



Infection mechanisms of *Rhizoctonia cerealis* in wheat

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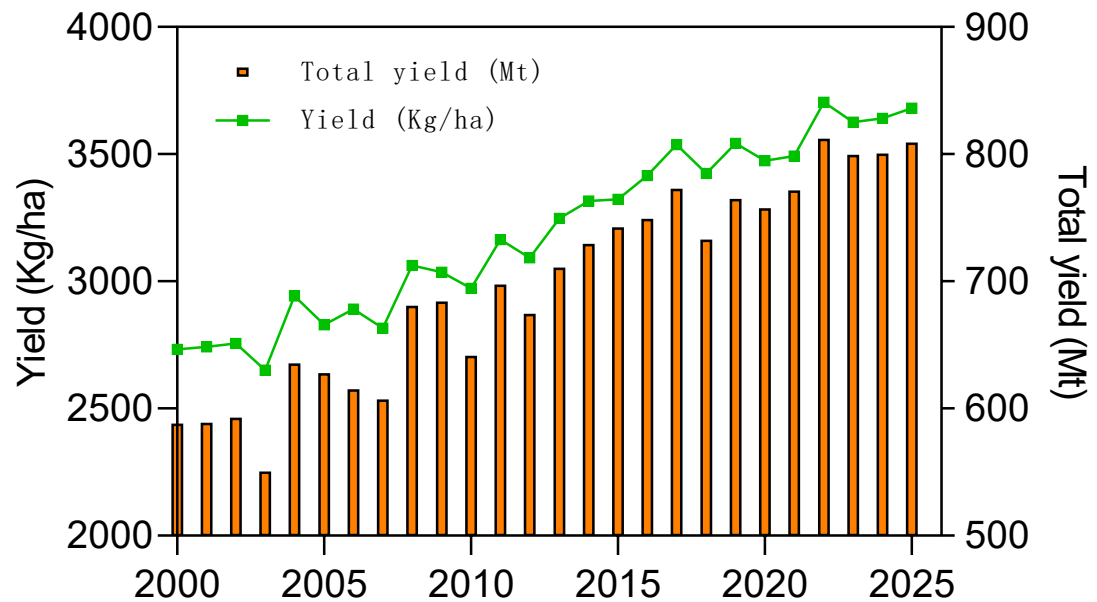


Research Background

- Wheat is one of the most important food crops, and its safe production is essential for global food security.
- Climate change and shifts in cultivation patterns bring increasing threats from multiple diseases, severely constraining stable and improved wheat yields.



Science, 2018



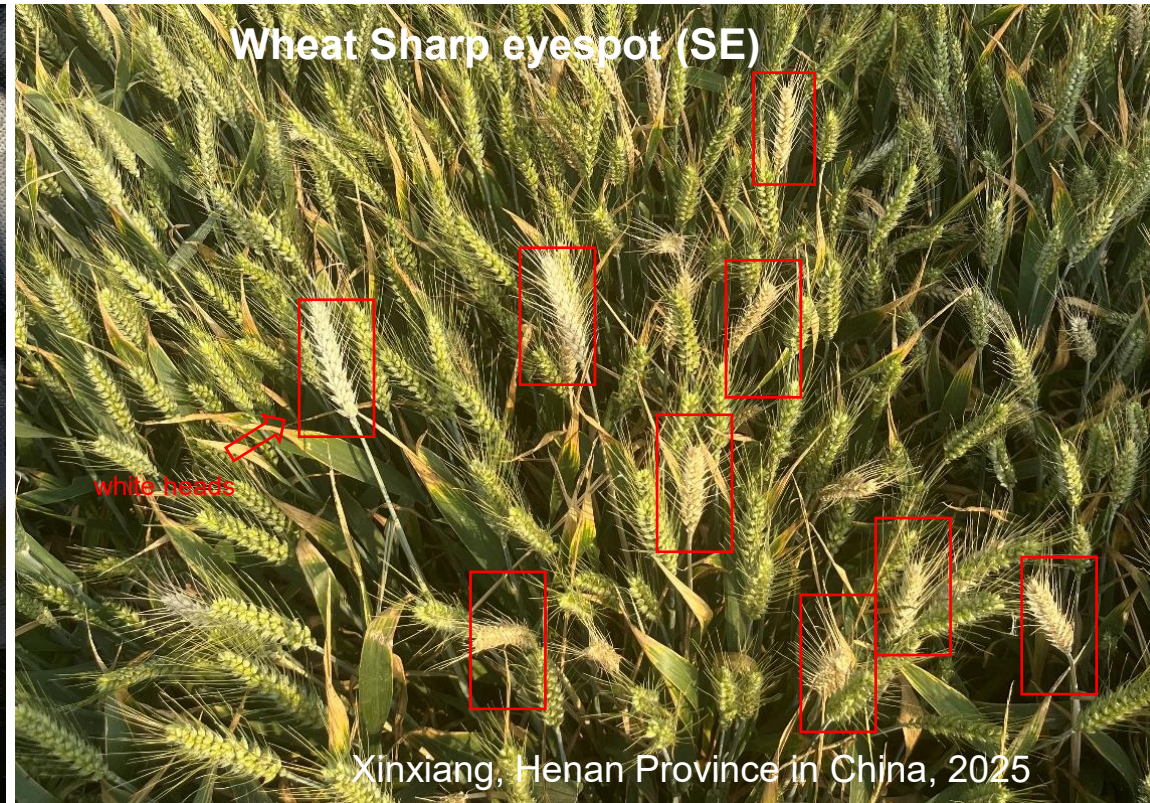
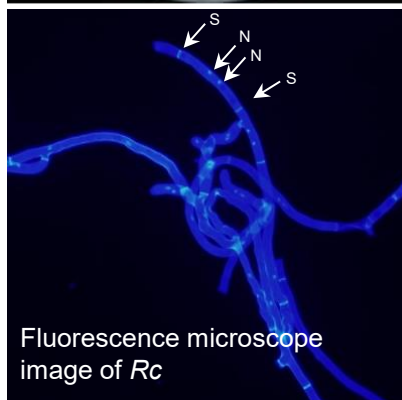
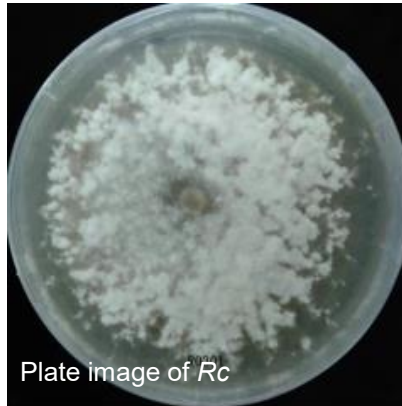
Global wheat production

Data source: FAO



Research Background

- Wheat sharp eyespot (SE), caused by *Rc*, is one of the most destructive diseases in wheat production in China.
- About 8 million hectares of wheat fields are infected with SE annually in China, accounting for 29% of the total area affected by wheat diseases.
- At present, most wheat cultivars are highly susceptible to SE, and chemical fungicides remain the primary control measure, despite causing severe environmental pollution.
- Dissecting the pathogenic mechanisms of *Rc* and identifying key regulatory genes will provide important theoretical support for resistance breeding against wheat SE.





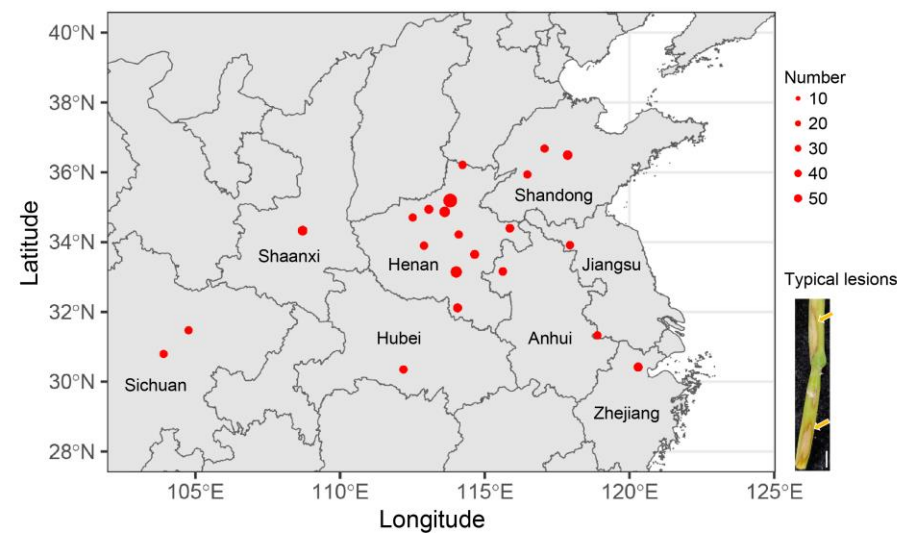
Research Objectives

- ❑ **To construct high-quality genome assemblies and genomic variation atlas for *Rc* isolates**
- ❑ **To unravel the core pathogenic mechanisms during *Rc* infection**
- ❑ **To Identify important regulatory genes for wheat sharp eyespot (SE)**
- ❑ **To provide new insights for SE management and resistance breeding of wheat**

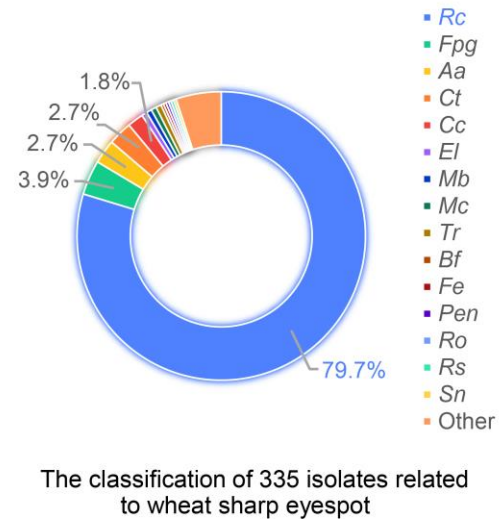


Research results

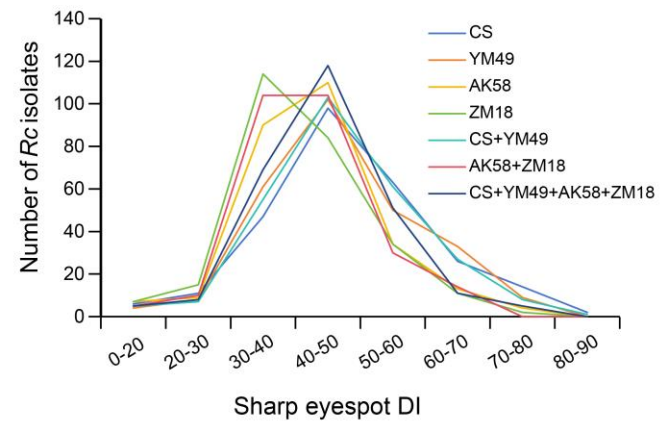
(A)



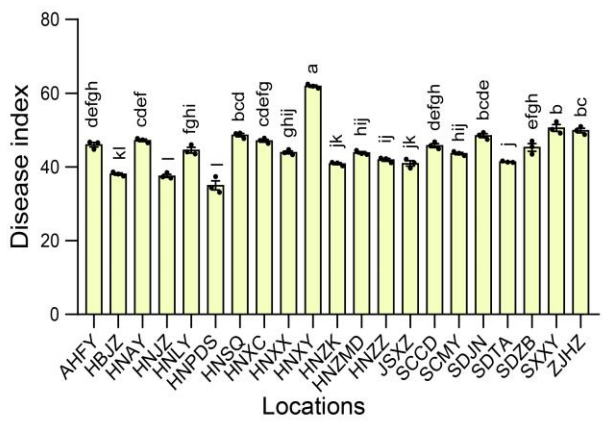
(B)



(C)

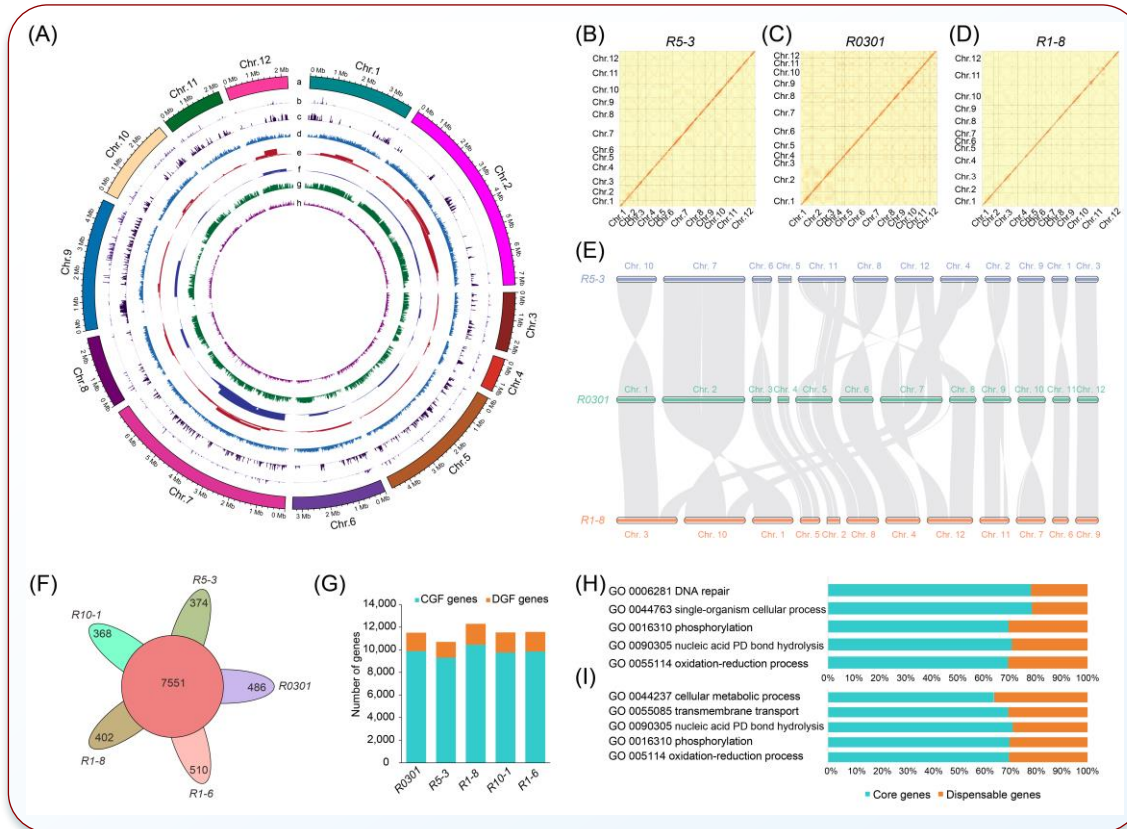


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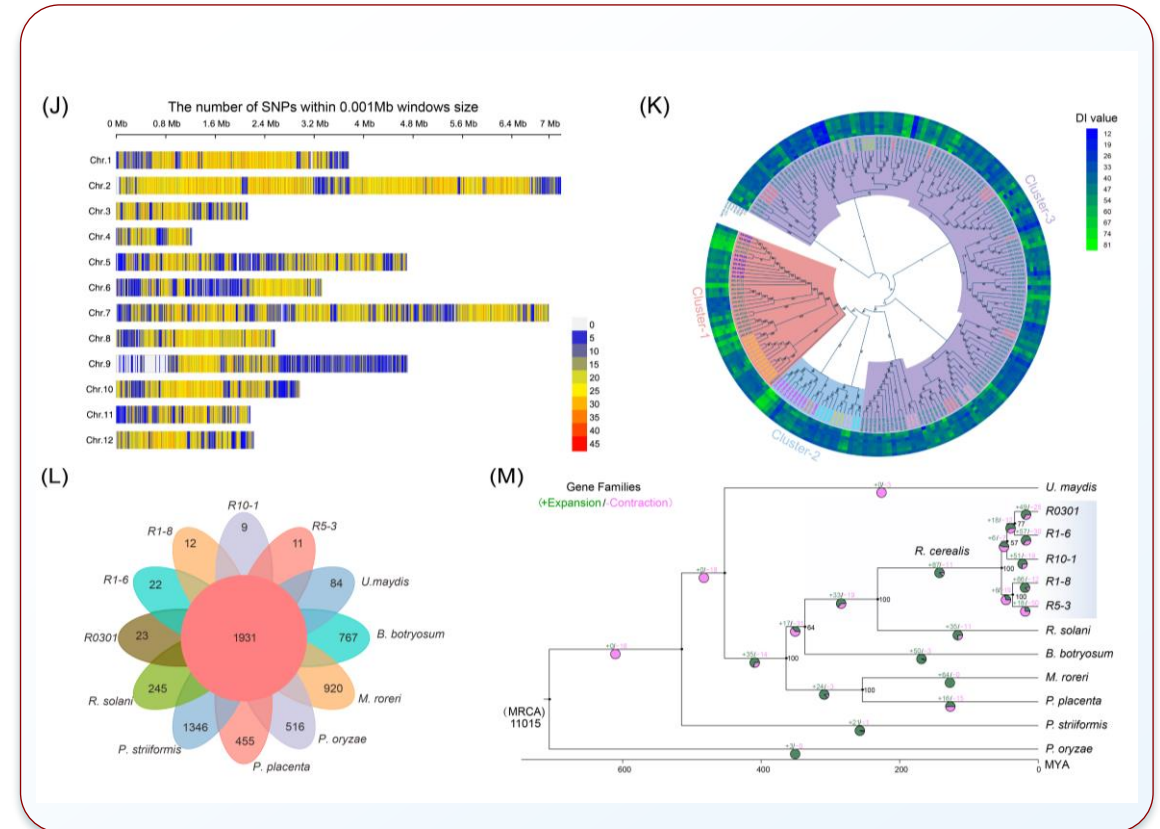


- A total of 1,683 SE-diseased wheat plants were collected from 30 locations in China.
- 335 isolates related to SE were identified, among which 79.7% belonged to *Rc*.
- *Rc* isolates from different locations showed significant differences in pathogenicity, suggesting regionally differences in pathogenicity.

Research results

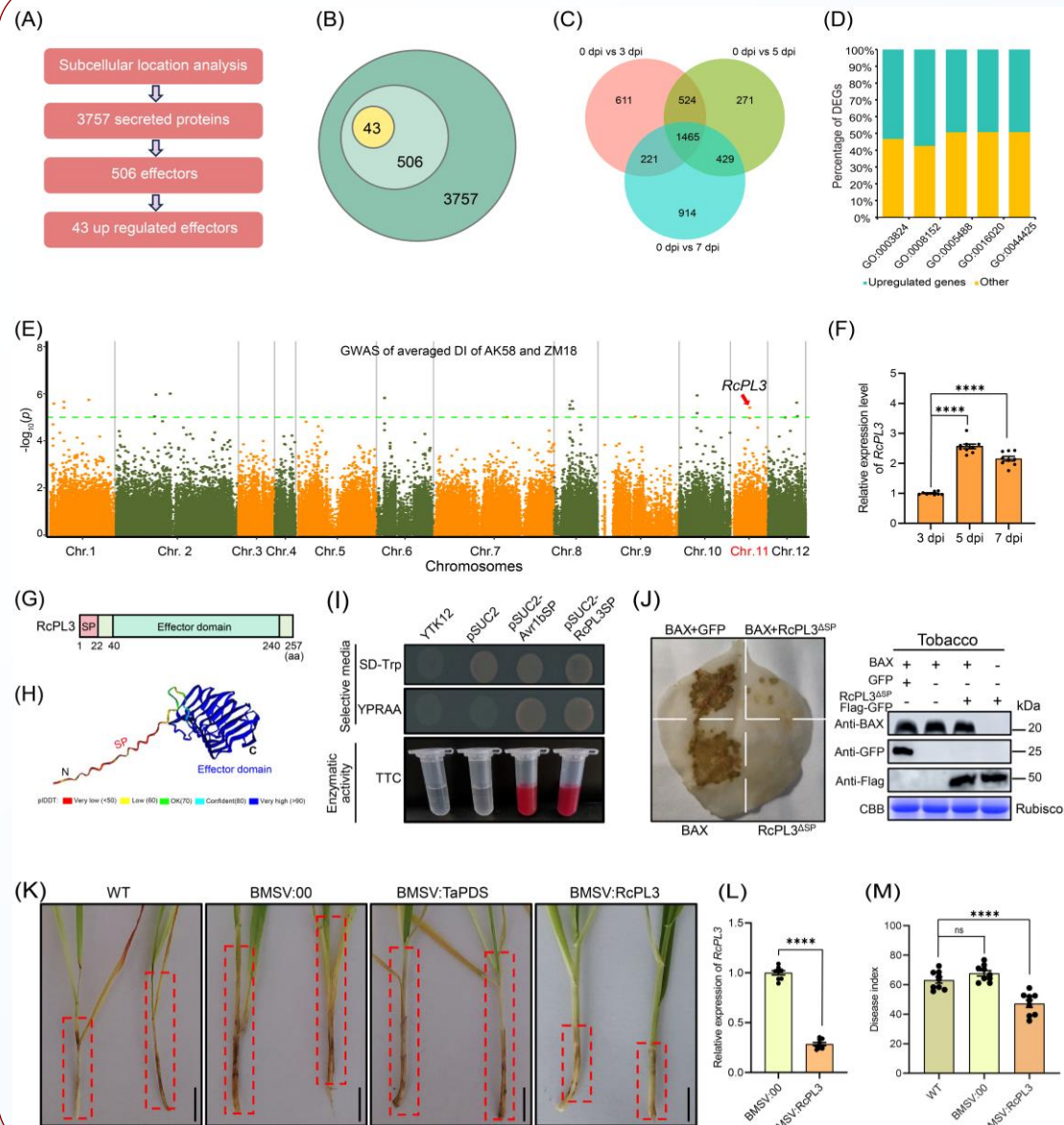


- The high-quality genome maps were assembled for five representative *Rc* isolates.
- *Rc* pan-genome was constructed, comprising 57,614 annotated genes; core genes occupied ~85.5% of the total genes within each isolate.

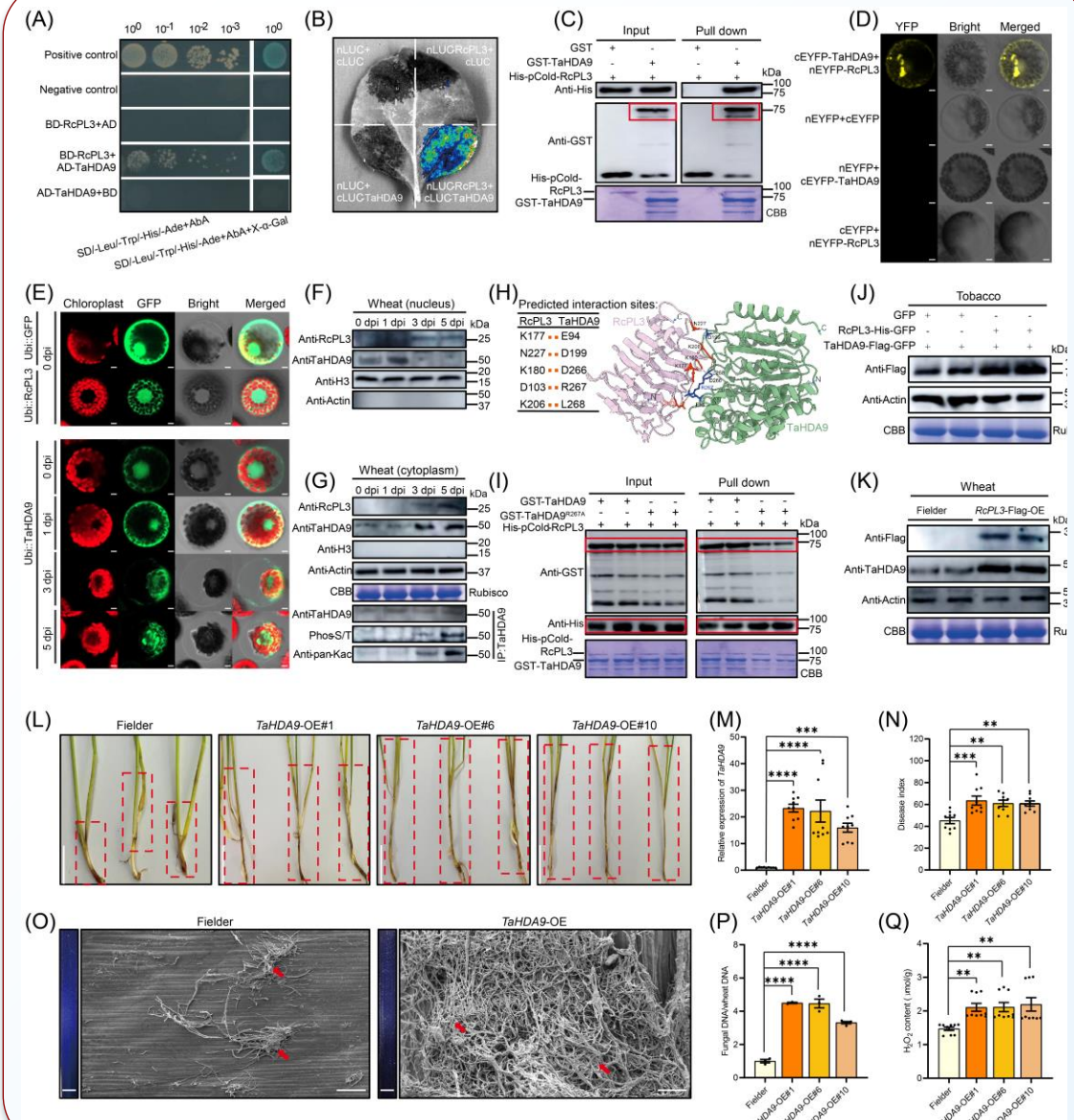


- We performed genome resequencing on 207 *Rc* isolates via the Illumina HiSeq platform to build a genomic-variation atlas.
- *Rc* is closest to *R. solani* among the 6 Basidiomycetes, and the divergence between them was predicted to have occurred ~232 million years ago.

Research results

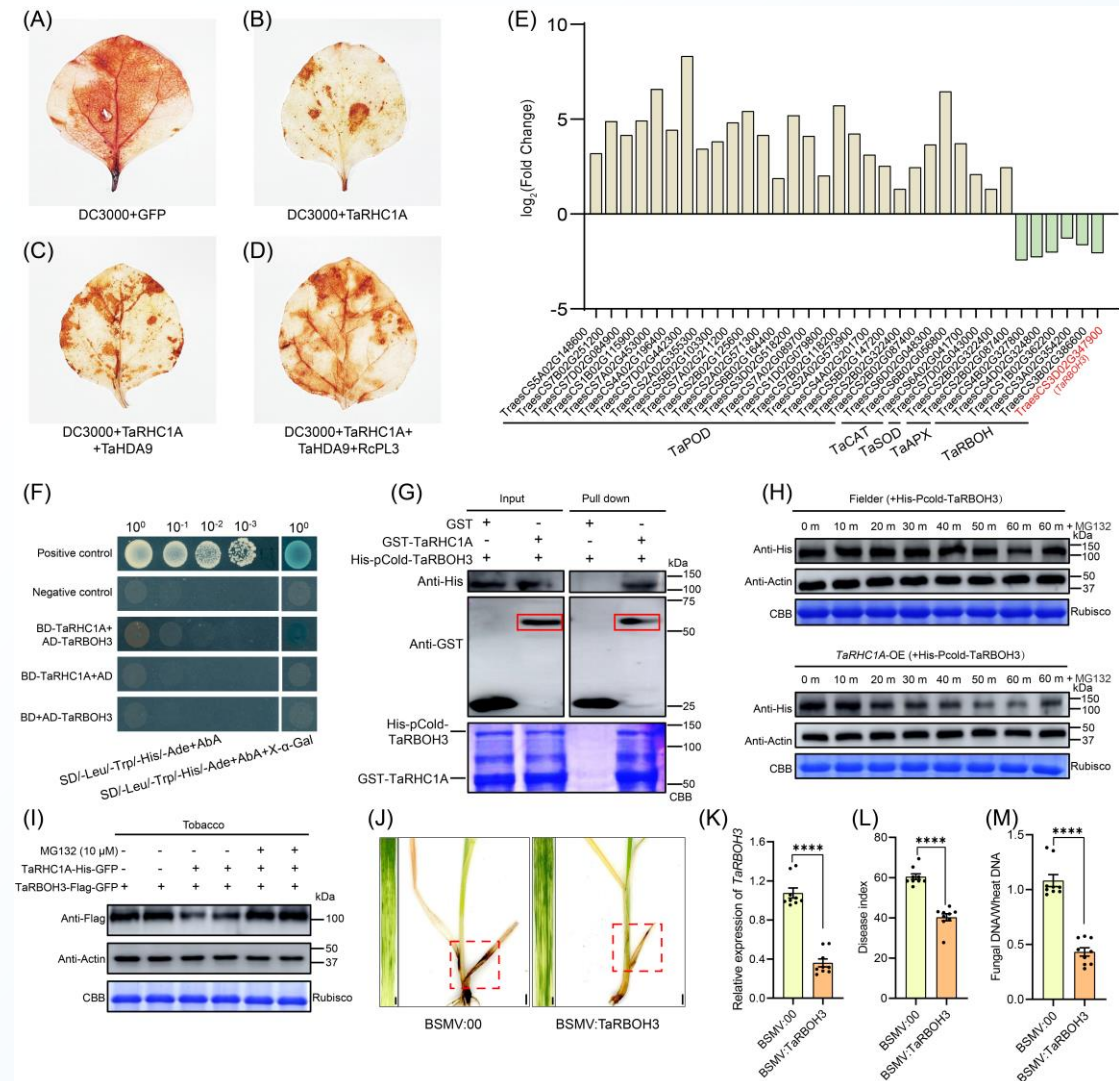
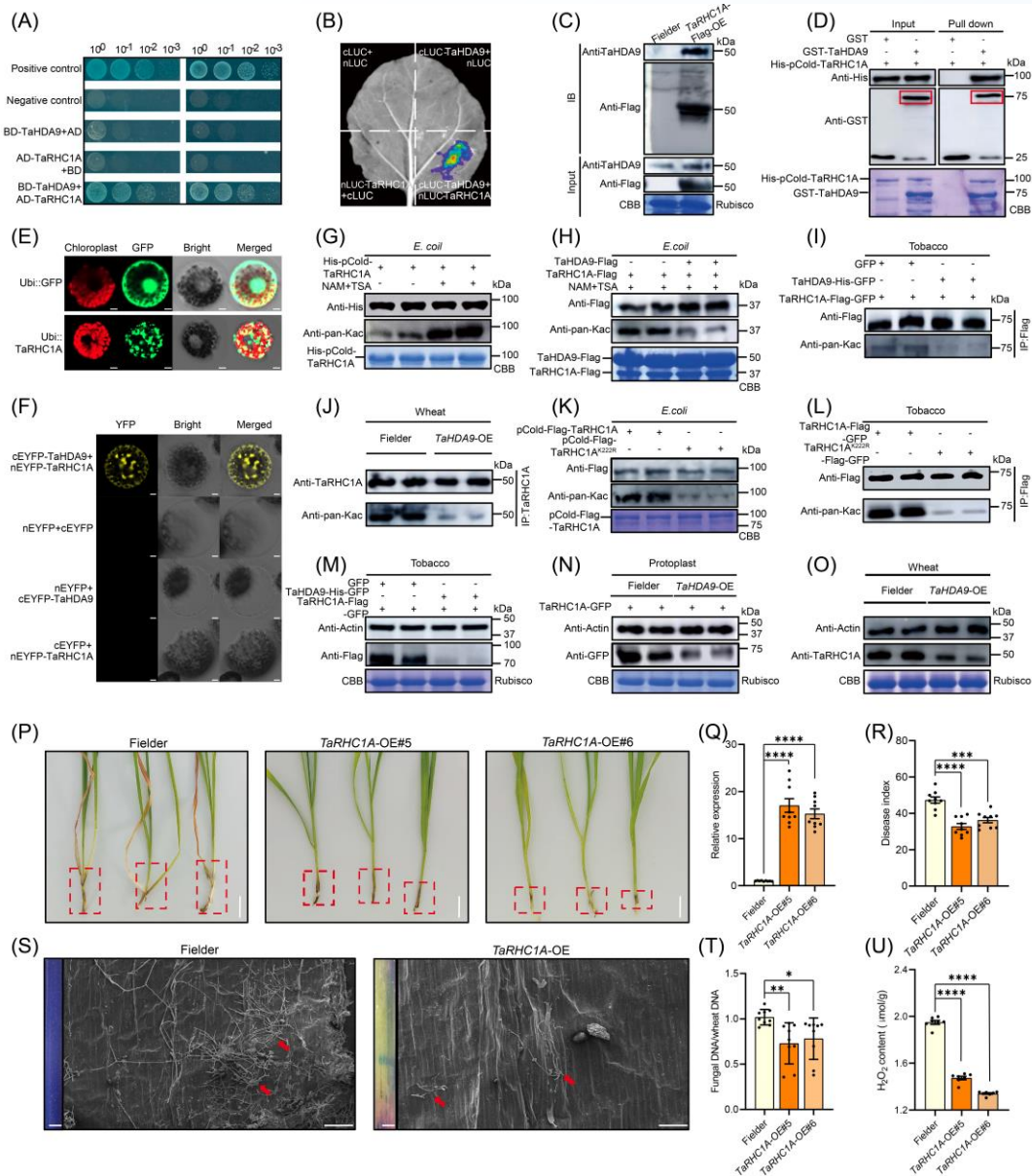


➤ Genome, GWAS and transcriptome analysis suggested that *RcPL3* was associated with *Rc* pathogenicity



➤ *RcPL3* increased the protein accumulation of *TaHDA9* possibly through post-translational modifications

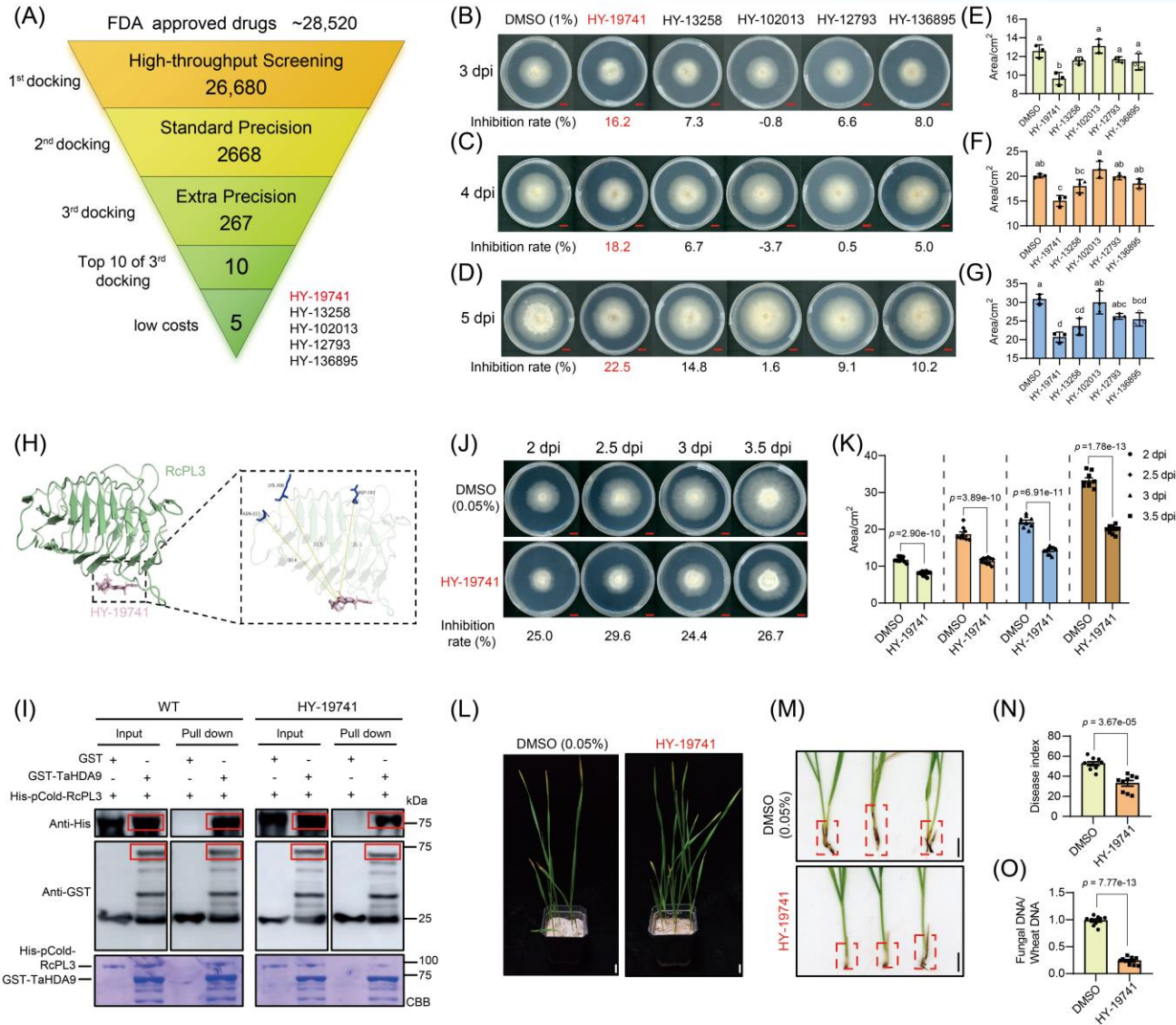
Research results



➤ TaRHC1A could be inhibited by TaHDA9 through deacetylation.

➤ TaRHC1A mediates wheat SE resistance by modulating ROS. On the one hand, it promotes TaRBOH3 degradation via ubiquitination; on the other hand, it up-regulates antioxidant enzyme genes and represses the expression of ROS-synthesizing enzyme genes.

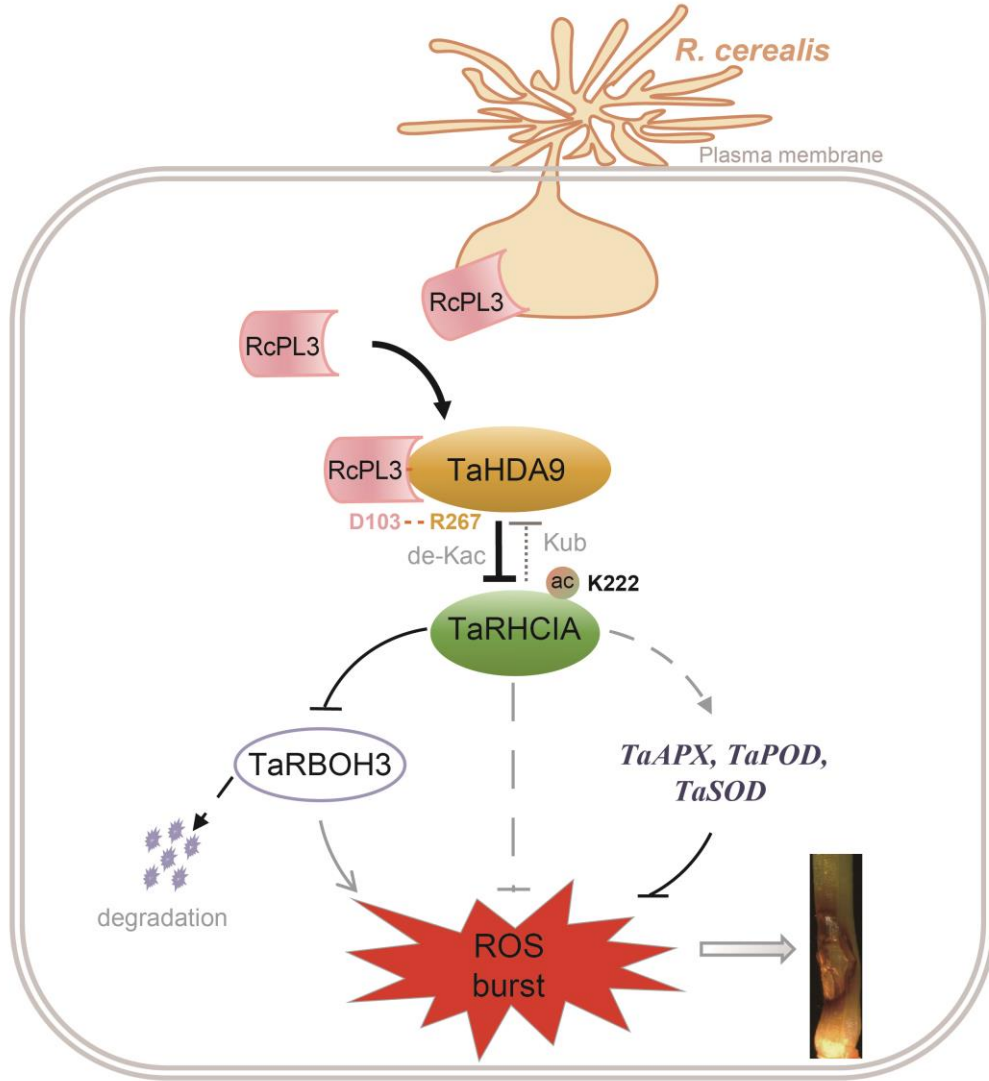
Research results



- Using virtual screening and agar diffusion assays, we identified a small-molecule compound HY-19741 from the FDA-approved drug library.
- HY-19741 effectively impedes *Rc* infection possibly by weakening the interaction of RcPL3 and TaHDA9.

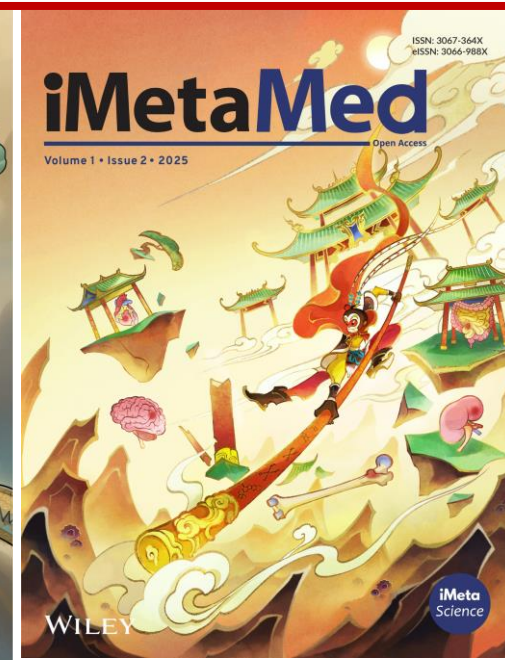
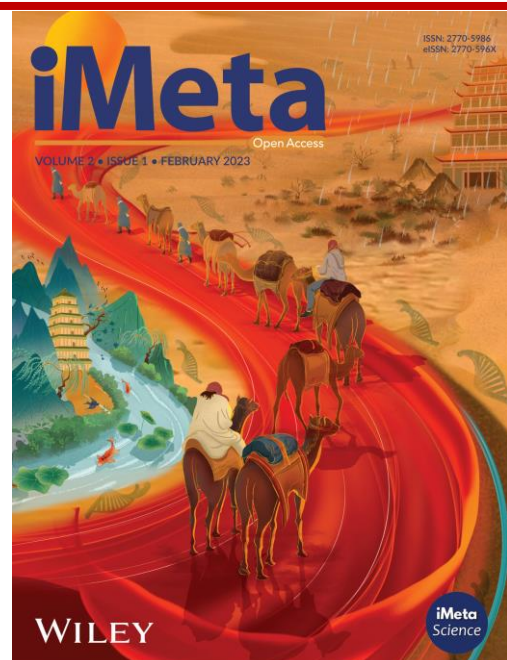


Summary



- ❑ We constructed high-quality genome maps of five representative *Rc* isolates by *de novo* sequencing and established its atlas of genomic variation.
- ❑ We identified a key effector RcPL3 conferring *Rc* pathogenicity and proposed a working model RcPL3-TaHDA9-TaRHC1A-TaRBOH3 regulating SE resistance in wheat.
- ❑ We found out HY-19741 as an antagonist to effectively impede *Rc* infection.

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