

张瑞福，1974 年出生于山东省泰安市。1998 年毕业于莱阳农学院（现青岛农业大学），2004 年 4 月在南京农业大学获理学博士学位，2004 年 6 月起先后在香港大学、美国德克萨斯农工大学、加州大学戴维斯分校从事博士后研究。2010 年 4 月起作为南京农业大学高层次引进人才任南京农业大学资源与环境科学学院教授，博士生导师。2013 年入选教育部新世纪优秀人才，2015 年 1 月破格晋升为三级教授，兼任中国农科院农业资源与农业区划研究所微生物资源与利用研究室研究员，博士生导师，创新团队首席科学家，国家菌种资源库常务副主任，中国农业微生物菌种保藏管理中心主任，农业部农业微生物资源收集保藏重点实验室主任。主要从事根际微生物与生物肥料、农业有机废弃物微生物降解转化与有机肥料研究。发表 SCI 论文 80 多篇，论文被 SCI 论文引用 2000 多次。

一、教育经历

1994.9-1998.6 山东莱阳农学院 农学系 农学学士

1998.9-2004.4 南京农业大学微生物学系 硕博连读 理学博士

二、工作经历

2004.6-2006.6 Department of Biodiversity & Ecology, Hong Kong University, Postdoctoral Research Fellow

2006.6-2008.9 Department of Microbiology & Plant Pathology, Texas A&M University, Postdoctoral Research Associate.

2008.9-2010.5 Department of Biological & Agricultural Engineering, University of California, Davis, Postdoctoral Research Associate

2010.5-至今 南京农业大学资源与环境科学学院 教授

三、获奖情况

中国科协优秀科技论文奖，张瑞福，2008，中国科协。

中国自然资源学会青年科技奖，张瑞福，2013，中国自然资源学会。

教育部科技进步一等奖，沈其荣,徐阳春,杨帆,杨兴明,薛智勇,陆建明,徐茂,李荣,赵永志,黄启为,张瑞福,余光辉,冉炜,李荣,沈标，2013，有机肥作用机制和产业化关键技术与推广，教育部。

国家科技进步二等奖，沈其荣,徐阳春,杨帆,杨兴明,薛智勇,陆建明,徐茂,李荣,赵永志,黄启为,张瑞福,余光辉,冉炜,李荣,沈标，2015，有机肥作用机制和产业化关键技术与推广，国务院。

农业部中华农业科技奖优秀创新团队奖，沈其荣，徐阳春，张瑞福，邹建文，杨兴明，黄启为，冉炜，郭世伟，余光辉，沈标，2015，有机肥和土壤微生物创新团队，农业部。

大北农科技奖，沈其荣，黄启为，李荣，刘东阳，张建，蔡枫，缪有志，张瑞福，凌宁，徐阳春，冉炜，陈巍，王其传，谭石勇，陆建明 利用秸秆和废弃动物蛋白制造木霉固体菌种和木霉全元生物有机肥 2017，北京大北农科技集团股份有限公司。

教育部技术发明一等奖，沈其荣,黄启为,李荣,刘东阳,张瑞福,陈巍 2018，利用秸秆和废弃动物蛋白制造木霉固体菌种及木霉全元生物有机肥，教育部。

国家科技进步二等奖，李顺鹏，崔中利，沈标，刘智，何健，杨

新民，王新华，张瑞福，蒋建东，洪青，2005，农药残留微生物降解技术的研究与应用，国务院。

全国农牧渔业丰收三等奖，李顺鹏，崔中利，沈标，刘智，何健，顾向阳，张瑞福，蒋建东，王新华，傅立斌，荆留民，刘军，洪青，陈立伟，房金钺，2004，农药残留微生物降解技术的研究与应用，农业部。

四、教学情况

本科生教学：《资源与环境生物技术》

研究生教学：《土壤微生物研究进展》、《科技论文写作》、《农业资源与环境科学前沿》

五、学术兼职

SCI 杂志 International Biodeterioration & Biodegradation 编委

SCI 杂志 Journal of Integrative Agriculture 编委

《微生物学杂志》编委

《农业科技导报》编委

中国微生物学会常务理事

中国微生物学会微生物资源专委会主任

中国微生物学会农业微生物专委会委员

中国土壤学会理事

中国土壤学会土壤生物与生化专委会委员

中国植物营养与肥料学会生物与有机肥专委会副主任委员

中国植物营养与肥料学会植物营养生物学专委会委员

中国自然资源与区划学会 理事

中国农科院农业微生物资源创新团队首席科学家

国家菌种资源库常务副主任

中国农业微生物菌种保藏管理中心主任

农业部农业微生物资源收集与保藏重点实验室主任

江苏省固体有机废弃物资源化高技术研究重点实验室副主任

六、社会兼职

第七届农业部肥料评审登记委员会委员

第二届农业部耕地质量建设与管理专家指导组专家

第二届全国科技平台标准化技术委员会（TC486）

七、主持项目

“根际益生菌 **SQR9** 特异基因岛合成新型天然活性物质分析及其参与生物膜形成的自噬作用机制”，31870096，国家自然科学基金面上项目，59 万，2019.1-2022.12. 主持。

“两组分系统 **ResD/E** 调控根际促生菌解淀粉芽孢杆菌 **SQR9** 根际定殖的分子机理研究”，31572214，国家自然科学基金面上项目，75.8 万，2016.1-2019.12. 主持。

“根际有益菌在作物根表形成生物膜的机理模型与调控研究”，31330069，国家自然科学基金重点项目，312 万，2014.1-2018.12. 参加。

“根际促生菌 **Bacillus amyloliquefaciens SQR9** 与植物根系分泌物互作的分子机理研究”，41271271，国家自然科学基金面上项目，75

万，2013.1-2016.12. 主持。

“新型农业微生物肥效制剂的创制”，2013AA102802，科技部 863 项目，827 万，2013.1-2017.12，主持。

“教育部新世纪优秀人才资助计划”教育部，50 万元，2014.1-2016.12,主持。

“生防菌 *Bacillus amyloliquefaciens* SQR9 在植株根表原位条件下形成生物膜的蛋白组变化研究”，20110097110002，教育部博士点博导基金，12 万，2012.1-2014.12，主持。

“微生物有机肥产业发展中的关键技术研究”，2011BAD11B03，科技部科技支撑计划，255 万，2011.1-2015.12，课题主持。

“青年骨干人才培养与引进计划”03-80900205，江苏省优势学科建设项目，10 万，2011.7-2012.7，主持。

“高温木质纤维素酶制剂的研发及协同作用机理研究”，03-06J0425，中央高校基本科研业务费，40 万，2010.11-2012.11，主持。

“南京农业大学高层次引进人才科研启动经费”，680-804103，南京农业大学，50 万，2010.5-2015.5，主持。

“有机磷农药水解酶基因水平转移的分子基础研究”，30400014，国家自然科学基金青年基金，20 万，2005.1-2007.12，主持。

八、发表论文（第一与责任作者论文）

Liu Y, Feng H, Fu X, Zhang N, Du W, Shen Q and **Zhang R*** 2020. Induced root-secreted D-galactose functions as a chemoattractant and enhances the biofilm formation of *Bacillus amyloliquefaciens* SQR9 in an McpA-dependent manner

Applied Microbiology & Biotechnology (Published online DOI: 10.1007/s00253-019-10265-8)

Liu Y[†], Feng H[†], Chen L, Zhang H, Dong X, and **Zhang R* 2020**. Exploring the signals in root exudates sensed by the *Bacillus amyloliquefaciens* histidine kinase KinD. *Molecular Plant-Microbe Interactions* (Published online DOI:10.1094/MPMI-07-19-0201-R)

Xu Z, Mandic-Mulec I, Zhang H, Liu Y, Sun X, Feng H, Xun W, Zhang N, Shen Q and **Zhang R* 2019**. Antibiotic bacillomycin D affects iron acquisition and biofilm formation in *Bacillus velezensis* through a Btr-mediated FeuABC-dependent pathway *Cell Report* 29(5):1192-1202.

Li G, Chen X, Zhou X, Huang R, Li L, Miao Y, Liu D, and **Zhang R* 2019**. Improvement of GH10 family xylanase thermostability by introducing of an extra α -helix at the C-terminal. *Biochemical and Biophysical Research Communications* 515(3):417-422.

Wang D[†], Xu Z[†], Zhang G, Xia L, Dong X, Li Q, Liles MR, Shao J, Shen Q and **Zhang R* 2019**. A genomic island in a plant beneficial rhizobacterium encodes novel antimicrobial fatty acids and a self-protection shield to enhance its competition. *Environmental Microbiology* 21(9):3455-3471

Zhang W[†], Liu Z[†], Zhou S, Mou H* and **Zhang R*. 2019**. Cloning and expression of a β -mannanase gene from *Bacillus* sp. MK-2 and its directed evolution by random mutagenesis. *Enzyme and Microbial Technology* 124:70-78.

Xu Z[†], Zhang H[†], Sun X, Liu Y, Yan W, Xun W, Shen Q and **Zhang R* 2019**. *Bacillus velezensis* wall teichoic acids is required for biofilm formation and root colonization. *Applied and Environmental Microbiology* 85(5): e02116-18. (Cover Story)

Xun W, Li W, Xiong W, Ren Y, Miao Y, Xu Z, Zhang N, Shen Q* and **Zhang R* 2019**. Diversity-triggered deterministic microbiome assembly compromises ecosystem functions. *Nature Communications* 10(1):3833

Feng H[†], Zhang N[†], Fu X, Liu Y, Krell T, Du W, Shao J, Shen Q and **Zhang R* 2019**. Recognition of dominant attractants by key chemoreceptors mediates recruitment of plant growth-promoting rhizobacteria. *Environmental Microbiology* 21(1):402-415.

Xu Z, Xie J, Zhang H, Wang D, Shen Q and **Zhang R*. 2019**. Enhanced control of plant wilt disease by a xylose-inducible degQ gene engineered into *B. velezensis* strain SQR9XYQ. *Phytopathology* 109(1):36-43.

Dong X[†], Zhang G[†], Xiong Q, Liu D, Wang D, Liu Y, Wu G, Li P, Luo Y and **Zhang R***. 2018. *Paracoccus salipaludis* sp. nov., isolated from saline-alkaline soil. *International Journal of Systematic and Evolutionary Microbiology* 68(12):3812-3817.

Dong X, Liu Y, Zhang G, Wang D, Zhou X, Shao J, Shen Q and **Zhang R***. 2018. Synthesis and detoxification of nitric oxide in the plant beneficial rhizobacterium *Bacillus amyloliquefaciens* SQR9 and its effect on biofilm formation. *Biochemical and Biophysical Research Communications* 503(2):784-790.

Xun W, Yan R, Ren Y, Jin D, Xiong W, Zhang G, Cui Z, Xin X* and **Zhang R*** 2018. Grazing-induced microbiome alterations drive soil organic carbon turnover and productivity in meadow steppe. *Microbiome* 6(1):170.

Miao Y, Kong Y, Li P, Li G, Liu D, Shen Q and **Zhang R***. 2018 Effect of CBM1 and linker region on enzymatic properties of a novel thermostable dimeric GH10 xylanase (Xyn10A) from filamentous fungus *Aspergillus fumigatus* Z5 *Applied Microbiology & Biotechnology Express* 8(1):44

Feng H, Zhang N, Du W, Zhang H, Liu Y, Fu X, Shao J, Zhang G, Shen Q and **Zhang R*** 2018. Identification of chemotaxis compounds in root exudates and their sensing chemoreceptors in plant growth-promoting rhizobacteria *Bacillus amyloliquefaciens* SQR9. *Molecular Plant-Microbe Interactions* 31(10):995-1005.

Li Q, Li Z, Li X, Xia L, Zhou X, Xu Z, Shao J, Shen Q and **Zhang R*** 2018. FtsEX-CwlO regulates biofilm formation by plant-beneficial rhizobacterium *Bacillus velezensis* SQR9. *Research in Microbiology* 169(3):166-176.

Xun W, Li W, Huang T, Ren Y, Xiong W, Miao Y, Ran W, Li D, Shen Q and **Zhang R*** 2018. Long-term agronomic practices alter the composition of asymbiotic diazotrophic bacterial community and their nitrogen fixation genes in an acidic red soil. *Biology and Fertility of Soils* 54(3):329-339.

Zhou X, Zhang N, Xia L, Li Q, Shao J, Shen Q and **Zhang R*** 2018. ResDE two-component regulatory system mediates oxygen limitation-induced biofilm formation of *Bacillus amyloliquefaciens* SQR9. *Applied and Environmental Microbiology* 84(8):e02744-17

Wu G[†], Liu Y[†], Xu Y, Zhang G, Shen Q and **Zhang R*** 2018. Exploring elicitors of beneficial rhizobacterium *Bacillus amyloliquefaciens* SQR9 to induce plant systemic resistance and their interactions with the signaling pathways *Molecular Plant-Microbe Interactions* 31(5):560-567.

Xun W, Huang T, Li W, Ren Y, Xiong W, Ran W, Li D, Shen Q and **Zhang R***

2017. Alteration of soil bacterial interaction networks driven by different long-term fertilization management practices in the red soil of South China. *Applied Soil Ecology* 120:128-134.

Zhang R, Vivanco MJ, and Shen Q*, **2017.** The unseen rhizosphere root-soil-microbe interactions for crop production. *Current Opinion in Microbiology* 37:8-14.

Miao Y, Li P, Li G, Liu D, Druzhinina IS, Kubicek CP, Shen Q and **Zhang R***. **2017** Two degradation strategies for overcoming the recalcitrance of natural lignocellulosic xylan by polysaccharides-binding GH10 and GH11 xylanases of filamentous fungi *Environmental Microbiology* 19(3):1054-1064.

Chen L[#], Liu Y[#], Wu G, Zhang N, Shen Q and **Zhang R*** **2017.** Beneficial rhizobacterium *Bacillus amyloliquefaciens* SQR9 induces plant salt tolerance through spermidine production. *Molecular Plant-Microbe Interactions* 30(5):423-432.

Liu Y, Chen L, Feng H, Xu Y, Li Z, Wu G, Zhang N, Zhang G, Shen Q and **Zhang R*** **2017.** Identification of root secreted compounds involved in the communication between soil-borne pathogen-cucumber-*Bacillus amyloliquefaciens* SQR9. *Molecular Plant-Microbe Interactions* 30(1):53-62.

Liu Y[†], Yang D[†], Zhang N, Chen L, Cui Z, Shen Q, **Zhang R*** **2016.** Characterization of uncultured genome fragment from soil metagenomic library exposed rare mismatch of internal tetranucleotide frequency. *Frontiers in Microbiology* 7:2081

Zhang N[†], Yang D[†], Kendall JR, Miao Y, Zhang G, Druzhinina, IS, Kubicek CP, Shen Q and **Zhang R*** **2016.** Comparative genomic analysis of *Bacillus amyloliquefaciens* and *Bacillus subtilis* reveals evolutionary traits for adaptation to plant-associated habitats. *Frontiers in Microbiology* 7:2039

Xun W, Xu Z, Li W, Ren Y, Huang T, Ran W, Wang B, Shen Q and **Zhang R*** **2016.** Long-term organic-inorganic fertilization ensures great soil productivity and bacterial diversity after natural-to-agricultural ecosystem conversion *Journal of Microbiology*. 54(9):611-617.

Njeri KV, Chen L, Liu Y, Raza W, Zhang N, Mungai LK, Shen Q and **Zhang R*** **2016.** Characterization of extracellular polymeric substances of *Bacillus amyloliquefaciens* SQR9 induced by root exudates of cucumber. *Journal of Basic Microbiology*. 56, 1183–1193

Sun L, Xun W, Huang T, Zhang G, Gao J, Ran W, Li D, Shen Q and **Zhang R*** **2016.** Alteration of the soil bacterial community during the parent materials

maturation driven by different fertilizations *Soil Biology & Biochemistry* 96:207-215.

Liu Y, Chen L, Zhang N, Li Z, Zhang G, Xu Y, Shen Q and **Zhang R*** 2016. Plant-microbe communication enhances auxin biosynthesis by a root-associated plant beneficial bacterium *Bacillus amyloliquefaciens* SQR9. *Molecular Plant-Microbe Interactions* 29(4):324-330.

Xun W, Zhao J, Xue C, Zhang G, Ran W, Wang B, Shen Q and **Zhang R*** 2016. Significant alteration of soil bacterial communities and organic carbon decomposition by different long-term fertilization management conditions of extremely low-productivity arable soil in South China. *Environmental Microbiology* 18(6):1907-1917.

Xun W, Xiong W, Huang T, Ran W, Li D, Shen Q, Li Q and **Zhang R*** 2016. Swine manure and quicklime have different impacts on chemical properties and composition of bacterial communities of an acidic soil. *Applied Soil Ecology* 100:38-44.

Shao J, Li S, Zhang N, Cui X, Zhou X, Zhang G, Shen Q and **Zhang R*** 2015. Analysis and cloning of the synthetic pathway of the phytohormone indole-3-acetic acid in the plant-beneficial *Bacillus amyloliquefaciens* SQR9 *Microbial Cell Factories*. 14:130.

Zhang N[†], Yang D[†], Wang D, Miao Y, Shao J, Zhou X, Xu Z, Li Q, Feng H, Li S, Shen Q* and **Zhang R*** 2015. Whole transcriptomic analysis of the plant beneficial rhizobacterium *Bacillus amyloliquefaciens* SQR9 during enhanced biofilm formation regulated by maize root exudates. *BMC Genomics* 16:685

Xun W, Huang T, Zhao J, Ran W, Wang B, Shen Q and **Zhang R*** 2015. Environmental conditions rather than microbial inoculum composition determine the bacterial community, microbial biomass and enzyme activity of reconstructed soil microbial communities. *Soil Biology & Biochemistry* 90:10-18.

Miao Y, Liu D, Li G, Li P, Xu Y, Shen Q and **Zhang R***. 2015 Genome wide transcriptomic analysis of a superior biomass degrading strain of *Aspergillus fumigatus* revealed the active lignocelluloses degrading genes. *BMC Genomics* 16:459

Miao Y, Li J, Xiao Z, Shen Q and **Zhang R*** 2015. Characterization and identification of thermostable xylanolytic enzymes from *Aspergillus fumigatus* Z5. *BMC Microbiology* 15:126

Sun L, Gao J, Huang T, Kendall JR, Shen Q and **Zhang R*** 2015. Parental material and cultivation determine soil bacterial community structure and fertility.

FEMS Microbiology Ecology. 91:1-10.

Shao J, Xu Z, Zhang N, Shen Q and **Zhang R*** 2015. Contribution of indole-3-acetic acid in the plant growth promotion by the rhizospheric strain *Bacillus amyloliquefaciens* SQR9. *Biology and Fertility of Soils* 51(3):321-330

Qiu M, Xu Z, Li X, Li Q, Zhang N, Shen Q and **Zhang R*** 2014. Comparative proteomics analysis of *Bacillus amyloliquefaciens* SQR9 revealed the key proteins involved in in situ root colonization. *Journal of Proteome Research*. 13(12):5581-5591.

Li B, Li Q, Xu Z, Zhang N, Shen Q and **Zhang R*** 2014. Responses of beneficial *Bacillus amyloliquefaciens* SQR9 to different soilborne fungal pathogens through the alteration of antifungal compounds production *Frontiers in Microbiology* 5:636

Xu Z[†], **Zhang R[†]**, Wang D, Qiu M, Feng H, Zhang N and Shen Q*. 2014. Enhanced control of cucumber wilt disease by *Bacillus amyloliquefaciens* SQR9 by altering the regulation of its DegU phosphorylation. *Applied and Environmental Microbiology* 80:2941-2950.

Chen L, Xun W, Sun L, Zhang N, Shen Q and **Zhang R***. 2014. Effect of different long-term fertilization regimes on soil viral community in a red soil of southern China. *European Journal of Soil Biology* 62:121-126.

Liu Y, Zhang N, Qiu M, Feng H, Vivanco JM, Shen Q and **Zhang R***. 2014. Enhanced rhizosphere colonization of beneficial *Bacillus amyloliquefaciens* SQR9 by pathogen infection *FEMS Microbiology Letters*. 353:49-56.

Zhao J, Ni T, Li Y, Xiong W, Ran W, Shen B, Shen Q and **Zhang R***. 2014. Responses of bacterial communities in arable soils under a rice-wheat cropping system to different fertilizer regimes and sampling time *Plos One*. 9(1): e85301.

Zhao J[†], **Zhang R[†]**, Xue C, Xun W, Sun L and Shen Q*. 2014. Pyrosequencing reveals contrasting soil bacterial diversity and community structure in two main winter wheat growing areas of China. *Microbial Ecology* 67:443-453.

Qiu M, Li S, Zhou X, Cui X, Vivanco JM*, Shen Q and **Zhang R*** 2014. De-coupling root-microbiome association followed by antagonist inoculation improves rhizosphere soil suppressiveness. *Biology and Fertility of Soils* 50:217-224.

Zhang N, Wang D, Liu Y, Li S, Shen Q and **Zhang R*** 2014. Effects of different plant root exudates and their organic acid components on chemotaxis, biofilm

formation and colonization by beneficial rhizosphere-associated bacterial strains *Plant Soil*. 374: 689-700.

Li S[†], **Zhang R[†]**, Wang Y, Zhang N, Qiu M, Shen B, Yin X, Shen Q*. **2013**. Promoter analysis and transcription regulation of fus gene cluster responsible for fusaricidin synthesis of *Paenibacillus polymyxa* SQR-21 *Applied Microbiology & Biotechnology* 97(21):9479-9489.

Zhang R[†], Xu C[†], Shen Q, Kusuga T, Wu W, Szewczyk E, Ma D and Fan Z*. **2013**. Characterization of two cellobiose dehydrogenases and comparison of their contributions to total activity in *Neurospora crassa*. *International Biodeterioration & Biodegradation* 82:24-32

Badri DV[†], Chaparro JM[†], **Zhang R***, Shen Q, Vivanco JM*. **2013**. Application of natural blends of phytochemicals derived from the root exudates of *Arabidopsis* to the soil reveal that phenolic related compounds predominantly modulate the soil microbiome. *Journal of Biological Chemistry*. 288(7):4502-4512

Weng J[†], Wang Y[†], Li J, Shen Q and **Zhang R***. **2013**. Enhancing root colonization and biocontrol activity of *Bacillus amyloliquefaciens* SQR9 by *abrB* gene disruption *Applied Microbiology & Biotechnology* 97(19):8823-8830.

Xu Z, Shao J, Li B, Yan X, Shen Q and **Zhang R***. **2013**. Contribution of Bacillomycin D in *Bacillus amyloliquefaciens* SQR9 to antifungal activity and biofilm formation *Applied and Environmental Microbiology* 79(3):808-815

Qiu M[†], **Zhang R[†]**, Xue C, Zhang S, Li S, Zhang N and Shen Q*. **2012**. Application of bio-organic fertilizer can control *Fusarium* wilt of cucumber plants by regulating microbial community of rhizosphere soil. *Biology and Fertility of Soils* 48:807-816

Zhang R, Pan L, Zhao Z and Gu J-D*. **2012** High Incidence of Plasmids in Marine *Vibrio* Species Isolated from Mai Po Nature Reserve of Hong Kong *Ecotoxicology*, 21:1661-1668

Huo Z, Zhang N, Waseem Raza, Shen Q and **Zhang R***. **2012**. Comparison of the spores of *Paenibacillus polymyxa* SQR-21 prepared at different temperatures. *Biotechnology Letters* 34:925-933.

Huo Z[†], Zhang N[†], Xu Z, Li S, Zhang Q, Qiu M, Huang Q, **Zhang R*** and Shen Q. **2012**. Optimization of survival and spore formation of *Paenibacillus polymyxa* SQR-21 during bioorganic fertilizer storage. *Bioresource Technology*. 108:190-195.

Zhang R, Fan Z* and Kusuga T. **2011**. Heterologous expression of cellobiose

dehydrogenase from *Neurospora crassa* in *Pichia pastoris* and its purification and characterization. *Protein Expression & Purification*. 75:63-69.

Zhang R, Lipuma JJ and Gonzalez CF*. 2009 Two type IV secretion systems with different functions in *Burkholderia cenocepacia* K56-2. *Microbiology* 155:4005-13.

Zhang R and Gu J-D*. 2009. Complete sequence of plasmid pMP-1 from the marine environmental *Vibrio vulnificus* and location of its replication origin. *Marine Biotechnology*. 11(4):456-62.

Zhang R, Wang Y, Leung P and Gu J-D*. 2007. pVC, a small, cryptic plasmid from the environmental isolate of *Vibrio cholerae* MP-1. *Journal of Microbiology*. 45:193-198.

Zhang, R., Wang Y and Gu J-D*. 2006. Identification of environmental plasmid-bearing *Vibrio* species isolated from polluted and pristine marine environments of Hong Kong and resistance to antibiotics and mercury. *Anton Leeuw Int J G*, 89:307-315.

Zhang, R., Jiang J, Gu J-D and Li S*. 2006. Long term effect of methylparathion contamination on soil microbial community diversity estimated by 16S rRNA gene cloning. *Ecotoxicology*

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九、相关著作

中国生物种质与试验材料资源发展报告, 2016, 科学技术文献出版社 参编

十、专利成果

授权专利:

国家发明专利, 张瑞福 邵佳慧 张楠等, 高产吡啶-3-乙酸的重组细胞及其构建方法与应用。专利号: CN 201410675072.6 授权日: 2017.5.24

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CN201610003589.X, 申请日: 2016.1.4 授权日: 2019.1.18

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申请专利:

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国家发明专利, 张瑞福 陈小娟 徐志辉 荀卫兵 邵佳慧 张楠 冯海超 一株促进作物耐盐碱生长的巨大芽孢杆菌及盐碱地专用微生物

肥料和应用 申请号：201910300563.5 申请日：2019.4.15

国家发明专利,张瑞福 陈小娟 李盼 刘云鹏 徐志辉 邵佳慧 一株增强作物耐盐能力的根际促生菌及其微生物肥料和应用 申请号：201910359879.1 申请日：2019.4.30