

Editorial: plant disease management in the post-genomic era: from functional geno...

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Editorial on the Research Topic

Plant Disease Management in the Post-genomic Era: From Functional Genomics to Genome Editing

The growing world population requires an efficient management and control of diseases in crop production to guarantee both food security and safety ([FAO, 2018](#) ; [Sarrocco and Vannacci, 2018](#)). The development of the so called NGS (Next Generation Sequencing) techniques has been positively welcomed as a new tool for understanding the nature of plant diseases, even if the potential for their use has not yet been fully discovered.

This Research Topic arises from the idea to give an updated and exhaustive overview of the exploitation of genome sequencing, genome comparison, transcriptomics, metagenomics, RNA based technologies, and genome editing strategies as a new frontier to contribute to plant disease management.

The knowledge of the complex relationship occurring among plants, pathogens, the environment and, eventually, beneficial organisms, is now increasing thanks to the ecological application of genomics (ecogenomics), both at single strain and at community level ([Martin, 2014](#)). Metagenomics and metatranscriptomics can be of help to describe the whole microbial community not only in terms of its ecology, but also to detect that fraction of the microbiome that, modulating the activity of plant pathogens in favor of the plant host, could be developed (as single isolate or in consortia) as biopesticides. Cobo-Díaz et al. used a concurrence culture-independent metabarcoding approach to characterize the microbial communities

associated to the incidence and composition of *Fusarium* spp. on maize stalk and other bacterial and fungal genera, using co-occurrence network analysis. Such approach could be a useful tool as part of a screening strategy for novel antagonist candidates against toxigenic *Fusarium* spp.

The wide range of beneficial microorganisms does not only include those isolates directly interacting with harmful pathogens but also consists of endophytes that, thanks to their mutualistic relationship with the host, can increase plant tolerance to biotic and abiotic stress. Pereira et al. grouped into operational taxonomic units (OTU) ITS sequences amplified from culturable fungi associated to *Festuca rubra* subsp. *pruinosa* (FRP) roots thus demonstrating a set of seven species. These seem to be the components of the core mycobiome of FRP and include very promising candidates in the adaptation of FRP plants to salinity, a characteristic stress factor of their habitat. Indeed a *Diaporthe* strain could help ryegrass (*Lolium*) to adapt to high salinity. The genome of bacterial endophyte *Paraburkholderia phytofirmans* was extensively studied by Esmaeel et al. , allowing the identification of all gene clusters which contribute to the adaptive mechanisms under different environmental conditions and explaining the high ecological competence of this microorganism, able to promote plant growth and to induce resistance to abiotic and biotic stresses.

The number of fully-sequenced and released genomes is increasing rapidly. This genomics “ revolution” gave an important contribution in plant pathology, rapidly increasing our knowledge of the molecular mechanisms underpinning pathogenesis, resistance and the mode of action of beneficial

microorganisms ([Klosterman et al., 2016](#)). Firrao et al. , through the analysis of Illumina sequence data-sets of 11 European and one non-European *Pseudomonas syringae* pv. *actinidia* (Psa) genomes, gave a picture of the significant differences in the genome evolution of this bacterium before and after a clonal expansion, thus furnishing information of great value for epidemic management. In the same way, the genome-wide analysis of the plant pathogenic bacteria *Ralstonia solanacearum* and *Xantomonas oryzae* pv. *oryzae* , performed by Cho et al. , and Doucouré et al. , respectively, will have important effect in the sustainable deployment of broad-spectrum and durable resistance to these serious pathogens.

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