

Stop the Rot Onion Bacterial Project
Stakeholder Advisory Panel meeting
27 March 2024



Objective A2a

Pathogenomics

<https://alliumnet.com/projects/stop-the-rot/>

USDA NIFA SCRI Project No. 2019-51181-30013



United States
Department of
Agriculture

National Institute
of Food and
Agriculture

Pathogenomics of *Pantoea* onion pathogens

Why *Pantoea agglomerans*?

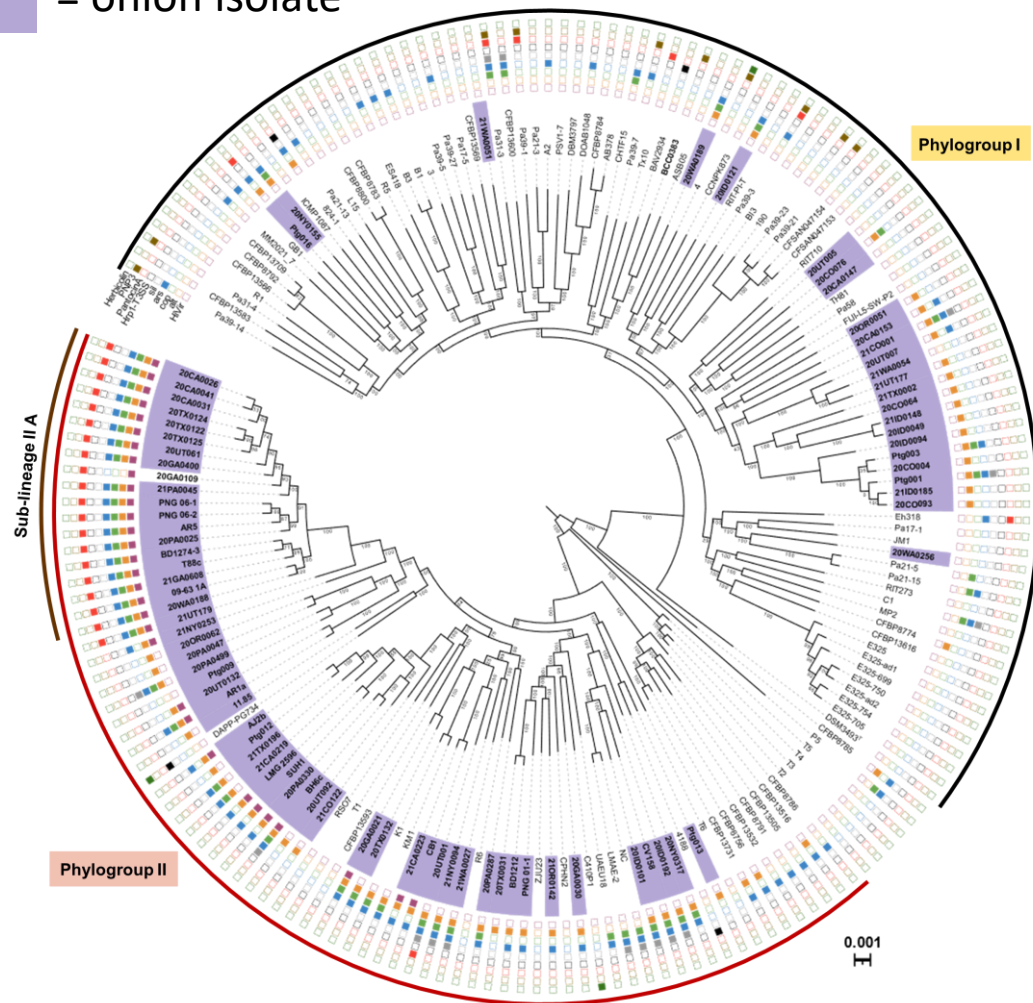
- *P. agglomerans* is isolated routinely from symptomatic onions nationwide. However, not all *P. agglomerans* strains cause disease in onions.
- Pathogenomics approach: Couple disease phenotyping with comparative genomics to identify genes associated with pathogenic strains.

What's the goal?

- Identify *Pantoea* onion pathogen-specific gene targets for development of improved diagnostic tools.
- Leverage genomic insights (e.g. distribution of copper resistance genes) to help inform management strategies for various regions of onion production around the USA.

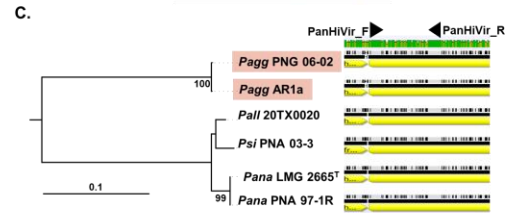
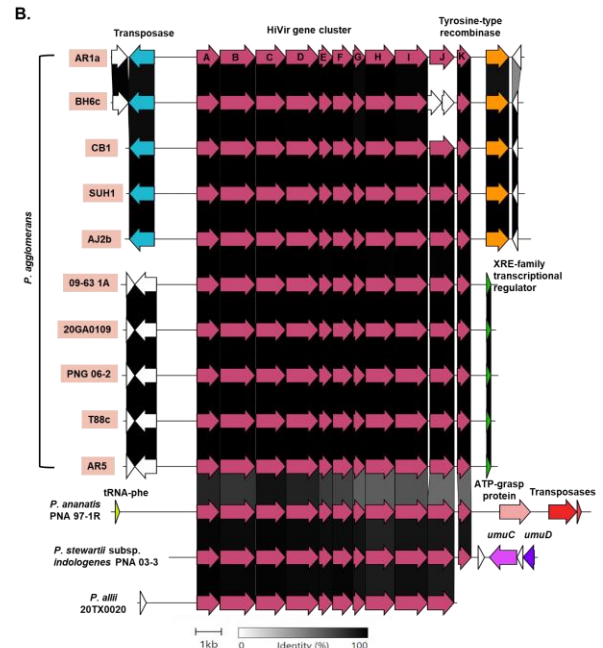
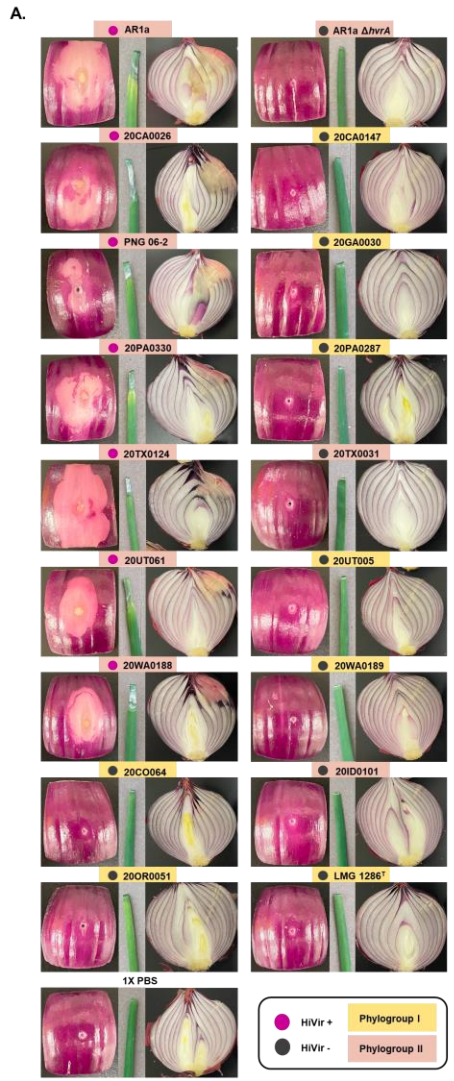
P. agglomerans genomic family tree

■ = onion isolate

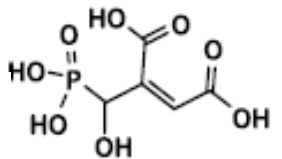


- Generated genome assemblies for 81 *P. agglomerans* (Pagg) strains (79 from onion)
- Combined with 100 high quality public Pagg genome assemblies for analysis
- Pagg strains in 2 large groups
- Onion isolates from both groups but more commonly from Phylogroup II
- Most onion isolates have *alt* genes for thiosulfate tolerance ■
- Necrosis-inducing HiVir encoding strains only in Phylogroup II ■

P. agglomerans HiVir+ strains can cause onion necrosis



Polidore et al. 2021



2-hydroxyphosphonomethyl-maleate (pantaphos)

D.

		Genotype	
		HiVir +	HiVir -
Phenotype	RSN +	59	0
	RSN -	0	247

306 *P. agglomerans* strains

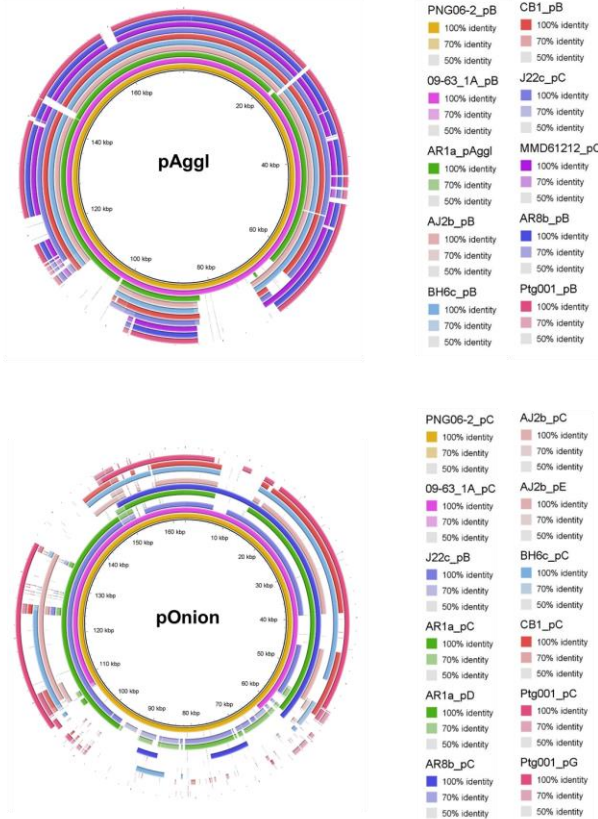
- HiVir = 11-gene cluster that codes for synthetic pathway for herbicide-like phytotoxin pantaphos
- HiVir encoding *Pagg* strains caused red scale necrosis, bulb necrosis, and foliar necrosis
- HiVir genes were similar (not identical) to HiVir cluster of other *Pantoea* spp.
- 59 RSN+ *Pagg* strains were HiVir+ and in Phylogroup II

P. agglomerans HiVir and *alt* virulence genes and copper resistance genes are found on plasmids

A.

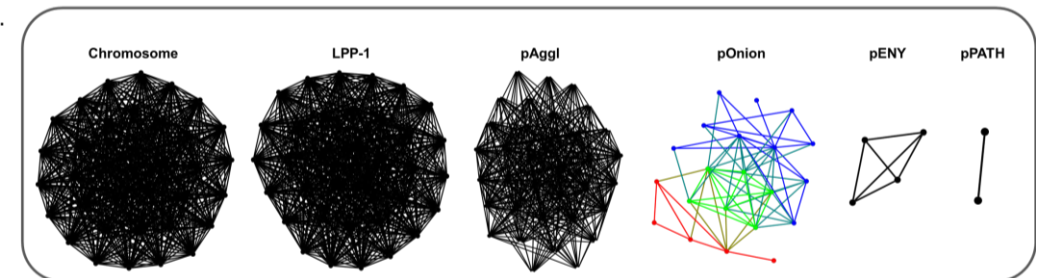


B.

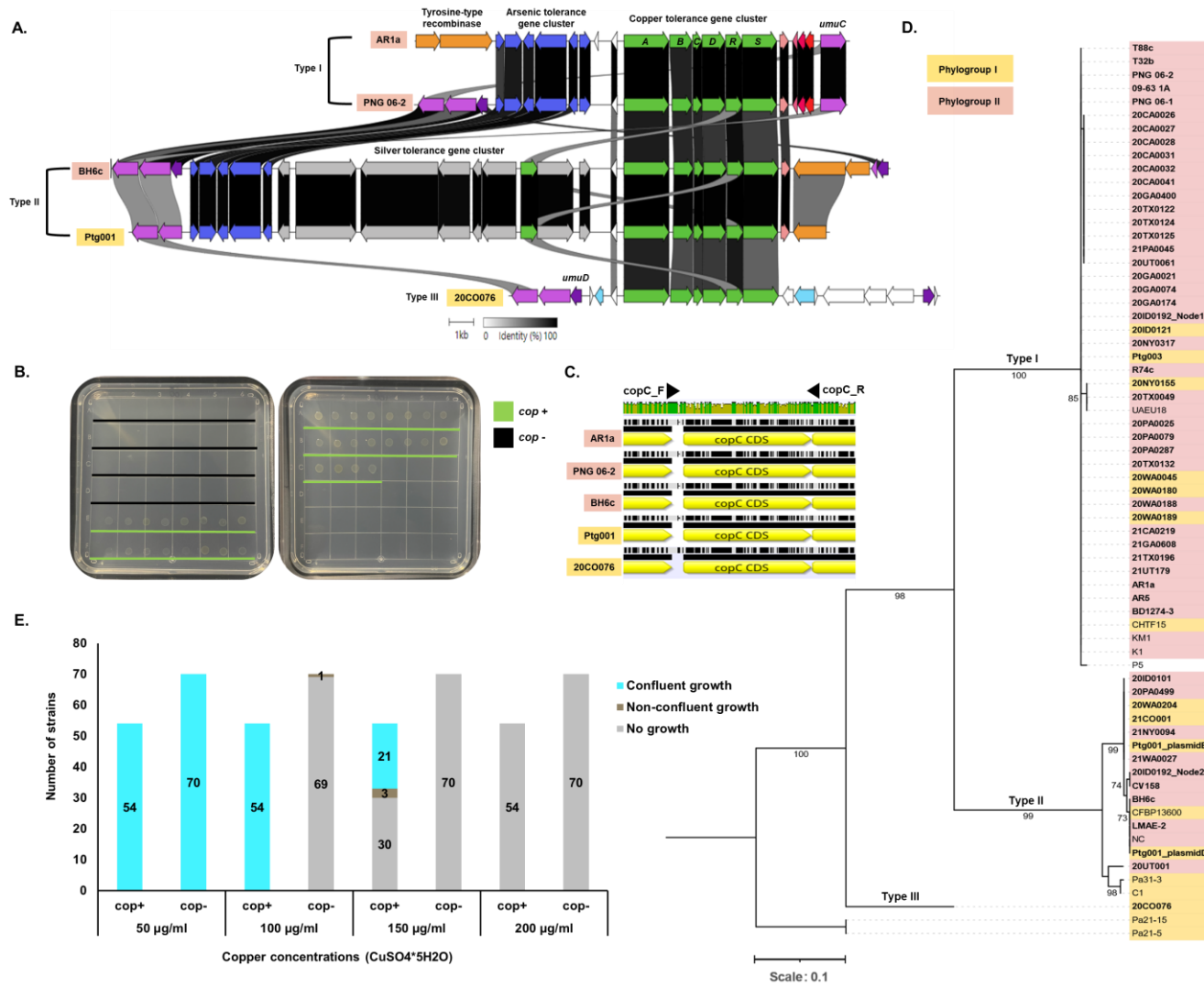


- Pagg HiVir genes encoded on two different types of plasmid
 - pAggl (conserved across Pagg)
 - pOnion (mosaic in Pagg onion isolates)
- pOnion plasmids encode *alt* genes and sometimes copper resistance genes

C.



P. agglomerans frequently encodes copper resistance genes



- Pagg 6-gene copper resistance clusters (*copABCDRS*) divided into three types
- Copper resistance genes found in both Phylogroup I and II strains
- All 3 types of copper resistance gene clusters associated with elevated copper resistance in laboratory assays

Recommendations & questions from Stakeholder Advisory Panel on pathogenomics & copper tolerance