1 Introduction

The relationships between bacteria and their hosts has recently exploded into the forefront of scientific thought and discussion especially in regards to the modulating effect they have on human health[11]. This revelation is nothing not new in the plant science community as it has long been known that legumes, for example, harbor communities of bacteria in their root nodules which fix atmospheric nitrogen and release it in usable form into the soil-root interface, or rhizosphere—ultimately allowing the plant and the surrounding microbiota to benefit[28]. The excitement currently observed in this 'revolution', especially in the therapeutic benefits that may derived[5,6] are primarily human-centered and is largely the after-effect of sequencing technologies having come of age. As the costs of these technologies have gone down it has been possible to sequence larger and larger amounts of genetic information which can then leveraged find new therapeutic avenues, not only in human medicine but as well to plant sciences.

As the techniques to study these microbial communities evolve they have given rise to new questions that large collections of genetic information alone cannot answer. While the current paradigm can identify subsets of beneficial bacteria and their relative abundances which impart benefits to their host, the underlying mechanism that govern their establishment and stability are not well understood. In order to better understand the interactions that allow communities to coalesce into beneficial forms as well as to asses those which are detrimental to plant health, new techniques have to be developed which can leverage the genetic data that can be derived from them. Towards this extent, the Garrido-Oter lab at the Max Planck Institute for Plant Breeding Research is developing a system which aims to do just that. This system employs rationally designed synthetic communities which can be monitored in real-time through absorbance spectrophotometry and subsequently sequenced during times of observable differences in their abundances which may have an underlying genetic cause.

The system, currently under development, employs soil-derived bacterial taxa, which form part of the core root microbiota [21,23] and the ubiquitous freshwater algae, *Chlamydomonas reinhardtii* as host, in aqueous conditions. Preliminary results have indicated that, together,

these organisms behave as would be expected in true phycospheres—the aquatic analogue of the rhizosphere. Through designing synthetic communities and inoculating them in a photobioreactor which is able simulate the conditions of phycospheres and sequencing them as necessary, they can begin to unravel some of the unanswered questions that remain in the field. Through these revelations, future synthetic communities can be designed which would yield phenotypes that confer certain levels of protection to their host plant and promote their growth.

The resolution of the concentrations of the components (bacteria or Chlamydomonas) in the system, however, remains at large. Through the use of models based on the Beer-Lambert law, the relative composition in these modeled phycospheres can begin to be determined. Ongoing experiments have amassed data which are given to conduct this work. In these data, specific strains of bacteria are co-inoculated with Chlamydomonas and, once their measured signals are resolved, should yield those which have impart benefits or detriments to said host. Thus the work ahead aims establish the models which can resolve the measured absorbance data obtained from synthetic phycospheres, modeled in microplates and a photobioreactor, and extract the desired strains. Subsequently, these models will also be tested to determine model transferability from Tecan-measured absorbance calibration data to the photobioreactor system. If the transfer of the models are successful they will then be correlated with measured against 16S relative abundance data and cell count estimations in order to optimally enhance the phycosphere modeling system.