Editorial: Molecular interactions between crops and phytopathogens volume III: Vegetables and other crops

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Plant diseases cause substantial annual yield losses of crops, and pose a major threat to global food security and agricultural sustainability. Improving crop resistance against diverse diseases plays a crucial role in safeguarding sustainable crop production to nourish the increasing world population. Deciphering the molecular mechanisms underlying the interactions between crops and phytopathogens will provide a valuable basis for the improvement of crop resistance and disease management.

In the context of long-term coevolution, crops have developed sophisticated strategies to cope with phytopathogens. Invading phytopathogens, on the other hand, have evolved various defensive mechanisms to facilitate their invasions and infection. Understanding different crop-pathogen interactions will broaden our knowledge toward the dynamic coevolutionary arm races engaged by plants and pathogens. In this context, we organized this Research Topic on “Molecular Interactions between Crops and Phytopathogens Volume III: Vegetables and other crops.” Besides the three major...
food crops in the world, this Research Topic mainly focused on the valuable vegetables and other crops. This topic was presented by ten outstanding articles, which cover cabbage (Liu et al.), bell peppers (Yang et al.), litchi (Li et al.), tobacco (Yang et al.), Brassica napus Canola Adhikary et al.), barley (Yuan et al; Xu et al.), rose (Tian et al.), soybean (Feng et al.), and a new model plant within the family Gramineae, Brachypodium distachyon (Peng et al.). According to the research content and research perspective, we broadly divided these ten articles into the following four themes:

Identification of key genes involved in crop-pathogen interactions by omics approach

Technical breakthroughs in sequencing technology, and the rapid development of bioinformatics, including multi-omics tools, offer many new clues for understanding the molecular mechanisms of crop-pathogen interactions. The TRICHOME BIREFRINGENCE-LIKE (TBL) family participates in the O-acetylation of cell wall polysaccharides. Tian et al. profiled TBL gene family in rose genome and explored their functions during plant resistance to gray mold. Twelve of 50 RcTBL genes were down-regulated upon Botrytis cinerea infection, and knocking down of RcTBL16 significantly enhanced plant resistance to B. cinerea, highlighting the importance of the function of TBL proteins for future studies. Plant-specific lateral organ boundaries domain (LBD)-containing transcription factors are involved in plant responses to various stresses. Feng et al. investigated the LBD gene family in soybean on a genome-wide scale, and identified differentially expressed LBD genes upon Phytophthora sojae infection. They further showed that GmLBD9 and GmLBD23 negatively regulate plant defense against P. sojae, whereas GmLBD16 and GmLBD88 contribute to soybean defense against P. sojae. This study expands our knowledge about the origin and evolution of GmLBD gene family in soybean and promotes the potential application of these genes in disease resistance improvement. MicroRNAs (miRNAs) are one of the key components that control the transcriptional responses of plant to pathogen infection. Peng et al. identified the differentially expressed miRNA and their target genes in Brachypodium distachyon upon infection by Magnaporthe oryzae, providing an unraveling complex miRNA-mediated regulatory networks during B. distachyon-M. oryzae interactions. A NAC transcription factor BdNAC21 gene was validated as a target of the differentially expressed mir164c. Identification of differentially abundant proteins (DAP) using proteomics reveals their direct functional role in plant-pathogen interactions. Adhikary et al. explored the DAPs associated with Plasmodiophora brassicae resistance in Brassica napus canola at different infection stages. Seventy-three DAPs annotated as orthologs to clubroot-resistant proteins and eight quantitative trait loci (QTLs) were identified, providing potential candidates conferring immune response to P. brassicae in canola.

Characterization of pathogenicity-related genes in crop pathogens

Litchi downy blight caused by Peronophythora litchii, an oomycete pathogen, is a major disease in litchi. Cytochrome b5, an electron transport component, is essential in the Class II cytochrome P450 monoxygenation system. Li et al. identified a Cyt-b5 domain protein, PCBL51, in P. litchi and, for the first time, reported that this cytochrome b5 superfamily member contributed to the mycelial growth, stress response, and pathogenicity in P. litchi. The P4-ATPases, aminophospholipid translocases (APTs), play essential roles in the growth and pathogenesis of fungal pathogens. Yang et al. identified a P4-ATPase Drs 2 homolog PcApt1 in Phytophthora capsici, and demonstrated that PcApt1 participated in phosphatidylserine (PS) transport across the plasma membrane, the hyphal growth, extracellular laccase activity, and P. capsici virulence. Since both PCBL51 and PcApt1 are well conserved in oomycetes, these two studies provide new insights into the development of plant pathogenic oomycetes and hence are helpful for the control of related diseases. Powdery mildew, a biotrophic pathogen, secretes various effectors to manipulate plant cell death. Yuan et al. discovered a secreted effector protein CSEP0027 from the barley powdery mildew pathogen Blumeria graminis f. sp. hordei (Bgh) as a cell death inducer. CSEP0027 contributed to Bgh virulence in barley by directly interacting with barley catalase HvCAT1 and altering its subcellular localization, indicating that powdery mildew pathogen promotes its virulence by manipulating reactive oxygen species homeostasis during infection.

Jasmonic acid signaling in crop-pathogen interactions

The plant hormone jasmonic acid (JA) plays essential roles in many biological processes, including plant defense against pathogens. Xu et al. explored transcriptomic, proteomic and metabolomic data of powdery mildew (PM)-susceptible and PM-resistant accessions to systemically examine the mechanisms of PM resistance. They found that the resistance to PM in qingke, also called “naked barley,” involves the accumulation of aromatic phenolamides through jasmonate-mediated activation of defense-related genes. N-acyl-homoserine lactones (AHLs) are the most common signal molecules in Gram-negative bacteria. Liu et al. found that AHL improved the resistance of Chinese
cabbage and *Arabidopsis* to the hemibiotrophic bacteria *Pectobacterium carotovorum* ssp. *carotovorum*. In this process, the JA signaling pathway participates in AHL priming by coordinating with the auxin signaling pathway.

**Characterization of the Nep1-like proteins from biocontrol agent *Pythium oligandrum***

Necrosis and ethylene-inducing peptide 1-like proteins (NLPs) exhibit dual functions in plant-pathogen interactions, acting as both toxin-like virulence factors and triggers of plant immune responses. Yang et al. showed that the cytotoxin and immunity induction activity of NLPs are largely divergent. Both non-cytotoxic and cytotoxic PyolNLPs from the biocontrol agent *Pythium oligandrum* enhanced plant resistance to a wide range of pathogens. In addition, they found that the conserved nlp24-like peptide pattern is required for this process uncoupled with reactive oxygen species and cell death.

In summary, the collected articles in this Research Topic identified some key genes or pathways involved in crop-pathogen interactions, characterized their functions, and preliminarily explored their functional mechanisms. Data in these articles provide valuable gene resources for controlling crop diseases and further dissecting the molecular mechanisms underlying crop-phytopathogen interactions.

**Author contributions**

All authors have made a substantial and intellectual contribution to the work and have acted as co-editors of this special issue.

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