

## Best talk / Post-Doc

### Long-term maintenance and expansions of dozens of pathogenic *Pseudomonas* strains within *A. thaliana* populations.

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Crop disease outbreaks are commonly associated with the clonal expansion of single pathogenic lineages, until new genetic resistances are deployed by plant breeders. Whether similar boom-and-bust scenarios hold for natural plant pathogens is mostly unknown. To address this question, we are studying the bacterial genus, *Pseudomonas*, known to contain important plant pathogens, and its colonization of a wild host, *Arabidopsis thaliana*. We initially carried out a multi-year 16S rDNA survey of *Pseudomonas* in *A. thaliana* leaves at hundred-km scales. The most common lineage, defined as a 16S rDNA operational taxonomic unit (OTU), corresponded to a pathogenic clade present in all sites. It was the most successful plant colonizer and was significantly correlated with total microbial load. To determine whether this OTU ubiquity indicated the clonal expansion of a single *Pseudomonas* lineage, or whether the 16S rDNA similarity masked greater underlying diversity, we cultured and sequenced 1,524 *Pseudomonas* genomes from more than 130 *A. thaliana* individuals. We found that this persistent OTU was composed of dozens of pathogenic lineages that differ in gene content and disease phenotype. This clade diverged more than 100,000 years ago, prior to *A. thaliana* recolonization after the last glacial maximum. Single lineages reached high frequencies within plants, but different lineages dominated across plants. The abundance of this OTU, along with the maintenance of diversity in this pathogen lineage, suggests not only that genetic innovations underlying the success of the lineage are rooted deeply in the OTU phylogeny, but also that in contrast to crop systems, no single strain overtook *A. thaliana* populations. An important question for the future is how much of this is explained by host genetic diversity, and how much by an environment more complex than that in agricultural systems.

**Keywords:** Pathogen diversity, clonal expansion, wild vs. agricultural populations, from metagenomics to strains.