张红生,教授,博士生导师。现任农学院种业科学系主任、南京农业大学国际交流与合作处处长、国际教育学院院长。1978-1982 年南京农学院农学系农学专业本科毕业,获农学学士学位;1982-1988 年南京农业大学植保系植物病理系研究生毕业,1985 年和 1988 年分别获农学硕士和博士学位;1991-1992 年荷兰 Wageningen 农业大学植物育种系博士后;1998-2000 年美国Cornell 大学访问学者。主要从事(1)水稻种质资源收集、鉴定、评价和利用;(2)水稻重要农艺性状的遗传机制与基因的分子定位;(3)水稻抗病虫和抗逆境基因的克隆与功能分析。先后承担国家863、国家自然科学基金、转基因重大专项和高校博士点基金等课题30多项。授予发明专利16项。在PNAS, Plant Cell, Rice, J Exp Bot, Plant Mol Biol, TAG, PLOS One, FEBS Letters等国内外期刊发表研究论文100多篇;获教育部科技进步一等奖一次,中国农科院科技进步二等奖一次。

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近 5 年发表的文章:

Identification and fine mapping of qGR6.2, a novel locus controlling rice seed germination under salt stress. BMC Plant Biology, 2021

A Cys2/His2 zinc finger protein acts as a repressor of green revolution gene SD1/OsGA20ox2 in rice (Oryza sativa L.). Plant and Cell Physiology, 2020

Natural variation in OsGASR7 regulates grain length in rice. Plant Biotechnology Journal, 2020 WPMIAS: Whole-degradome-based Plant MicroRNA-Target Interaction Analysis Server. Bioinformatics, 2020

Comparative Analysis of Salt Responsive Gene Regulatory Networks in Rice and Arabidopsis.

Computational Biology and Chemistry, 2020

A Little Membrane Protein with 54 Amino Acids Confers Salt Tolerance in Rice (Oryza sativa L.). Acta Physiologiae Plantarum, 2020

Genome-wide association analysis of panicle exsertion and uppermost internode in rice (Oryza sativa L.). Rice, 2019

Physiological characteristics of cold stratification on seed dormancy release in rice. Plant Growth Regulation, 2019

Fine mapping of a panicle blast resistance gene Pb-bd1 in Japonica landrace Bodao and its application in rice breeding. Rice, 2019

Rice qGL3/OsPPKL1 Functions with the GSK3/SHAGGY-Like Kinase OsGSK3 to Modulate Brassinosteroid Signaling. Plant Cell, 2019

Influence of isopropylmalate synthase OsIPMS1 on seed vigour associated with amino acid and energy metabolism in rice. Plant Biotechnology Journal, 2019

A microRNA biogenesis-like pathway for producing phased small interfering RNA from a long non-coding RNA in rice. Journal of Experimental Botany, 2019

Construction and analysis of degradome-dependent microRNA regulatory networks in soybean.

BMC Genomics, 2019

Comparative analysis of microRNAs and their targets in the roots of two cultivars with contrasting salt tolerance in rice (Oryza sativa L.). Plant Growth Regul, 2019

OsSYP121 accumulates at fungi penetration sites and mediates host resistance to rice blast. Plant Physiology, 2019

A quantitative trait locus, qSE3, promotes seed germination and seedling establishment under salinity stress in rice. Plant J, 2018

A zinc finger transcriptional repressor confers pleiotropic effects on rice growth and drought tolerance by down-regulating stress-responsive genes. Plant Cell Physiol, 2018

Natural variation reveals that OsSAP16 controls low-temperature germination in rice. J Exp Bot, 2018

DPMIND: degradome-based plant miRNA-target interaction and network database. Bioinformatics, 2018

OsNHX2, an Na+/H+ antiporter gene, can enhance salt tolerance in rice plants through more effective accumulation of toxic Na+ in leaf mesophyll and bundle sheath cells. Acta Physiol Plant, 2017

A Novel RNA-Binding Protein Involves ABA Signaling by Post-transcriptionally Repressing ABI2. Front Plant Sci, 2017

Arabidopsis RabF1 (ARA6) Is Involved in Salt Stress and Dark-Induced Senescence (DIS). Int J Mol Sci, 2017

QTL Identification and Fine Mapping for Seed Storability in Rice (Oryza sativa L.). Euphytica, 2017

Characterization and fine mapping of a blast resistant gene Pi-jnw1 from the japonica rice landrace Jiangnanwan. PLOs one, 2016

Knock-down of a RING finger gene confers cold tolerance. Bioengineered, 2016

Identification and Characterization of Quantitative Trait Loci for Shattering in Rice Landrace

Jiucaiqing from Taihu Lake Valley, China. The Plant Genome, 2016

QTL mapping of panicle blast resistance in Japonica landrace Heikezijing and its application in rice breeding. Mol Breeding, 2016

Identification of genes involved in rice seed priming in the early imbibition stage. Plant Biology, 2016

Population structure analysis and association mapping of bacterial blight resistance inindica rice (Oryza sativa L.) accessions. Plant Growth Regul, 2016

OsSNAP32, a SNAP25-type SNARE protein-encoding gene from rice, enhanced resistance to blast fungus. Plant Growth Regulation, 2016

Population structure analysis and association mapping of blast resistance in indica rice (Oryza sativa L.) landrace. Genet Mol Res, 2016

Fine mapping of a new race-specific blast resistance gene Pi-hk2 in Japonica Heikezijing from Taihu region of China. Phytopathology, 2016

A Novel Little Membrane Protein Confers Salt Tolerance in Rice (Oryza sativa L.). Plant Mol Biol Rep, 2016

Identification of QTLs with Additive, Epistatic, and QTL × Seed Maturity Interaction Effects for Seed Vigor in Rice. Plant Mol Biol Rep, 2016

## 近5年获得的项目:

国家自然科学基金,高盐胁迫下水稻幼苗形成关键基因 qSE3 克隆与功能分析,2018,主持。 国家自然科学基金,水稻 A20/AN1 型 E3 泛素连接酶提高抗逆性的分子机理研究,2015,主持。

国家自然科学基金,OsPPKL基因家族调控水稻籽粒发育的遗传网络解析, 2014, 主持。

国家自然科学基金, E3 泛素连接酶 ZFRG1 在水稻抗逆应答反应中的作用, 2011, 主持。

国家科技重大专项,粳稻地方品种抗稻瘟病基因 pi-bd/的克隆及功能研究, 2014, 主持。

农业农村部项目,农产品质量安全监管,2020,主持。

江苏省农业自主创新子课题,江淮稻区稻瘟病菌群体遗传分析及抗穗颈瘟基因的发掘与利用, 2019,参与。

省部级项目,水稻高活力种子关键基因发掘和种质创新及育种材料创制,2016,主持。