

# Microbial community roles and chemical mechanisms in the parasitic development of *Orobanche cumana*

Jiao Xi<sup>1#</sup>, Beilei Lei<sup>1,2#</sup>, Yong-Xin Liu<sup>3</sup>, Zanbo Ding<sup>1</sup>, Jiayi Liu<sup>1</sup>, Tengqi Xu<sup>1</sup>,  
Lijun Hou<sup>4</sup>, Siqi Han<sup>1</sup>, Xun Qian<sup>5</sup>, Yongqing Ma<sup>6</sup>, Quanhong Xue<sup>7</sup>,  
Jinming Gao<sup>8</sup>, Jie Gu<sup>5\*</sup>, James M. Tiedje<sup>5,9\*</sup>, Yanbing Lin<sup>1\*</sup>

<sup>1</sup>College of Life Sciences, Northwest A&F University, Shaanxi, China

<sup>2</sup>State Key Laboratory of Crop Stress Biology for Arid Areas, Northwest A&F University, Shaanxi, China

<sup>3</sup>Institute of Genetics and Developmental Biology, Chinese Academy of Sciences, Beijing, China



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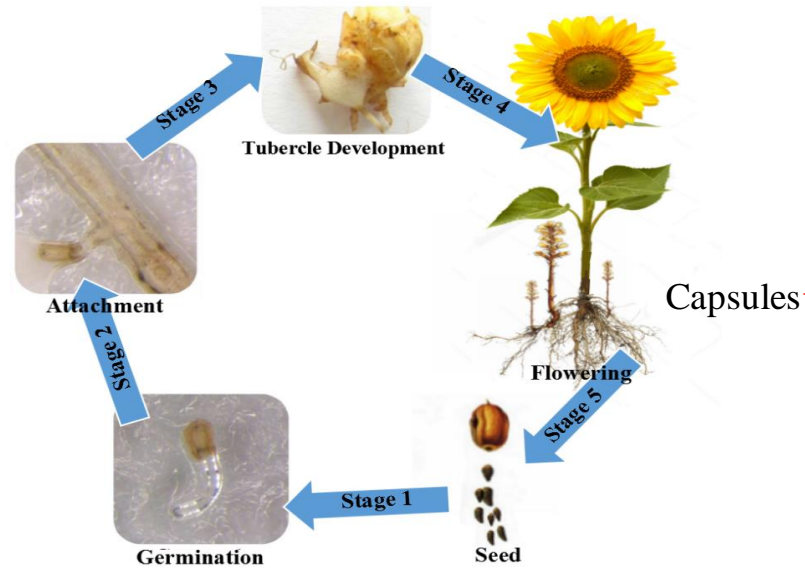
# Introduction



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# Introduction



Capsules

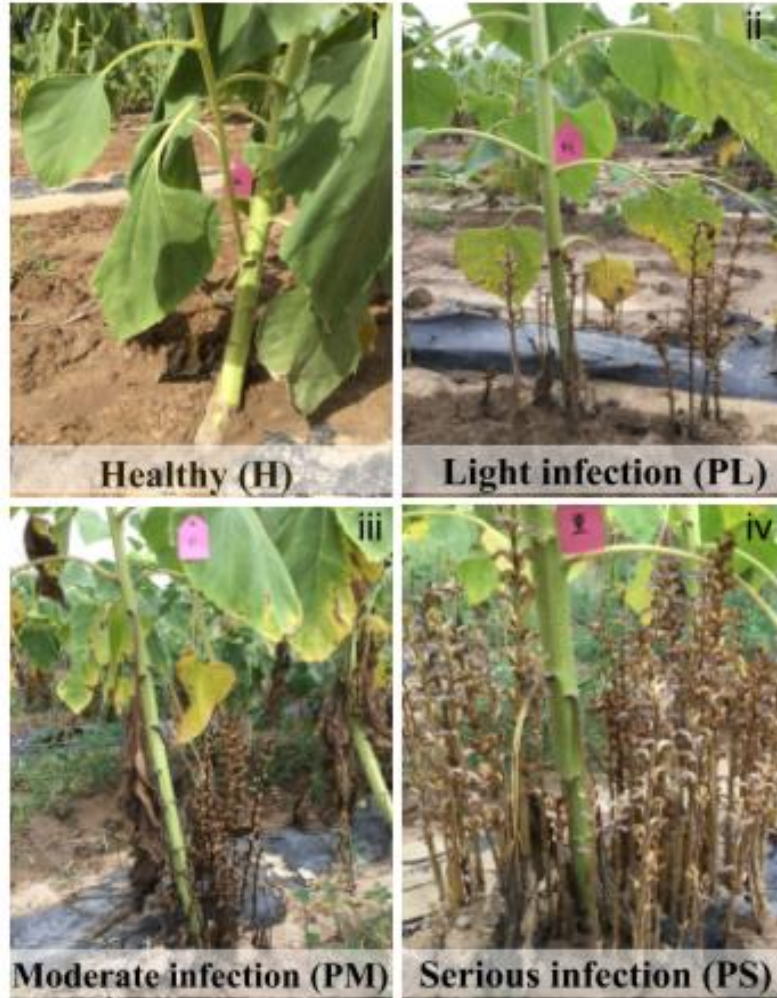


Output 68 capsules/plant,  
1000-grains weight: 4.14 mg  
totally 174,000 seeds

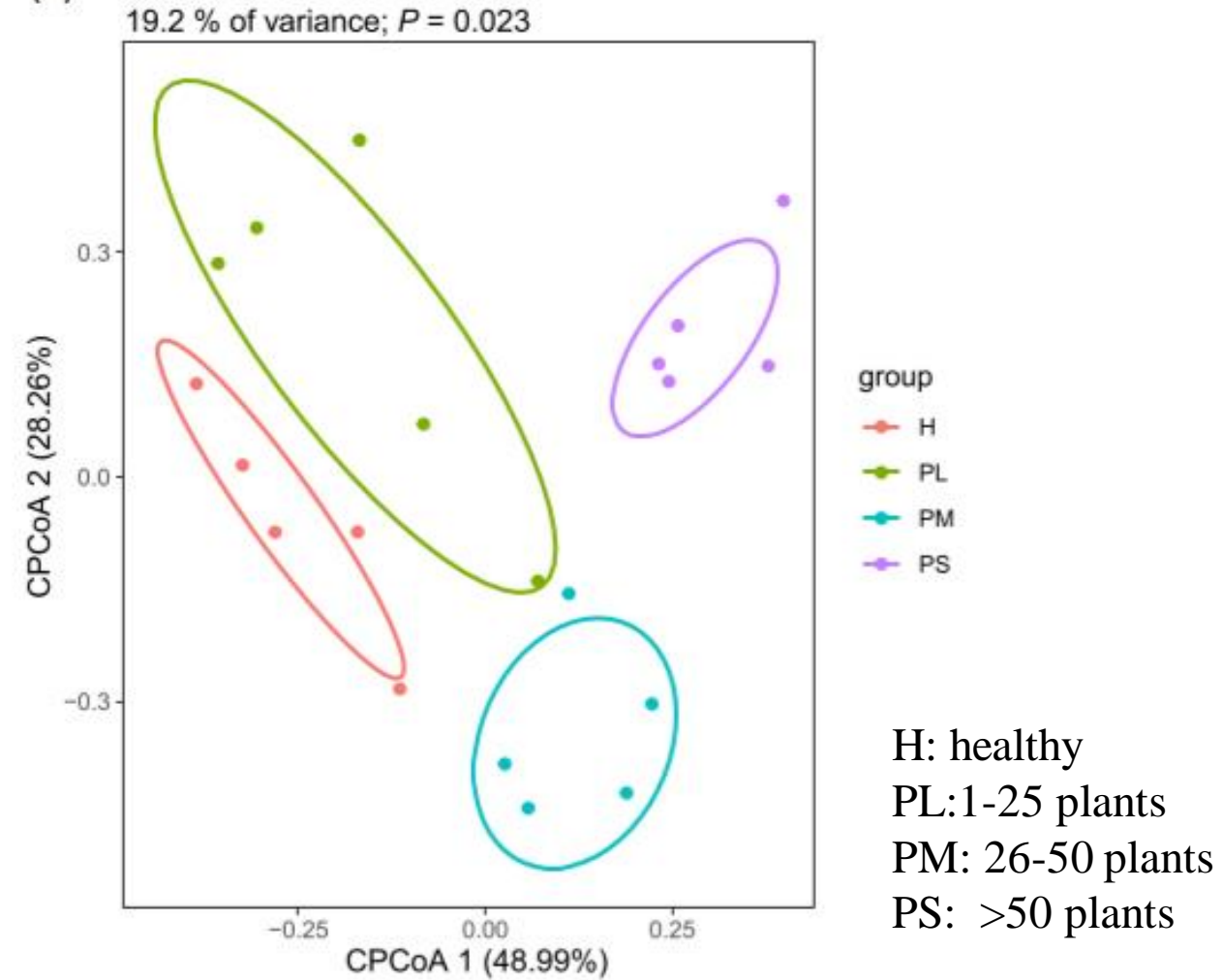
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# Results

(A)



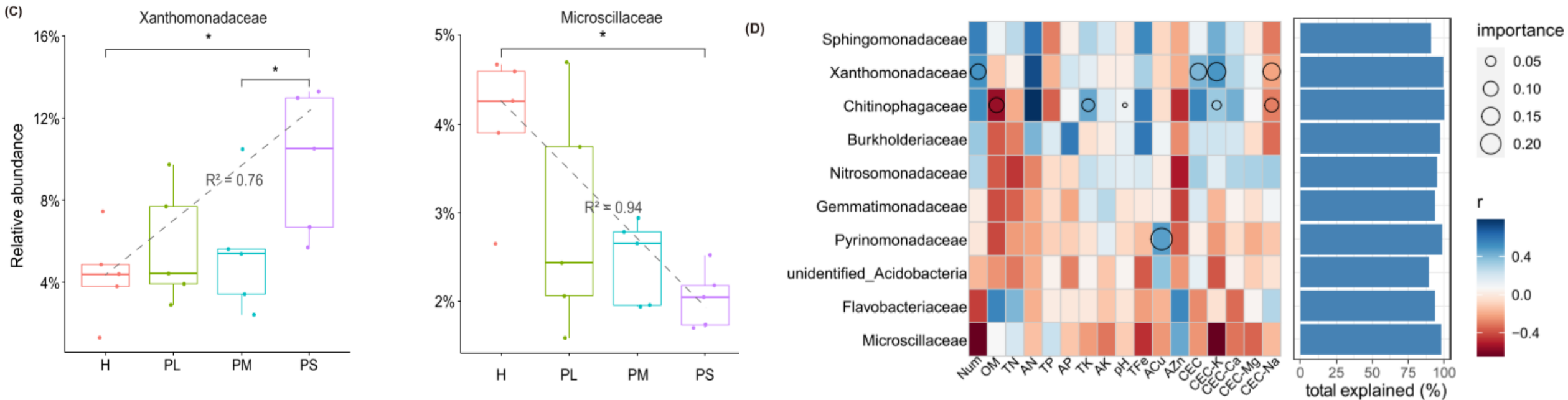
(B)



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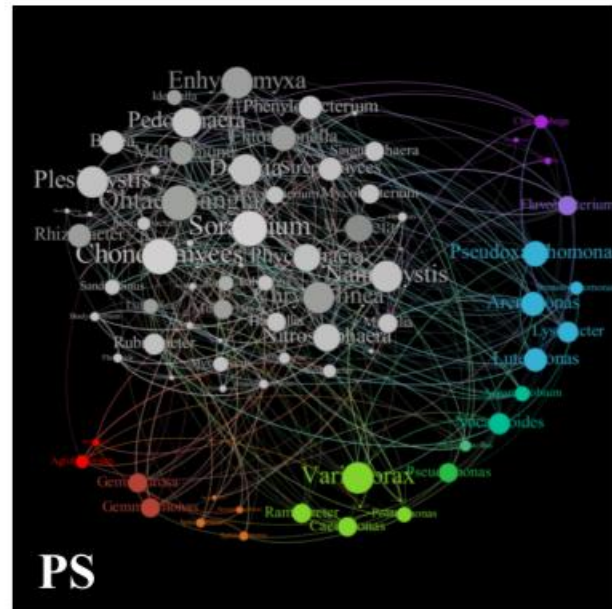
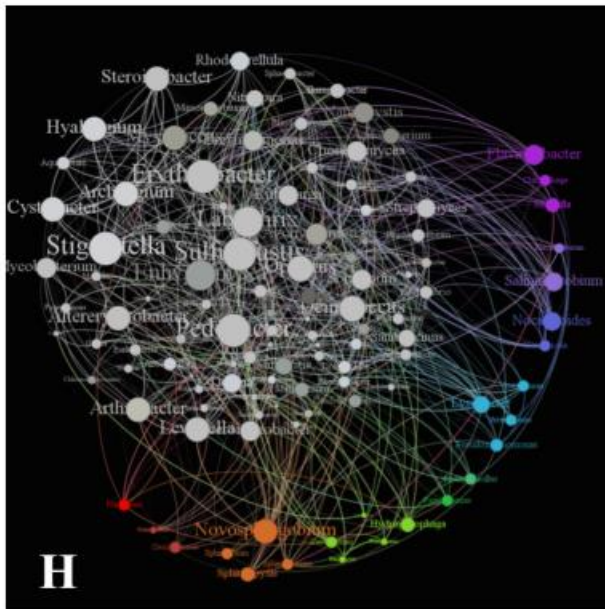
# Results



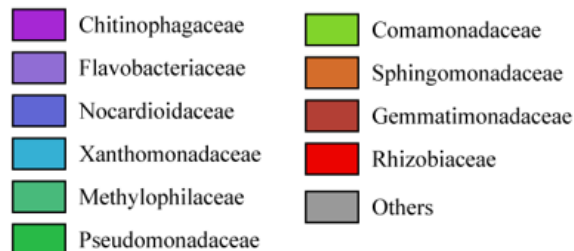
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# Results

(A)



## Family

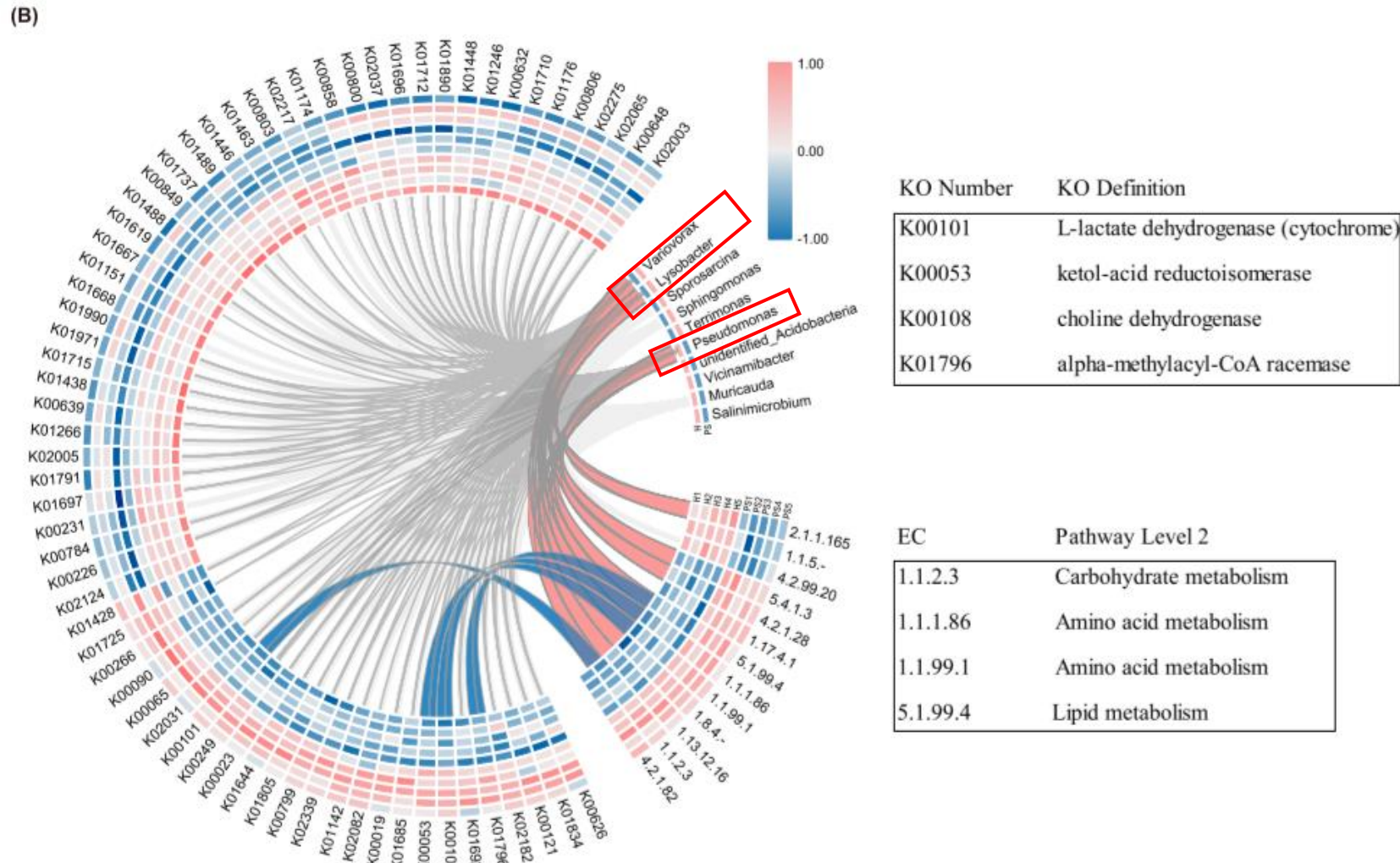


The parameter comparison of co-occurrence network

Settings		H	PS
Network Overview	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
	Average Path length	3.68	3.53
	Graph Density	0.09	0.10
	Modularity	3.91	3.67
Node Overview	Modularity with resolution	3.64	3.67
	Number of Communities	7	5
	Number of Weakly Connected Con	1	1
	Average Clustering Coefficient	0.58	0.46
	Total triangles	1388	581
Sum change		0.021	0.011

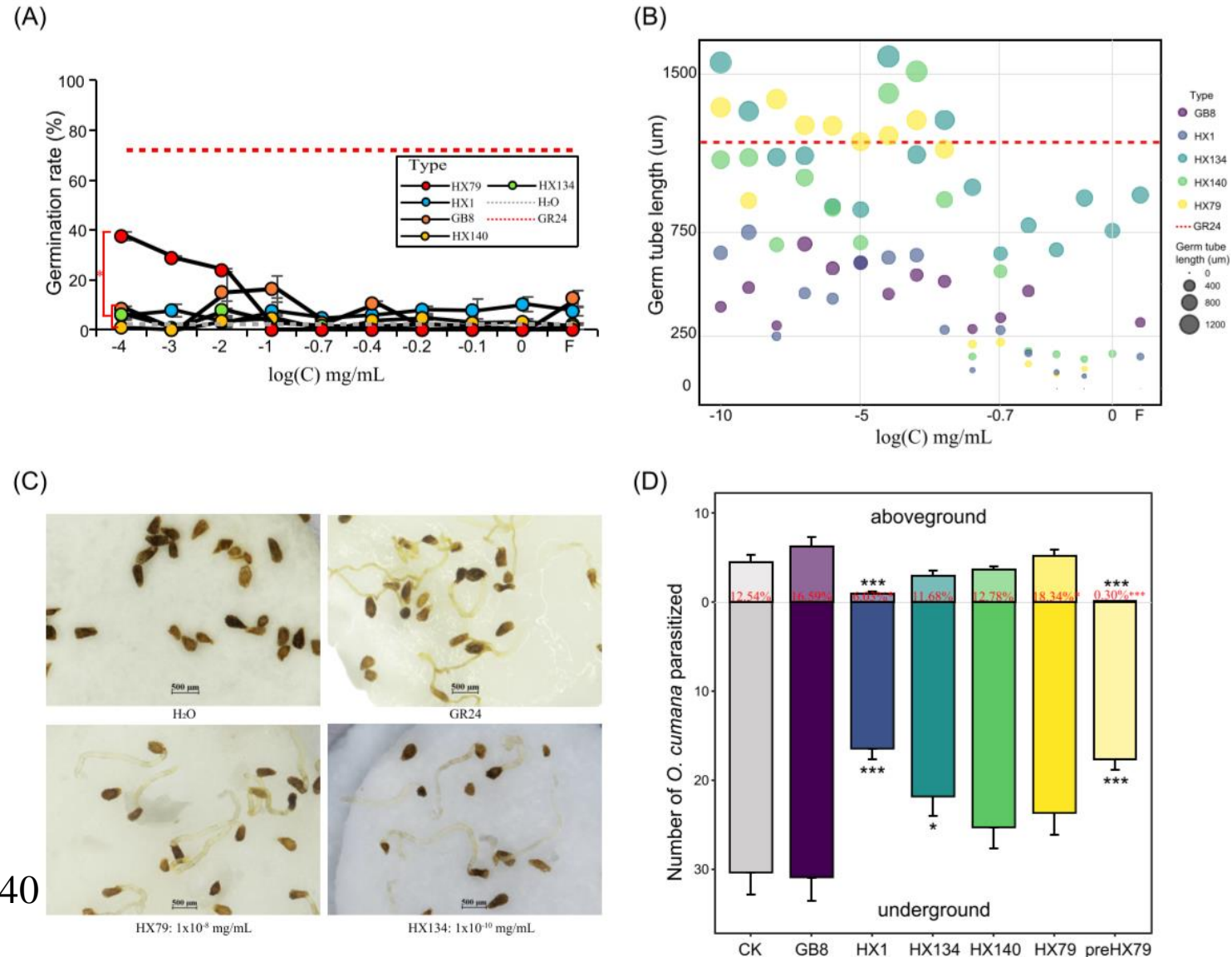
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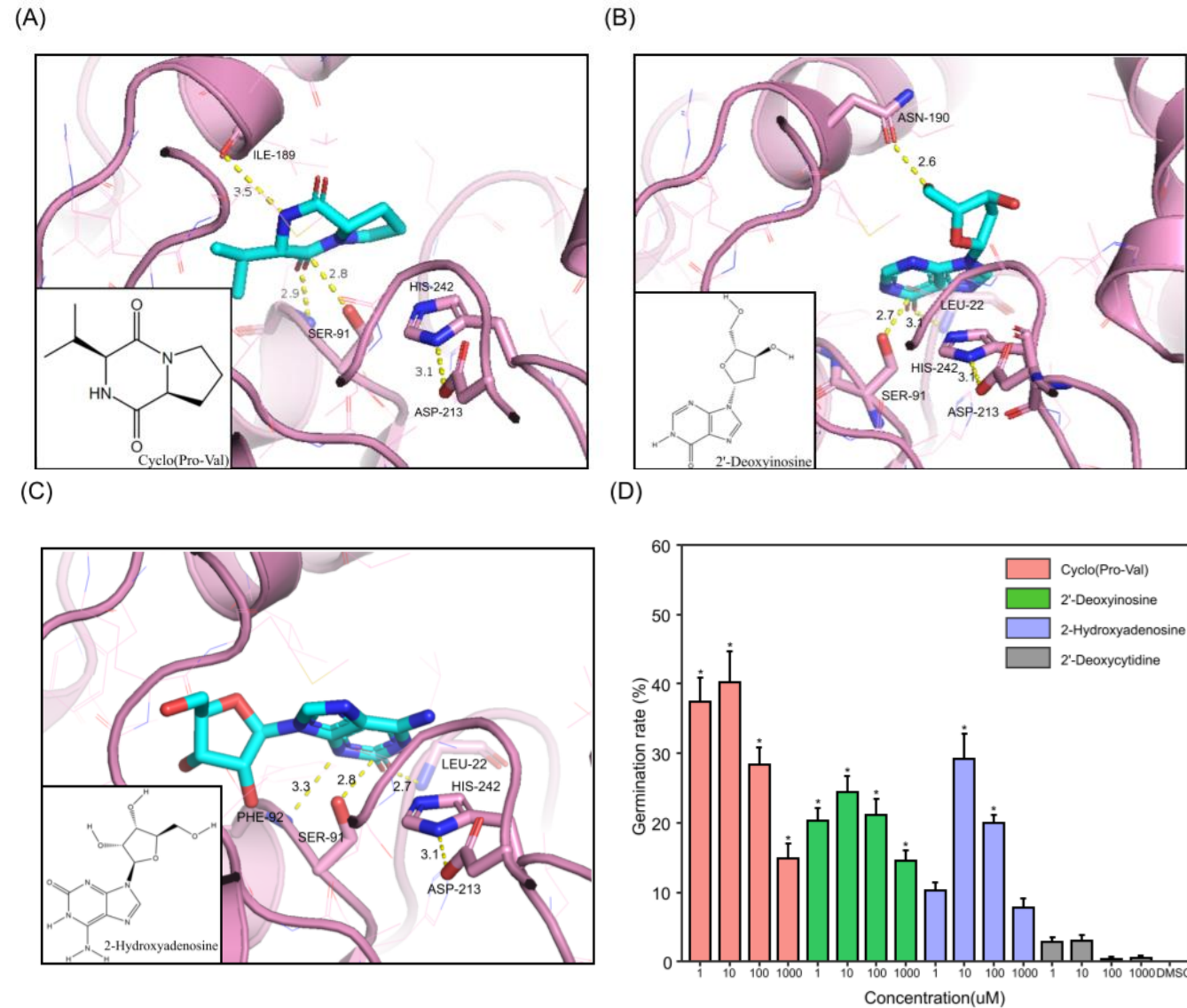


*Lysobacter*: HX79  
*Variovorax*: GB8  
*Pseudomonas*: HX1, HX134, HX140

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# Conclusions

1. To investigate the mechanism controlling the parasitism of *O. cumana*, we performed integrated multi-omics analysis in this study. It was demonstrated that rhizosphere microbes have a regulatory effect on the parasitism of *O. cumana*.
2. By constructing a molecular binding model, we successfully predicted three compounds that promote the germination of *O. cumana* and clarified their molecular recognition mechanisms.
3. For practical purpose, the strategy of screen compounds appears applicable to other parasitic weeds, including *Phelipanche* species.





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