

## Genomic characterization reveals insights into patulin biosynthesis and pathogenicity in *Penicillium* species

With the support by the National Natural Science Foundation of China, the Ministry of Science and Technology of China, and the Chinese Academy of Sciences (CAS), the research group led by Prof. Tian ShiPing (田世平) at the CAS Key Laboratory of Plant Resources, Institute of Botany, revealed molecular basis of patulin (an acetate-derived tetraketide mycotoxin) biosynthesis and pathogenicity in *Penicillium* species based on genome structure analysis and gene knockout assay, which was published in *Molecular Plant-Microbe Interactions* (2015, 28(6): 635–647) as a cover story.

*Penicillium* species are fungal pathogens devastate crop plants and annually cause huge economic losses worldwide. *P. expansum* and *P. italicum* are well known post-harvest pathogens and differ in host range and patulin production ability. The former has broader fruit hosts and serves as a patulin producer; whereas the latter is restricted to citrus fruits and does not produce patulin. The molecular basis of host-specificity and mycotoxin biosynthesis of fungal pathogens is a longstanding biological puzzle. Prof. Tian's group provided the high-quality genome drafts of *P. expansum* (33.52 Mb) and *P. italicum* (28.99 Mb), and uncovered the differences in genome structure, important pathogenic characteristics, and secondary metabolite (SM) gene clusters in the *Penicillium* species. A total of 55 gene clusters related to secondary metabolism, including a cluster of 15 genes responsible for patulin biosynthesis, are identified in *P. expansum*. Functional studies confirmed that *PePatL* and *PePatK* play crucial roles in the biosynthesis of patulin, and patulin is not related to fungal virulence. Moreover, *P. expansum* contains more pathogenic genes and SM gene clusters, in particular an intact patulin cluster, as compared to *P. italicum*. These findings provide important information relevant to understanding the molecular network of patulin biosynthesis and mechanisms of host-specificity in *Penicillium* species.

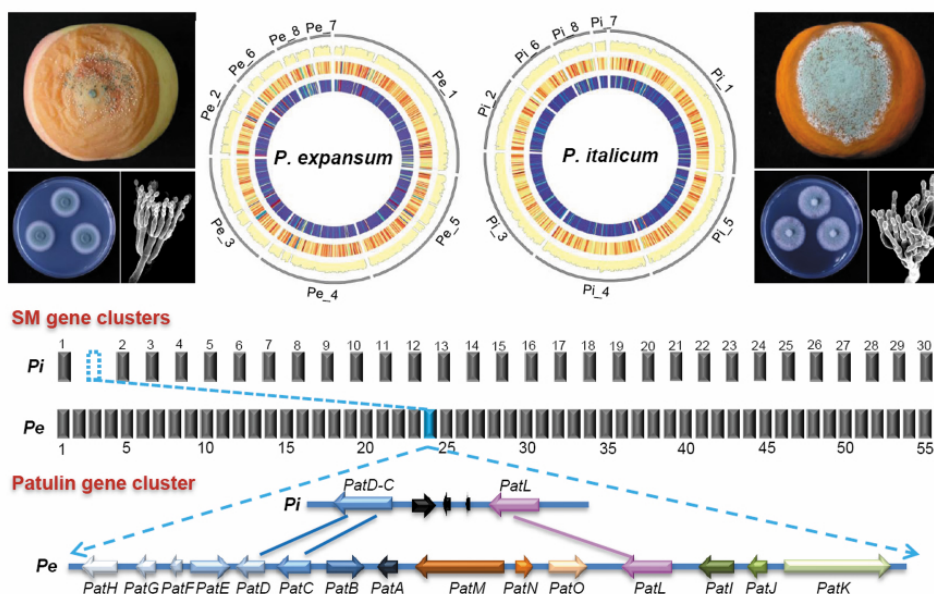


Figure Genome features of *Penicillium* spp. and gene cluster responsible for patulin biosynthesis.