•研究报告•

新疆伊犁马铃薯根际芽胞杆菌纯培养多样性

刘国红¹ 刘 波^{1*} 车建美¹ 陈倩倩¹ 林乃铨² 崔卫东³

1 (福建省农业科学院农业生物资源研究所, 福州 350003)

2 (福建农林大学植物保护学院, 福州 350002)

3 (新疆农业科学院微生物应用研究所, 乌鲁木齐 830000)

摘要: 了解马铃薯根际土壤中芽胞杆菌种类多样性, 可为挖掘芽胞杆菌新资源提供基础。从新疆伊犁州9个地点采集了30份马铃薯根际土壤样品, 采用可培养法从中分离芽胞杆菌, 通过16S rRNA基因同源性鉴定了分离菌株的分类地位。共获得芽胞杆菌349株, 基于菌落形态特征和16S rRNA基因序列确定了66个代表菌株, 其中14株与近缘种模式菌株的16S rRNA基因序列相似性介于93.0–98.5%之间, 为潜在芽胞杆菌新种。349株芽胞杆菌属于9属66种, 分别为芽胞杆菌属(*Bacillus*)的41个种(41/66, 62.1%), 为最优势属; 类芽胞杆菌属(*Paenibacillus*)有9种(9/66, 13.6%), 赖氨酸芽胞杆菌属(*Lysinibacillus*)共6种(6/66, 9.1%), 嗜冷芽胞杆菌属(*Psychrobacillus*)共4种(4/66, 6.1%), 虚构芽胞杆菌属(*Fictibacillus*)有2种(2/66, 3.0%), 短芽胞杆菌属(*Brevibacillus*)、大洋芽胞杆菌属(*Oceanobacillus*)、鲁梅尔芽胞杆菌属(*Rummelibacillus*)和解硫胺素芽胞杆菌属(*Aneurinibacillus*)皆为1种。新疆9个地点马铃薯根际土壤中芽胞杆菌含量为 $2.20\text{--}8.86 \times 10^4$ cfu/g, 其中特克斯蒙古乡马铃薯根际土壤中芽胞杆菌的菌落含量和种类最多, 分别为 8.86×10^4 cfu/g和37种; 尼勒克县马场马铃薯根际土壤中的芽胞杆菌含量最少, 特克斯去昭苏路上和阜康西沟村的芽胞杆菌种类最少, 仅9种。但每个地点的优势种均相同, 均为简单芽胞杆菌(*Bacillus simplex*)和阿氏芽胞杆菌(*B. aryabhatai*)。芽胞杆菌种类可划分为高频度分布型(简单芽胞杆菌等4种)、中频度分布型(植物内生芽胞杆菌等12种)和低频度分布型(其余51种芽胞杆菌, 如蕈状芽胞杆菌)。新疆9个地点芽胞杆菌种类分布可分为高含量高丰度型(特克斯蒙古乡和农技推广园)和低含量低丰度型(如尼勒克县马场等地)。相关性分析发现, 马铃薯根际芽胞杆菌种类分布与海拔高度无显著相关性。新疆马铃薯根际土壤蕴含种类丰富的芽胞杆菌资源, 可为芽胞杆菌功能菌株开发提供丰富的菌种来源。

关键词: 芽胞杆菌, 马铃薯根际土壤, 多样性

Diversity of *Bacillus*-like species isolated from potato rhizosphere soils in Yili, Xinjiang

Guohong Liu¹, Bo Liu^{1*}, Jianmei Che¹, Qianqian Chen¹, Naiquan Lin², Weidong Cui³

1 Agricultural Bio-Resource Institute, Fujian Academy of Agricultural Sciences, Fuzhou 350003

2 College of Plant Protection, Fujian Agriculture and Forestry University, Fuzhou 350002

3 Institute of Applied for Microorganism of Xinjiang Academy of Agricultural Sciences, Urumqi 830000

Abstract: This study aims to understand the diversity of *Bacillus*-like species found in potato rhizosphere soils in Xinjiang, and provide a basis for mining new resources. *Bacillus*-like bacteria were isolated from potato rhizosphere soils using the cultivable method and preliminarily identified based on the 16S rRNA gene sequences. The spatial distribution pattern of the *Bacillus*-like bacteria was analyzed using frequency distribution and number. A total of 349 *Bacillus*-like isolates were obtained from 30 soil samples, and identified as 66 species belonging to 9 genera and 2 families (Bacillaceae and Paenibacillaceae) within Bacilli by 16S rRNA gene sequences. Sixty six selective strains were chosen to be further analyzed based on colony morphology and 16S rRNA gene sequences, and 14 strains were potential novel species based on the lower

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* 通讯作者 Author for correspondence. E-mail: fzliubo@163.com

similarities found between 93.0–98.5% in their closed references type strains. The species numbers of each genus were 41 for *Bacillus* (41/66, 62.1%), 9 for *Paenibacillus* (9/66, 13.6%), 6 for *Lysinibacillus* (6/66, 9.1%), 4 for *Psychrobacillus* (4/66, 6.1%), 2 for *Fictibacillus* (2/66, 3.0%), and 1 for *Brevibacillus*, *Oceanibacillus*, *Rummelibacillus* and *Aneurinibacillus*, respectively. In the potato rhizosphere soils, the content range of *Bacillus*-like species were $2.20\text{--}8.86\times 10^4$ cfu/g. The highest colony content and *Bacillus*-like species, e.g. 8.86×10^4 cfu/g and 37 species, respectively, occurred in the Mongolian township of Tekes, while the lowest colony content was found in a stud-farm in Nilka County and the lowest *Bacillus*-like species (9 species) were found in Xigou Village of Fukang City and on the way from Tekes to Zhaosu County. There was large difference in the distribution of *Bacillus*-like species in the potato rhizosphere soils, but each site was characterized by the same dominant species, *Bacillus simplex* and *Bacillus aryabhattai*. Based on their occurrence frequency, the *Bacillus*-like species could be discriminated as high frequency species including *Bacillus simplex*, middle frequency species including *Bacillus endophyticus*, and low frequency species including *Bacillus mycoides*. Based on the number of *Bacillus*-like species, 9 collecting sites were divided into two groups, namely high content and richness and low content and richness. Moreover, there was no significant correlation between the distribution of *Bacillus*-like species and altitude. Thus, there were many *Bacillus*-like species in potato rhizosphere soils, which provide rich resources for exploring functional strains.

Key words: *Bacillus* species; potato rhizosphere soil; diversity

马铃薯是世界上很多国家非常重要的食品, 目前有130个国家将其作为重要的非谷物食品(Calvo et al, 2010; 徐海泉等, 2015)。芽胞杆菌是一类重要的微生物资源, 在自然界中广泛分布(Liu et al, 2016), 其大多数种类能够产生多种功能代谢产物, 有些种类能防治马铃薯软腐病(Rahman et al, 2012)和青枯病(Calvo et al, 2010; Saber et al, 2015), 有些种类对马铃薯生长具有促生作用(Calvo et al, 2010; Hanif et al, 2015)。目前, 尽管已有300多种芽胞杆菌被分离鉴定(LPSN), 但仍有大量的芽胞杆菌资源及其活性物质有待挖掘。土壤是芽胞杆菌及其生物活性物质的一个重要来源, 植物根际土壤的芽胞杆菌能够保护植物根部不被病原菌侵染, 且其中一些种类还对植物具有促生长能力(Asari et al, 2016; Huang et al, 2015; Liu et al, 2016a)。植物根际微生物组研究变得越来越重要, 健康的微生物组能促进植物的生长, 而植物根际土壤中的芽胞杆菌是健康微生物组的重要成员之一。

新疆是我国马铃薯主要种植基地之一, 昌吉回族自治州和哈萨克自治州(简称伊犁州)种植了大量的马铃薯。秦越等(2015)利用末端限制性片段长度多态性(T-RFLP)技术分析了连作栽培对马铃薯根际微生物多样性的影响, 发现芽胞杆菌是根际微生物的优势属, 占比例最大。王娜等(2016)也通过T-RFLP分析发现间作后马铃薯根际土壤细菌数量增加, 多样性指数高于连作栽培, 而且间作栽培能

够有效改善马铃薯根际土壤细菌菌群结构, 使一些有益菌属比例上升, 潜在致病菌比例下降甚至消失, 且出现了新的益生菌。白洋(2014)^①采用T-RFLP技术探究了用稻草包芯栽培方式在马铃薯不同生长期土壤细菌种类的变化, 表明整个生育时期稻草包芯处理后土壤细菌种类波动较小, 根际细菌中病菌数量较少, 益生菌(如芽胞杆菌等)的比例较大, 有益芽胞杆菌主要是侧孢短芽胞杆菌(*Brevibacillus laterosporus*)、短短芽胞杆菌(*Brevibacillus brevis*)、短小芽胞杆菌(*Bacillus pumilus*)等。

我们从新疆9个地点采集了马铃薯种根际土壤样本, 采用可培养法从中分离芽胞杆菌, 通过16S rRNA基因系统发育分析芽胞杆菌的分类地位, 以期为进一步挖掘利用马铃薯根际土壤中芽胞杆菌资源提供参考。

1 材料与方法

1.1 土壤样品采集

2013年7月27–30日, 于新疆伊犁州9个地点采集了马铃薯根际土壤样品30份(表1), 保存于无菌自封袋, 室温保存带回实验室放于4℃冰箱保存, 进行芽胞杆菌分离。

1.2 培养基和试剂

PCR仪和凝胶成像分析仪购自Bio-Rad公司;

^① 白洋 (2014) 马铃薯稻草包芯栽培的土壤酶活与细菌种群变化研究. 硕士学位论文, 福建农林大学, 福州.

表 1 新疆马铃薯根际土壤样本采集信息
Table 1 Information of potato rhizosphere soil samples from Xinjiang

编号 No.	采集地点 Collection site	海拔 Altitude (m)	经纬度 Location
S1	尼勒克县尼勒克镇公社种子队 Seed Team of Nilka Township, Nilka County	1,138	43°46'28" N, 82°35'01" E
S2	阜康市上户沟乡西沟村 Xigou Village, Shanghugou Township, Fukang City	1,261	44°00'17" N, 88°33'46" E
S3	尼勒克县马场 Machang, Nilka County	1,139	43°45'58" N, 82°34'43" E
S4	尼勒克县沙勒漫乡 Shaleman Township, Nilka County	1,110	43°47'08" N, 82°32'15" E
S5	昭苏县农业局试验场 Testing Ground of Agricultural Bureau, Zhaosu County	1,856	44°09'46" N, 81°09'14" E
S6	特克斯蒙古乡(施药) Mongolia Township, Tekes County (pesticide applied)	1,171	43°13'25" N, 81°54'27" E
S7	特克斯蒙古乡 Mongolia Township, Tekes County	1,181	43°13'17" N, 81°52'33" E
S8	特克斯去昭苏路上 On the way from Tekes to Zhaosu County	1,808	—
S9	特克斯县农业技术推广园 Agro Technical Extension Garden, Tekes County	1,181	43°13'17" N, 81°52'33" E

恒温培养箱(BI-250AG)购自施都凯仪器设备(上海)有限公司; 2×PCR Master Mix购自上海铂尚生物技术有限公司; 引物由上海铂尚生物技术有限公司合成。LB培养基配制参考葛慈斌等(2015)的描述。

1.3 芽胞杆菌的分离与鉴定

土壤中芽胞杆菌的分离主要参考刘国红等(2014)的方法。称取土壤样品10 g至90 mL无菌水, 震荡混匀20 min后, 80℃水浴10 min, 土壤悬浮液依次稀释成浓度为10⁻¹、10⁻²、10⁻³。取100 μL悬浮液至LB平板并涂布均匀, 30℃培养2天后观察菌落生长情况。根据菌落形态特征等进行芽胞杆菌种类归类、统计计数及纯化, 采用-80℃甘油冷冻法进行保存。采用Tris-饱和酚法提取芽胞杆菌基因组DNA, 参考Cheng和Jiang (2006)描述的方法。采用通用细菌16S rRNA引物进行扩增、测序, 主要参考Liu等(2016b)描述的方法。16S rRNA基因扩增引物为27F(5'-AGAGTTTGTACCTGGCTCAG-3')和1492R(5'-GGTTACCTTGTTACGACTT-3')。检测出有条带的菌株PCR产物送至上海铂尚生物技术有限公司进行测序。

1.4 芽胞杆菌的系统发育分析

根据所得到序列在网站(<http://www.ezbiocloud.net/>)上进行序列比对分析后(Kim et al, 2012), 结合BLASTn和RDP数据库比对初步判断得出芽胞杆菌种的分类地位。选择相关的参考菌株序列, 再经Clustal X对齐后(Thompson et al, 1997), 用软件Mega 6.0采用邻接法和Jukes-Cantor模型构建系统发育树(Jukes & Cantor, 1969; Felsenstein et al, 1985; Saitou & Nei, 1987; Tamura et al, 2013)。

1.5 芽胞杆菌种类多样性分析

统计各采样点马铃薯根际土样本芽胞杆菌种类数、数量总和, 比较各样本芽胞杆菌种类的变化, 分析芽胞杆菌种类在各个采样点土壤样本中出现的频次和数量。

1.6 芽胞杆菌种群数量、分离频度、海拔间的相关性分析

对9个地点的芽胞杆菌, 用DPS统计软件进行在土壤中的数量与海拔之间, 以及分离频度与在土壤中的数量之间的相关性分析。

2 结果

2.1 芽胞杆菌的分离与鉴定

根据分离菌株的菌落形态特征进行归类统计, 共分离获得芽胞杆菌349株, 通过对菌株16S rRNA基因序列的同源性进行比对, 对349个菌株进行16S rRNA基因序列分析并最终确定66个代表菌株进行后续分析。

基于16S rRNA基因系统发育分析结果表明, 在细菌属水平上的种群多样性非常丰富, 349株菌隶属9个属的66个种。芽胞杆菌属(*Bacillus*) 41个种(41/66, 62.1%), 类芽胞杆菌属(*Paenibacillus*) 9个种(9/66, 13.6%), 赖氨酸芽胞杆菌属(*Lysinibacillus*) 6个种(6/66, 9.1%), 嗜冷芽胞杆菌属(*Psychrobacillus*) 4个种(4/66, 6.1%), 虚构芽胞杆菌属(*Fictibacillus*) 2个种(2/66, 3.0%), 短芽胞杆菌属(*Brevibacillus*)、大洋芽胞杆菌属(*Oceanobacillus*)、鲁梅尔芽胞杆菌属(*Rummelibacillus*)和解硫胺素芽胞杆菌属(*Aneurinibacillus*)皆为1个种。16S rRNA相似性

在93–100%之间,说明部分分离菌株与其亲缘关系最近的模式种之间可能存在一定的遗传差异。

2.2 芽胞杆菌资源系统发育分析

66种芽胞杆菌的16S rRNA基因序列系统发育分析见图1。其中,FJAT-21955、FJAT-21963、FJAT-21352、FJAT-18003、FJAT-21351和FJAT-18019与其最相近模式菌株的16S rRNA基因相似性皆低于97.0%,分别为93.5% (*Bacillus altitudinis* 41KF2b^T)、94.1% (*Psychrobacillus psychrodurans* DSM 11713^T)、94.3% (*Bacillus simplex* NBRC 5720^T)、96.5% (*Bacillus drentensis* LMG 21831^T)、96.9% (*Bacillus paraflexus* RC2^T)和97.0% (*Paenibacillus uliginis* N3/975^T)。FJAT-18017、FJAT-22090和FJAT-18069与其亲缘关系最近模式菌株的16S rRNA基因相似性位于97–98%之间,分别为97.4% (*Bacillus thioparans* BMP-1^T)、97.7% (*Psychrobacillus psychrodurans* DSM 11713^T)和97.8% (*Lysinibacillus macroides* LMG 18474^T)。FJAT-22048、FJAT-22140、FJAT-22098、FJAT-22121和FJAT-18000与其最近模式菌株的相似性介于98–98.5%之间,分别为98.2% (*Bacillus horneckiae* DSM 23495^T)、98.3% (*Bacillus decolorationis* LMG 19507^T)、98.3% (*Lysinibacillus varians* GY32^T)、98.4% (*Bacillus fortis*)和98.4% (*Psychrobacillus insolitus* DSM 5^T)。根据原核生物种的界定阈值标准,上述菌株可能为芽胞杆菌潜在新种,为最终确定其分类地位,我们正在用包括生理生化特征、MLST序列分析、DNA-DNA杂交以及脂肪酸分析等多相分类方法对其进行鉴定,以确定其准确的分类地位。

2.3 芽胞杆菌种类分布频次

马铃薯根际芽胞杆菌种类分布可分为三大类:高频度分布型、中频度分布型和低频度分布型。

高频度分布类型包含4个种即简单芽胞杆菌(*Bacillus simplex*)、阿氏芽胞杆菌(*B. aryabhattai*)、矮缩芽胞杆菌(*B. atrophaeus*)和短小芽胞杆菌(*B. pumilus*)。其中简单芽胞杆菌和阿氏芽胞杆菌存在于9个采集地点的所有土壤样本中,矮缩芽胞杆菌在除特克斯去昭苏路上之外的其他8个地点的样本中获得(8/9, 88.9%),短小芽胞杆菌在除尼勒克县尼勒克镇公社种子队一队和尼勒克县沙勒漫乡外的7个地点获得(7/9, 77.8%)。

中频度类型分布在4–6个地点的土壤样本中,

包含12种芽胞杆菌,分别为植物内生芽胞杆菌(*Bacillus endophyticus*)、耐寒芽胞杆菌(*B. frigoritolerans*)、地衣芽胞杆菌(*B. licheniformis*)、烟酸芽胞杆菌(*B. niacini*)、嗜气芽胞杆菌(*B. aerophilus*)、苏云金芽胞杆菌(*B. thuringiensis*)、图瓦永芽胞杆菌(*B. toyonensis*)、含低硼赖氨酸芽胞杆菌(*Lysinibacillus parviboronicapiens*)、忍冷嗜冷芽胞杆菌(*P. psychrodurans*)、蜡状芽胞杆菌(*B. cereus*)、病研所芽胞杆菌(*B. idriensis*)和沙福芽胞杆菌(*B. safensis*)。其中沙福芽胞杆菌分布在尼勒克县尼勒克镇公社种子队一队、尼勒克县马场、尼勒克县沙勒漫乡、昭苏县农业局试验场、特克斯蒙古乡和特克斯农业科技推广园6个地点。

低频度类型分布在少数几个地点,分布极不均一。分布在1–3个地点的土壤样品中,包含其余的51种芽胞杆菌,其中14种为潜在芽胞杆菌新种。

2.4 芽胞杆菌种类及数量多样性

芽胞杆菌种类含量分布结果见表2。9个地点马铃薯根际土壤中芽胞杆菌含量不同,菌落含量范围为2.20–8.86×10⁴ cfu/g,尼勒克县马场土壤样品中的芽胞杆菌含量最少(2.20×10⁴ cfu/g),特克斯蒙古乡芽胞杆菌的含量最多(8.86×10⁴ cfu/g)。

马铃薯根际土芽胞杆菌优势菌群都是简单芽胞杆菌,每个地点分离到的芽胞杆菌种类不一致:特克斯蒙古乡马铃薯根际土中分离到的芽胞杆菌种类最多,为37种;其次是特克斯农技推广园(31种),最少的为特克斯→昭苏和阜康西沟村,皆为9种。

表2 新疆马铃薯根际土壤中芽胞杆菌含量分布(样品编号同表1)

Table 2 The content of *Bacillus* species in the potato rhizosphere soil from Xinjiang. Soil sample number see Table 1.

样本编号 Sample no.	芽胞杆菌含量 <i>Bacillus</i> colonies content (×10 ⁴ cfu/g)	种类数 Species number
S1	3.25	19
S2	5.00	9
S3	2.20	11
S4	6.60	15
S5	3.97	15
S6	7.70	15
S7	8.86	37
S8	4.30	9
S9	3.76	31

Fig. 1 Phylogenetic analysis of *Bacillus* species based on 16S rRNA gene sequence. n represents number of isolates, and percent values represent the 16S rRNA gene sequence similarities between isolates and related type species.

图 2 马铃薯根际土壤样品采集点的聚类分析。编号 S1-9 同表 1。

Fig. 2 Analysis of collection sites of potato rhizosphere soils. Soil samples S1-9 are the same as Table 1.

2.5 芽胞杆菌含量聚类分析

以表2数据构建矩阵进行聚类分析(图2), 当 $\lambda = 15$ 时, 9个采集地点的芽胞杆菌种类分布可划分为3大类: 第I类为高含量高丰度型, 包含特克斯蒙古乡和农技推广园; 第II类为低含量低丰度型, 包含其余7个土壤样本采集点, 可分为两大亚类型, 分别为低含量中丰度型和中含量低丰度型。

3 讨论

本研究结合纯培养法和16S rRNA基因系统发育分析法, 对新疆伊犁马铃薯根际土壤中芽胞杆菌种类多样性进行了调查。研究表明, 马铃薯根际土壤中可培养的芽胞杆菌种群多样性非常丰富, 获得的349株芽胞杆菌隶属于芽胞杆菌目9个属的66个种。其中多数菌株属于芽胞杆菌属, 该属的简单芽胞杆菌和阿氏芽胞杆菌几乎分布在所有采集的土壤样本中。马铃薯根际土壤存在一定量的芽胞杆菌潜在新资源, 目前已正式发表了2个新种, 即茄科芽胞杆菌(*Bacillus solani* FJAT-18043^T) (Liu et al, 2015)和茄科类芽胞杆菌(*Paenibacillus solani* FJAT-22460^T) (Liu et al, 2016b), 其余14株与其最相近模式菌株的16S rRNA基因序列同源性在93.0-98.5%之间。这些潜在新种的分类地位和生物学特性需进一步深入研究。

国内外学者基于16S rRNA基因的系统发育法分析了番茄(马宁宁, 2013)、烟草、玉米、田七、甘蔗、小麦、毛竹等植物根际土壤中芽胞杆菌物种分布。将本研究结果与上述结果进行比较, 发现本研究获得的芽胞杆菌在上述植物根际土壤中均有分布, 皆为作物根际的优势属。马铃薯块茎表面含有

丰富的芽胞杆菌, 主要为短小芽胞杆菌(Weinert et al, 2010), 且部分菌株具有一定的抗病原菌活性, 而本研究从马铃薯根际土壤中也获得了一定量的短小芽胞杆菌资源, 可能具有作为马铃薯病原菌生防制剂研发的潜力。毛竹根际土壤中含有大量的芽胞杆菌属和类芽胞杆菌属菌群, 优势种是蜡状芽胞杆菌和蕈状芽胞杆菌, 这与本文调查分析结果不同, 而且毛竹根际获得的类芽胞杆菌种类在马铃薯根际也不存在(李潞滨等, 2008), 这可能与植株本身的特性相关。烟草根际和非根际土壤中均含有丰富的芽胞杆菌资源, 优势种为巨大芽胞杆菌, 与同为茄科作物的马铃薯根际的优势种不同(林凤敏等, 2011)。田七和马铃薯根际的阿氏芽胞杆菌均为优势种, 但田七的优势种苏云金芽胞杆菌和*Bacillus siamensis* (Fan et al, 2016)在马铃薯根际含量不多, 而本研究获得的优势种简单芽胞杆菌和萎缩芽胞杆菌(*B. atrophaeus*)和田七根际含量也很少。同为粮食作物的玉米根际土壤中的优势芽胞杆菌种类与本文研究结果相同(刘国红等, 2014), 但含有的芽胞杆菌种类远低于马铃薯根际, 这可能与采集样本的数量和作物特性相关。Verma等(2016)在小麦根际获得的优势种群为蜡状芽胞杆菌类群(*Bacillus cereus* group)、枯草芽胞杆菌类群(*Bacillus subtilis* group)和巨大芽胞杆菌(*Bacillus megaterium*), 而纺锤形赖氨酸芽胞杆菌(*Lysinibacillus fusiformis*)和解木糖赖氨酸芽胞杆菌(*Lysinibacillus xylanilyticus*)在马铃薯根际均存在, 为低频率分布型。芽胞杆菌属是甘蔗根际土壤厚壁菌门的优势属(Pisa et al, 2011), 连作花生田根际土壤的优势菌为简单芽胞杆菌和巨大芽胞杆菌(颜艳伟等, 2011), 但本研究未分离获得巨大芽胞杆菌。

Sikorski等(2008)调查发现以色列“进化谷”芽胞杆菌种群结构丰富多样, 其中简单芽胞杆菌分布在所有采集样本中, 本文研究发现马铃薯土壤样品中亦含有高频率分布的简单芽胞杆菌, 这可能与该种自身生物特性有一定的相关性。简单芽胞杆菌能产生挥发性有机化合物, 提高马铃薯的产量(Velivelli et al, 2015), 还可以高效消除化学需氧量, 用于降解土壤中的氯磺隆和除草剂氟乐灵(Erguven et al, 2016)。阿氏芽胞杆菌亦具有广泛的分布特性, Lee等(2012)发现贫瘠土壤含有丰富的阿氏芽胞杆菌且对意大利苍耳(*Xanthium italicum*)具有促生作用, 具

有作为植物生长促生剂的潜力。藏红花(*Crocus sativus*)根际土壤和非根际土中均含有大量的阿氏芽胞杆菌(Ambardar & Vakhlu, 2013)。Zhang等(2013)首次报道萎缩芽胞杆菌能产生3种抗真菌物质, 高效抑制多种病原真菌生长, 可用于植物病原菌防治, 笔者亦从马铃薯根际获得了高频率分布的萎缩芽胞杆菌资源, 该种群可能对马铃薯的病害防治具有很大的作用。Verma等(2016)首次报道小麦根际土壤中的植物内生芽胞杆菌(*B. endophyticus*)和食木糖类芽胞杆菌(*Paenibacillus xylanexedens*)具有多功能的促生作用, 本文从马铃薯根际土壤中也获得了中频率分布的植物内生芽胞杆菌和低频率分布的食木糖类芽胞杆菌, 这2种芽胞杆菌可能对马铃薯生长具有一定的促进作用。

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