

**欢迎报考或保送本实验室的研究生！本实验室具有开放的思维、严谨的逻辑、浓厚的学术氛围、广泛的国际交流与合作渠道、紧密的产学研合作、一流的设备、优厚的补助、高效的产出，定能助力你的成才。**

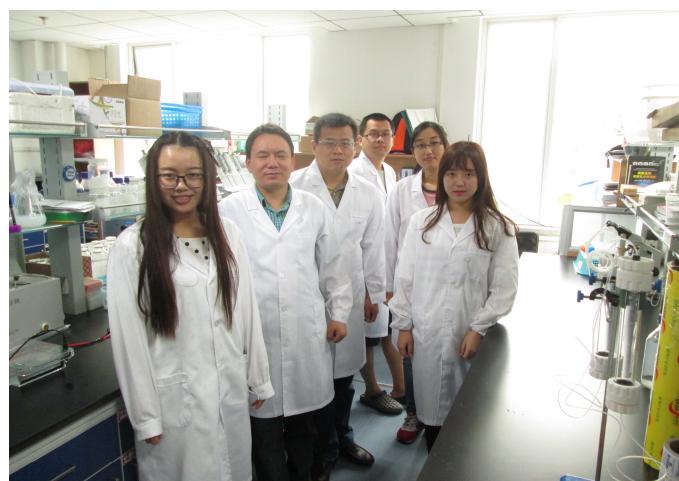
**简介：**张瑞福，山东泰安人，1974年出生于山东省泰安市。2004年4月在南京农业大学获理学博士学位，2004年6月起先后在香港大学、美国德克萨斯农工大学、加州大学戴维斯分校从事博士后研究。2010年4月起作为南京农业大学高层次引进人才任南京农业大学资源与环境科学学院教授，博士生导师。2013年入选教育部新世纪优秀人才，2014年6月入选中国农科院英才计划，2016年入选科技部中青年科技创新领军人才。兼任中国农科院农业资源与农业区划研究所微生物资源与利用研究员，博士生导师。主要从事根际微生物与生物肥料、农业废弃物资源化利用、微生物菌种保藏研究。



实验室：资环楼 A609  
办公室：资环楼 C602  
Tel: 025-84396477  
Email:rfzhang@njau.edu.cn  
zhangruifu@caas.cn



南京实验室人员



北京实验室人员

### 教育及工作经历：

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

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- 南京农业大学资源与环境科学学院 教授 博士生导师。

2014.7- 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

### 学术与社会兼职：

(1) SCI 杂志 International Biodeterioration & Biodegradation 编委 (2008 年至今);

(2) 中国微生物学会常务理事

(3) 中国微生物学会资源微生物专委会主任

(4) 中国微生物学会农业微生物专委会委员

(5) 中国土壤学会理事

(6) 中国土壤学会土壤生物与生化专委会委员

(7) 中国植物营养与肥料学会生物与有机肥专委会委员

(8) 中国农科院微生物资源收集、保藏与发掘利用创新团队首席科学家

(9) 中国农科院农业资源与农业区划研究所微生物学科点点长

(10) 中国农业微生物菌种保藏管理中心主任

(11) 国家微生物资源共享服务平台工作委员会常务副主任（负责人）

(12) 农业部农业微生物资源收集与保藏重点实验室主任

(13) 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

(14) 第七届农业部肥料评审登记委员会委员

(15) 农业部耕地质量建设与管理专家指导组专家

(16) 《微生物学杂志》编委

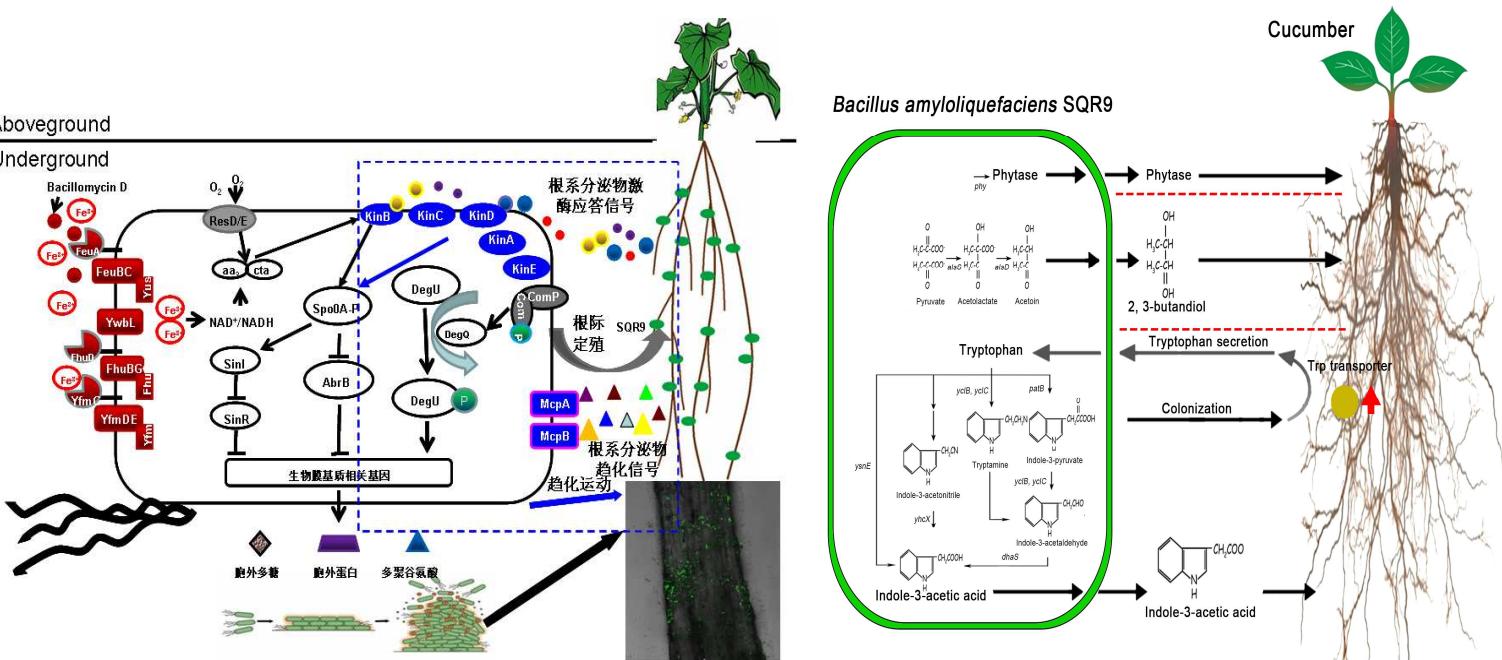
## 教学工作

本科生教学：《资源环境生物技术》专业必修课程

研究生教学：《土壤微生物研究进展》、《科技论文写作》

## 研究方向：

(1) **根际微生物与微生物肥料：**植物根际微生物被看作是植物的第二个基因组，具有促进植物生长、提高养分的有效性和吸收、诱导宿主植物抵抗生物与非生物逆境、协助宿主植物抑制土传病害等功能，对植物生长和健康有重要影响。根际微生物对于开发绿色环保的生物肥料等农用微生物制剂具有重要价值。生物肥料已成为我国肥料产业重要成员之一，在促进化肥减施增效、提高农产品品质方面发挥重要作用。近年来，我国生物肥料产业以年均20%的速度增长，到2015年，达到了1100多家生产企业、2200多个登记产品、产能超过1000万吨、产值近200亿元的规模。但从肥料总体上看，我国生物肥料规模还较小。限制生物肥料应用的主要瓶颈之一是其田间应用效果的不稳定性。对生物肥料中的微生物在复杂根际环境中的竞争定殖机制和生物肥料的作用机理研究将有助于从根本上发展突破生物肥料瓶颈的技术和产品提供理论支撑。芽孢杆菌、假单胞菌、木霉菌、根瘤菌等是主要应用菌种，其中分离自植物根际的促生芽孢杆菌占登记生物肥料产品使用菌种的55%以上。本实验室围绕根际有益微生物资源收集利用，建立了根际有益微生物资源库，指导企业开发了多个功能微生物肥料产品。以生物肥料中广泛使用的根际促生芽孢杆菌及其与根系互作为研究对象，解析了其在植物根际定殖的分子调控网络以及植物根系分泌物的介导作用，发现了菌-根互作协同促进植物生长的新机制，阐释了生物肥料和有机类肥料提高土壤质量的土壤微生物学机理。



根际促生芽孢杆菌与宿主植物根系互作机制模式图

芽孢杆菌根际促进植物生长的作用机理

## (2) 农业废弃物资源化利用

我国目前每年产生约 6000 万吨纯养分资源的固体有机废弃物，与此同时，我国目前每年要消耗 5900 多万吨纯养分资源的化肥，生产这些化肥则要消耗我国 5% 左右的煤炭和天然气等不可再生资源，而这些化肥养分只有 30-40% 被作物当季利用，很大部分被损失浪费了。充分利用农业有机废弃物资源生产有机类肥料或其他高附加值产品，既消纳了农业废弃物而保护了农业环境，也通过肥料化利用提升了耕地质量，通过其他资源化利用途径提高了农业产值，为循环农业发展提供技术支撑。本实验室广泛收集筛选农业有机废弃物高效转化的微生物资源，研究废弃物转化过程中的微生物及生化过程，开发了提高转化效率的微生物接种剂及其工艺。对木质纤维素类的微生物转化降解进行了重点研究，独自完成了一株高效堆肥曲霉菌株的全基因组测序、拼接、注释，以及该菌株对不同碳源底物（蔗糖、纤维素、木聚糖、稻秆）的转录响应，通过转录组分析确定了菌株参与木质纤维素类转化的关键酶系及其基因，建立了这些基因异源高效表达的酵母及丝状真菌表达宿主体系。对其中的外切葡聚糖酶、内切葡聚糖酶、葡萄糖苷酶、纤维二糖脱氢酶、木聚糖酶及一些辅助酶等进行了纯化和酶学性质及协同作用机制研究，获得了部分复合酶制剂，阐释了纤维二糖脱氢酶促进纤维素酶效率的分子机制。

## 主持课题：

- (1) “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。
- (2) “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。
- (3) “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。
- (4) “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。
- (5) “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。
- (6) “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。

- (7) “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。
- (8) “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。
- (9) “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。
- (10) “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。
- (11) “有机磷农药水解酶基因水平转移的分子基础研究”, 30400014, **国家自然科学青年基金**, 20 万, 2005.1-2007.12, 主持。
- (12) “农业资源与环境学科生物学研究创新引智基地（111 项目）”, B12009, 教育部、国家外国专家局, 2012.1-2016.12, 中方骨干参加。

## 专利:

- (1) 美国专利 Zhiliang Fan, Takao Kasuga, Weihua Wu, Xiaochao Xiong, **Ruifu Zhang**, 2012, Biochemical platform for fuels and chemicals production from cellulosic biomass, US Patent: 20120129221A1
- (2) 国家发明专利, 李顺鹏, **张瑞福**, 蒋建东, 戴青华, 崔中利, 何健, 2005, 一种三唑磷农药残留降解菌及其生产的菌剂, CN200410044951.5。
- (3) 国家发明专利, 李顺鹏, 顾立锋, 何健, 洪青, **张瑞福**, 蒋建东, 2006, 一种辛硫磷农药残留降解菌及其生产的菌剂, CN200510022545.3。
- (4) 国家发明专利, 沈其荣; 李荣; 刘红军; 黄蓉; 文春燕; **张瑞福**; 乔策策; 邵铖 一种脱毒水解菜籽饼生产农用氨基酸肥的菌剂及工艺 2014/6/25, CN201410089043.1
- (5) 国家发明专利, 沈其荣; 梁晓琳; 李荣; 黄蓉; 文春燕; **张瑞福**; 沈标 一种全元复合微生物肥料及其制备方法和应用 2014/8/20, CN201410114967.2.
- (6) 国家发明专利, 沈其荣; 李荣; 刘红军; 马婧; 沈标; 邵铖; 乔策策; **张瑞福** 一种利用病死猪蛋白生产的液体氨基酸复合物及其应用 2014/5/21, CN201410042218.3.
- (7) 国家发明专利, 沈其荣; 王世梅; 梁银; **张瑞福** 一种防除连作黄瓜枯萎病的拮抗放线菌及其微生物有机肥料, 2013/9/4, 江苏, 2010.04.13 申请 2011.06.01 授权中华人民共和国国家专利局 已公开, CN201310177972.3.
- (8) 国家发明专利, **张瑞福**; 邵佳慧; 张楠 高产吲哚-3-乙酸的重组细胞及其构建方法与应用。申请日: 2014.11.21 申请号: 201410675072.6
- (9) 国家发明专利, **张瑞福**; 邵佳慧; 张楠 生物合成吲哚-3-乙酸的成套蛋白及其应用。申请日: 2014.11.21 申请号: 201410677417.1
- (10) 国家发明专利, **张瑞福**; 张如; 沈其荣; 崔晓双; 李荣 利用秸秆和滤泥生产木霉生物有机肥的方法和获得的产品。申请日: 2016.1.4 申请号: 201610003589.X

## 科技奖励:

- (1) 中国科协优秀科技论文奖, 张瑞福, 2008, 中国科协。
- (2) 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。
- (3) 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研究与推广, 教育部。

- (4) **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研究与推广, 国务院。
- (5) **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, 农业部。
- (6) **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。
- (7) **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, 房金钱, 2004, 农药残留微生物降解技术的研究与应用, 农业部。

## 发表文章:

近年根际微生物与生物肥料方面发表论文:

- (1) Zhang R and Shen Q\*, 2017. The unseen rhizosphere root-soil-microbe interactions for crop production. *Current Opinion in Microbiology* (Invited Review, In Press)
- (2) Zhao J, Ni T, Xun W, Huang X, Huang Q\*, Ran W, Shen B, Zhang R and Shen Q. 2017. Influence of straw incorporation with and without straw decomposer on soil bacterial community structure and function in a rice-wheat cropping system. *Applied Microbiology & Biotechnology* (Pressed online, doi:10.1007/s00253-017-8170-3.)
- (3) 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* (In revision)
- (4) 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* (Pressed online, DOI:10.1094/MPMI-07-16-0131-R)
- (5) Raza W, Ling N, Zhang R, Huang Q, Xu Y, Shen Q\* 2017. Success evaluation of the biological control of Fusarium wilts of cucumber, banana, and tomato since 2000 and future research strategies. *Critical Review of Biotechnology*. 37(2):202-212.
- (6) Zhou C, Shi L, Ye B, Feng H, Zhang J, Zhang R, Yan X\* 2017. pheS\*, an effective host-genotype-independent counter-selectable marker for marker-free chromosome deletion in *Bacillus amyloliquefaciens*. pheS\*, an effective host-genotype-independent counter-selectable marker for marker-free chromosome deletion in *Bacillus amyloliquefaciens*. *Applied Microbiology & Biotechnology* 101:217-227.
- (7) Liu Y<sup>†</sup>, Yang D<sup>†</sup>, 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.
- (8) Zhang N<sup>†</sup>, Yang D<sup>†</sup>, 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 evolutional traits for adaptation to plant-associated habitats. *Frontiers in Microbiology* 7:2039.
- (9) 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.
- (10) Zhou X, Fornara D, Ikenaga M, Akagi I, Zhang R, Jia Z\* 2016. The resilience of microbial community under drying and rewetting cycles of three forest soils. *Frontiers in Microbiology* 7:1101.
- (11) 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.
- (12) 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.
- (13) Chen L, Liu Y, Wu G, Njeri KV, Shen Q, Zhang N\* and Zhang R 2016. Induced maize salt tolerance by rhizosphere inoculation of *Bacillus amyloliquefaciens* SQR9. *Physiologia Plantarum* 158: 34-44.

- (14) 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.
- (15) 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.
- (16) Li R, Shen Z, Sun L, **Zhang R**, Fu L, Deng X, Shen Q\* 2016. Novel soil fumigation method for suppressing cucumber *Fusarium* wilt disease associated with soil microflora alterations. *Applied Soil Ecology* 101:28-36.
- (17) 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.
- (18) Zhao J, Ni T, Li J, Lu Q, Fang Z, Huang Q, **Zhang R**, Li R, Shen B\*, Shen Q 2016. Effects of organic-inorganic compound fertilizer with reduced chemical fertilizer application on crop yields, soil biological activity and bacterial community structure in a rice-wheat cropping system. *Applied Soil Ecology* 99:1-12.
- (19) Zhang J, Akcapinar GB, Atanasova L, Rahimi MJ, Przylucka A, Yang D, Kubicek CP, **Zhang R**, Shen Q\* and Druzhinina IS. 2016. The neutral metallopeptidase NMP1 of *Trichoderma guizhouense* is required for mycotrophy and self-defense. *Environmental Microbiology* 18(2):580-597.
- (20) 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.
- (21) 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*. 13:5581-5591.
- (22) Zhang N<sup>†</sup>, Yang D<sup>†</sup>, 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. (共同通讯)
- (23) 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.
- (24) Xu Z<sup>†</sup>, **Zhang R<sup>†</sup>**, 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. (并列第一)
- (25) 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* 79:808-815 (Nominated by Editors as the Spotlight article)
- (26) 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*. 288:4502-4512. (共同通讯)
- (27) 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.
- (28) 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* 51:321-330.
- (29) 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.
- (30) 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.
- (31) 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.
- (32) 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: e85301.

- (33) 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.
- (34) 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.
- (35) 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.
- (36) Weng J<sup>†</sup>, Wang Y<sup>†</sup>, 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* 97:8823-8830.
- (37) Qiu M<sup>†</sup>, **Zhang R<sup>†</sup>**, 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. (并列第一)
- (38) Li S<sup>†</sup>, **Zhang R<sup>†</sup>**, 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* 97:9479-9489. (并列第一)
- (39) 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.
- (40) 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.
- (41) Chen L, Liu Y, Wu G, Njeri KV, Shen Q, Zhang N\* and **Zhang R** 2016. Induced maize salt tolerance by rhizosphere inoculation of *Bacillus amyloliquefaciens* SQR9. *Physiologia Plantarum* (doi:10.1111/ppl.12441)
- (42) Wang Y, Weng J, Raza W, Yin X, **Zhang R** and Shen Q\*. 2012. *Bacillus subtilis* genome editing using ssDNA with short homologous fragments. *Nucleic Acids Research*. 40:e91.
- (43) Zhang J, Akcapinar GB, Atanasova L, Rahimi MJ, Przylucka A, Yang D, Kubicek CP, **Zhang R**, Shen Q\* and Druzhinina IS. 2015. The neutral metallopeptidase NMP1 of *Trichoderma guizhouense* is required for mycotrophy and self-defense. *Environmental Microbiology* 18:580-597.
- (44) Raza W, Ling N, **Zhang R**, Huang Q, Xu Y, Shen Q\* 2016. Success evaluation of the biological control of Fusarium wilts of cucumber, banana, and tomato since 2000 and future research strategies. *Critical Review of Biotechnology*. 26:1-11.
- (45) Yuan J, Chaparro JM, Manter DK, **Zhang R**, Vivanco JM\*, Shen Q. 2015. Roots from distinct plant developmental stages are capable of rapidly selecting their own microbiome without the influence of environmental and soil edaphic factors. *Soil Biology & Biochemistry* 89:206-209.
- (46) Li R, Shen Z, Sun L, **Zhang R**, Fu L, Deng X, Shen Q\* 2016. Novel soil fumigation method for suppressing cucumber Fusarium wilt disease associated with soil microflora alterations. *Applied Soil Ecology* 101:28-36.
- (47) Zhao J, Ni T, Li J, Lu Q, Fang Z, Huang Q, **Zhang R**, Li R, Shen B\*, Shen Q 2016. Effects of organic-inorganic compound fertilizer with reduced chemical fertilizer application on crop yields, soil biological activity and bacterial community structure in a rice-wheat cropping system. *Applied Soil Ecology* 99:1-12.
- (48) Xiong W, Li Z, Liu H, Xue C, **Zhang R**, Wu H, Li R, Shen Q\* 2015. The Effect of long-term continuous cropping of black pepper on soil bacterial communities as determined by 454 pyrosequencing. *Plos One*. 10:e0136946.
- (49) Xue C, Ryan PC, Shen Z, **Zhang R**, Huang Q, Li R, Ruan Y, Shen Q\* 2015. Manipulating the banana rhizosphere microbiome for biological control of Panama disease. *Scientific Report*. 5:11124.
- (50) Xiong W, Zhao Q, Zhao J, Xun W, Li R, **Zhang R**, Wu H and Shen Q\*. 2015. Different continuous cropping spans significantly affect microbial community membership and structure in a vanilla-grown soil as revealed by deep pyrosequencing. *Microbial Ecology* 70:209-218.
- (51) Huang XF, Chaparro JM, Reardon KF, **Zhang R**, Shen Q and Vivanco JM\*. 2014. Rhizosphere interactions: root exudates, microbes, and microbial communities. *Botany* 92: 267-275.
- (52) Li S, Yang D, Qiu M, Shao J, Guo R, Shen B, Yin X, **Zhang R**, Zhang N and Shen Q\*. 2014. Complete genome sequence of *Paenibacillus polymyxa* SQR-21, a plant growth-promoting rhizobacteria with antifungal activity and rhizosphere colonization ability. *Genome Announcement* 2:e00281-14.

- (53) 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.
- (54) Huang X, Yong X, Zhang R, Shen Q and Yang X\*. 2013. The supernatant of *Bacillus pumilus* SQR-N43 has antifungal activity towards Rhizoctonia solani. *Journal of Basic Microbiology*. 53:657-63.
- (55) Yong X, Zhang R, Zhang N, Chen Y, Huang X, Zhao J and Shen Q\*. 2013. Development of a specific real-time PCR assay targeting the poly- $\gamma$ -glutamic acid synthesis gene, *pgsB*, for the quantification of *Bacillus amyloliquefaciens* in solid-state fermentation. *Bioresource Technology*. 129:477-484.
- (56) Ding C, Shen Q, Zhang R, and Chen W\*. 2013. Evaluation of rhizosphere bacteria and derived bio-organic fertilizers as potential biocontrol agents against bacterial wilt (*Ralstonia solanacearum*) of potato. *Plant Soil*. 366: 453-466.
- (57) Li S, Zhang N, Zhang Z, Luo J, Shen B, Zhang R and Shen Q\*. 2013. Antagonist *Bacillus subtilis* HJ5 controls Verticillium wilt of cotton by root colonization and biofilm formation. *Biology and Fertility of Soils* 49:295-303.
- (58) Zhang N, Wu K, He X, Li S, Zhang Z, Shen B, Yang X, Zhang R, Huang Q and Shen Q\*. 2011. A new bioorganic fertilizer can effectively control banana wilt by strong colonization with *Bacillus subtilis* N11. *Plant Soil*. 344:87-97.
- (59) 王伟, 岳政府, 刘孝文, 张瑞福\*. 2017. 低温适应型植物根际促生细菌的筛选及促生效应研究. *南京农业大学学报*. 40(1):93-100.
- (60) 赵军, 李勇, 冉炜, 张瑞福, 沈标\*, 沈其荣. 2016. 有机肥替代部分化肥对稻麦轮作系统产量及土壤微生物区系的影响. *南京农业大学学报* 39(4):594-602.
- (61) 崔晓双, 王伟, 张如, 张瑞福\* 2015. 基于根际竞争能力的植物根际促生菌的筛选及促生效应研究. *南京农业大学学报*. 38(6):958-966.
- (62) 张楠, 吴凯, 沈怡斐, 张瑞福, 沈其荣, 黄启为 2014. 根际益生菌解淀粉芽孢杆菌 SQR9 在香蕉根表的定殖行为研究. *南京农业大学学报*. 37(6):59-65.
- (63) 张瑞福\*, 颜春荣, 张楠, 李俊, 沈其荣 2013. 微生物肥料研究及其在耕地质量提升中的应用前景. *中国农业科技导报*. 15:8-16.
- (64) 张瑞福, 沈其荣\* 2012. 抑病型土壤的微生物区系特征及调控. *南京农业大学学报*. 35:125-132.

#### 近年发表的农业废弃物资源化利用相关文章:

- (65) 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* (Pressed online, doi:10.1111/1462-2920.13614)
- (66) Liu H, Chen D, Zhang R, Hang X, Li R\*, Shen Q. 2016. Amino acids hydrolyzed from animal carcasses are a good additive for the production of bio-organic fertilizer. *Frontiers in Microbiology* 7:1290.
- (67) 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.
- (68) 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.
- (69) Yang D, Pomraning K, Kopchinskiy A, Karimi Aghcheh R, Atanasova L, Chenthamara K, Baker SE, Zhang R, Shen Q, Freitag M, Kubicek CP, Druzhinina IS. 2015. Genome sequence and annotation of *Trichoderma parareesei*, the ancestor of the cellulase producer *Trichoderma reesei*. *Genome Announcement* 3: e00885-15.
- (70) 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 Biodegradation & Biodegradation* 82:24-32.
- (71) 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.
- (72) Liu D, Li J, Zhao S, Zhang R, Wang M, Miao Y, Shen Y and Shen Q\*. 2013. Secretome diversity and quantitative analysis of cellulolytic *Aspergillus fumigatus* Z5 in the presence of different carbon sources. *Biotechnology for Biofuels* 6:149.
- (73) Liao H, Xu C, Tan S, Wei Z, Ling N, Yu G, Raza W, Zhang R, Shen Q and Xu Y\*. 2012. Production and characterization of acidophilic xylanolytic enzymes from *Penicillium oxalicum* GZ-2. *Bioresource Technology*. 123:117-124.

- (74) Fan Z, Wu W, Hildebrand A, Kusuga T, **Zhang R** and Xiong X. 2012. A novel biochemical platform for fuels and chemicals production from cellulosic biomass. *Plos One* 7:e31693.
- (75) Liu D, **Zhang R**, Yang X, Zhang Z, Song S, Miao Y and Shen Q\*. 2012. Characterization of a thermostable beta-glucosidase from *Aspergillus fumigatus* Z5, and its functional expression in *Pichia pastoris* X33. *Microbial Cell Factories*. 11:25.
- (76) Liu D, **Zhang R**, Yang X, Wu H, Xu D, Tang Z and Shen Q\*. 2011. Thermostable cellulase production of *Aspergillus fumigatus* Z5 under solid-state fermentation and its application in degradation of agricultural wastes. *International Biodeterioration & Biodegradation* 65:717-725.
- (77) Liu D, **Zhang R**, Yang X, Xu Y, Tang Z, Tian W and Shen Q\*. 2011. Expression, purification and characterization of two thermostable endoglucanases cloned from a lignocellulosic decomposing fungi *Aspergillus fumigatus* Z5 isolated from compost. *Protein Expression & Purification* 79:176-86.
- (78) Liu D, **Zhang R**, Wu H, Xu D, Tang Z, Yu G, Xu Z and Shen Q\*. 2011. Changes in biochemical and microbiological parameters during the period of rapid composting of dairy manure with rice chaff. *Bioresource Technology* 102:9040-9049.

### 其他文章及 2010 年之前发表文章：

- (1) Zhang G, Fauzi Haroon M, **Zhang R**, Hikmawan T, Stingl U\*. 2016. Draft genome sequences of two *Thiomicrospira* strains isolated from the brine-seawater interface of Kebrit Deep in the Red Sea. *Genome Announcement*. 4(2):e00110
- (2) Zhang G, Fauzi Haroon M, **Zhang R**, Hikmawan T, Stingl U\*. 2016. Draft genome sequence of *Pseudoalteromonas* sp. strain XI10 isolated from the brine-seawater interface of Erba Deep in the Red Sea. *Genome Announcement*. 4(2):e00109
- (3) Zhang G, Gu J, **Zhang R**, Rashid M, Haroon MF, Xun W, Ruan Z, Dong X and Stingl U\* 2017. Halopropundus marisrubri gen. nov., sp. nov., an extremely halophilic archaeon isolated from the Discovery Deep brine-seawater interface in the Red Sea. *Int J Syst Evol Microbiol*. (Pressed online, doi:10.1099/ijsem.0.001559)
- (4) Zhang G, Fauzi Haroon M, **Zhang R**, Hikmawan T, Stingl U\*. 2016. Draft genome sequences of two *Thiomicrospira* strains isolated from the brine-seawater interface of Kebrit Deep in the Red Sea. *Genome Announcement*. 4(2):e00110.
- (5) Zhang G, Fauzi Haroon M, **Zhang R**, Hikmawan T, Stingl U\*. 2016. Draft genome sequence of *Pseudoalteromonas* sp. strain XI10 isolated from the brine-seawater interface of Erba Deep in the Red Sea. *Genome Announcement*. 4(2):e00109
- (6) **Zhang R**, Lipuma JJ and Gonzalez CF\*. 2009 Two type IV secretion systems with different functions in *Burkholderia cenocepacia* K56-2. *Microbiology* 155:4005-4013.
- (7) **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.
- (8) **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*. 11:456-62.
- (9) **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.
- (10) Jiang, J., **Zhang R**, Cui Z, He J, Gu L and Li S\*. 2007. Parameters controlling the gene targeting frequency in *Sphingomonas* species *rrn* site and expression of the methyl parathion hydrolase. *Journal of Applied Microbiology*. 102:1578-1585.
- (11) Jiang, J., **Zhang R**, Li R, Gu J-D and Li S\*. 2007. Simultaneous biodegradation of methyl parathion and carbofuran by a genetically engineered microorganism constructed by mini-Tn5 transposon. *Biodegradation*, 18:403-412.
- (12) **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.
- (13) **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*, 15:523-530.
- (14) **Zhang, R.**, Cui Z, Zhang X, Jiang J, Gu J-D and Li S\*. 2006. Cloning of the organophosphorus pesticide hydrolase gene clusters of seven degradative bacteria isolated from a methyl parathion contaminated site and evidence of their horizontal gene transfer. *Biodegradation*, 17:465-472.
- (15) **Zhang, R.**, Cui Z, Jiang J, He J, Gu X and Li S\*. 2005. Diversity of organophosphorus pesticide-degrading bacteria in a polluted soil and conservation of their organophosphorus hydrolase genes. *Canada Journal of Microbiology*. 51: 337~343.

- (16) 戴青华, 张瑞福, 蒋建东, 邱珊莲, 李顺鹏\* 2007. 三唑磷水解酶基因的克隆及水解产物的确定. **中国环境科学** 6:777-780.
- (17) 张瑞福, 吴旭平, 樊奔, 何健, 蒋建东, 李顺鹏\* 2005. 有机磷农药污染土壤中有机磷农药降解菌的分离与多样性研究, **生态学报**. 25(6):1502-1508.
- (18) 张瑞福, 蒋建东, 代先祝, 顾立锋, 李顺鹏\* 2005. 污染环境中降解基因的水平转移及其在生物修复中的作用, **遗传**. 27(5):845-851.
- (19) 蒋建东, 张瑞福, 何健, 张小舟, 崔中利, 李顺鹏\* 2005. 细菌对环境污染物的趋化性及其在生物修复中的作用, **生态学报**. 25(7):1764-1771.
- (20) 戴青华, 张瑞福, 蒋建东, 顾立锋, 李顺鹏\* 2005. 一株三唑磷降解菌 mp-4 的分离鉴定及降解特性的研究, **土壤学报**. 42(1):111-115.
- (21) 张瑞福, 戴青华, 何健, 代先祝, 李顺鹏\* 2004. 七株有机磷农药降解菌的降解特性比较研究, **中国环境科学**. 24(5):584-587.
- (22) 张瑞福, 崔中利, 李顺鹏\* 2004. 土壤微生物群落结构研究方法进展, **土壤**. 36(5):476-480.
- (23) 张瑞福, 崔中利, 何健, 黄婷婷, 李顺鹏\* 2004. 甲基对硫磷长期污染对土壤微生物的生态学效应, **农村生态环境**. 20(4):1-5.
- (24) 张瑞福, 蒋建东, 崔中利, 李顺鹏\* 2004. 菌株 DLL-1 降解土壤和韭菜中甲基对硫磷的研究, **应用生态学报**. 15 (2): 295-298.
- (25) 蒋建东, 曹慧, 张瑞福, 张明星, 李顺鹏\* 2004. 有机磷农药对韭菜虫害的防治效果及农药的微生物降解, **应用生态学报**. 15(8):1459-1462.
- (26) 顾立锋, 何健, 张瑞福, 李顺鹏\* 2004. 一株耐盐苯酚降解菌的分离及降解特性研究, **土壤学报**. 41(5):756-760.
- (27) 张瑞福, 曹慧, 崔中利, 李顺鹏\*, 樊奔 2003. 土壤微生物总 DNA 的提取与纯化, **微生物学报**. 43 (2): 276-282. (获第六届中国科协期刊优秀论文奖)
- (28) 张瑞福, 朱卫, 崔中利, 李顺鹏\* 2003. 辛硫磷降解菌 X-1 的分离鉴定及降解性状的初步研究, **环境科学学报**. 23 (3): 411-413.
- (29) 朱卫, 张瑞福, 崔中利, 李顺鹏\* 2003. 一株杀虫单降解细菌的筛选与生物学特性研究, **南京农业大学学报**. 26 (1): 100-103.
- (30) 崔中利, 张瑞福, 何健, 李顺鹏\* 2002. 对硝基苯酚降解菌 P3 的分离、降解性质及基因工程菌的构建, **微生物学报**. 42(1):19-26.