BioFrontiers - Biology Seminar

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Inter-Kingdom Signaling -- A *Populus* Case Study

Experimental evidence pointing to inter-kingdom signaling between *Populus* and its endophytic community will be presented specifically related to *Laccaria* colonization, Small Secreted Protein Signaling and Quorum Sensing. These data initially emerged from the sequenced, assembled and annotated *Populus* genome, where over 35 archaeal, bacterial and fungal genomes were detected and assembled. Since then over 500 bacterial endophytic and 35 fungal associates have been sequenced, assembled and annotated from *Populus*. As result of these efforts, *Populus* lectin receptor-like kinase has been identified that control *Laccaria* colonization. The *Populus* transgenes has been transformed into Arabidopsis, which resulted in the formation of a Hartig-net, the first report of a mycorrhizal association in Arabidopsis. The PtRLK gene induces metabolic changes in Arabidopsis that mimic fungal challenge but in the presence of *Laccaria* these responses subside. From the assembled *Populus* genome over 200 small secreted proteins have been identified and characterized. Several of these are actively taken up by fungal associates and are then subsequently localized to the nucleus of *Laccaria*. The presence of the *Populus* secreted proteins in the *Laccaria* nuclei cause changes in *Laccaria* hyphal branching. From the *Populus*-based, endophytic bacterial collection, several genera, i.e., *Rhizobium*, *Rahnella*, *Albidiferax* and *Pseudomonas*, were found to contain quorum sensing genes that respond to *Populus* leaf macerate. The plant signal is actively transported and is most likely a dipeptide, resembling a D-Ala-D-Leu dimer. It appears that *Populus* has metabolic signals that attract favorable bacteria via co-option of their quorum sensing machinery. Strategies for leveraging this information indicate we may be able to intentionally and specifically manage the *Populus* microbiome in an environmentally relevant manner. Inter-kingdom signaling between a plant host and its microbiome, through exchange of metabolites and proteins, appears to be pervasive.

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