

**The plant microbiome: beyond collecting stamps.** J.M. RAAIJMAKERS<sup>1,2</sup>, M. MEDEMA<sup>3</sup>, V. TRACANA<sup>3</sup>, M. DE HOLLANDER<sup>1</sup>, J. PEREZ-JARAMILLO<sup>1</sup>, V. CARRION BRAVO<sup>1</sup>. <sup>1</sup>Netherlands Institute of Ecology (NIOO-KNAW), Netherlands. <sup>2</sup>Institute of Biology, Leiden University, Netherlands. <sup>3</sup>Wageningen University, Department of Bioinformatics, Netherlands. E-mail: J.Raaijmakers@nioo.knaw.nl

Plant roots are colonized by many microorganisms, populations of which can reach cell densities much greater than the number of plant cells. Various studies have shown that members of the plant microbiome contribute to plant tolerance to abiotic (e.g. drought) and biotic (e.g. pathogens) stress factors, but also to plant nutrition, growth and development. For the majority of plant-associated microorganisms, however, there is limited knowledge on their support functions and the mechanisms involved. Novel -omics technologies have provided in-depth knowledge of the diversity and functioning of plant microbiomes and significant advances are being made to uncover mechanisms, genes and metabolites involved in the multi-trophic interactions in these microbiomes. To better understand this complexity, reductionist and systems approaches are needed to identify the biotic and abiotic factors involved in microbiome assembly and activity. New results are presented on the role of rhizosphere and endosphere bacteria in protection of plants against soil-borne pathogens. For rhizosphere bacteria, we have shown that representatives of the Proteobacteria protect plants from pathogen infection by the production of chlorinated peptides and alteration of root architecture and plant growth via modulation of sulfur assimilation. In-depth metagenomic sequencing of the endosphere allowed *de novo* assembly of high quality bacterial genomes, and revealed various yet unknown biosynthetic genes and pathways with potential for plant protection and antibiotic discovery. An overview is presented on the wealth of genes and functions of the plant microbiome.

**Innovative remote sensing and species distribution modeling to detect and predict the potential spread of *Xylella fastidiosa*.** J.A. NAVAS-CORTÉS. *Institute for Sustainable Agriculture (IAS), Spanish National Research Council (CSIC), Menéndez Pidal s/n, 14004 Córdoba, Spain. E-mail: j.navas@csic.es*

Control of *Xylella fastidiosa*, once established in a territory, is difficult to attain, so efforts should focus on development of preventive measures. Remote sensing has been shown to be a useful decision support tool for crop management, through early detection and implementation of surveillance programmes that assist limitation of pathogen spread to new areas. A collaboration between JRC-European Commission and the POnTE consortium was established to develop a robust and accurate method for the automatic classification of *X. fastidiosa* infection and disease severity at large scales. Remote sensing information can be combined with species distribution models (SDMs), that determine relationships between sampled locations for a species and associated environmental variables, and these are used to estimate the ecological requirements of the species. SDMs provide realistic scenarios to explain the influence of bioclimatic variables on the epidemiology of plant diseases, particularly those caused by “new” plant pathogens. We used correlative niche models to quantify and map the global patterns of the potential geographic distribution of *Xylella fastidiosa*. Overall, projected potential distribution from estimated models conformed well with the current known distribution of *X. fastidiosa*. The application of SDMs to the most prevalent *X. fastidiosa* subspecies will be discussed.

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**Grapevine trunk diseases: a need for clarity in concepts and definitions.** G. SURICO, L. MUGNAI. *Dipartimento di Scienze delle Produzioni Agroalimentari e dell’Ambiente, University of Florence, Piazzale delle Cascine 28, 50144 Firenze, Italy. E-mail: giuseppe.surico@unifi.it*

Grapevine wood diseases (more than 20 of these can be listed), usually called Grapevine Trunk Diseases (GTD), became a major and increasing problem for vinegrowers in the last decades. Besides the economic impacts of GTDs, there is in recognition, description, attribution and nomenclature for some of them. At the beginning of the 20<sup>th</sup> century, several authors