

# 列当寄生过程中微生物群落的作用 及其化学调节机制

席娇<sup>1#</sup>, 雷蓓蕾<sup>1,2#</sup>, 刘永鑫<sup>3</sup>, 丁赞博<sup>1</sup>, 刘佳茜<sup>1</sup>, 徐腾起<sup>1</sup>, 侯丽君<sup>4</sup>, 韩思琦<sup>1</sup>,  
钱勋<sup>5</sup>, 马永清<sup>6</sup>, 薛泉宏<sup>7</sup>, 高锦明<sup>8</sup>, 谷洁<sup>5\*</sup>, James M. Tiedje<sup>5,9\*</sup>, 林雁冰<sup>1\*</sup>

<sup>1</sup>西北农林科技大学生命科学学院  
<sup>2</sup>西北农林科技大学旱区作物逆境生物学国家重点实验室  
<sup>3</sup>中科院遗传所



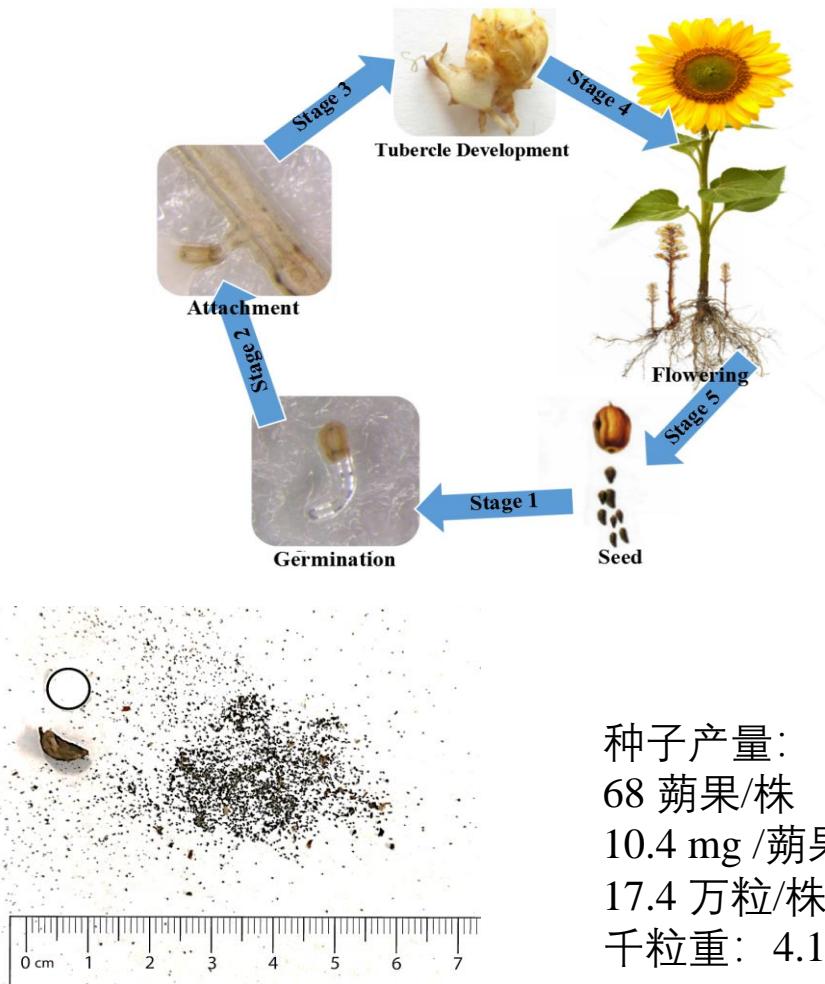
Jiao Xi, Beilei Lei, Yong-Xin Liu, Zanbo Ding, Jiaxi Liu, Tengqi Xu, Lijun Hou, et al. 2022. Microbial community roles and chemical mechanisms in the parasitic development of *Orobanche cumana*. *iMeta* e31. <https://doi.org/10.1002/imt2.31>

# 背景介绍



Jiao Xi, Beilei Lei, Yong-Xin Liu, Zanbo Ding, Jiaxi Liu, Tengqi Xu, Lijun Hou, et al. 2022. Microbial community roles and chemical mechanisms in the parasitic development of *Orobanche cumana*. *iMeta* e31. <https://doi.org/10.1002/imt2.31>

# 背景介绍



种子产量:  
68 蒴果/株  
10.4 mg /蒴果  
17.4 万粒/株  
千粒重: 4.14 mg



化学与生物制剂防



作物轮作

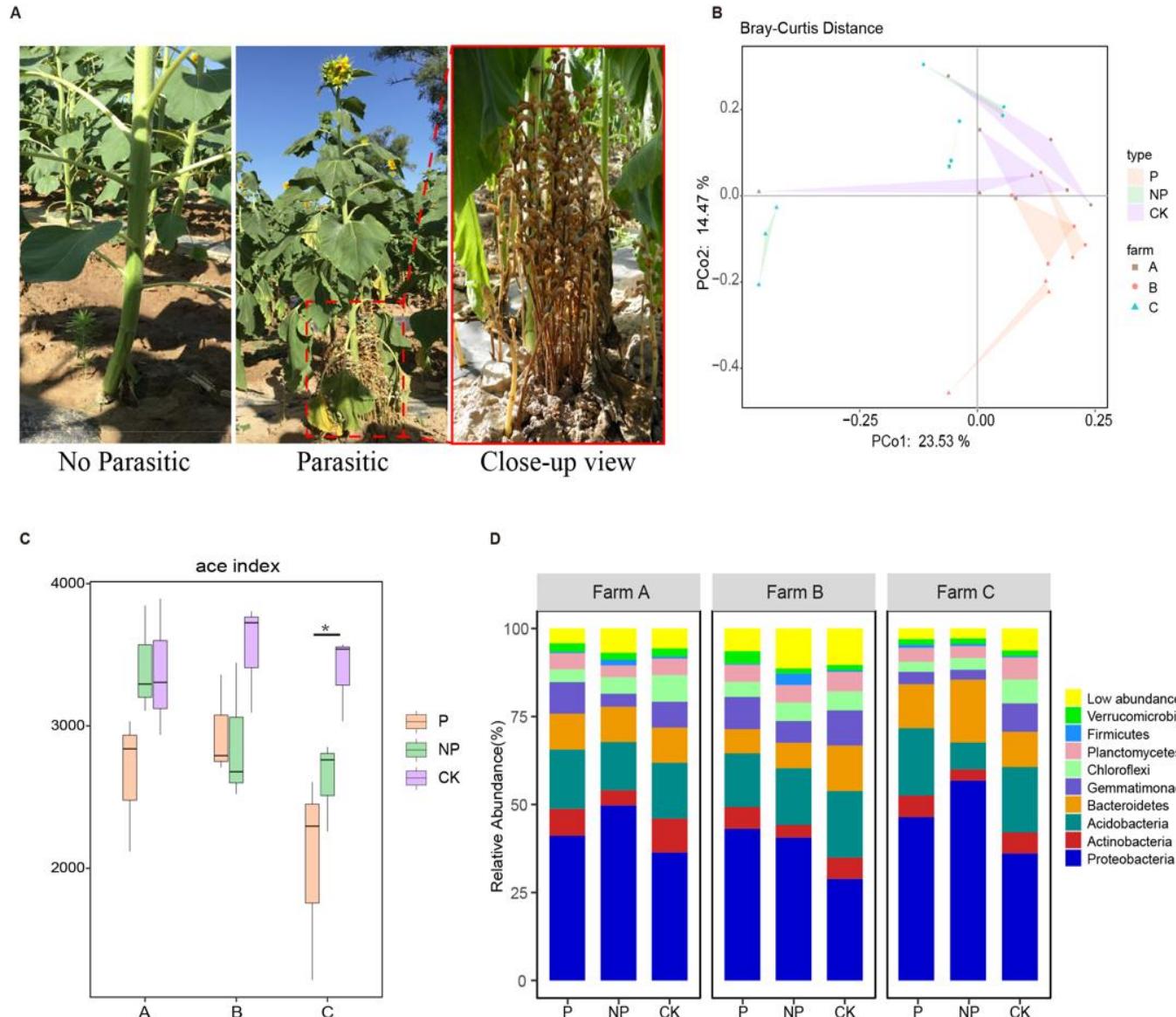


人工拔除



抗性品种培育

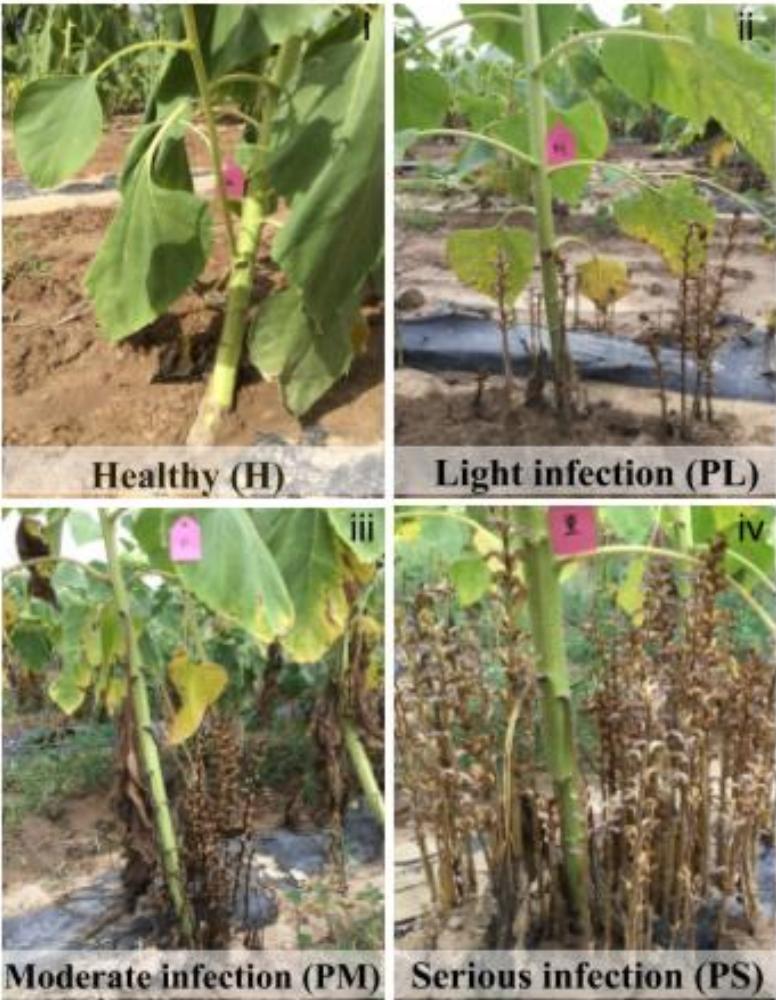
# 列当寄生影响微生物群落变化



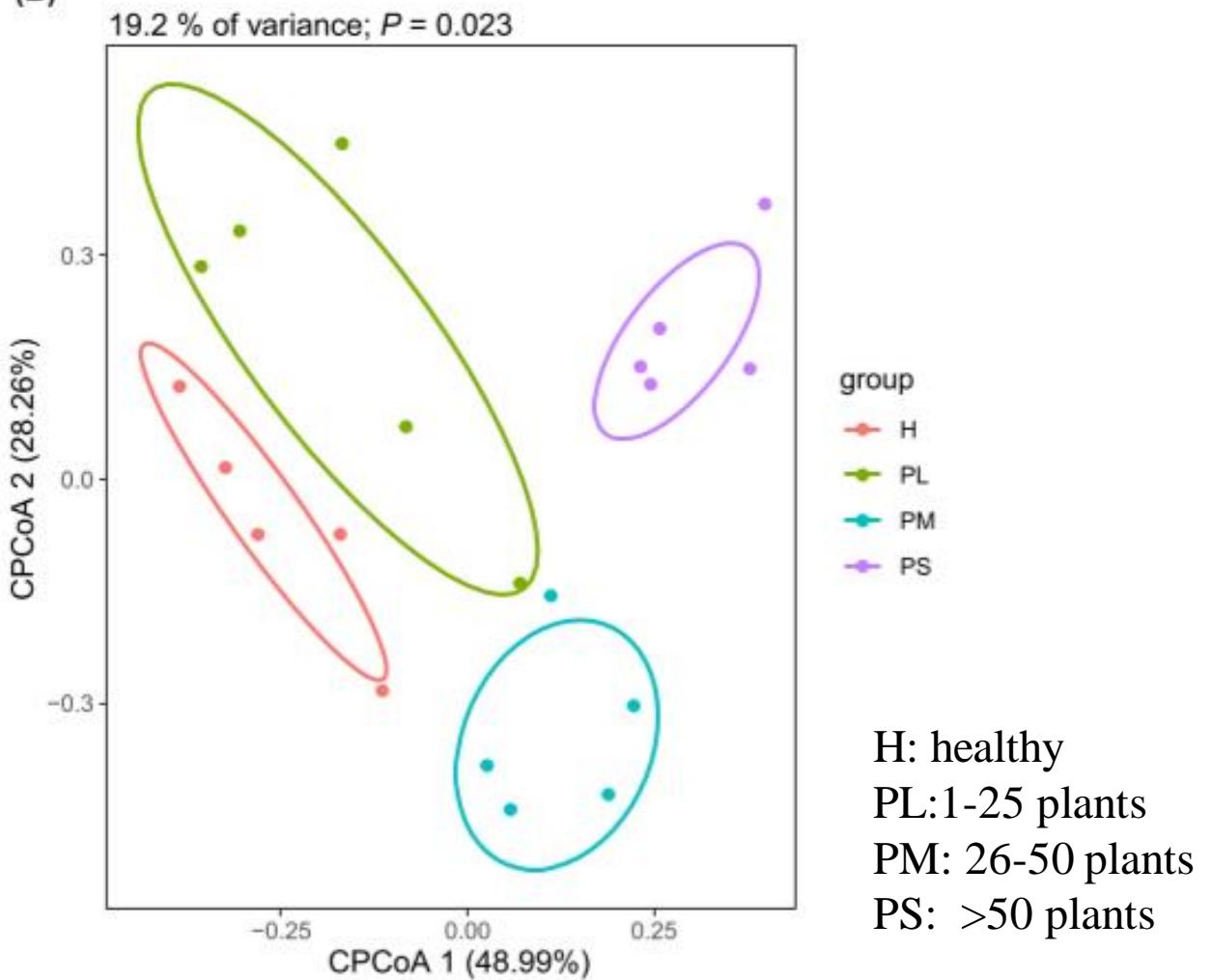
Jiao Xi, Beilei Lei, Yong-Xin Liu, Zanbo Ding, Jiaxi Liu, Tengqi Xu, Lijun Hou, et al. 2022. Microbial community roles and chemical mechanisms in the parasitic development of *Orobanche cumana*. *iMeta* e31. <https://doi.org/10.1002/imt2.31>

# 列当寄生影响微生物群落变化

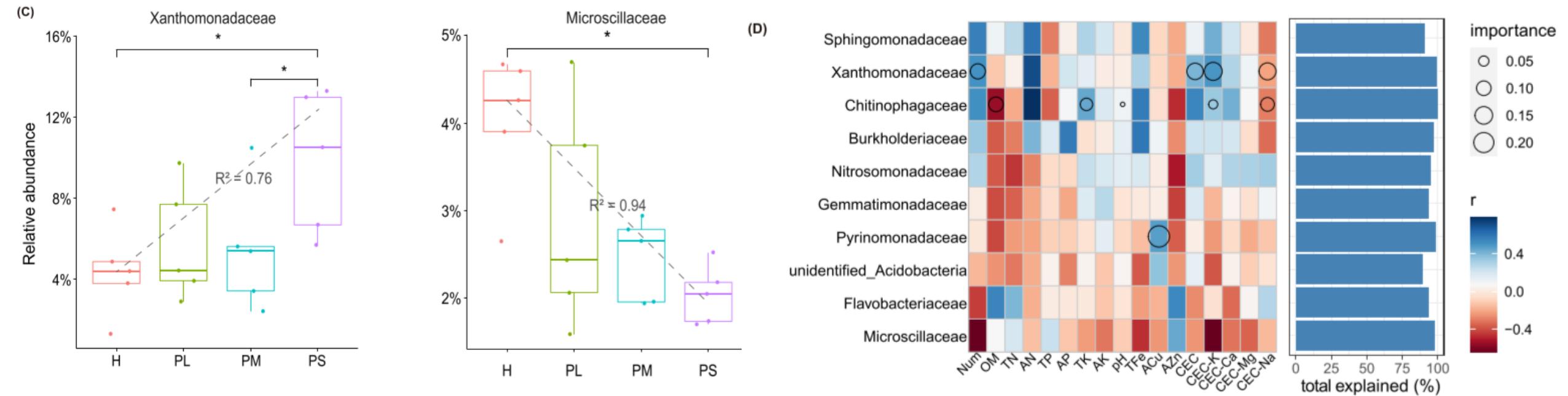
(A)



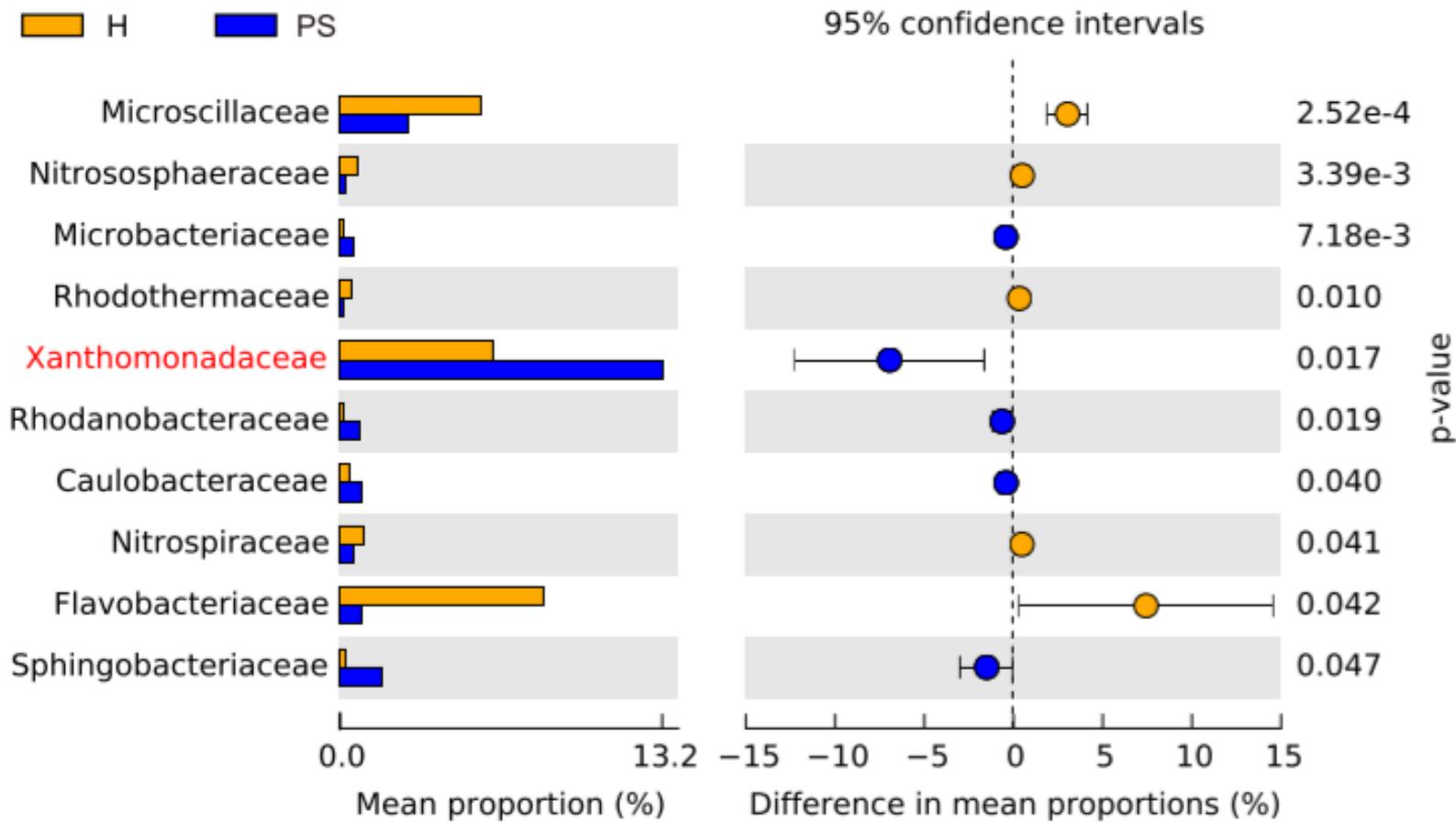
(B)



# 列当寄生影响微生物群落变化

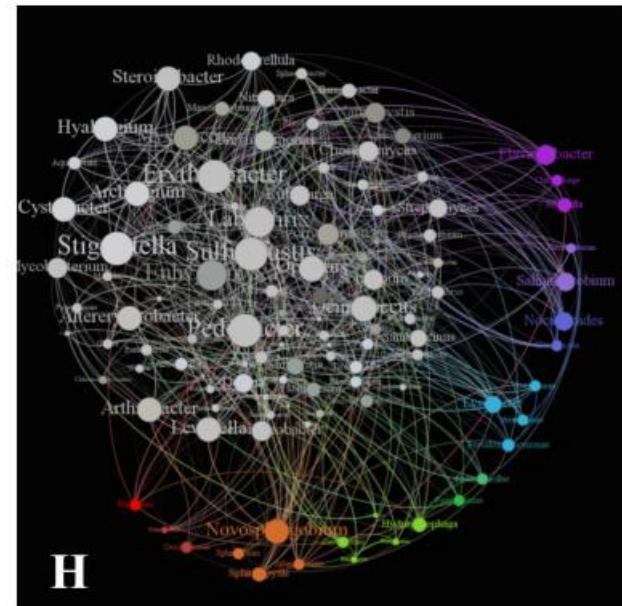


# 列当寄生影响微生物群落变化



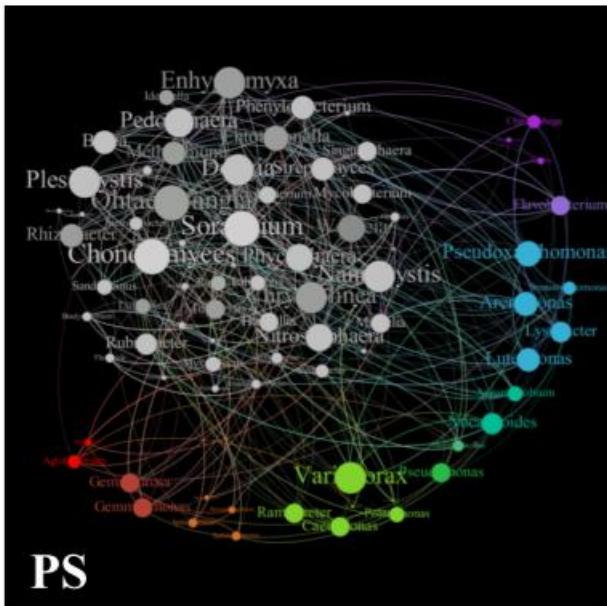
# 微生物群落功能分析与biomarker预测

(A)



**Family**

Chitinophagaceae	Comamonadaceae
Flavobacteriaceae	Sphingomonadaceae
Nocardioidaceae	Gemmimonadaceae
Xanthomonadaceae	Rhizobiaceae
Methylophilaceae	
Pseudomonadaceae	Others

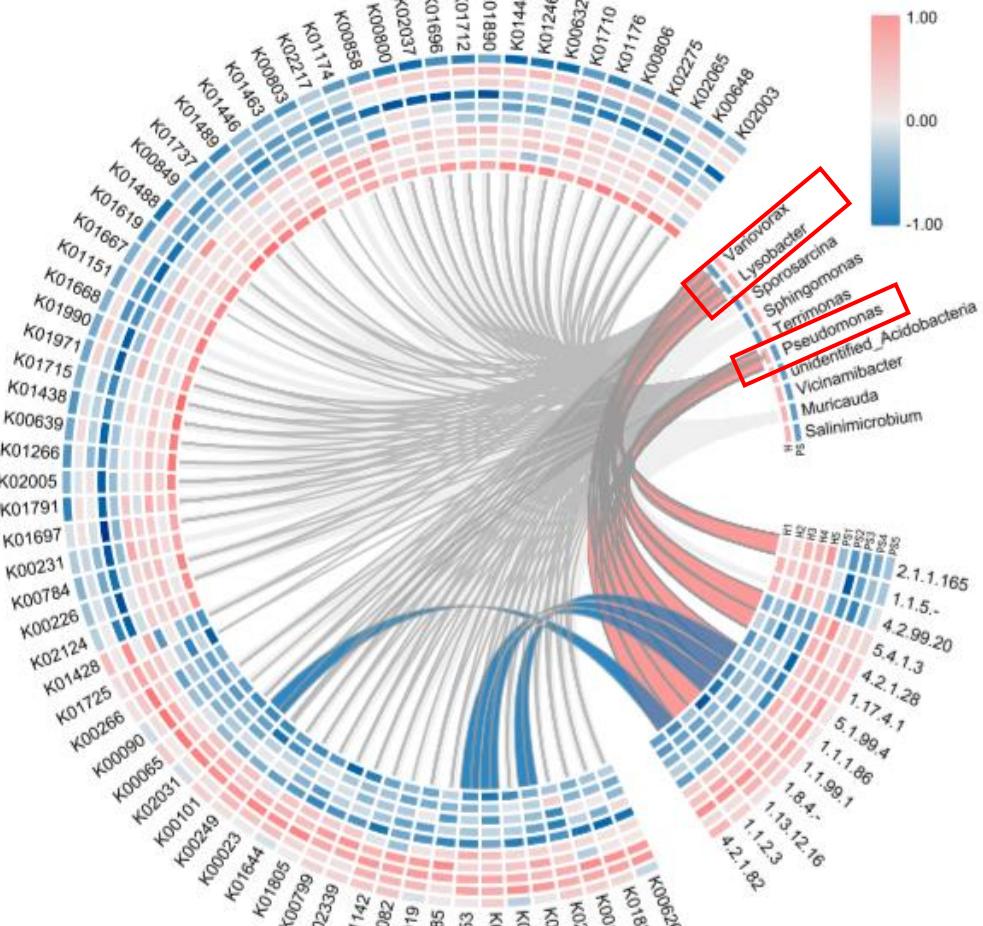


Co-occurrence network 相关参数

Settings	H	PS
Nodes	117	82
Edges	627	341
Type	Undirected Graph	Undirected Graph
Average Degree	10.72	8.32
Average Weighted Degree	1.57	1.15
Network Diameter	9	8
Network Radius	5	5
Network Overview	Average Path length	3.68
	Graph Density	0.09
	Modularity	3.91
	Modularity with resolution	3.64
	Number of Communities	7
	Number of Weakly Connected Con	1
Average Clustering Coefficient	0.58	0.46
Node Overview	Total triangles	581
	Sum change	0.011

# 微生物群落功能分析与biomarker预测

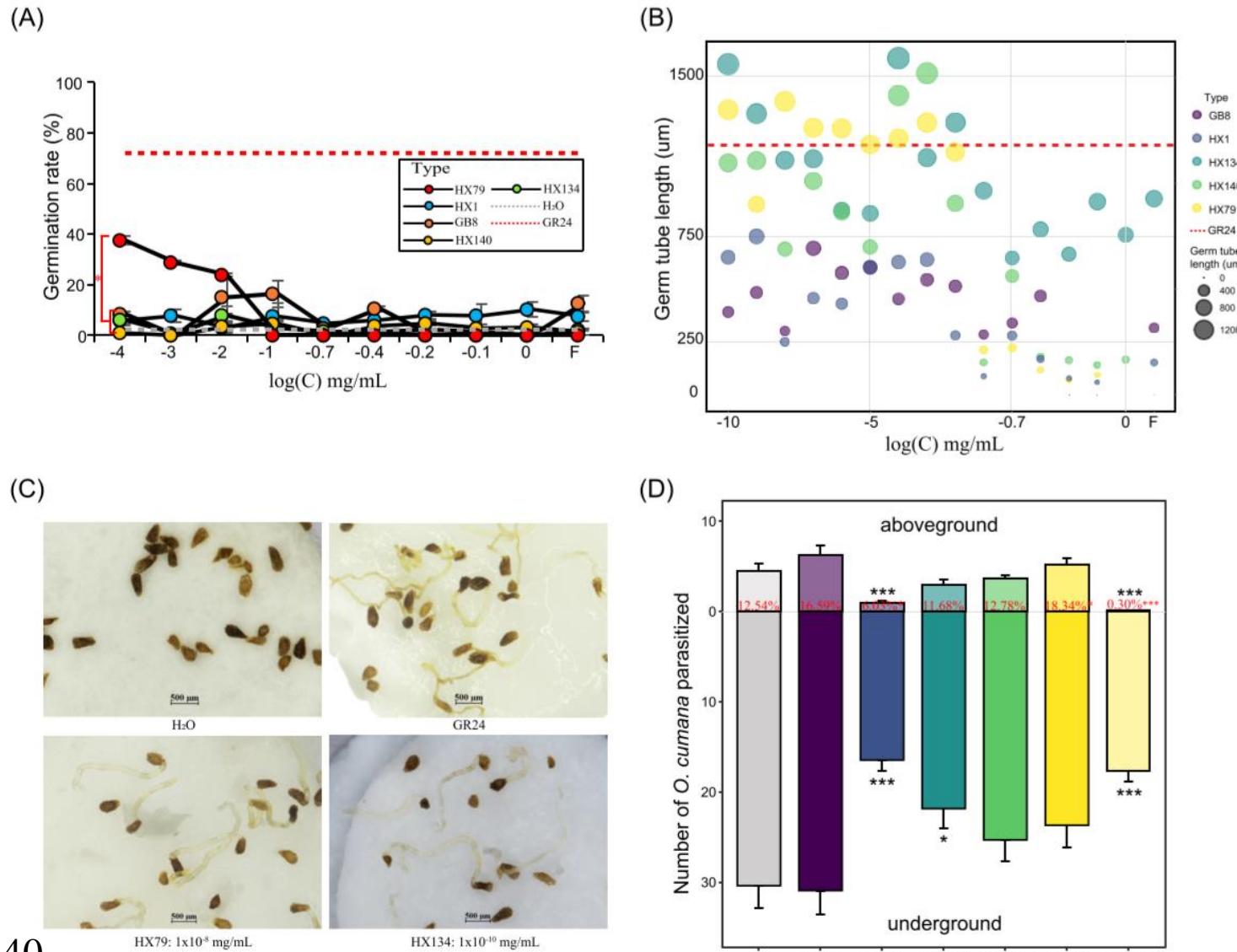
(B)



KO Number	KO Definition
K00101	L-lactate dehydrogenase (cytochrome)
K00053	ketol-acid reductoisomerase
K00108	choline dehydrogenase
K01796	alpha-methylacyl-CoA racemase

EC	Pathway Level 2
1.1.2.3	Carbohydrate metabolism
1.1.1.86	Amino acid metabolism
1.1.99.1	Amino acid metabolism
5.1.99.4	Lipid metabolism

# 细菌对列当萌发和寄生的影响及其化学机制



*Lysobacter*: HX79

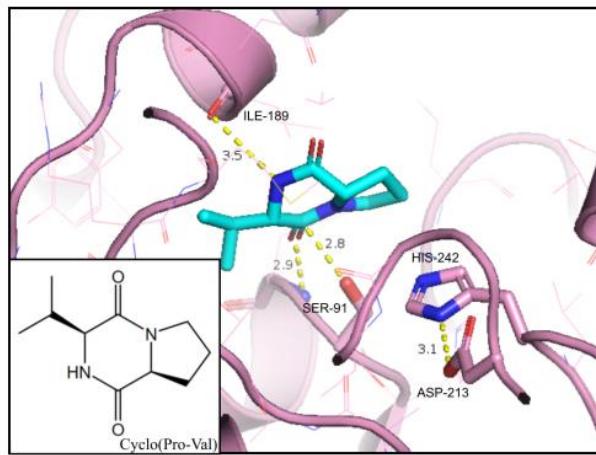
*Variovorax*: GB8

*Pseudomonas*: HX1, HX134, HX140

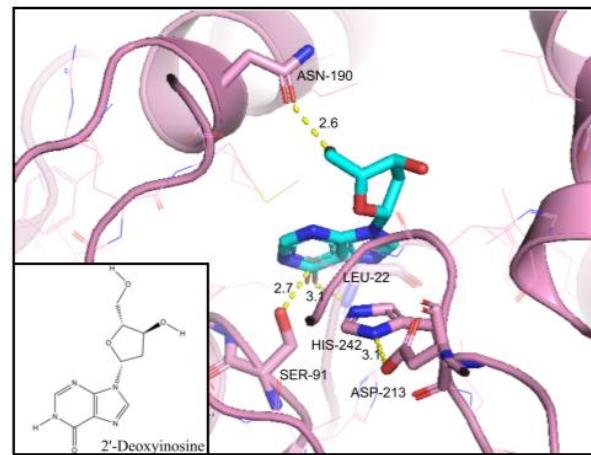
Jiao Xi, Beilei Lei, Yong-Xin Liu, Zanbo Ding, Jiaxi Liu, Tengqi Xu, Lijun Hou, et al. 2022. Microbial community roles and chemical mechanisms in the parasitic development of *Orobanche cumana*. *iMeta* e31. <https://doi.org/10.1002/imt2.31>

# 细菌对列当萌发和寄生的影响及其化学机制

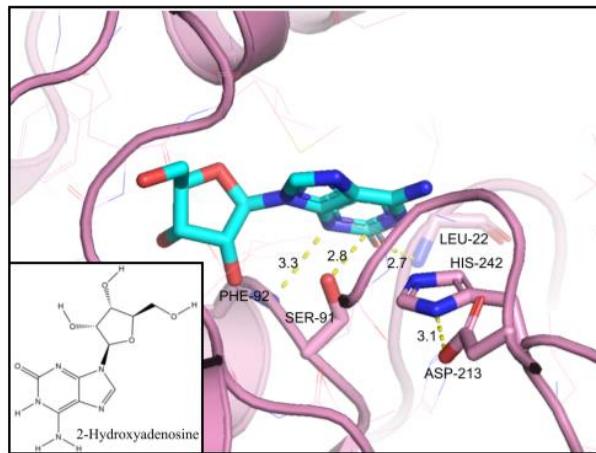
(A)



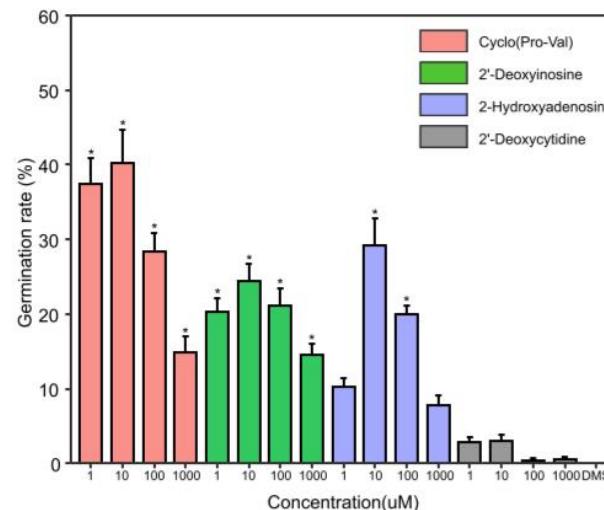
(B)



(C)



(D)



# 结论

1. 证明了向日葵根际微生物是可以调控列当的寄生，并且找到了两株细菌，一株是可以抑制列当萌发的假单胞菌HX1，另一株是可以促进列当萌发的溶杆菌HX79，并且它可以作为列当自杀萌发诱导剂，在种植向日葵前一个月使用，可以降低土壤中列当种子库含量，使后续作物生长时，减少寄生。
2. 通过建立的分子结合模型，成功预测出三种化合物对列当种子具有萌发活性。
3. 我们的研究策略也适用于其他寄生性杂草，如瓜列当等植物。



“*iMeta*”是由威立、肠菌分会和本领域数百位华人科学家合作出版的开放获取期刊，主编由中科院微生物所刘双江研究员和荷兰格罗宁根大学傅静远教授担任。目的是发表原创研究、方法和综述以促进宏基因组学、微生物组和生物信息学发展。目标是发表前10%(IF > 15)的高影响力论文。期刊特色包括视频投稿、可重复分析、图片打磨、青年编委、前3年免出版费、50万用户的社交媒体宣传等。2022年2月正式创刊发行！



主页: <http://www.imeta.science>

出版社: <https://onlinelibrary.wiley.com/journal/2770596x>



投稿: <https://mc.manuscriptcentral.com/imeta>



[office@imeta.science](mailto:office@imeta.science)



[iMeta](#)

