

Tracing bacterial and oomycete communities in lettuce greenhouse production

Cora S. McGehee and Rosa E. Raudales

Department of Plant Science and Landscape Architecture, University of Connecticut, 1376

Storrs Rd., Storrs, CT 06269, USA

The objective of this project was to characterize bacterial and oomycete communities associated with lettuce at different production stages in a commercial greenhouse. DNA was isolated from surfaces at the sowing station, seedlings trays, deep-water culture foam rafts, lettuce roots, nutrient solution liners and liquid samples from the water source as it entered in the greenhouse, water after carbon filtration, and nutrient solution. High-throughput sequencing was used to amplify the 16S rRNA regions of bacterial communities and metabarcoding of the internal transcribed spacer regions 6 and 7 with adapter overhang sequences to identify oomycetes. *Pythium* was detected in all samples with an abundance of 80% across all production stages. The predominant oomycete species detected in production stages were *Pythium aphanidermatum*, *Pythium dissotocum*, *Pythium myriotylum*, and *Phytophthora cryptogea*. The most commonly identified bacterial phyla and genus across all of the production stages was Proteobacteria (53%) and *Pseudomonas* (29%), especially in the sowing and seedling stages. The greatest alpha diversity of taxa based on Shannon-Weiner diversity index and Simpson's index of diversity occurred in the nutrient solution and late-stage surfaces for both bacteria and oomycete populations. The detection of pathogenic oomycetes and bacterial communities in production areas may assist with targeted control strategies.