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Autore	Nicolas Denance
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Sommario/riassunto	Phytopathogenic bacteria of the Xanthomonas genus cause severe diseases on hundreds of host plants, including economically important crops, such as bean, cabbage, cassava, citrus, hemp, pepper, rice, sugarcane, tomato or wheat. Diseases occurring in nature comprise bacterial blight, canker, necrosis, rot, scald, spot, streak or wilt. Xanthomonas spp. are distributed worldwide and pathogenic and nonpathogenic strains are essentially found in association to plants. Some phytopathogenic strains are emergent or re-emergent and, consequently, dramatically impact agriculture, economy and food safety. During the last decades, massive efforts were undertaken to decipher Xanthomonas biology. So far, more than one hundred complete or draft genomes from diverse Xanthomonas species have been sequenced (http://www.xanthomonas.org), thus providing powerful tools to study genetic determinants triggering pathogenicity and adaptation to plant habitats. Xanthomonas spp. employ an arsenal of virulence factors to invade its host, including extracellular polysaccharides, plant cell wall-degrading enzymes, adhesins and secreted effectors. In most xanthomonads, type III secretion (T3S) system and secreted effectors (T3Es) are essential to bacterial pathogenicity through the inhibition of plant immunity or the induction of plant susceptibility (S) genes, as reported for Transcription Activation-Like (TAL) effectors. Yet, toxins can also be major virulence determinants in some xanthomonads while nonpathogenic

Xanthomonas species do live in sympatry with plant without any T3S systems nor T3Es. In a context of ever increasing international commercial exchanges and modifications of the climate, monitoring and regulating pathogens spread is of crucial importance for food security. A deep knowledge of the genomic diversity of Xanthomonas spp. is required for scientists to properly identify strains, to help preventing future disease outbreaks and to achieve knowledge-informed sustainable disease resistance in crops. This Research Topic published in the 'Plant Biotic Interactions' section of Frontiers in Plant Science and Frontiers in Microbiology aims at illustrating several of the recent achievements of the Xanthomonas community. We collected twelve manuscripts dealing with comparative genomics or T3E repertoires, including five focusing on TAL effectors which we hope will contribute to advance research on plant pathogenic bacteria.