



卵菌与真菌分子生物学实验室

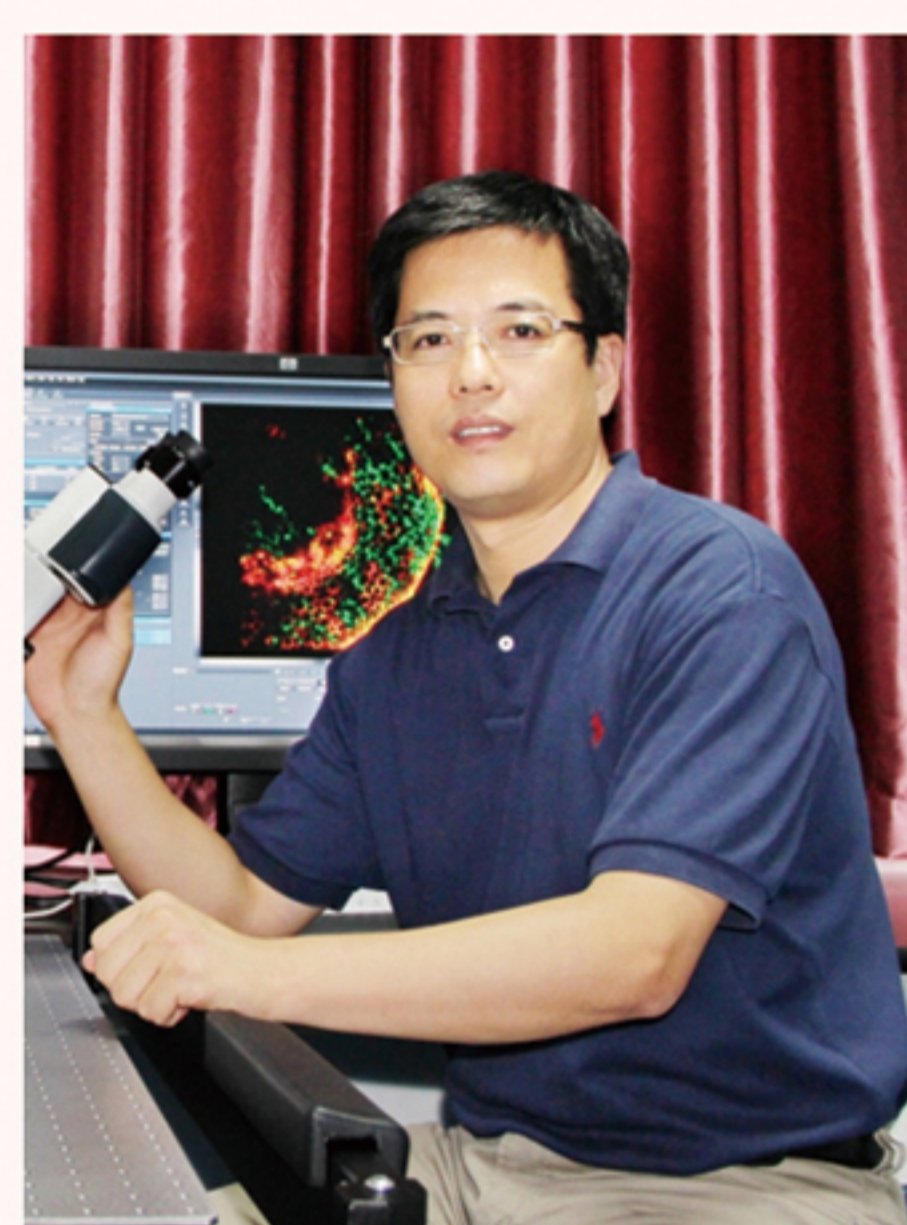
Lab of Oomycete & Fungal Molecular Biology

团队介绍

南京农业大学卵菌与真菌分子生物学研究室是我国从事植物病原菌物学研究历史最悠久的单位之一，对植物疫病菌、稻瘟病菌、棉花黄萎病菌和板栗疫病菌等的生物学、病理学和功能基因组学等进行了系统而深入的研究。目前承担国家973计划、863计划、农业行业科研专项、现代产业技术体系、自然科学基金重点项目、国家杰出青年科学基金等数十项重要国家科研项目。实验室现有教授4人、副教授1人、讲师1人和科研助理3人。



郑小波 教授
“973”项目首席专家
教育部跨世纪优秀人才
全国优秀科技工作者



王源超 教授
教育部长江学者特聘教授
国家杰出青年基金获得者
入选国家百千万人才工程
国家有突出贡献中青年专家



张正光 教授
国家杰出青年基金获得者
江苏省特聘教授
教育部新世纪优秀人才
PLoS One、Cur. Genetics编委



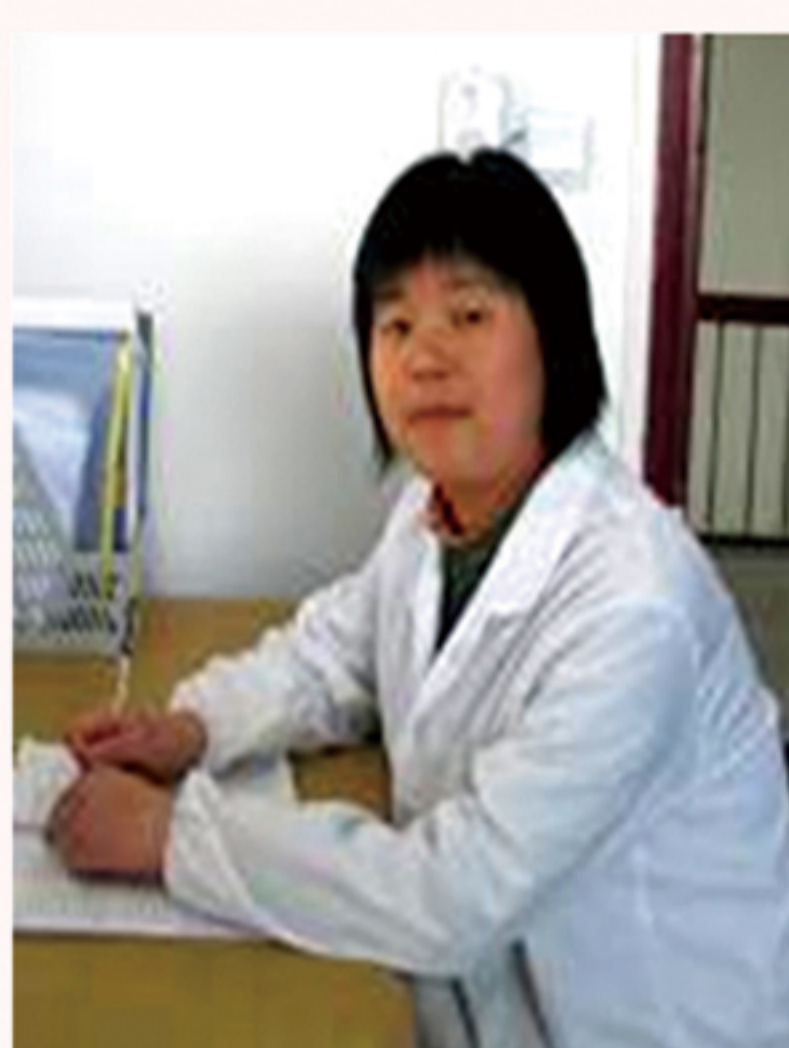
董莎萌 教授
国家优秀青年基金获得者
钟山学术新秀获得者



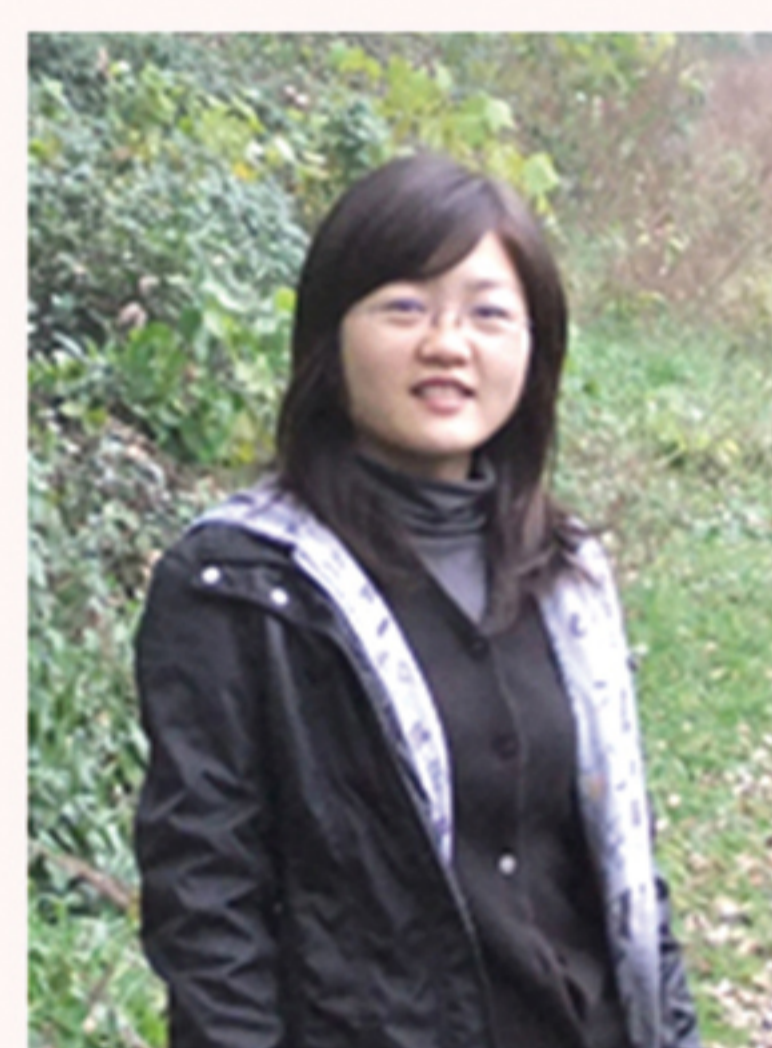
张海峰 副教授
江苏青蓝工程优秀骨干
钟山学术新秀获得者



叶文武 讲师



杨悦 实验师



王晓莉 科辅



杭宇 实验师

人才培养

已培养博士研究生45人、硕士研究生66人。其中1人获得全国百篇优秀博士学位论文奖、1人获提名奖，3人获省优博，2人获省优硕。多名毕业生在美国、英国、荷兰等地开展博士或博士后研究。



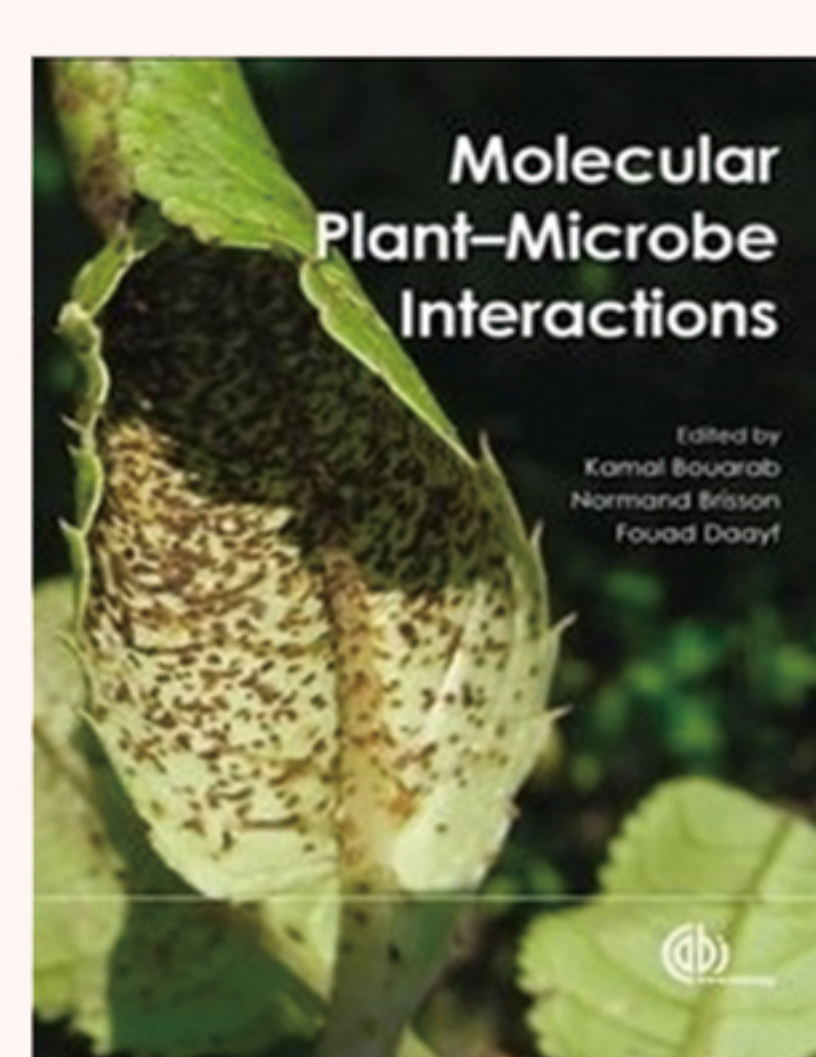
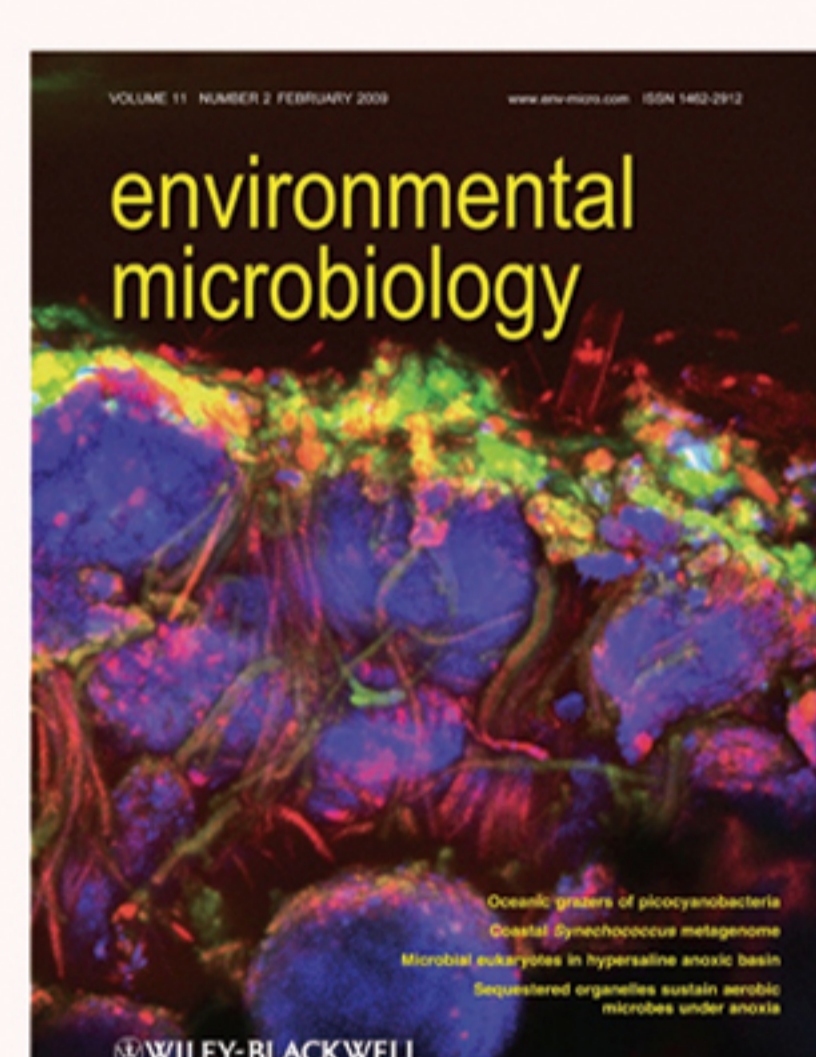
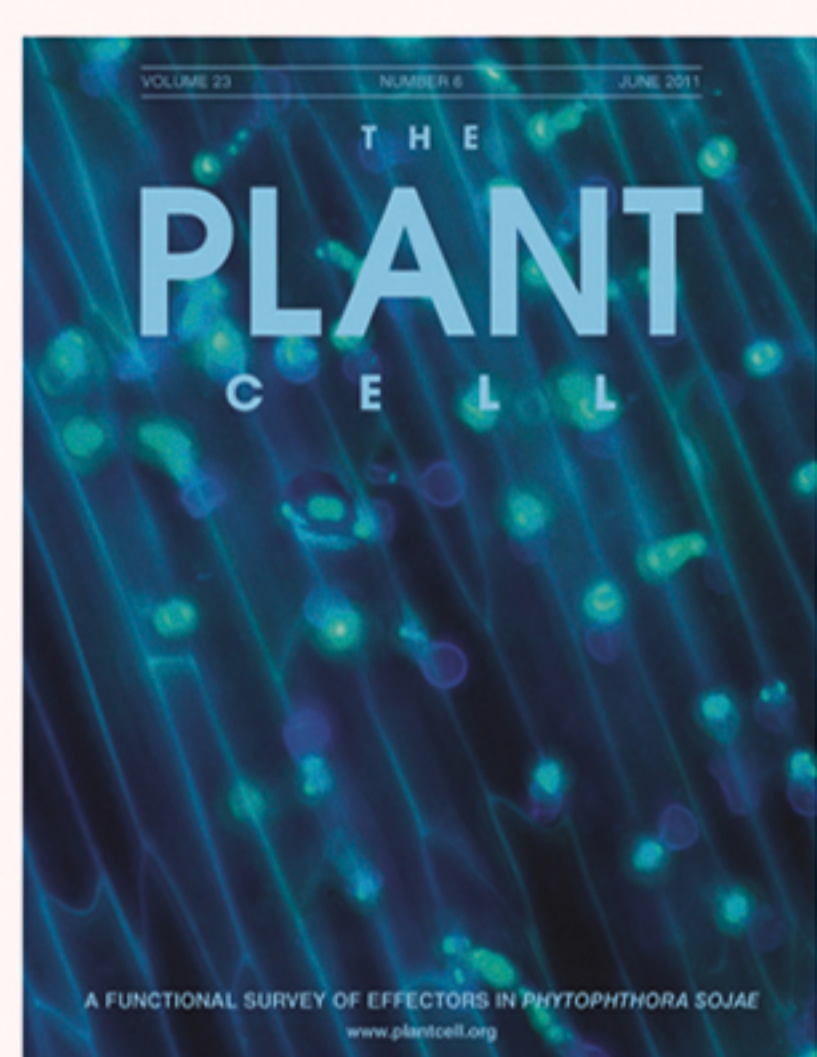


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研究成果

获教育部科技成果一、二等奖各1项，获授权发明专利12项，编写专著1部。在Science、Nature Genetics、Plant Cell、PLoS Pathogens、New Phytologist、Molecular Microbiology、Environmental Microbiology、Molecular Plant-Microbe Interaction、Eukaryotic Cell、Molecular Plant Pathology、Fungal Genetic Biology、Phytopathology等国际著名刊物发表SCI研究论文100多篇。

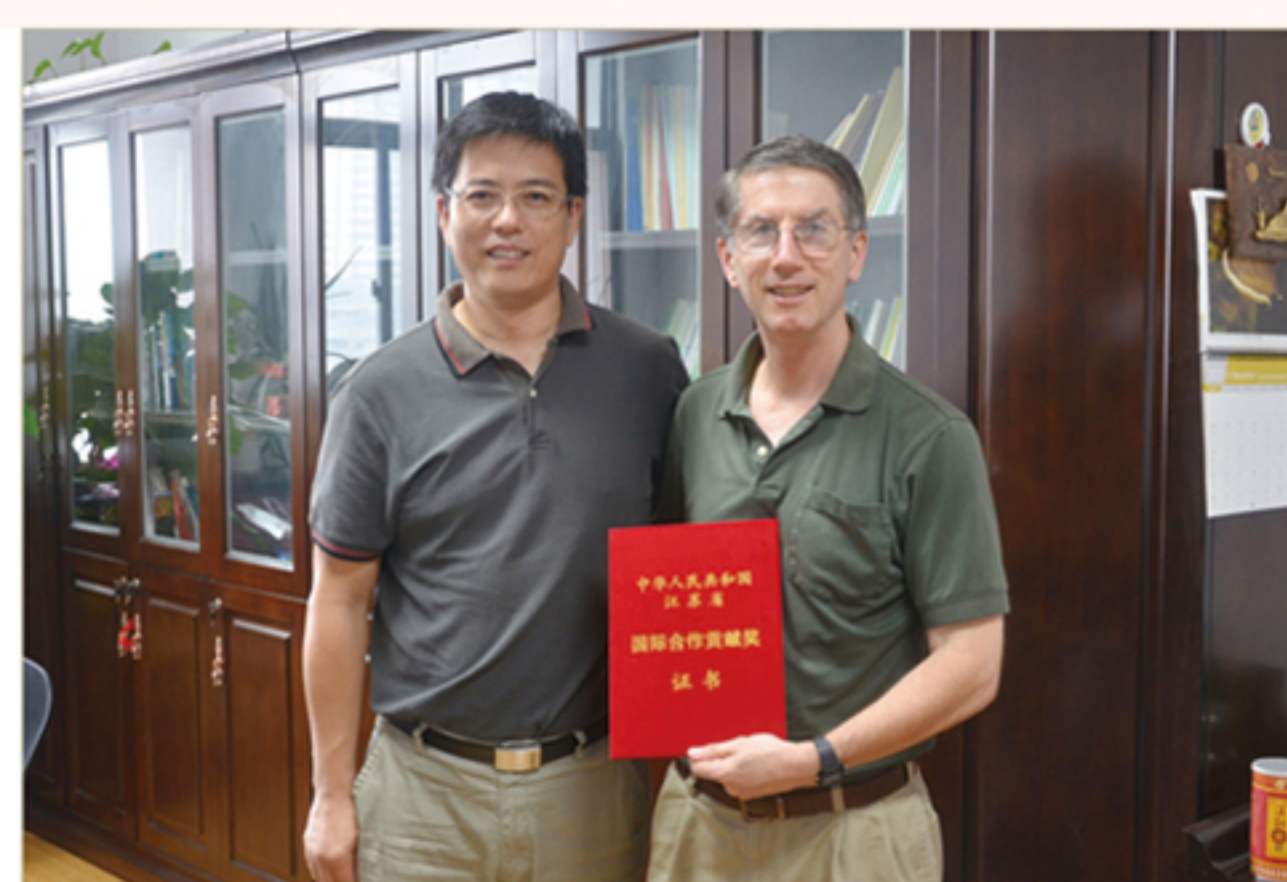


承担项目

- ◆ 农业公益性行业科研专项（201303018）2013-2017
- ◆ 国家 973计划子课题（2009CB119200）2010-2014
- ◆ 国家 863计划课题（2012AA101501）2012-2015
- ◆ 国家杰出青年基金项目-植物病原卵菌，2013-2017
- ◆ 国家杰出青年基金项目-植物病理学，2014-2018
- ◆ 国家优秀青年基金项目-植物病原卵菌学，2015-2019
- ◆ 中荷政府国际科技合作项目（2013DFG32030）2013-2015
- ◆ 国家大豆产业技术体系岗位科学家，2007-2015
- ◆ 国家自然科学基金重点项目（31430073）2015-2019
- ◆ 国家自然科学基金面上项目（31271998）2013-2016
- ◆ 国家自然科学基金面上项目（31471736）2015-2018
- ◆ 国家自然科学基金青年基金项目（31201471）2013-2015
- ◆ 国家自然科学基金青年基金项目（31401688）2015-2017
- ◆ 江苏省自然科学基金（BK2012362）2012-2015
- ◆ 江苏省自然科学基金（BK20140698）2014-2017

国际合作与交流

聘请了美国俄勒冈州立大学Brett Tyler博士和美国加州大学河滨分校Wenbo Ma博士为实验室兼职教授，并长期与荷兰瓦赫宁根大学Francine Govers、英国The Sainsbury Lab的Sophien Kamoun、加拿大农业部南方研究中心Mark Gijzen和美国路易斯安那州立大学健康科学中心Ping Wang等实验室保持着密切的合作关系。





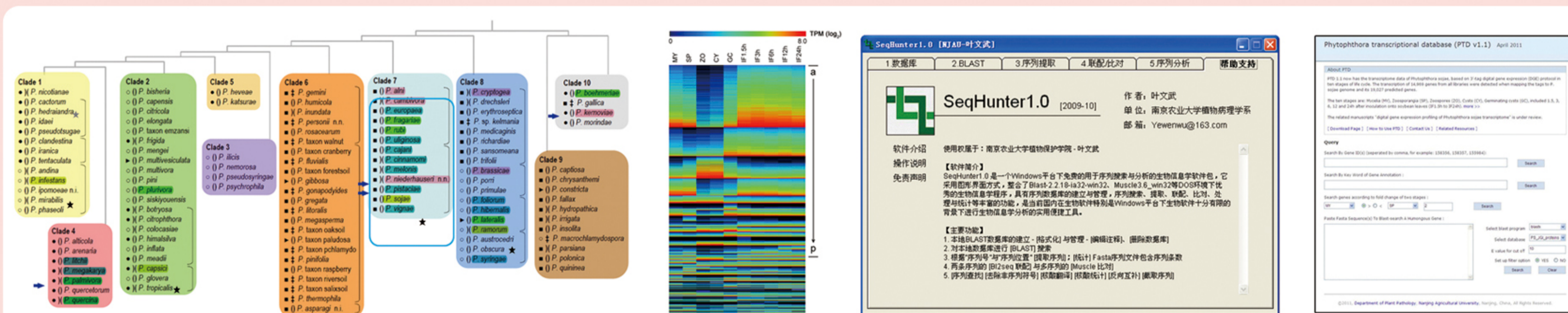
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OOMYCETE MOLECULAR GENETICS AND PLANT DISEASE CONTROL

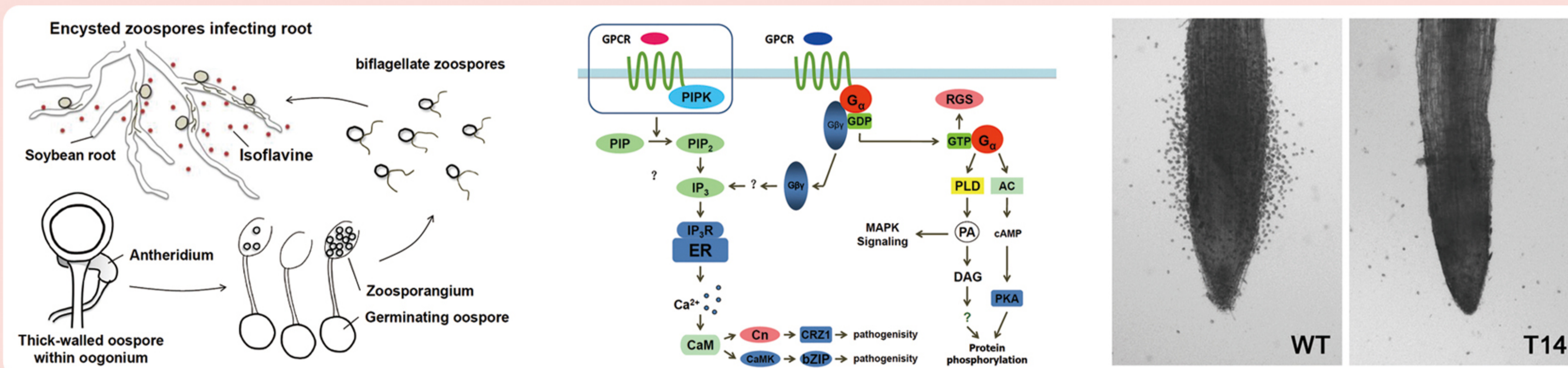
Oomycetes falls within the kingdom Stramenopiles and form a distinct phylogenetic lineage of fungus-like eukaryotic microorganisms. Many oomycetes species are economically important, aggressive plant pathogens, such as the *Phytophthora*, *Pythium*, and downy mildews. Our lab has focused on the oomycete plant diseases for over 30 years. We study the *Phytophthora* pathogens of soybean, cotton, and potato on taxonomy, biology, genetics, pathology, and disease control technology, and have set up the national information network of *Phytophthora* disease, Asia's largest *Phytophthora* strain preservation center, and oomycete omics database. Recently, we achieved a series of important advances in *Phytophthora* functional genomics, molecular mechanism of *Phytophthora*-plant interaction, and plant disease control technologies.

1. Genomics and Bioinformatics Platform (Molecular Plant-Microbe Interaction, 2011; BMC genomics, 2013)



Large scale genomic, transcriptomic, and proteomic data were generated and analyzed, and associated software and database were developed.

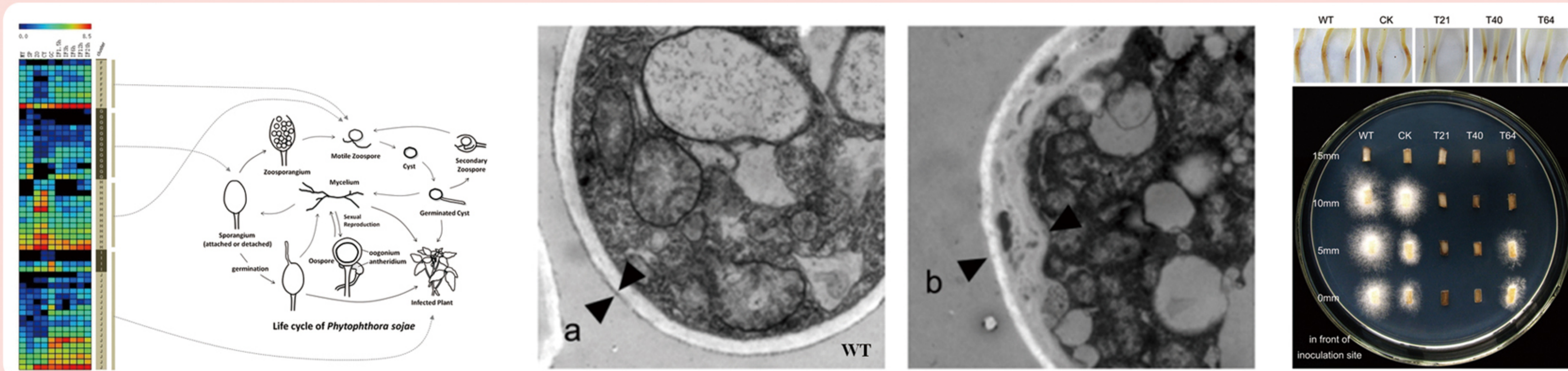
2. Molecular Mechanisms of *Phytophthora* Chemotaxis to host (Mol. Microbiol., 2013; Eukaryotic Cell, 2008)



GPCR-PIPK, G protein alpha-subunit 1 and its interacting protein PsHint1 are involved in chemotaxis to soybean isoflavones.

3. Transcriptional regulation of *Phytophthora* virulence factors

(Environmental Microbiology, 2014; Molecular Plant-Microbe Interaction, 2008; Molecular Plant Path., 2014; FGB, 2013)



Transcription regulators including many protein kinases and transcription factors have been identified.

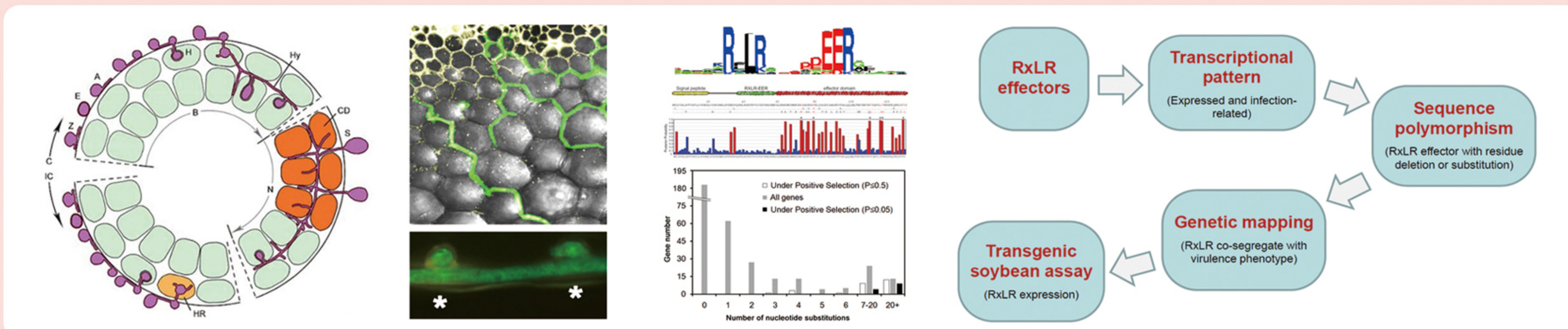


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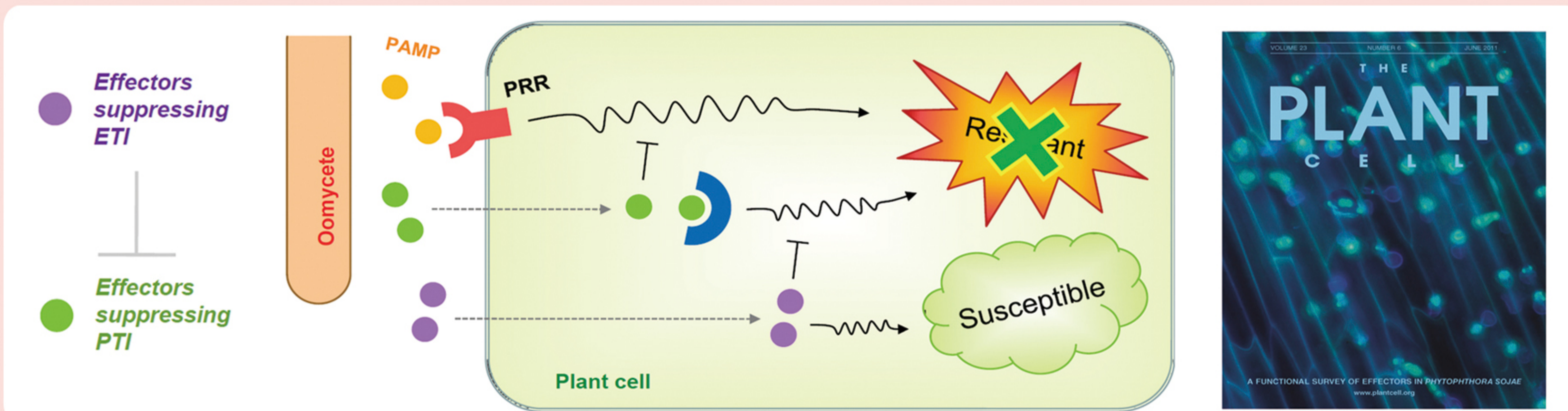
OOMYCETE MOLECULAR GENETICS AND PLANT DISEASE CONTROL

4. Virulence Variation and Avirulence Genes Identification (PLoS Pathogens, 2011; MPMI, 2013; Mol. Plant Path., 2012)



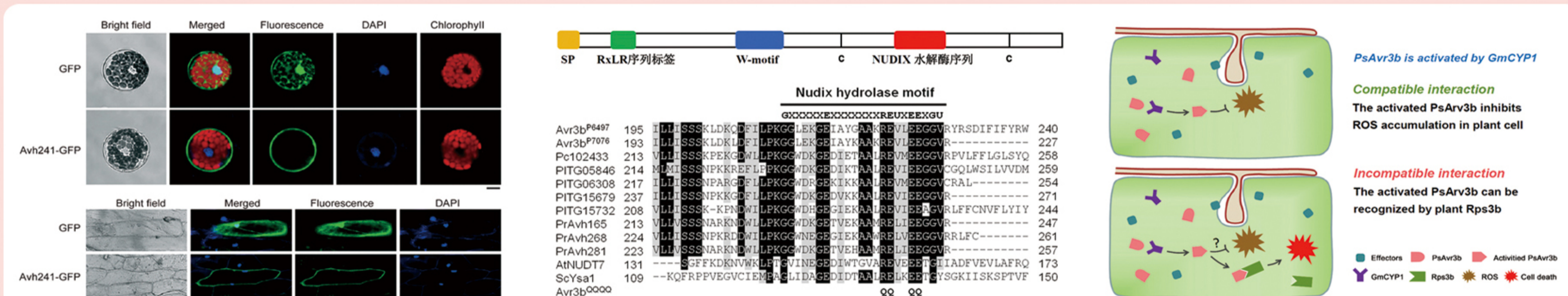
Two new avirulence genes, *Avr1d* and *Avr3b*, were identified from *Phytophthora sojae*, using a novel strategy.

5. Transcriptional Programming & Functional Interactions of *Phytophthora* Effectors (Plant cell, 2011)



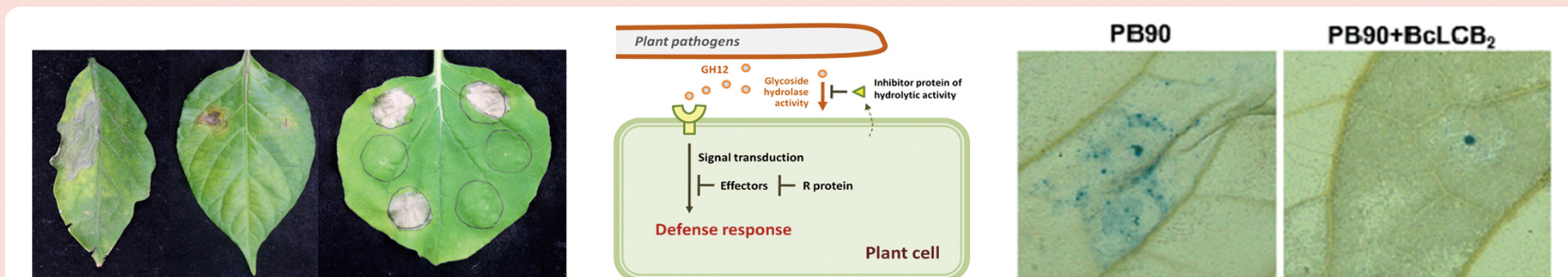
Two classes of RxLR effectors target different functional branches of the plant defense response. Cover story of The Plant Cell.

6. How do the *Phytophthora* Effectors Impair Plant Immunity? (PLoS Pathogens, 2011; New Phytologist, 2012)



P. sojae Avh241 is recognized by plants dependent on plasma membrane localization and promoting infection independent on the localization; *Avr3b* mimics plant immunity negative regulator; its avirulence and virulence functions are activated by a soybean cyclophilin.

7. Identification of new PAMPs from oomycetes (Plant, Cell and Environment, 2012; New Phytologist, 2009)



A glycoside hydrolase from oomycetes and other plant pathogens can cause widespread, dual plant defense responses.



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大豆有害生物种类与发生危害特点研究

我国大豆病虫害发生面积广、种类复杂、危害严重，是大豆产业发展的主要制约因素之一。本课题组在国家大豆产业技术体系、公益性行业科研专项和国家863计划等项目的资助下，系统开展了我国大豆有害生物的快速检测技术研究，进行了有害生物的种类调查，明确了大豆主要有害生物分布范围，阐明了大豆重要有害生物发生危害特点和演变趋势，为提高我国大豆病虫害的防控水平、保障国家大豆产业的安全提供了植保技术的支撑。

1. 我国大豆病虫害普查与病情监测

田间采样

保守基因序列分析

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440 450 460 470 480
AATGATTCGACGCGGCTTAAATAGGATCTTGAATTAATCGATAGAGAA
AATGATTCGACGCGGCTTAAATAGGATCTTGAATTAATCGATAGAGAA
AATGATTCGACGCGGCTTAAATAGGATCTTGAATTAATCGATAGAGAA
    
```

病原分离与鉴定

致病性测定

<ul style="list-style-type: none"> 尖镰孢菌 (<i>Fusarium oxysporum</i>) 腥黑穗孢菌 (<i>Fusarium proliferatum</i>) 木贼镰孢菌 (<i>Fusarium equiseti</i>) 茄镰孢菌 (<i>Fusarium solani</i>) 大豆疫霉菌 (<i>Phytophthora sojae</i>) 	<ul style="list-style-type: none"> 大豆黑斑病菌 (<i>Alternaria brassicae</i>) 大豆拟茎点种腐病菌 (<i>Phomopsis longicolla</i>) 大豆霜霉病菌 (<i>Peronospora manshurica</i>) 大豆白粉菌 (<i>Erysiphe glycines</i>) 大豆炭疽菌 (<i>Colletotrichum truncatum</i>) 	<ul style="list-style-type: none"> 大豆拟茎点种腐病菌 (<i>Phomopsis longicolla</i>) 大豆菌核病菌 (<i>Sclerotinia sclerotiorum</i>)
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2. 重要植物病原生物学的分子检测技术

Turbidity vs. Reaction time

Concentration	100 ng/μl	10 ng/μl	1 ng/μl	100 pg/μl	10 pg/μl	1 pg/μl	100 fg/μl	10 fg/μl
Reaction time (min)	~40	~45	~50	~55	~60	~65	~70	~75

Agarose Gel Electrophoresis

M: 1500bp, 500bp

Lanes: 100ng, 10ng, 1ng, 100pg, 10pg, 1pg, 100fg, 10fg

(Plant pathology, 2012; FEMS Micro. Letters, 2012)

3. 通过宣传册、讲座、在线信息平台及微信群等构建多渠道的作物病虫害宣传与交流平台

主要农作物病虫害识别手册

作物病虫害信息平台

大豆病虫害信息平台

大豆病虫害信息平台 (SOYBEAN PEST INFORMATION SYSTEM)

该平台提供大豆病虫害的识别、防治、预警等信息，旨在提高大豆生产者的病虫害防治水平，保障大豆产业的安全。



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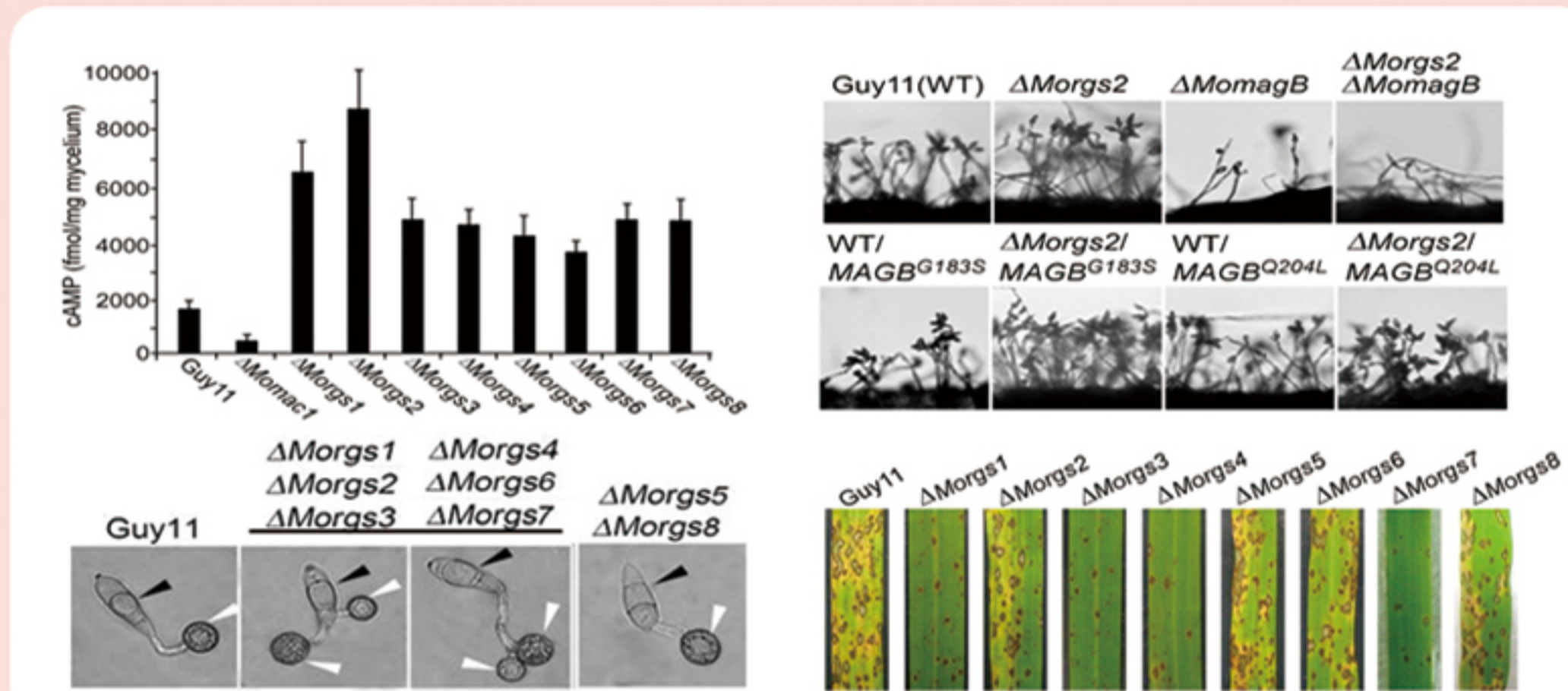
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PATHOGENESIS OF THE RICE BLAST FUNGUS

The plant pathogenic fungus *Magnaporth oryzae* is a causal agent of the rice blast disease and an important model for the understanding of molecular development and pathogenicity in lower eukaryotic organisms. Discovering of the mechanisms that regulate various developmental and pathological processes in the rice blast fungus will not only provide insights into the underlying molecular mechanism of the pathogenesis, but also strategies to the development of new disease management and control. For the past ten years, our group has been studying infection-related morphogenesis in *M. oryzae* and achieved several critical and significant results.

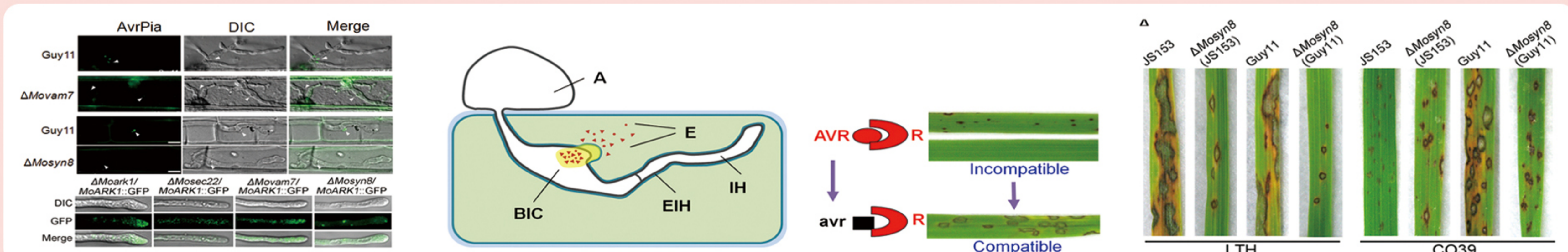
1. Regulatory Mechanisms of the G protein Signaling Pathway

- ① Eight RGS and RGS-like proteins were characterized in *M. oryzae*, which has been the largest number of RGS proteins ever described from a single fungal organism.
- ② RGS and RGS-like proteins are involved in a complex process to control asexual/sexual development, appressorium differentiation, penetration, and pathogenicity.
- ③ RGS proteins play a role in regulation of amino acid metabolism that is critical for growth and pathogenicity.



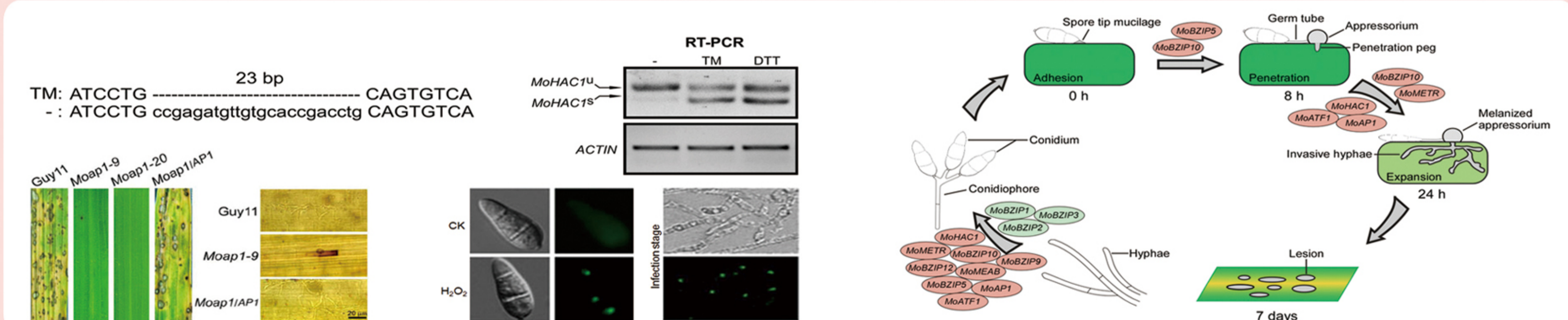
2. Endocytosis and Secretion Mediated by Vesicle Trafficking

- ① SNARE proteins mediate intracellular vesicle fusion among the eukaryotic cells.
- ② SNARE proteins MoSec22, MoVam7 and MoSyn8 play pleiotropic roles including avirulence effector secretion.
- ③ MoSec22, MoVam7 and MoSyn8 modulate vesicle transport to control the localization pattern of the MoArk1 kinase.
- ④ MoSyn8 mediated virulence attenuation follows gene-for-gene hypothesis.



3. System-wide Characterization of the bZIP Transcription Factor Proteins

- ① The bZIP transcription factor family is involved in differentiation and pathogenicity through either shared or distinct mechanisms.
- ② MoAp1 modulates homeostasis of the intracellular ROS to control the growth and development.
- ③ MoAp1 acts as a redox sensor to suppress the plant defense response induced by ROS during the pathogen and host interaction.
- ④ MoHac1 regulates the ER-stress response through a conserved UPR pathway.



Publications

Guo, M., et al. PLoS Pathogens, 2011, 7: e1001302.
Zhang, H., et al. PLoS Pathogens, 2011, 7: e1002450.
Chen, Y., et al. Environmental Microbiology, 2014, 16: 788.
Tang, W., et al. Environmental Microbiology, 2014.

Zhang, H., et al. Proteomics, 2014, 14: 2508.
Teng, W., et al. Journal of Experimental Botany, 2014, 65: 2483.
Wang, J., et al. Molecular Plant Pathology, 2013, 14: 470.
Zhang, H., et al. Molecular Plant-Microbe Interaction, 2014, 27: 446.
Guo, M., et al. Molecular Plant-Microbe Interaction, 2011, 23: 1053.