Risk Assessment of Endophytes

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A whole-genome comparison of virulence traits in endophytic genomes of enterobacteria

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Endophytes are roughly defined as microorganisms living inside plants without causing them harm. Plant pathogens and endophytes co-exist and often interact with the plant host and within its microbial community. The outcome of this interaction may lead to healthy plants or to plant disease, through the inducible production of molecules known as virulence factors.

It is now clear that some of the endophytes of grapevine have a human origin. For example, species known as human pathogens were transmitted to plants during the domestication of consumable species (Campisano et al., 2014). This is in agreement with other findings showing that the endosphere of grapevine is filled with species belonging to groups categorized as pathogenic (Yousaf et al., 2014). These studies suggest that there is a connection between endophytes and pathogens that might refer to the origin of endophytes as a group. However the very keys of the endophytic and pathogenic lifestyles rest in the genomes of bacteria.

Genomics is an outstanding tool for analysing the ecology, biotechnological properties and life history of microorganisms. Bacterial comparative genomics has highlighted how the genomes of endosymbionts and free living organisms differ, in that the former have drastically being reduced and re-arranged. Nontheless, the genomic differences between bacterial endophytes and plant pathogens are not quite clear.

In this study we compare the genomes of 7 endophytic strains belonging to the genera *Pantoea*, *Enterobacter* and *Erwinia* with a panel of reference strains known to be pathogenic or endophytic. A whole-genome alignment revealed that the genomes of endophytes seem to be smaller than the ones from pathogens and analysis of othologous-gene content showed that the core genomes contain 2648, 2301 and 2913 gene families in *Enterobacter*, *Erwinia* and *Pantoea* respectively. We show that pathogens and endophytes share genes coding virulence factors like cell wall degrading enzymes, protein secretion systems, siderophores and pathogenicity islands, but also genes that might be determinant for the association with plants and that to the best of our knowledge were never before reported, like the NUDIX complex and several two component systems.

Finally we quantify the number of virulence factors in endophytic and pathogenic strains in the core and the accesory genomes and show that endophytes and pathogens have very little differences in content of virulence factors, however the distribution and gene context varies between the two groups.

Campisano, A., Ometto, L., Compant, S., Pancher, M., Antonielli, L., Yousaf, S., Varotto, C., Anfora, G., Pertot, I., Sessitsch, A., and Rota-Stabelli, O. (2014). Interkingdom transfer of the acne-causing agent, Propionibacterium acnes, from human to grapevine.*Mol Biol Evol* 31**,** 1059-1065. doi: 10.1093/molbev/msu075.

Yousaf, S., Bulgari, D., Bergna, A., Pancher, M., Quaglino, F., Casati, P., and Campisano, A. (2014). Pyrosequencing detects human and animal pathogenic taxa in the grapevine endosphere. *Frontiers in Microbiology* 5.doi: 10.3389/fmicb.2014.00327.