nudus
AF519240	DNA	2	100.0%	100.0%	17	301	94.68%	AF519240	Sipunculus sp.
DQ300004	DNA	2	99.3%	99.3%	17	301	94.68%	DQ300004	Sipunculus norvegicus
AF519239	DNA	2	99.3%	99.3%	17	301	94.68%	AF519239	Sipunculus nudus
AF448166	DNA	2	99.1%	99.0%	9	301	97.34%	AF448166	Sipunculus nudus
MN729832	DNA	2	98.3%	98.3%	15	301	95.35%	MN729832	Sipuncula sp.
MN729831	DNA	2	98.3%	98.3%	15	301	95.35%	MN729831	Sipuncula sp.
MN729830	DNA	2	98.3%	98.3%	15	301	95.35%	MN729830	Sipuncula sp.
DQ300010	DNA	2	98.3%	98.3%	17	301	94.68%	DQ300010	Sipunculus polymyotus
DQ300009	DNA	2	98.3%	98.3%	17	301	94.68%	DQ300009	Sipunculus phalloides
MW204010	DNA	2	98.1%	98.1%	44	301	85.71%	MW204010	Sipunculus sp.

Selected sequences are only summaries    Download Full Sequence(s)

Alignment View    Distances    Dotplot    Text View    Download    Lineage    Info

← → Extract    R.C.    Translate    Add/Edit Annotation (restricted)    Allow Editing (restricted)    Annotate & Predict    Save

Identity

1. M02662:168:000000000-KLC6K1:.... ATGCATGTCTAAGTACAGGCTTTCAAAAGCGAAACCGGAATGGCTCATTAGGTCGGACATGGTTCCTTAGATCGTACACTCCTACTTGA  
 2. MW203228 ATGCATGTCTAAGTACAGGCTTTCAAAAGCGAAACCGGAATGGCTCATTAGGTCGGACATGGTTCCTTAGATCGTACACTCCTACTTGA

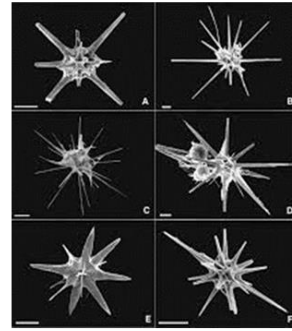
General  
 Colors: **CGT** - Base Call Quality  
 Graphs    Options  
 Annotations    Options  
 Consensus  
 Highlighting    Options

圖片來源：WIKIPEDIA

十字粘棘蟲 *Acanthocolla cruciata* (100%)

18S:

GCGCGCCTGCTGCCTTCCTTAGATGTGGTAGCCGTTTCTCAGGC  
 TCCCTCTCCGGAATCGAACCCCTAATCTCCGTTACCCGTCAAAGC  
 CATGGTAGTCCAATACACTACCATCGAAAGCTGATAGGGCAGAA  
 ATTTGAATGAAGCGTCTCCGAAGAGATCCGCTGAATTACTATGAT  
 TCACCGAAGCGCAAGCGCATTGGTGGGAAATCTAATAAGTGCA  
 ACCTGTTACCAGGCATGTAGTGCAAGTATTAGCTCTAGAATTATT  
 ACGGTTATCCTTGATGATTGACCATCAAA



Hit Table

Name	Scale Ty...	# Sequences	% Pairwise I...	% Identical Sites	Query start	Query end	Query cover...	Accession	Organism
JN811205	.	2	100.0%	100.0%	13	301	96.01%	JN811205	Staurolithium sp.
JN811195	.	2	100.0%	100.0%	19	301	94.02%	JN811195	Acanthocolla cruciata
JN811182	.	2	100.0%	100.0%	57	301	81.40%	JN811182	Staurolithium sp.
JN811174	.	2	100.0%	100.0%	11	301	96.68%	JN811174	Acanthocolla cruciata
HQ688754	.	2	99.7%	99.7%	15	301	95.35%	HQ688754	Uncultured eukaryote
HQ688745	.	2	99.3%	99.3%	15	301	95.35%	HQ688745	Uncultured eukaryote
JN811184	.	2	98.8%	98.8%	49	301	84.05%	JN811184	Acanthocolla solidissima
JN811202	.	2	98.3%	98.3%	11	301	96.68%	JN811202	Trizona brandti
JX188359	.	2	95.9%	95.9%	14	301	95.68%	JX188359	Uncultured eukaryote
KJ763536	.	2	90.4%	90.4%	9	301	97.34%	KJ763536	Uncultured eukaryote
KJ761023	.	2	90.4%	90.4%	9	301	97.34%	KJ761023	Uncultured eukaryote
KJ757192	.	2	90.0%	90.0%	9	301	97.34%	KJ757192	Uncultured eukaryote
KC172865	.	2	89.9%	89.9%	13	301	96.01%	KC172865	Acantharia sp.
JN811222	.	2	89.9%	89.9%	14	301	95.68%	JN811222	Litholophus sp.
AJ829834	.	2	89.7%	89.7%	9	301	97.34%	AJ829834	Uncultured marine
JX842106	.	2	89.7%	89.7%	9	301	97.34%	JX842106	Uncultured marine
KJ763045	.	2	89.4%	89.4%	9	301	97.34%	KJ763045	Uncultured eukaryote

Alignment View

Identity

1. M02662:168:000000000-KLC6K:1...  
 2. JN811195

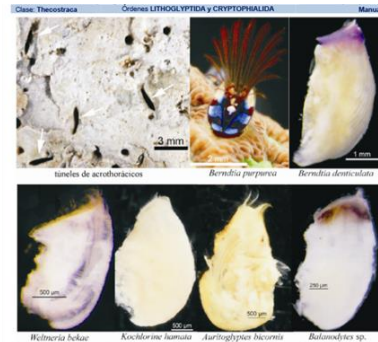
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 ATATGCTTGTCTCAAAGCAAGCAATGCTCTAAGTTAAAGGATTGGAAGCTGGAGACTGCGGACGGCTCATTATCAGTTATAGTTTCATTGATG

圖片來源：De Deckker, P. (2004). On the celestite-secreting Acantharia and their effect on seawater strontium to calcium ratios. *Hydrobiologia*, 517, 1-13.

藤壺 *Auritoglyptes bicornis* (100%)

18S:

AGATGTGGTAGCCGTTTCTCAGGCTCCCTCTCCGGAATCGAACC  
 CTGATCCCCGTTACCCGTTATTGCCATGGTAATCATAGAAATTAC  
 CATCGAAAGCTGATAAGGCAGACATTTGAAAGATGCGTCGCCG  
 GTACGTGACCGTGCGATCCGCACAAAATTATTCAGAGTACCCAA  
 GAGGCACGGCCCCGAGAGGCCGATTGGTTTTGATCTAATAAAA  
 GCGCTCTCCCCGCAACGCCGCCGAAACGACGCCACAAGTCGG  
 AGCTGGAGTGCATG



Name	# Sequences	% Pairwise I...	% Identical Sites	Query start	Query end	Query cover...	Accession	Organism
KM087448	2	100.0%	100.0%	31	301	90.03%	KM087448	Lithoglyptes sp.
KM087444	2	100.0%	100.0%	31	301	90.03%	KM087444	Kochlorine sp.
KM087430	2	100.0%	100.0%	31	301	90.03%	KM087430	Kochlorine hamata
KM087428	2	100.0%	100.0%	31	301	90.03%	KM087428	Kochlorine hamata
KM087414	2	100.0%	100.0%	31	301	90.03%	KM087414	Lithoglyptes ivanovi
KM087410	2	100.0%	100.0%	31	301	90.03%	KM087410	Auritoglyptes sp.
FJ751887	2	100.0%	100.0%	17	301	94.68%	FJ751887	Auritoglyptes bicornis
KM087413	2	99.6%	99.6%	31	301	90.03%	KM087413	Auritoglyptes sp.
L26520	2	98.7%	98.3%	9	301	97.34%	L26520	Trypetes lampas
KM087437	2	98.5%	98.5%	31	300	89.70%	KM087437	Berndtia sp.
KM087424	2	98.5%	98.5%	31	301	90.03%	KM087424	Balanodytes sp.
KM087406	2	98.5%	98.5%	31	301	90.03%	KM087406	Balanodytes sp.
KM087405	2	98.5%	98.5%	31	301	90.03%	KM087405	Balanodytes sp.
KM087403	2	98.5%	98.5%	31	301	90.03%	KM087403	Armatoglyptes mitis
KM087431	2	98.2%	98.2%	31	300	89.70%	KM087431	Berndtia sp.
KM087421	2	98.2%	98.2%	31	300	89.70%	KM087421	Weltneria bekae
KM087416	2	98.2%	98.2%	31	300	89.70%	KM087416	Berndtia sp.

Selected sequences are only summaries    Download Full Sequence(s)

Alignment View   Distances   Dotplot   Text View   Download   Lineage   Info

← → Extract R.C. Translate Add/Edit Annotation (restricted) Allow Editing (restricted) Annotate & Predict Save

Identity

1. M02662:168:000000000-KLC6K:1...  
 2. FJ751887

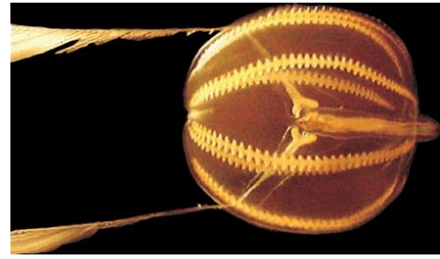
TCATATGCTTGTCTCAAAGATTAAGCCATGCATGCTAAGTACAGGCCCTAACTAAGGCGAGACCGGAATGGCTCTAAATCAGTTAAGTTCCCTTAGATC  
 TCATATGCTTGTCTCAAAGATTAAGCCATGCATGCTAAGTACAGGCCCTAACTAAGGCGAGACCGGAATGGCTCTAAATCAGTTAAGTTCCCTTAGATC

General  
 Colors: CGT - Base Call Quality  
 Graphs    Options  
 Annotations    Options  
 Consensus  
 Highlighting    Options

圖片來源：Kolbasov GA (2015). Orders Lithoglyptida & Cryptophialida. Revista IDE@ - SEA, n° 101B (30-06-2015): 1–6. (ISSN 2386-7183).

櫛水母 *Pukia falcata* (100%)

GC GCGCCTGCTGCCTTCCTTGGATGTGGTAGCCGTTTCTC  
 GGGCTCCCTCTCCGGAATCGAACCCCTAATTCCTCCGTTACC  
 CGTTGTACCATGGTAAGCCAATACCTTACCATCGAAAGT  
 TGATAGGGCAGAAACTCGAATGAAACATCGCCGGCTCGA  
 GGCCATGCGATTGGAACAGTTATTATGAATCACCAAGAAG  
 CGTCGTGAAACGCATTGGCTTTAATCTAATAAATACATCCC  
 TTCCAGAAGTCGGGACTTTTCGCATGTATTAGCTCTAGAAT  
 TACTACGGTTATCCAT



Hit Table

Name	le Ty...	# Sequences	% Pairwise L...	% Identical Sites	Query start	Query end	Query cover...	Accession	Organism
MF599322		2	100.0%	100.0%	5	301	98.67%	MF599322	<i>Pukia falcata</i>
KJ859219		2	100.0%	100.0%	5	301	98.67%	KJ859219	<i>Pleurobrachia globosa</i>
MW647069		2	99.7%	99.7%	5	301	98.67%	MW647069	<i>Pleurobrachia bachei</i>
MF599335		2	99.7%	99.7%	5	301	98.67%	MF599335	<i>Pleurobrachia</i> sp.
MF599334		2	99.7%	99.7%	5	301	98.67%	MF599334	<i>Pleurobrachia</i> sp.
MF599326		2	99.7%	99.7%	5	301	98.67%	MF599326	<i>Pleurobrachidae</i> sp.
MF599313		2	99.7%	99.7%	5	301	98.67%	MF599313	<i>Pleurobrachia pileus</i>
MF599304		2	99.7%	99.7%	5	301	98.67%	MF599304	<i>Pleurobrachia</i> sp.
KJ754154		2	99.7%	99.7%	5	301	98.67%	KJ754154	<i>Pleurobrachia brunnea</i>
KJ754153		2	99.7%	99.7%	5	301	98.67%	KJ754153	<i>Pleurobrachia pileus</i>
KJ193811		2	99.7%	99.7%	5	301	98.67%	KJ193811	<i>Pleurobrachia pileus</i>
HM799973		2	99.7%	99.7%	5	301	98.67%	HM799973	Uncultured marine
AF293677		2	99.7%	99.7%	5	301	98.67%	AF293677	<i>Pleurobrachia bachei</i>
AF100944		2	99.7%	99.7%	5	301	98.67%	AF100944	<i>Hormiphora</i> sp.
AF293678		2	99.3%	99.3%	5	301	98.67%	AF293678	<i>Pleurobrachia pileus</i>
AF293675		2	99.3%	99.3%	5	301	98.67%	AF293675	Undescribed pleurobrachiid
MF599328		2	99.0%	99.0%	5	301	98.67%	MF599328	<i>Hormiphora californensis</i>

Alignment View

Identity

1. M02662:168:000000000-KLC6K:1:...  
 2. MF599322

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 GGGCTCCCTCTCCGGAATCGAACCCCTAATTCCTCCGTTACC  
 CGTTGTACCATGGTAAGCCAATACCTTACCATCGAAAGT  
 TGATAGGGCAGAAACTCGAATGAAACATCGCCGGCTCGA  
 GGCCATGCGATTGGAACAGTTATTATGAATCACCAAGAAG  
 CGTCGTGAAACGCATTGGCTTTAATCTAATAAATACATCCC  
 TTCCAGAAGTCGGGACTTTTCGCATGTATTAGCTCTAGAAT  
 TACTACGGTTATCCAT

Selected sequences are only summaries

Download Full Sequence(s)

General

Colors: C G T - Base Call Quality

Annotations

Consensus

Highlighting

圖片來源：Gershwin, L. A., Zeidler, W., & Davie, P. J. (2010). Ctenophora of Australia. *Memoirs of the Queensland Museum*, 54(3), 1-45.



附錄四、以 12S 基因序列發現之南沙太平島環境 DNA 海水魚物種名錄

物種	111年								110年							
	TP01	TP02	TP03	TP04	TP05	TP06	TP07	TP08	TP01	TP02	TP03	TP04	TP05	TP06	TP07	TP08
黃鰭鮨	v	v														
長鰭鮨								v								
鮨魚	v															
東方齒鮨								v								
鮨科				v												
鮨科				v												
鯉魚								v								
圓鯛科				v												
後刺尾鯛					v											
黃尾刺尾鯛					v											
褐斑刺尾鯛	v					v										
黑尾刺尾鯛					v											
雙斑櫛齒刺尾魚									v	v	v	v	v	v	v	v
粗棘鼻魚									v	v	v	v				
擬鮨鼻魚					v											
大眼鼻魚	v			v												
鼻魚				v												
單角鼻魚	v			v												
黑背鼻魚				v												

物種	111年								110年							
	TP01	TP02	TP03	TP04	TP05	TP06	TP07	TP08	TP01	TP02	TP03	TP04	TP05	TP06	TP07	TP08
刺尾鯛科	v			v	v				v							
隆頭魚科	v		v	v												
豔麗絲綉鸚鯛						v				v		v	v	v	v	v
長頭馬鸚哥魚				v												
哈氏錦魚	v	v		v												
雜色尖嘴魚				v												
五帶錦魚	v	v	v	v			v									
詹氏錦魚				v												
邵氏豬齒魚	v			v												
斑點海豬魚	v	v														
三斑海豬魚	v			v												
福氏鸚哥魚	v															
鈍頭錦魚	v			v												
新月錦魚	v			v												
三葉唇魚	v			v												
藍尖尾無鬚鱈	v		v													
勃氏刻齒雀鯛	v		v													
白帶固齒鯛				v												
眼斑海葵魚									v	v	v					

物種	111年								110年							
	TP01	TP02	TP03	TP04	TP05	TP06	TP07	TP08	TP01	TP02	TP03	TP04	TP05	TP06	TP07	TP08
雀鯛科	v		v													
螢光星衫魚	v															
大洋短鰓燈魚					v											
多耙眶燈魚					v											
長領珍燈魚					v											
七星底燈魚				v			v		v	v	v	v	v	v	v	v
眶下眶燈魚				v	v		v									
天紐珍燈魚		v	v				v									
大洋短鰓燈魚			v				v									
麥氏珍燈魚		v		v	v		v									
仿珍燈魚		v	v		v		v									
燈籠魚							v									
燈籠魚科		v	v		v		v									
蒂爾鱗鰭烏尾鯨			v													
淡網紋裸胸鯨					v											
尖吻鱸						v										
鮫魚科						v										
低鰭舵魚									v		v					
銀漢魚科						v										

物種	111年								110年							
	TP01	TP02	TP03	TP04	TP05	TP06	TP07	TP08	TP01	TP02	TP03	TP04	TP05	TP06	TP07	TP08
細斑刺鼻單棘魷				v												
黑邊角鱗魷				v												
褐擬鱗魷				v												
皮剝魷科				v												
皮剝魷科				v												
單棘魷科				v												
雙棘三刺魷						v			v	v	v	v	v	v	v	v
蝴蝶魚科				v												
耳帶蝴蝶魚													v			v
囊頭魷科				v												
長臂囊頭魷				v			v									
棘鱗		v	v	v			v	v								
脂眼凹肩鰲						v	v									
尖棘角魚								v								
虱目魚								v								
白腹小沙丁魚							v									
縫鱗小沙丁魚							v									
花蓮小沙丁魚									v	v	v	v	v	v		v
鋪眼銀帶鯆				v												

物種	111年								110年							
	TP01	TP02	TP03	TP04	TP05	TP06	TP07	TP08	TP01	TP02	TP03	TP04	TP05	TP06	TP07	TP08
日本海鯨									v		v	v	v	v	v	
環球海鯨										v	v	v			v	
銀灰半稜鯢	v		v	v	v											
島嶼側帶小公魚									v	v	v	v	v	v	v	v
側帶小公魚屬									v	v	v	v	v	v	v	v
斑石鯛							v		v	v	v					v
日本帶魚							v			v						
黃背牙鯛							v									
雙邊魚科															v	
黑背叉尾鶴鱗										v	v					v
尼羅口孵非鯽										v					v	
奧利亞口孵非鯽															v	
海鯢												v				
大棘鑽嘴魚									v	v	v	v	v	v	v	v
斑點竿蝦虎									v		v			v		
大吻蝦虎															v	
蝦虎科	v															
雨傘旗魚									v	v	v	v	v	v	v	v
四鱗旗魚									v	v	v	v	v	v		v

物種	111年								110年							
	TP01	TP02	TP03	TP04	TP05	TP06	TP07	TP08	TP01	TP02	TP03	TP04	TP05	TP06	TP07	TP08
劍旗魚									v	v	v	v	v	v	v	v
條紋旗魚									v	v	v	v	v	v	v	v
旗魚科											v					
旗魚科									v	v	v	v	v	v	v	
旗魚科									v							
黑邊布氏鰨									v	v						
黃斑光胸鰨									v	v		v	v	v	v	v
銀紋笛鯛									v		v					
笛鯛科									v			v		v		
黃鰭紫魚									v	v	v					
日本馬頭魚										v	v	v	v	v	v	v
薛氏凡鯧												v				
烏魚										v	v	v		v	v	
大鱗梭										v	v	v	v	v		v
似鯧銀漢魚科									v	v	v			v		
南方擬金眼鯛									v	v	v	v	v	v	v	v
香魚															v	
金錢魚									v	v	v	v	v	v	v	v
紅鼓魚									v	v	v		v			v

物種	111年								110年							
	TP01	TP02	TP03	TP04	TP05	TP06	TP07	TP08	TP01	TP02	TP03	TP04	TP05	TP06	TP07	TP08
婆羅叫姑魚												v				
鞍帶石斑魚									v	v	v					
六角石斑魚				v												
鮨科				v												
短嘴格				v												
銀臭肚魚									v	v	v	v				v
褐藍子魚									v	v	v	v	v	v	v	v
白沙鯪												v				
太平洋棘鯛									v	v	v	v	v	v	v	v
金頭鯛												v				
棘鯛屬									v	v				v	v	v
魷鯊	v						v									
大青鯊													v	v		v
尖吻鯖鯊		v	v		v		v									
長臂鯖鯊									v	v		v	v	v	v	v
淺海狐鯊			v													
深海狐鯊	v	v	v		v	v	v	v	v	v	v	v	v	v	v	v
長尾鯊科					v											



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