a putative virulence gene, *srfA* and *srfB*, respectively, in *P. syringae* pv. *syringae* B728. Little is known about the functions of these genes in DC3000. Knockout mutants of *srfABC* operon were constructed in DC3000 and currently being characterized. The results indicate that the carbonic anhydrase, CynT is a key regulator for bacterial factors related to pathogenesis and virulence.

Versatile activities of *Arabidopsis berberine* bridge enzyme-like (BBE-l) proteins

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The oligogalacturonide oxidase 1 (OGOX1) and cellodextrin oxidase (CELLOX) are BBE-l enzymes that oxidize, respectively, oligogalacturonides (OGs) and cellodextrins (CDs), thereby inactivating their elicitor nature and concomitantly releasing H_2O_2. By using a multienzyme–based assay, we demonstrated that the H_2O_2 generated downstream of the combined action of a fungal polygalacturonase and OGOX1 on pectin, or an endoglucanase and CELLOX on cellulose, can be directed by plant peroxidases (PODs) either towards reactions possibly involved in plant defense (e.g., oxidation of monolignol) or others possibly involved in a developmental event (e.g., oxidation of auxin), pointing to these cell wall oxidases as enzymatic transducers between microbial glycoside hydrolases and plant PODs. Moreover, we identified a novel reaction mechanism through which the activity of BBE-l oxidases on cell wall oligosaccharides scavenged the radical cation $ABTS^{\bullet+}$ with an efficiency dependent on the type and length of the oxidized oligosaccharides. In contrast to the oxidation of longer oligosaccharides, the activity on short galacturonan- and cellulose-oligomers successfully counteracted the radical cation-generating activity of a fungal laccase, suggesting that BBE-l oxidases can generate radical cation scavenging activity in the apoplast with a power proportional to the extent of degradation of the plant cell wall, with possible implications for redox homeostasis and defense against oxidative stress.

The elephant in the plant: Let's talk about a lesser known 'omonas

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The bacterial genus *Sphingomonas* from the class Alphaproteobacteria is common on leaves and roots of a wide variety of plants, and is widespread in soil and water. However, despite high abundances little is known, in contrast to the (in)famous abundant genus *Pseudomonas*, with which its name rhymes. Analyzing the genomes of over 400 plant-associated *Sphingomonas* reveals an arsenal of genes for biotic interactions and great genomic diversity, especially compared to *Pseudomonas* isolated from the same plants. As there are no important *Sphingomonas* plant pathogens, such genes are presumably either involved in positive interactions with the plant or interactions with other microbes. Some *Sphingomonas*, including some of our isolates, can protect against bacterial and fungal pathogens, and others are reported to promote plant growth through other means. Fascinatingly, *Sphingomonas* seem to rely on healthy plant cells for their success, as they are quickly outcompeted in injured plant tissue. Using a subset of isolates from which we have closed the genomes, we are undertaking in my new group a deeper study of the genes involved in association with plants using experimental mutant screens, studying bacterial transcription in various environments, and characterizing its namesake sphingolipids that replace lipopolysaccharides to comprise its outer cell membrane.

Understanding the hypervariability of HYP effectors in potato cyst nematodes

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Plant-parasitic nematodes have evolved a large repertoire of effectors. Like many effectors, HYPs are secreted into the host and are necessary for infection. HYP genes consist of a 'hyper-variable' domain characterized by variable number, organization, and subfamily-specific repeats. The hyper-variable domain is flanked by 410 and 94 nucleotides that have remained 95% identical for ~30 million years of evolution. The objective of this research is to understand how it is possible for the genome of an animal to permit such variability in a single domain of a gene family, while maintaining the stability of the genome in general, and HYPs in particular. In order to capture the entire HYP gene in a single read we sequenced the genomes of *Globodera pallida* and *G. rostochiensis* using long-read sequencing technologies. Strikingly, we found that the dominant majority of HYP variation is allelic. To unravel the extent of such unprecedented diversity in an allelic series of a single gene, we have performed Cas9-based targeted Nanopore sequencing to enrich for HYP gene containing locus. Additionally, we have performed amplicon sequencing of multiple individuals across the lifecycle using Pacbio HiFi sequencing to understand when and how HYP variation is introduced. Latest results from these efforts at understanding the extent and nature of HYP diversity, and potentially yet unknown biology underlying HYP variation will be presented.

The tomato-*Phytophthora cinnamomi* pathosystem

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Phytophthora cinnamomi Rands (Pc), is considered one of the most virulent and invasive phytopathogens in the world, with a high incidence in non-forest and forest species such as chestnut, cork and holm oaks, avocado, blackberry, or tomato, causing leaf and root rot, crown, and trunk canker. The life cycle of Pc involves the production of highly virulent mobile asexual zoospores (Zs), which allows their dispersion of them through soil and water currents by the aquatic environment, stablishing a high biodiversity of belowground interactions with several host. At this work we will show new approaches for the management of Zs under strictly controlled conditions, at the laboratory. Those techniques allowed us to simulate nature in the laboratory, for inoculating tomato seedlings with Zs. This poor studied pathosystem, allowed us to expand our current knowledge about the biodiversity of Pc's abilities to interact with plant host.