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Sommario/riassunto	Crop plants are continuously under attack by pathogens, both during pre and post-harvest stages, often causing economically important food losses. Chemical treatments can pose a serious treat to human health and the environment. Furthermore, there is an increasing market, especially in OECD countries for organic produce, for which most pesticides and inorganic fertilisers are unacceptable. There is therefore a pressing need to develop more effective, sustainable and environmentally friendly tools for disease control. The use of beneficial microorganisms for the control of plant pathogens is very attractive, and the availability of novel molecular techniques and a plethora of genomic information open unexplored avenues for plant protection approaches. Genome-enabled integration of research became a major strategy in the era of the 2000's (the post-genomic era) and set the basis for a different way to understand interactions in plant-pathogen-beneficial microorganisms systems. In recent decades we have moved from the sequencing of single genomes, to the comparison of different genomes, their expression (from single organism to communities) and, more recently, we can apply novel techniques to edit a genome in a precise manner. Together with the complete sequencing of plant genomes, the genome sequences of plant pathogens as well as that of

some beneficial organisms (bacteria, fungi, viruses), and the furnished information on their virulence, gave support to relatively new strategies such as transcriptome, proteome, metabolome and secretome analysis. Analyses of avirulence and resistance genes, their products and the cross-talking mechanisms, as well as proteins and metabolites - at an "omics" level - in highly performing beneficial microorganisms/pathogens interactions, represents a major contribution to plant protection, providing information at an unprecedented level of resolution. While single genomes are explored to infer the range of biological activities accomplished by a single organism or species, and comparative genomics allows evaluating the diversity and evolution of biochemical pathways adopted by individual species to perform a common function, information is being obtained about processes carried out by a diverse set of organisms interacting with each other. Environmental genomics, popularized by the metagenome concept, can generate billions of DNA sequences from a given environment furnishing a comparative assessment of a community in situ. Metagenomics (sequence-based approaches applied across genomes in an environment) provides information about functional capabilities and responses of organism (plant, pathogen and beneficial agent) assemblages in different niches, giving a different perspective in the management of plant diseases at a multitrophic level. Advances in functional genomics and genome editing approaches have recently provided new tools to manage the plant-pathogen-beneficial microorganism system, for preventing or controlling disease. The use of RNA-based technologies is extremely appealing, and these include artificial micro-RNA and transacting small interfering RNA, which are currently being used for generating plant virus-resistant plants, thus fostering plant virus control researches. Finally, targeted genome editing strategies - exemplified by, but not limited to, the CRISPR-Cas technique - are among the most modern ways for inducing targeted deletions, insertions and precise changes in the genome of host plants or pathogens, as well as in the genomes of beneficial microorganisms. The aim of the present Research Topic is to give an exhaustive and up to date overview of examples of genomic techniques (genome sequencing, genome comparison, transcriptomics, metagenomics, RNA based technologies and genome editing strategies) applied to plants, pathogens or beneficial microorganisms to promote the exploitation of these modern tools as a new frontier in plant disease management.
