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青藏高原纳木错夏季沿岸水体可培养细菌多样性 及其与理化因子的相关性

郑艳艳, 郭小芳, 四郎玉珍, 德吉

(西藏大学理学院, 西藏拉萨 850000)

摘 要: 纳木错位于青藏高原中南部, 是该地区独具特色的咸水湖泊。对纳木错夏季沿岸水体可培养细菌物种多样性进行研究, 并揭示细菌群落多样性及物种分布与水质理化指标间的相关性。运用直接涂布平板法与稀释涂布平板法来分离湖水中的可培养细菌, 细菌菌株的鉴定采用16S rDNA基因序列分析结合经典分类方法, 并使用R 4.1.1、SPSS 20.0等软件分析细菌群落多样性。结果显示, 从纳木错夏季沿岸水体20个样点中共分离得到681株可培养细菌, 鉴定分为16属43种, 其中优势种为 *Acinetobacter johnsonii*。Spearman 相关系数显示, 总磷与总氮均为影响细菌群落多样性的主要理化指标, 总磷显著影响细菌总丰度 ($P<0.05$), 总氮显著影响 Simpson 多样性指数 ($P<0.05$)。RDA 结果显示, 氨氮是影响细菌群落分布的主要理化指标 ($P<0.05$)。本研究初步揭示了纳木错夏季沿岸水体可培养细菌群落多样性, 并获得较丰富的细菌菌株资源。

关键词: 青藏高原; 纳木错; 湖泊; 细菌多样性; 环境因子; 冗余分析; 16S rDNA

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0 引言

湖泊在生物圈、大气圈、岩石圈和水圈之间的物质能量循环中充当重要载体^[1]。青藏高原拥有全球海拔最高、面积最大、数量最多的高原湖群区, 其湖泊总面积约占全国湖泊总面积的二分之一^[2]。湖泊微生物在湖泊生态系统中发挥着不可或缺的作用^[3], 开展湖泊微生物研究对于揭示湖泊生态系统对外界条件变化的响应规律及深入了解湖泊生态系统来说有着重要意义^[4]。细菌是湖泊生态系统中的重要一员, 湖泊中细菌的数量庞大且物种丰富, 它们在湖泊生态系统绝大多数生物活性元素的形态转化和地球化学循环中起着重要作用^[5], 近年来, 不少专家学者已逐步对其开展了相关研究^[6-10]。

青藏高原是中国最大、世界平均海拔最高的高原, 也是中国湖泊的主要分布区之一^[11]。纳木错是典型的青藏高原湖泊, 孙丹^[12]通过高通量测序等方法, 揭示了纳木错表层湖水与岸边土壤环境中的微生物群落构成; 刘金波等^[13]用定量PCR和克隆文库方法, 研究了纳木错湖水中 *cbbL* ID 基因丰度和固碳微生物群落组成, 并分析了其与环境参数的关系; 王鑫^[14]运用宏基因组测序等技术研究了湖中微生物的物种组成、物种分布及物种多样性; 刘晓波等^[15]通过流式细胞计数等技术分析了纳木错水体中细菌的群落组成。然而关于纳木错湖泊可培养微生物的研究报道较少, 潘文娟等^[16]从纳木错沉积物中分离得到6株放线菌, 填补了西藏湖泊放线菌资源的空白; 张红光等^[17]研究了纳木错水体可培养微生物丰度是否受海拔梯度造成的气候环境因素

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作者简介: 郑艳艳, 硕士研究生, 主要从事微生物生态学研究. E-mail: 1529243754@qq.com

通信作者: 德吉, 高级实验师, 主要从事微生物生态学教学与研究. E-mail: dg971103@163.com

的影响,结果表明纳木错可培养微生物的数量与温度呈显著正相关。但关于纳木错水体可培养细菌群落多样性及其对水质理化指标的响应规律的研究鲜有报道,探究青藏高原湖水可培养细菌群落多样性,将有着重要的生态学意义。

1 材料与方法

1.1 研究区域概况及水样采集

纳木错(90°16′~91°03′ E, 30°30′~30°55′ N)位于青藏高原,湖泊面积达2 020 km²^[18],流域面积达10 610 km²,跨越范围89°21′~91°23′ E, 29°56′~31°7′ N,流域周边的冰川融水会汇入纳木错湖泊^[19],成为湖泊水体的重要来源之一。

2020年夏季沿纳木错设20个样点采集水样,本

研究区域由于条件限制,无法达到湖面,因此仅在沿岸区设置样点。其中2号样点在扎西半岛,5号样点与主湖间隔了一道天然河坝,10号样点在多加寺附近,11号样点采样时水中长有水草,15号样点湖岸边上有很多动物粪便,19号样点在观景台,20号样点在湖泊入口处(图1)。用无菌采集器在距湖岸边约15 m、距水体表面约50 cm处进行水样采集^[20]。直接在采样地用多参数测试笔测定水样pH、温度、总溶解固体量、电导率和盐度,每个参数测定3次^[21]。每个样点共采集约7.5 L水样,平均装入3个无菌塑料桶。1份水样立即送至西藏博源环境检测有限公司测定水体理化因子,包括总氮、总磷、氨氮、化学需氧量与浊度;1份水样带回实验室立即分离其中的可培养细菌^[20]。

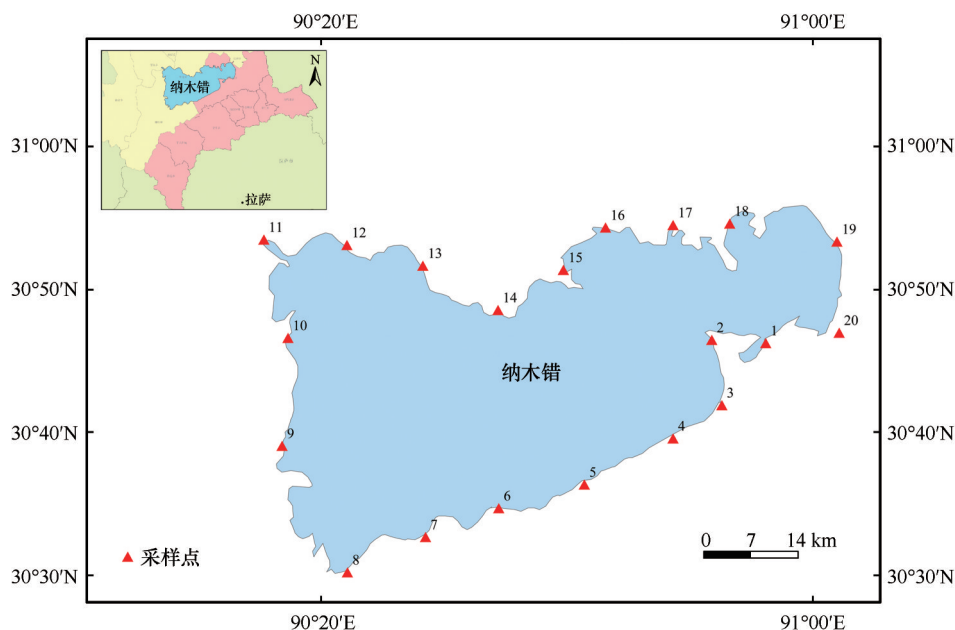


图1 纳木错采样点分布图

Fig. 1 Distribution of sampling sites in Nam Co

1.2 细菌的分离纯化与保藏

细菌的分离培养采用直接涂布平板法与稀释涂布平板法相结合。将20个样点的水样使用移液枪分别取200 μL接种于固体培养基平板(牛肉膏蛋白胨培养基:牛肉膏10 g,蛋白胨10 g,氯化钠5 g,琼脂粉20 g,水1 L, pH 7.4~7.6)上,采用涂布器将水样涂布均匀后放入恒温箱中倒置培养,温度设置为28℃。其中菌落数过多的样点重新采用稀释涂布平板法进行分离培养(5号、10号、11号、15号和19号)。每个处理设3个重复。待平板上长出清晰可见的菌落时依次进行计数、分离、纯化及保藏等

步骤,详见文献[20]。

1.3 细菌的分子鉴定及代表菌株系统发育树的构建

菌株的鉴定采用16S rDNA基因序列分析法进行。本实验使用的上、下游引物序列如下:27F:5'-AGAGTTTGATCCTGGCTCA-3';1492R:5'-GGT-TACCTTGTTACGACTT-3'^[22]。聚合酶链式反应完成后采用1%琼脂糖凝胶检测PCR扩增产物,将其送至上海生工生物工程股份有限公司进行双向测序,各序列均测通。

对供试菌株16S rDNA序列测序结果进行人工

校对,去除引物及双峰序列后在 GenBank 数据库中进行比对,从而确定菌株的分类地位^[20]。将供试菌株的基因序列上传至 GenBank 核酸数据库,登录号为 MW799879~MW799953,共 75 条序列。下载与代表菌株基因序列相似性高的菌株序列,使用 MEGA 7.0 软件中的邻接(neighbour-joining)法构建基于 16S rDNA 基因序列的系统发育树,其中检验次数设为 1 000 次^[23],确定本研究中菌株的系统发育学地位^[20]。

1.4 纳木错水体理化因子的测定

各项理化因子的测定详见文献[20]。

1.5 数据处理与分析

运用 R 4.1.1、SPSS 20.0、CANOCO 4.5、Arc-GIS 10.5 与 Origin 2019b 等软件进行数据的处理分析及图形的绘制。采用 Excel 2010 计算细菌的相对丰度、出现频率及总丰度,其中相对丰度指某一种细菌菌株数占有所有细菌菌株数的百分比,出现频率

为某一种细菌出现的样点数占有所有样点数的百分比,总丰度为某一个样点分离的细菌菌落数量,即 1 mL 水样中分离到的细菌菌落数,用 $\text{cfu} \cdot \text{mL}^{-1}$ 表示;采用 R 4.1.1 中 vegan 包进行多样性指数的计算;单因素方差分析(One-way ANOVA)采用 SPSS 20.0 软件中 Duncan 检验法进行;相关性分析采用 R 4.1.1 中的 Spearman 相关系数法进行;使用 CANOCO 4.5 软件进行细菌群落分布与环境因子之间的排序分析。

2 结果与分析

2.1 纳木错夏季水体理化指标的测定

对纳木错夏季 10 项水体理化指标进行了测定,并运用 SPSS 20.0 中的 Duncan 检验法对各样点的理化因子进行单因素方差分析。由表 1 可以看出,纳木错夏季 20 个水样间,除浊度(turbidity)外,其余 9 个理化因子均存在着不同程度的差异($P < 0.05$)。

表 1 纳木错各样点水体理化因子差异性分析

Table 1 Difference analysis of aquatic physicochemical factors of different sampling sites in Nam Co

采样点	pH	EC/($\mu\text{s} \cdot \text{cm}^{-1}$)	TDS/($\text{mg} \cdot \text{L}^{-1}$)	Salt/($\text{mg} \cdot \text{L}^{-1}$)	T/°C	COD/($\text{mg} \cdot \text{L}^{-1}$)	$\text{NH}_4^+-\text{N}/$ ($\text{mg} \cdot \text{L}^{-1}$)	TP/ ($\text{mg} \cdot \text{L}^{-1}$)	TN/ ($\text{mg} \cdot \text{L}^{-1}$)	Turbidity/ NTU
1	9.56bcd	1 759.33f	1 253.33g	877.33g	16.33b	8.00bc	0.18f	0.02cd	0.29fg	1a
2	9.40h	1 857.00c	1 320.00cd	923.67c	12.13k	4.00e	0.06q	0.02cd	0.15k	1a
3	9.48ef	1 690.00h	1 196.67i	831.67i	13.30ef	5.00de	0.07p	0.01d	0.22ij	1a
4	9.59b	1 810.00e	1 283.33f	891.67f	11.60l	8.00bc	0.19e	0.01d	0.54b	1a
5	8.72i	290.67n	206.67o	132.67o	9.70m	4.00e	0.17g	0.01d	0.40cd	1a
6	9.57bcd	1 655.00i	1 176.67j	817.33j	12.80ghi	6.00cde	0.16h	0.02cd	0.32ef	1a
7	9.56bcd	1 711.33g	1 213.33h	845.00h	13.07efg	7.00cd	0.08o	0.02cd	0.15k	1a
8	9.54bcd	1 445.33k	1 023.33l	708.67l	13.43e	8.00bc	0.27c	0.02cd	0.36de	1a
9	9.53cde	1 767.00f	1 256.67g	874.33g	13.40e	7.00cd	0.24d	0.02cd	0.30f	1a
10	9.52de	1 862.33c	1 320.00cd	920.00cd	12.37jk	4.00e	0.13j	0.02cd	0.28fgh	1a
11	9.66a	1 334.00l	947.00m	650.00m	12.57ij	10.00b	0.35b	0.03bc	0.42c	1a
12	9.59b	1 830.33d	1 296.67e	903.67e	12.53ij	7.00cd	0.15i	0.03bc	0.39cd	1a
13	9.57bcd	1 884.00b	1 336.67ab	932.67b	12.67hij	7.00cd	0.08o	0.02cd	0.25ghi	1a
14	9.58bc	1 872.00bc	1 330.00bc	926.67bc	12.53ij	5.00de	0.08n	0.02cd	0.29fg	1a
15	9.58bcd	1 901.67a	1 346.67a	950.00a	16.37b	13.00a	0.27c	0.04ab	0.39cd	1a
16	9.53cde	1 862.33c	1 323.33bcd	926.00bc	12.97fgh	4.00e	0.11k	0.03bc	0.18jk	1a
17	9.46fg	1 839.00d	1 310.00d	913.00d	13.00fgh	8.00bc	0.11m	0.02cd	0.23i	1a
18	9.44fgh	1 858.67c	1 320.00cd	922.33c	13.87d	7.00cd	0.11l	0.03bc	0.41c	1a
19	9.42gh	1 615.00j	1 150.00k	799.33k	14.83c	6.00cde	0.17g	0.03bc	0.24hi	1a
20	9.56bcd	706.67m	501.67n	343.00n	20.57a	15.00a	0.71a	0.05a	0.97a	1a

注:EC:电导率;TDS:总溶解固体量;T:温度;COD:化学需氧量; NH_4^+-N :氨氮;TP:总磷;TN:总氮。用不同字母标注的数据表明存在显著差异($P < 0.05$) [EC: electric conductivity; TDS: total dissolved solids; T: temperature; COD: chemical oxygen demand; NH_4^+-N : ammonium nitrogen; TP: total phosphorus; TN: total nitrogen. The data marked with different alphabets indicated that difference was significant ($P < 0.05$)]

2.2 纳木错夏季各样点水体可培养细菌多样性

2.2.1 纳木错夏季各样点水体可培养细菌物种组成

从纳木错夏季水体中共分离到681株细菌,鉴定分为16属43种(图2)。由出现频率数据可知,43个物种中,*Acinetobacter johnsonii*有着最高的出现频率,其次为*Shewanella putrefaciens*,而*Bacillus aryabhattai*、*Bacillus cereus*等12个物种的出现频率均最低。相对丰度数据显示,*A. johnsonii*相对丰度最高,其次为*S.*

putrefaciens,*Exiguobacterium undae*等8个物种的相对丰度均最低。综合分析相对丰度与出现频率可知,纳木错夏季水体可培养细菌优势种为*A. johnsonii*。

就属水平而言,*Acinetobacter*、*Aeromonas*与*Pseudomonas*出现频率最高,其次是*Shewanella*。相对丰度数据显示,*Acinetobacter*相对丰度最高,其次为*Shewanella*,*Flavobacterium*属仅分离到一株细菌。结果表明,纳木错夏季水体中细菌优势属为*Acinetobacter*。

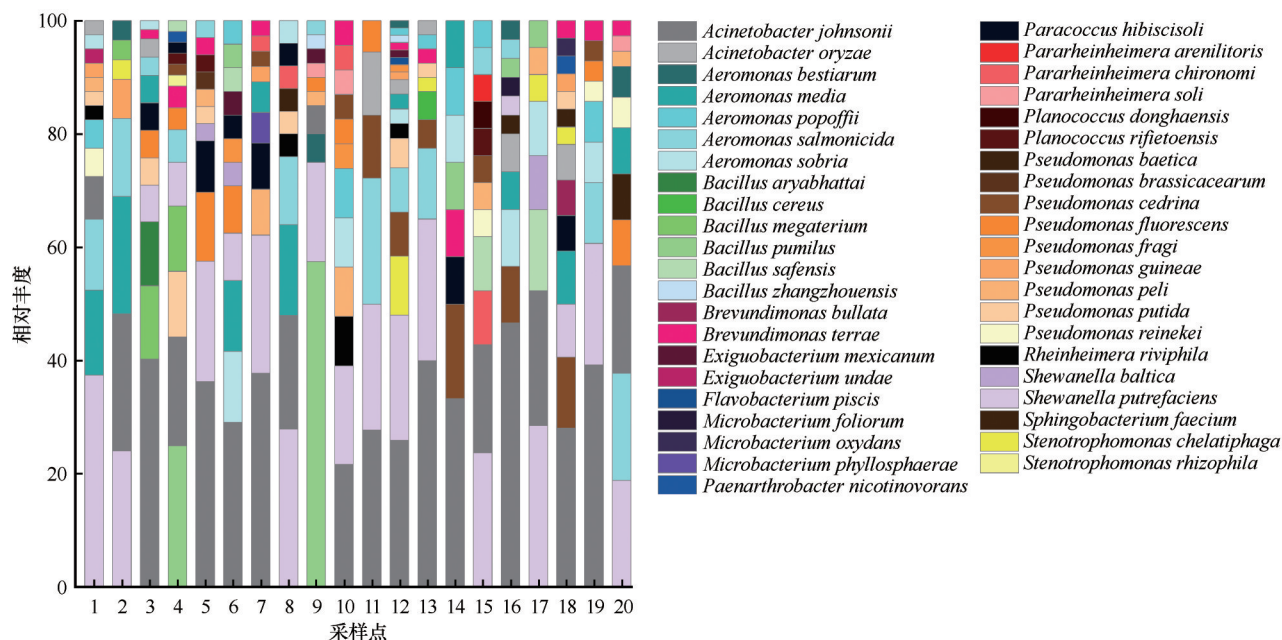


图2 纳木错各样点可培养细菌种水平的分布

Fig. 2 Species distribution of culturable bacteria of different sampling sites in Nam Co

2.2.2 基于16S rDNA基因序列构建代表菌株的系统发育树

为了解各供试菌株的系统发育地位,对其进行系统发育学分析,681个菌株归为43个系统发育型以构建供试菌株的系统发育树(图3)。

2.2.3 纳木错夏季各样点水体可培养细菌群落组成特征

图4显示,12号样点物种数最多(18种),其次是4号样点(14种),11号样点物种数最少(6种)。*A. johnsonii*为20个样点的共有细菌物种,除此之外,20个样点间无其他共有物种。*B. aryabhattai*、*B. cereus*及*Brevundimonas. bullata*等12个物种均只在1个样点当中出现,为该样点的特有种。

2.2.4 纳木错夏季各样点水体可培养细菌多样性指数

采用软件SPSS 20.0对各样点细菌总丰度进

行单因素方差分析,结果显示11号样点与其余19个样点间存在显著差异($P < 0.05$)。由图5(a)可见,11号样点细菌总丰度最高,其余各样点之间并没有显著差异。3组多样性指数显示[图5(b)],10号样点Shannon-Wiener多样性指数最高,9号样点Shannon-Wiener多样性指数最低,Simpson多样性指数、Pielou均匀度指数与Shannon-Wiener多样性指数变化趋势基本一致。这3项指数综合表明,10号样点有着最高的物种多样性,且物种分布最均匀,而9号样点物种多样性与均匀度均最低。

2.3 纳木错夏季水体可培养细菌多样性与理化因子相关性分析

由图6可看出,总磷与细菌总丰度、总氮与Simpson多样性指数均呈显著正相关($P < 0.05$),其余理化因子与多样性指数则没有显著相关性。

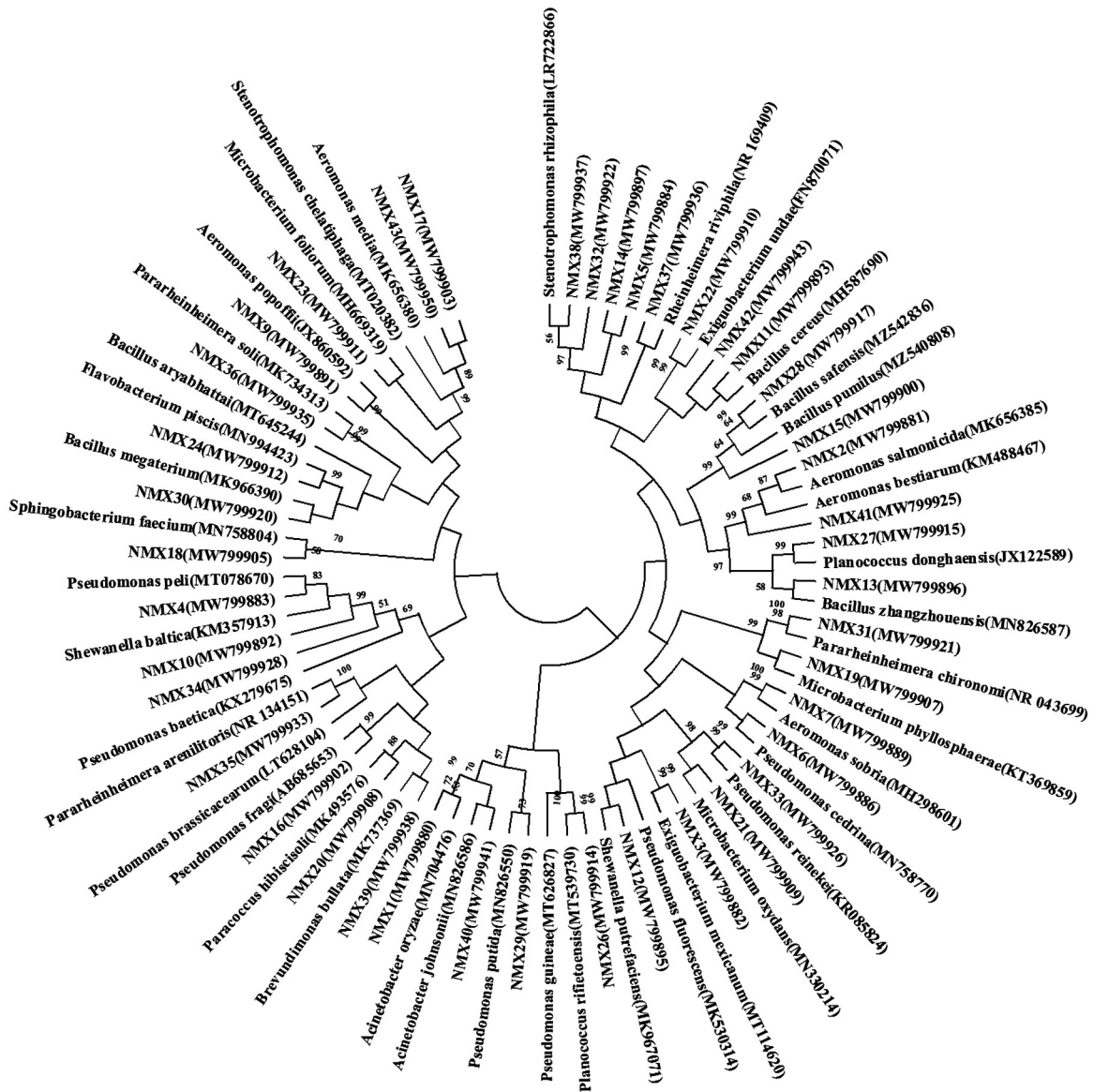


图3 基于16S rDNA序列的系统发育树

Fig. 3 Phylogenetic tree based on 16S rDNA sequence

2.4 纳木错夏季水体可培养细菌物种分布与理化因子排序分析

为更直观地反映细菌物种分布对于水质理化指标的响应规律,采用软件CANOCO 4.5对其进行排序分析。先进行除趋势对应分析,即DCA以确定合理的排序模型,DCA结果显示第一轴梯度长度值小于3,因此选择冗余分析,即RDA更加合理^[20]。在所有理化指标中, $\text{NH}_4^+\text{-N}$ 为对细菌群落分布具有显著影响的理化指标($P=0.03$)。为避免排序图杂乱,将低丰度物种排除后进行排序分析,图中仅展现相对丰度最高的10种细菌(图7)。

细菌物种分布对环境因子的响应规律在排序图中能够被直观看出,例如具有显著影响的环境因

子 $\text{NH}_4^+\text{-N}$ 与*S. putrefaciens*和*Aeromonas. salmonicida*间呈较强的正相关,而 $\text{NH}_4^+\text{-N}$ 与*A. johnsonii*间呈较强的负相关。

3 讨论

从纳木错夏季水体20个样点中共获得681株细菌,分属于16属43种。本研究结果显示,*Acinetobacter*、*Aeromonas*与*Pseudomonas*为纳木错夏季水体细菌的优势属。王永霞等^[24]从云南湖泊滇池中也分离到了这3个属,其中*Pseudomonas*为滇池的优势属,其次是*Acinetobacter*与*Aeromonas*,这3个属均为反硝化细菌属^[24]。张宇翔等^[25]从三种冷冻鸡肉样品中分离到100株耐冷细菌,其中*Pseudomo-*

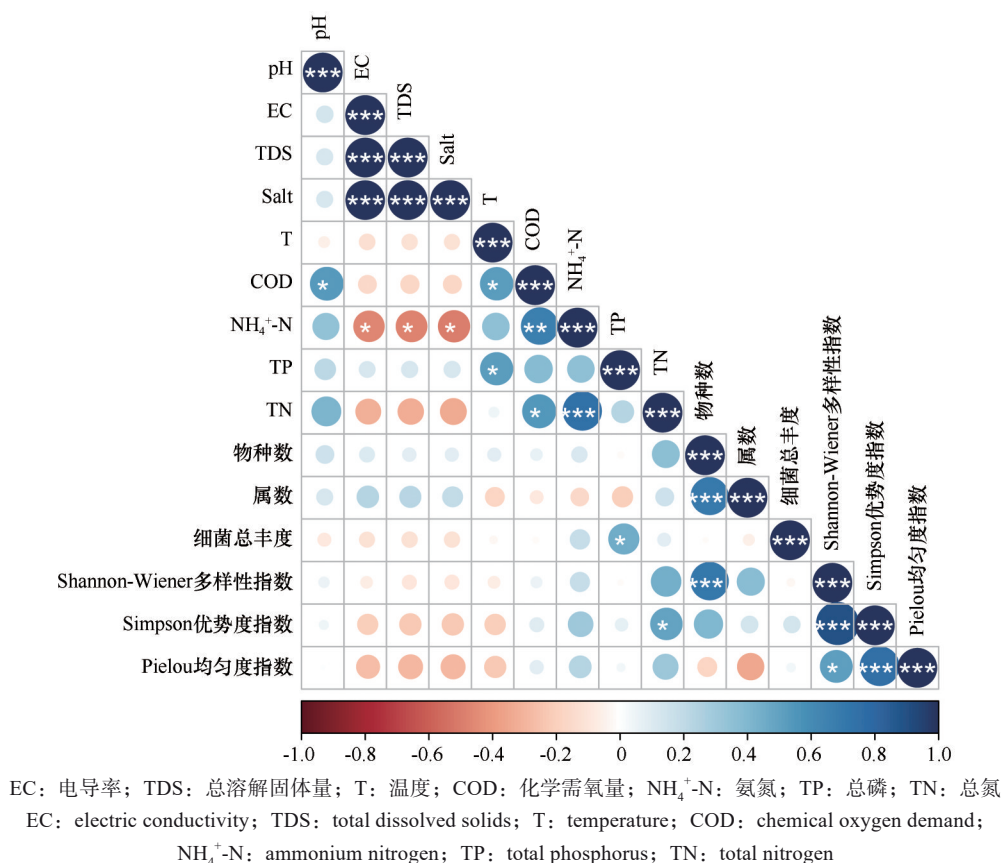
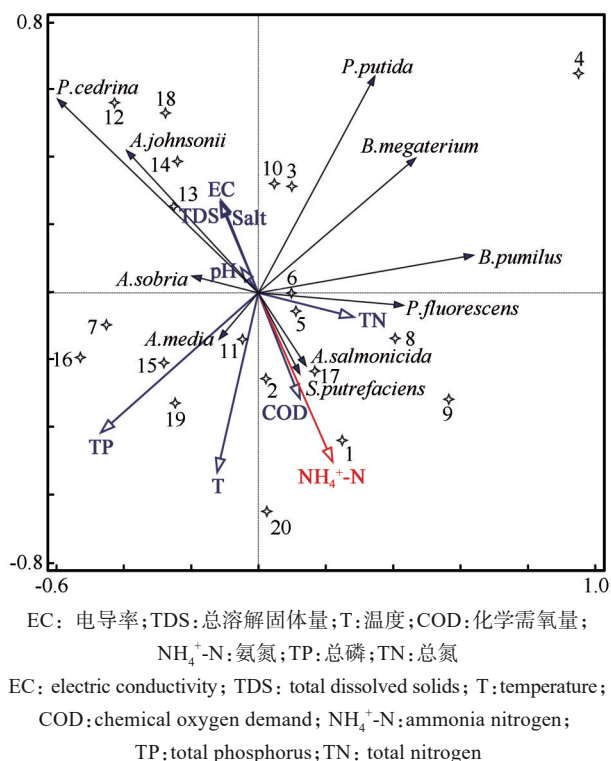


图6 纳木错各样点可培养细菌多样性与理化因子相关性

Fig. 6 Correlation between culturable bacteria diversity and physicochemical factors of different sampling sites in Nam Co

图7 纳木错可培养细菌群落分布与理化因子 RDA 排序图
 Fig. 7 RDA ordination diagram of culturable bacterial community distribution and physicochemical factors in Nam Co

A. johnsonii 有着一定的除磷能力; Zhao 等^[39] 研究发现 *A. johnsonii* 能够生活在极度受污染的水体中; 还有研究表明, *A. johnsonii* 能够与其他菌株相互作用^[40], 以此来进行水体的生物修复; 张阳等^[41] 研究发现 *A. johnsonii* 具有氮转化能力, 有着较强的反硝化功能; 张传丽等^[42] 研究发现 *A. johnsonii* 产脂肪酶活性较高, 有一定应用价值; Xue 等^[43] 从深海沉积物中分离出的一种产木聚糖酶的细菌菌株, 该菌株被鉴定为物种 *A. johnsonii*, 其可以在低温环境下生长。总之, *A. johnsonii* 应用价值突出, 对于该菌株资源的开发及利用具有重要意义。

单因素方差分析结果显示, 各样点理化因子均存在不同程度的差异。例如 5 号、11 号、15 号与 20 号样点与其余样点理化因子差异较大, 分析原因, 可能由于各采样点的自然生境有所差异: 5 号样点采样处与主湖之间隔了一道天然河坝, 11 号样点采样时水中长有水草, 15 号样点在河谷地带, 湖旁有很多动物粪便, 20 号样点在湖泊入口处, 因此这 4 个样点理化因子与其余样点之间差异较大。再则湖岸边的植被类型、放牧情况等自然因素也会对相应

的理化因子有所影响。

根据地表水环境质量标准基本项目标准限值可知,本研究所测得的化学需氧量、氨氮、总氮及总磷4项理化因子数据均未超过极限值。另外,本研究所设置的采样点位于纳木错沿岸区,水样采集位点较低,可能会将少许底部淤泥带入水样中,因此本文水质理化指标参数数据对于反映纳木错水质为清洁或者较清洁程度具有一定参考性。

各样点水体细菌多样性指数表明,11号样点总丰度显著高于其他样点($P<0.05$);12号样点的种数和属数相对较多,10号样点和6号样点细菌多样性较高,而9号样点则相对较低。分析各样点地理位置可以看出,11号样点离公路较近,有一定的人为活动影响,且取样位置水中长有大量水草,水样pH、COD与 $\text{NH}_4^+\text{-N}$ 等相对其他样点偏高,因此可能导致11号样点细菌总丰度显著高于其他样点;10号样点湖岸周围有大量土拨鼠、旱獭等野生动物栖居,且位于多加寺附近,人为活动较频繁,可能会导致10号样点多样性高于其他样点。

纳木错夏季各样点水体细菌多样性指数与水体理化因子相关性分析显示,TP是影响纳木错夏季各样点水体细菌总丰度的主要理化因子;TN是影响纳木错夏季各样点水体细菌多样性指数的主要理化因子。RDA结果显示, $\text{NH}_4^+\text{-N}$ 是影响纳木错夏季水体可培养细菌群落分布的主要环境因子。其他学者对高海拔湖泊细菌的研究中也有类似的结果。Liu等^[44]曾指出细菌多样性的变化随着TN的浓度变化而起伏,Wu等^[45]研究发现Salt是控制青藏高原东部海拔2 817~5 134 m的16个高山湖泊中细菌群落组成的主要环境因子,Liu等^[46]发现TN对高原湖泊卡拉库里湖的细菌多样性具有重大影响,细菌群落组成与T和pH均显著相关,Song等^[47]研究表明高原湖泊托素湖的细菌多样性和分布受到Salt和pH的高度影响。Liu等^[48]研究发现高原湖泊班公湖细菌群落组成与TN的浓度密切相关。Wang等^[49]研究发现 $\text{NH}_4^+\text{-N}$ 是亚高山湖泊细菌群落多样性的主要影响因素。Xia等^[50]研究发现西南高原湖泊细菌的群落组成受T、 $\text{NH}_4^+\text{-N}$ 、pH或TP的显著影响。Liu等^[51]发现细菌的 α 多样性随季节而变化,并且与EC呈极显著的负相关。

青藏高原地理位置及自然生境独特,该地区湖泊也蕴含着特殊的微生物资源,但高原湖泊生态系统由于极易受到外界影响及破坏,其中的微生物物

种组成也易随之发生更替。湖泊水体细菌对于湖泊生态系统的变化具有响应规律,开展高原湖泊水体可培养细菌物种多样性的研究,不仅能够为极端环境下特殊细菌资源的开发利用提供理论参考,还能够为高原湖泊生态系统的保护提供理论依据^[52]。

4 结论

本研究通过传统纯培养方法分离纯化纳木错夏季水体中的可培养细菌,揭示了其中可培养细菌的物种多样性,并对细菌群落多样性及群落结构分布对理化因子的响应规律做了初步探究,主要结论如下:

(1)从纳木错夏季水体中共分离得到681株细菌,鉴定分为16属43种,优势种为*A. johnsonii*。

(2)单因素方差分析结果显示,11号样点细菌总丰度显著高于其他样点($P<0.05$)。

(3)Spearman相关系数显示,TP、TN是影响纳木错各样点细菌总丰度和多样性的主要环境因子,冗余分析结果显示, $\text{NH}_4^+\text{-N}$ 是影响纳木错夏季水体可培养细菌群落分布的主要环境因子。

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Diversity of culturable bacteria and its correlation with physicochemical factors in summer coastal waters of Nam Co, Tibetan Plateau

ZHENG Yanyan, GUO Xiaofang, Silang Yuzhen, DE Ji

(School of Science, Tibet University, Lhasa 850000, China)

Abstract: Nam Co, located in the central and southern part of the Tibetan Plateau, is a unique saline lake in the region. To carry out the study on the composition and diversity of culturable bacterial species in coastal water bodies in the summer season in Nam Co and to reveal the response pattern of bacterial species diversity and community distribution to physicochemical factors will not only be able to provide valuable resources and references for the study of microbial diversity and the development and utilization of special bacterial resources under extreme environment, can provide a theoretical basis for the conservation of lake ecosystems on the Tibetan Plateau. In this study, 20 sampling sites were selected based on lake water distribution combined with geographical differences in coastal areas of Nam Co in the summer of 2020. Water samples were collected with sterile samplers at approximately 15 m from the shore and 50 cm from the water surface, the collected water samples were packed in sterile plastic buckets and brought back immediately to the laboratory to isolate the culturable bacteria inside. The direct coating plate method combined with the dilution coating plate method was used to isolate culturable bacteria from lake water, and the plate four zone streaking method was used to purify the whole bacterial strains, and bacterial strains were stored by freezing in glycerol tubes at -20°C . The medium used in the experiment was beef extract peptone medium, when isolated the cultivable bacteria strains from water samples, the water added in the medium was Nam Co lake water: sterile water=1:1, when purified the bacterial strains, all the added water in the medium was sterile water. The identification of bacterial strains was performed by the combination of classical taxonomy and 16S rDNA gene sequence analysis, and relevant statistical software, such as R 4.1.1 and SPSS 20.0, etc., was used to analyze the community distribution and species diversity of bacteria and their correlation with aquatic physicochemical factors. A total of 681 cultivable bacteria were isolated from 20 sampling sites of coastal water in the summer season in Nam Co, and all strains identified were classified into 43 species in 16 genera, of which the dominant species was *Acinetobacter johnsonii* and the dominant genus was *Acinetobacter*, and *Acinetobacter johnsonii* was a common bacterial species among 20 sampling sites. Among the 20 sampling sites, number 12 had the highest number of species, and it had 18 species; the second is number 4, which had 14 species, and number 11, which had the lowest number of species, which had only six species. The Shannon-Wiener diversity indexes, Simpson diversity indexes, and Pielou evenness indexes showed generally consistent trends among 20 sampling sites, the three indexes synthetically indicated that number 10 had the highest species diversity and the most even distribution, whereas the number 9 had the lowest species diversity and the most uneven distribution. Spearman correlation coefficient showed that both total nitrogen and total phosphorus were the main physicochemical factors affecting the diversity of cultivable bacterial species in water bodies in summer in Nam Co, and there was a significant correlation between total bacterial abundance and total phosphorus ($P<0.05$), and the Simpson diversity indexes was also significantly correlated with total nitrogen ($P<0.05$). Redundancy analysis results showed that ammonia nitrogen was the main environmental factor affecting the distribution of cultivable bacterial communities in water body during summer in Nam Co ($P<0.05$). This study initially revealed the species diversity and community distribution of culturable bacteria in coastal water bodies and their correlations with environmental factors in the summer season in Nam Co, and obtained a relatively rich resource of bacterial strains, in the hope of providing a theoretical basis for the conservation of lake ecosystems in the Tibetan Plateau and the exploitation and utilization of special bacterial resources.

Key words: Tibetan Plateau; Nam Co; lake; bacterial diversity; physicochemical factors; redundancy analysis; 16S rDNA

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