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Omics in Plant Disease Resistance

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OMICS in Plant Disease Resistance

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Abstract

The term OMICS, which look into the global profiling and analysis of various cellular molecules, has gained new heights with the advancement of next-generation sequencing and mass spectrometry technologies. It has broader implication in genetic improvement of crops for resistance against various diseases of economic significance. This focus issue entitled **OMICS in Plant Disease Resistance** highlights the implication of OMICS (genomics, transcriptomics, proteomics and metabolomics) in agricultural research.

Genomics and post-genomics era OMICS technologies have broader implication in genetic improvement of crops for disease resistance (Bhadauria et al., 2010a, 2010b, 2014). This focus issue summarizes the technological innovations in the area of OMICS for enhancing genetic resistance of crops to various pests, such as fungi,

oomycetes and insects (Figure 1). Below are some of the highlights of the focus issue on **OMICS in plant disease resistance**.

Wild germplasm is being utilized to enhance genetic resistance in lentil (*Lens culinaris*) against fungal diseases using next generation sequencing-based genotyping and comparative genomics approaches (Bhadauria et al.). Such approaches allow pinpointing and mapping the genomic regions in wild species (*Lens ervoides*) conferring resistance against diseases like anthracnose (*Colletotrichum lentis*), Ascochyta blight (*Ascochyta lentis*) and Stemphylium blight (*Stemphylium botryosum*). Similar approaches in pests could lead to identification of effectors (avirulence proteins; effectoromics) that can then be used in fishing out pathogen recognition specificities encoded by NBS-LRR class of resistance (*R*) genes in wild germplasm. The *R* genes can be introgressed in cultivars through marker-aided backcrossing to enhance genetic performance against fungal diseases.

Plants respond to pathogen attacks by deploying antimicrobial metabolites, such as phytoanticipins (like glucosinolates that are converted to toxic molecules after pathogen recognition), phytoalexins and altered volatile organic compounds. Liquid and gas chromatography coupled with mass spectrometry allow the global

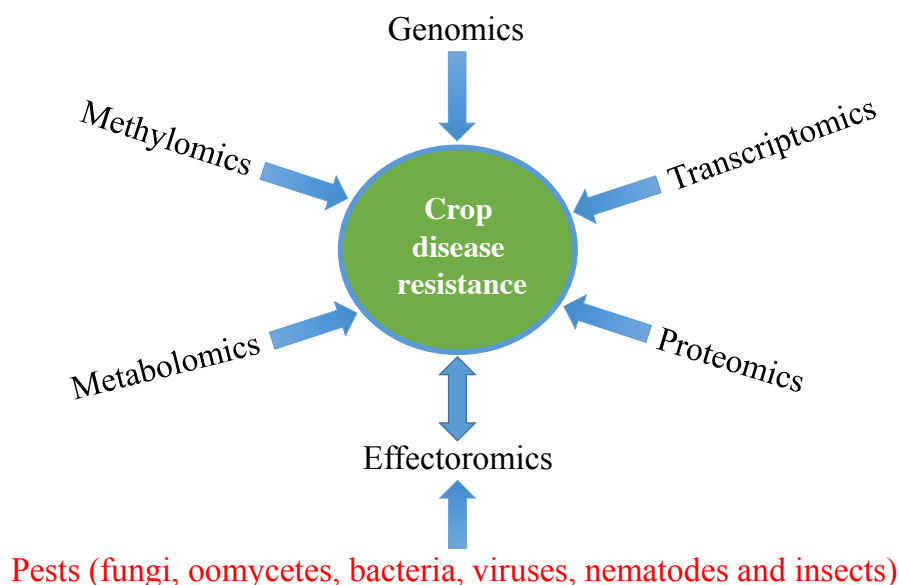


Figure 1. Omics in plant disease resistance.

identification of metabolites (Arbona and Gómez-Cadenas). Nitric oxide (NO) is considered as a signaling molecule and produced during biotic and abiotic stresses. Pérez et al., describe the role of cDNA-amplification fragment length polymorphism and RNA-Seq to unravel NO-based plant disease resistance and catalogue NO-responsive genes. Rodríguez's group at Misión Biológica de Galicia (MBG-CSIC), Spain (Francisco et al.) describes the advancement in OMICS (genomics, transcriptomics, proteomics and metabolomics) with the aim of identifying key components of brassica resistance against clubroot (*Plasmodiophora brassicae*), blackleg (*Leptosphaeria maculans*), etc. Cui et al., provide a comprehensive overview on interaction at transcriptome (RNA-Seq) and proteome levels between rice and planthopper-borne viruses, such as rice stripe virus (Tenuivirus), rice dwarf virus (Reoviridae), rice gall dwarf virus (Reoviridae), rice ragged stunt virus (Reoviridae), rice yellow stunt virus (Rhabdoviridae), rice grassy stunt virus (Tenuivirus), rice black-streaked dwarf virus (Reoviridae) and southern rice black-streaked dwarf virus (Reoviridae). Escobar's group (Cabrera et al.) describes the power of OMICS in identifying susceptibility and resistance factors in host to root-knot nematodes *Meloidogyne* spp. Burra et al., highlight technological advancements and pitfalls of transcriptomics and proteomics to unravel the molecular basis of complex plant-oomycete interaction and shed light on oomycete effector biology. Gomez-Casati's group at Universidad Nacional de Rosario, Argentina discussed the implication of OMICS in generating pathogen-resistant crops. Grandellis and colleagues summarize various gel and non-gel based protein separation methods coupled mass spectrometry to decipher plant defense against pathogens.

One of the best researched pathosystems (plant-fungal pathogen) is Rice-*Magnaporthe oryzae* not only because of economic significance but also genetic and molecular tractability of both host and pathogen. Sharma's group at ICAR-National Research Centre on Plant Biotechnology, India discuss transcriptomics-based oscillating interactome especially regulation of rice resistance genes and *M. oryzae* effectors, including avirulence proteins. Chen et al., discussed proteomics-based approaches to decipher molecular mechanisms underlying rice defense against broad spectrum of pathogens, such as viruses, bacteria and fungi, and in rice lesion mimic mutants.

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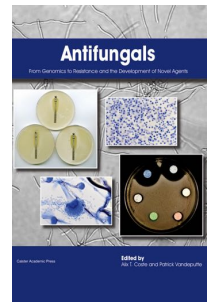
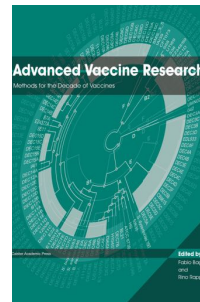
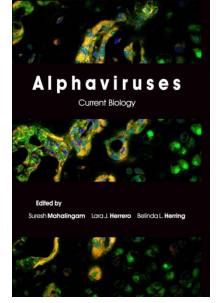
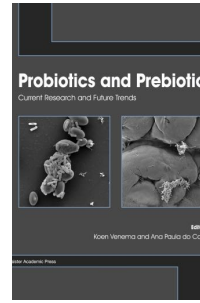
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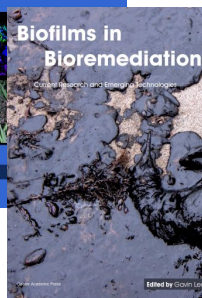
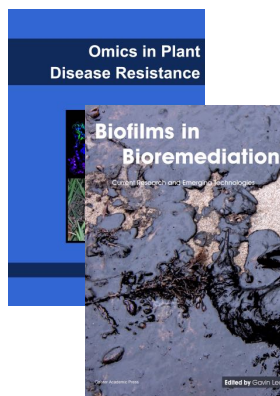
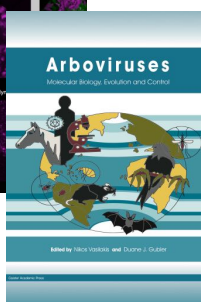
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