

Applications of Omics in Agriculture Production for Disease Resistance Crops

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Introduction

With a wealth of new crop plant genome data, the discovery of new resistance and defense-related genes and the characterization of variation in resistance loci has become a data-rich reality. How do we best take advantage of this knowledge? The perspective piece from Burdon *et al.* (2016) provides a critical view of the past, present, and developing genomic era strategies for rationale improvement and management of disease resistance.

Bacteria present their own peculiar challenges for disease management. Since the publication of the first genome sequence of a plant pathogenic bacterium in the year 2000, breath-taking progress in understanding bacteria–plant interactions has been achieved in a short time. Sundin *et al.* (2016) document the progress made in their concise review, and lay out how this progress is being translated into real advances in disease management. Among others, applications include more sensitive and precise diagnostics, genome-edited disease resistance, and the development of small molecules that target virulence genes in the pathogens themselves.

NGS has not only allowed us to unravel the diversity of bacterial plant pathogens but has also opened new vistas into the analysis of microbial diversity associated with plants directly or within the environment in which plants live. The emerging field of plant microbiome or phytobiome research shows much promise in elucidating the intricate interactions between plants and their phytobiomes. This accumulating information could even be employed to engineer phytobiomes to reduce disease incidence and severity or by using phytobiome members as biopesticides to control specific pathogens. Poudel *et al.* (2016) propose in their article a systems framework to elucidate microbiome networks, and more importantly, identify candidate microbes to manage plant diseases.



The genomics revolution and associated tools have also advanced strategies for control of plant viruses. The last three decades saw enormous success in engineered resistance to plant viruses using transgenes derived from viral and non-viral sequences. In recent years, gene editing and functional genomics are being used to develop novel virus resistant plants. Fondong *et al.* (2016) reviewed these technologies, viz. artificial mi-RNA, transacting small interfering RNA, and some which are more popular by their acronyms, viz. Clustered Regularly Interspaced Short Palindromic Repeat (CRISPR)-associated protein 9 (Cas9) technology and Targeting Induced Local Lesions IN Genomes (TILLING). Some of these technologies do not need a selectable marker for the selection of transgenic plants and agro infection.

With the increasing genome resources tools at our disposal, it has also become possible to tease apart complex interactions between pathogens and insect vectors. Plant viruses vectored by insects are often controlled by insecticides, which have come under increasing scrutiny in recent years. Kaur *et al.* (2016) review how NGS can be used to unravel insect genes that are up-regulated during insect–virus interactions following the acquisition of the virus. Their review specifically focuses on the interaction of a Begomo virus, Tomato yellow leaf curl virus, and a crini virus, Tomato chlorosis virus, with the whitefly vector *Bemisia tabaci* and of a tospovirus, Tomato spotted wilt virus, with Thrips *Frankliniella occidentalis*. In addition, they discuss how this new information may be exploited for the insect vector control by RNA interference.

Genomics applications for pathogen population analysis and diagnostics

Draft sequencing of pathogen genomes can provide a rapid and cost-effective means to understanding life and disease cycle attributes and provide resources for tool development required for more detailed analyses. This strategy was used to characterize the genetic diversity and population structure of the gray leaf spot pathogen of maize in South Africa (Muller *et al.* 2016). Comparing draft genomes from South Africa and the United States provided a streamlined process for identifying polymorphic small sequence repeat (SSR) markers.

Withers *et al.* (2016) describe the use of NGS to develop species-specific molecular diagnostics for the Oomycete pathogen, *Pseudoperonospora cubensis*. The study first entailed generation of NGS data for two very closely related species, *Pseudoperonospora cubensis* and *Peronospora humuli*. Sequence comparisons through bioinformatics approaches led to the finding of seven sets of markers conserved in *Pseudoperonospora cubensis* but absent from



the genomic sequence of *Peronospora humuli*. The markers were also tested against isolates of the same species and other oomycetes to provide further confirmation of specificity

Grapevine red blotch-associated virus (GRBaV) was recently identified as an emerging pathogen, which has impacted both the nurseries and premium wine grape production in the United States. In particular, the virus has impacted the wine industry in the state of California, transmission under vineyard conditions. Bahder *et al.* (2016) conducted a phylogenetic study on the amino acid sequence of the coat protein sequences of Gemini viruses and found that the coat protein of GRBaV was closely related to that of Tomato pseudo-curly top virus, a Gemini virus transmitted by treehoppers of the family Membracidae. Following this, they found that the three-cornered alfalfa hopper, *Spissistilus festinus* (Say), considered a minor pest of grapevines, was able to transmit the virus between grapevines. A quick diagnosis of the virus in the recipient plants was achieved using digital PCR technology.

Genomics accelerates development of plant disease resistance

The broadening availability of high-quality crop plant genomes is opening doors to an ever-increasing set of tools for plant breeders. This is particularly welcoming to breeders of crops with large and complex genomes such as wheat. With the wheat genome and advanced breeding genotype resources as a backdrop, Mahoney *et al.* (2016) describe taking advantage of next generation sequencing technologies to establish a genotyping-by-sequencing (GBS) strategy to map quantitative traits loci for tolerance to *Rhizoctonia* root rot. This soil borne disease is of economic concern in spring-planted wheat in the Pacific Northwest. Identification of markers for loci conferring increased levels of tolerance provides a foundation for cultivar improvement, marker development, and a new genetic resource for the management of root rot.

Also taking advantage of wheat genome resources, Pariyar *et al.* (2016) describe the use of association mapping to identify associations between phenotypic variations in susceptibility to the cyst nematode *Heterodera filipjevi* and single nucleotide polymorphisms (SNPs). Of seven quantitative trait loci (QTLs) identified by the authors, those on chromosomes 1AL, 2AS, 2BL, 3AL, and 4AL of wheat were linked to genes with predicted roles in biotic stress and plant pathogen interactions. The genome-wide association study included 161 modern winter wheat accessions, and the study of Pariyar *et al.* (2016) represents the first report of QTLs conferring resistance to *H. filipjevi* in wheat.



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