Understanding microbial interactions in infectious diseases to improve diagnostic and therapeutic success

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The human microbiome project changed the fundamental understanding of how microorganism interact with the human host, wherein synergistic and antagonistic interactions can be observed. Classical biomedical research focused on understanding how bacterial-host interactions could influence disease progression. Yet less explored, bacterial-bacterial interactions can also contribute to disease progression and to therapeutic failure. Examples of microbial interactions leading to disease include cystic fibrosis, dental caries or bacterial vaginosis. While the first two are currently easily diagnosed, bacterial vaginosis presents an increased challenge, mainly because its etiology is yet fully understood. Bacterial vaginosis is the most frequent cause of vaginal discomfort worldwide, and is also linked to serious medical conditions, including preterm birth and increased risk of acquisition of HIV. The bacterial interactions occurring during bacterial vaginosis are thought to be responsible for therapeutic failure, leading to very high recurrence rates. Despite the worldwide prevalence and the significant economic cost, researchers haven't yet identified bacterial vaginosis etiology, but current consensus is that a polymicrobial biofilm is involved.

During this talk, I will highlight two projects wherein my research group is aiming to (i) provide a better picture of how these bacterial species interactions enhance protection against current and/or potential novel antimicrobial agents or (ii) using the presence of key bacterial interactions as a mean to develop robust molecular diagnosis methods.