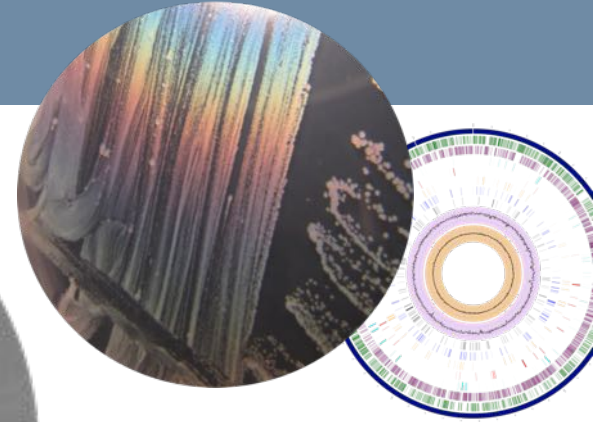
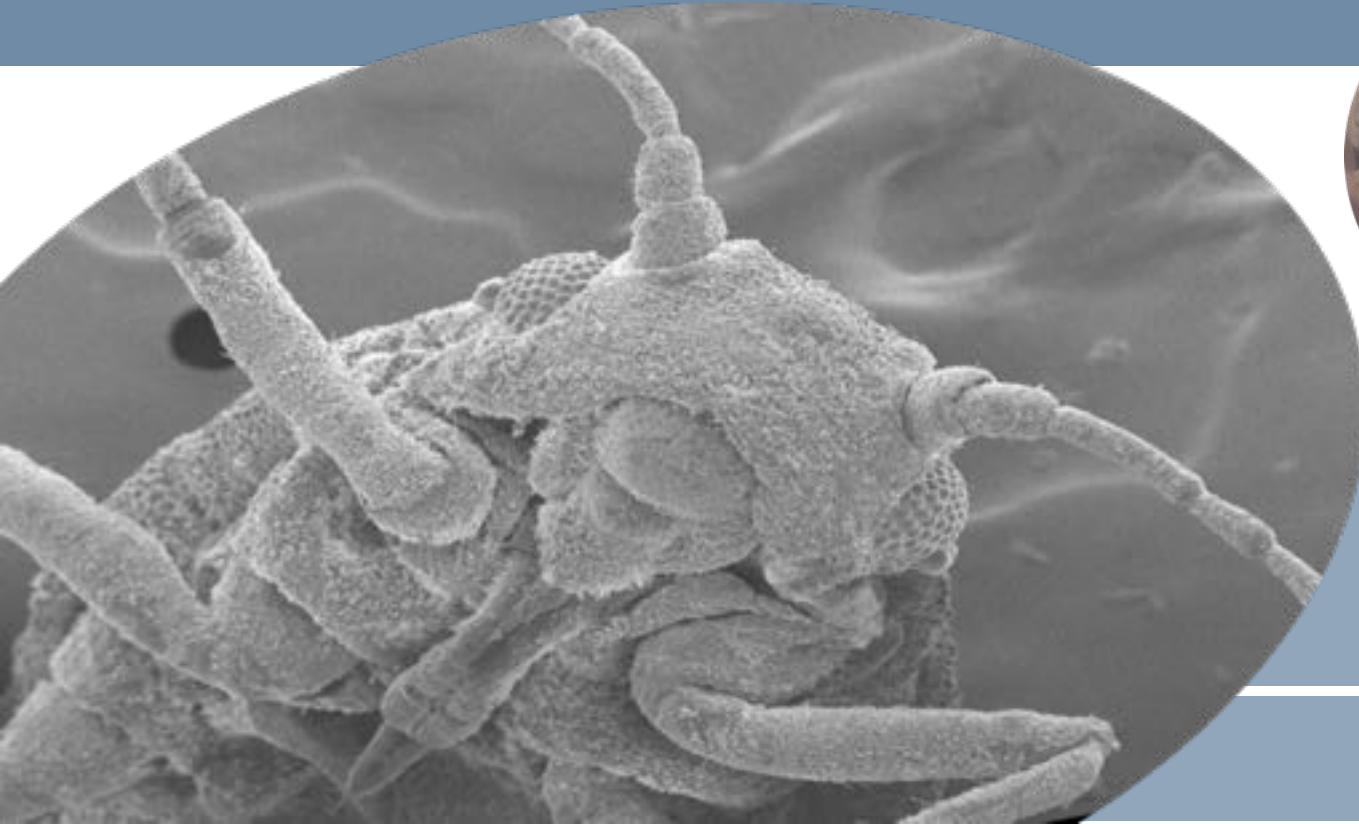


# Insect-Bacteria-Plant Interactions: Microbiomes of Russian wheat aphid contain bacteria that increase virulence to wheat



**Emily Luna**

Colorado State University

PAG-San Diego  
January, 2019





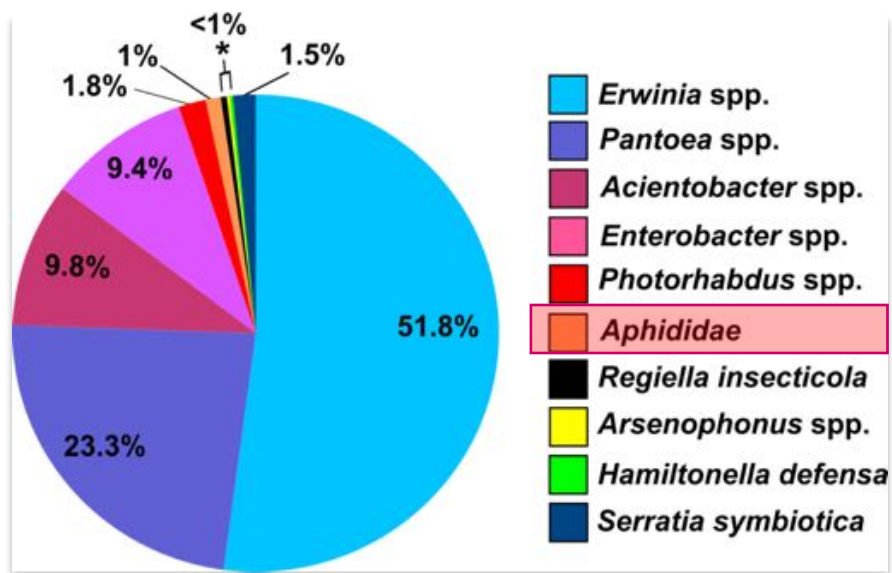


Do **bacteria**  
associated with  
Russian wheat **aphids**  
(RWA) enhance aphid  
virulence to **plants**?





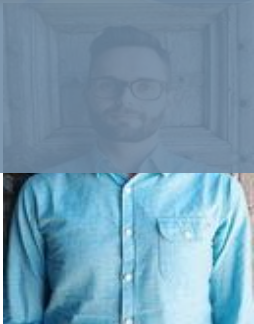
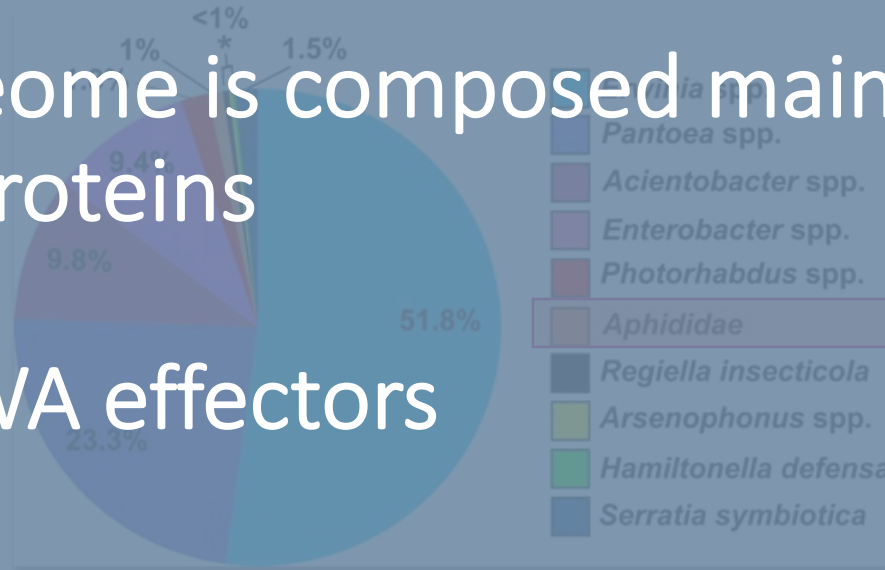
Leon van Eck





Salivary proteome is composed mainly  
of bacterial proteins

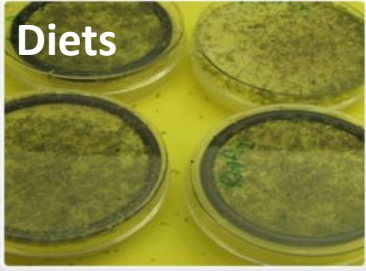
No known RWA effectors



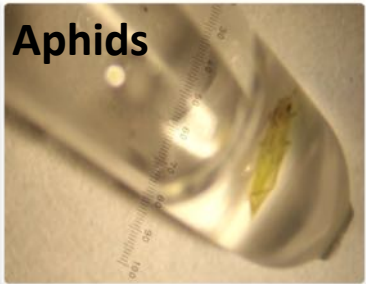
Leon van Eck

# Which bacteria are present in the system?

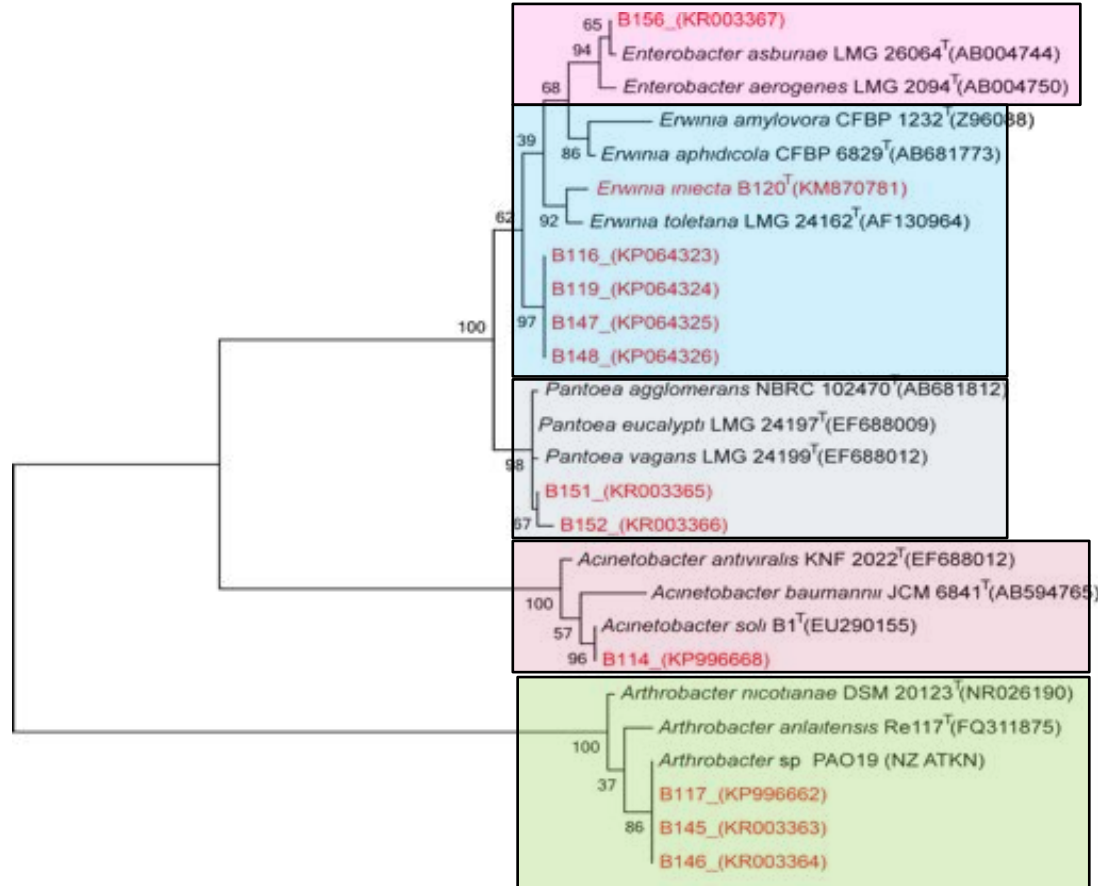
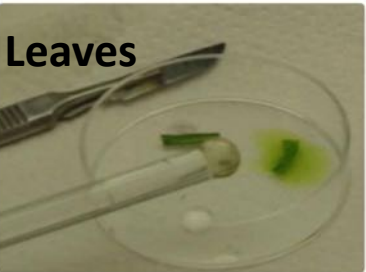
Diets



Aphids

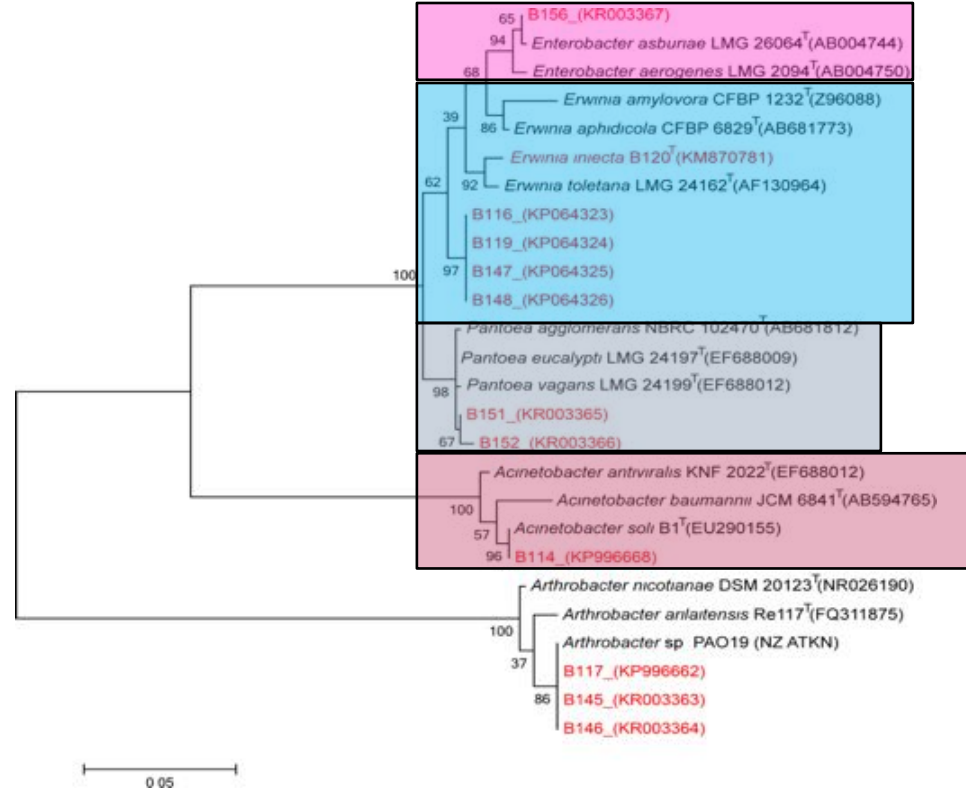
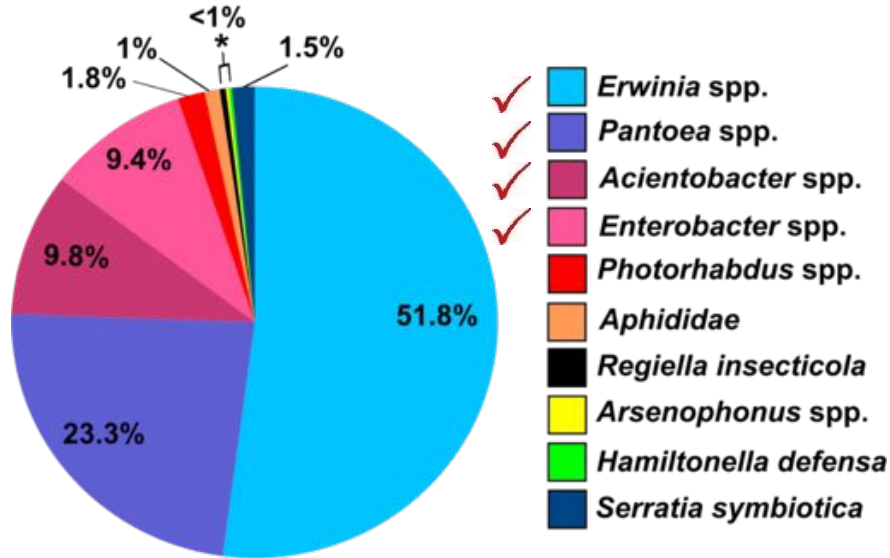


Leaves

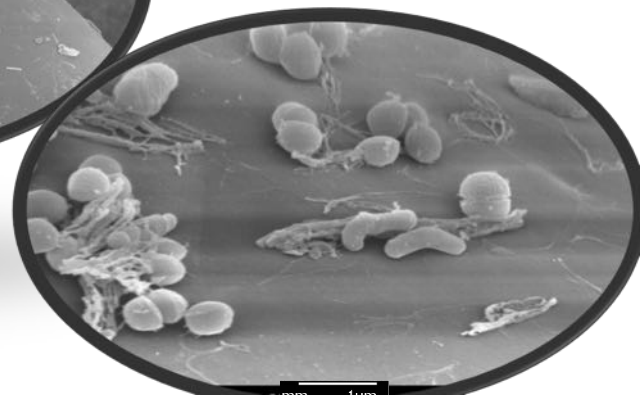
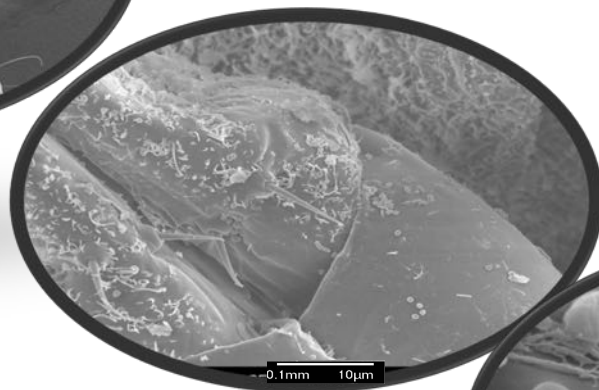
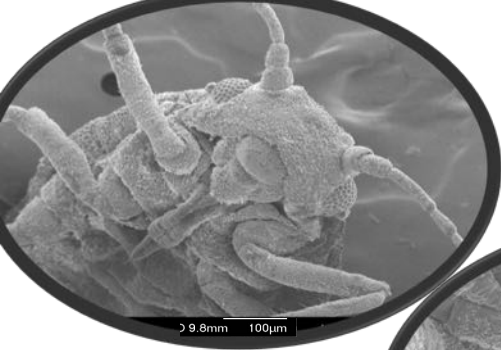


Tony Campillo

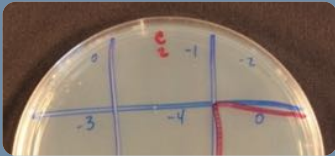
# Isolated bacteria recapitulates proteins found in RWA saliva



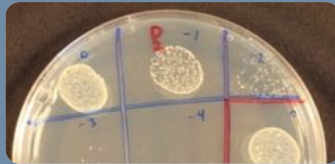




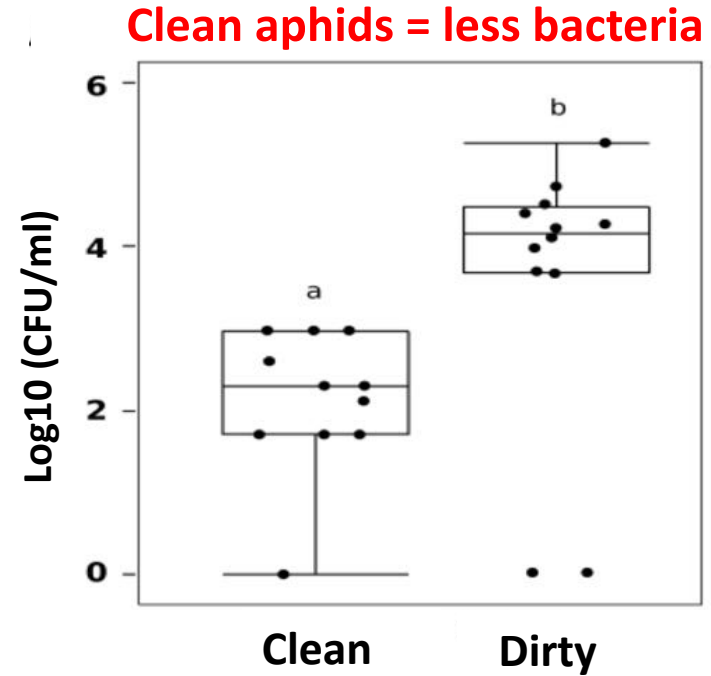
# Rearing aphid colonies with less bacteria



Clean



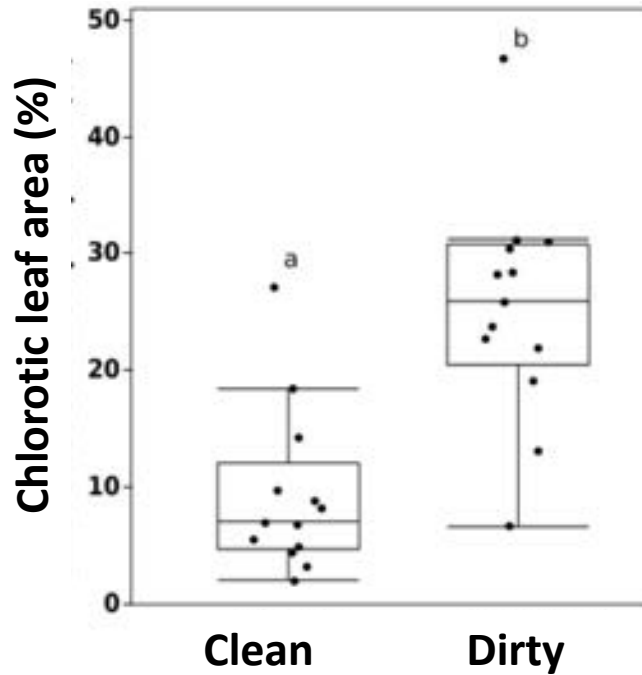
Dirty



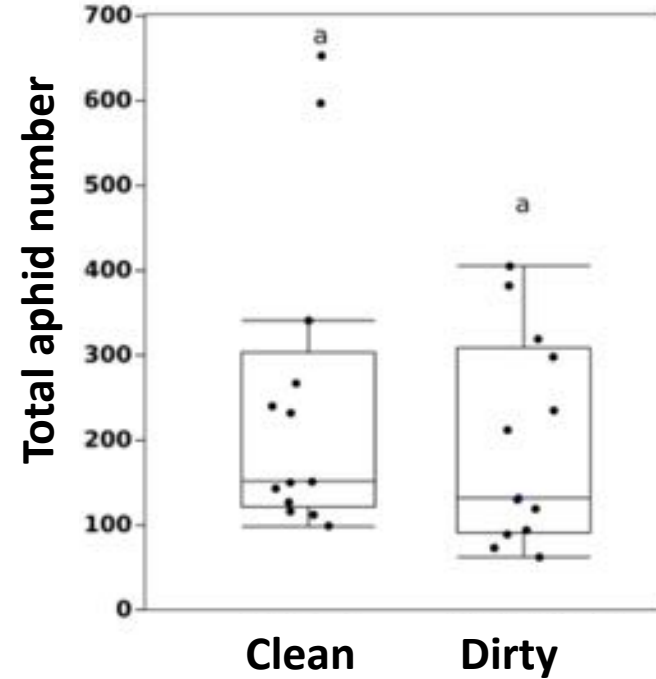
# Do bacteria contribute to plant damage?



Clean aphids = less chlorosis



Aphid number is same





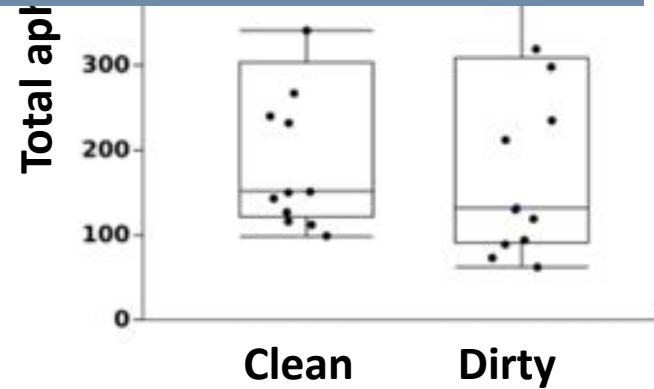
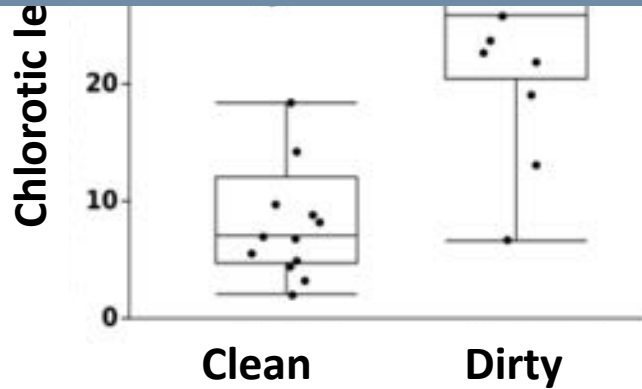
# Do bacteria contribute to plant damage?



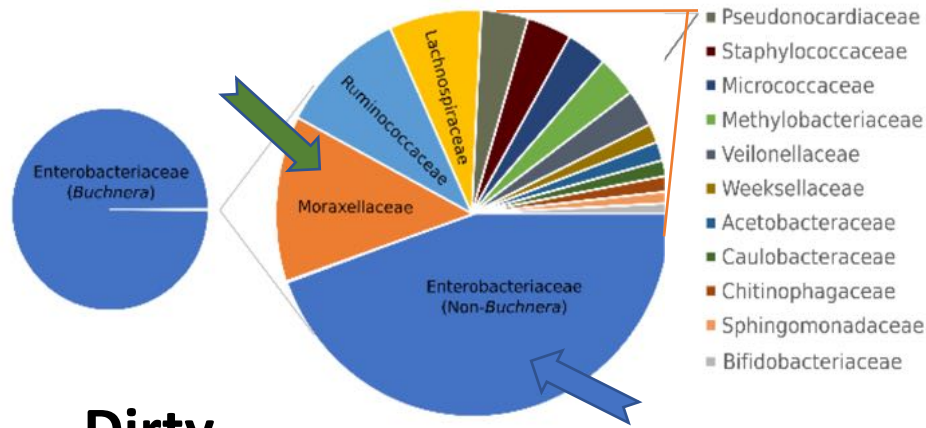
Clean aphids = less chlorosis

Aphid number is same

**Bacteria contribute to aphid virulence**

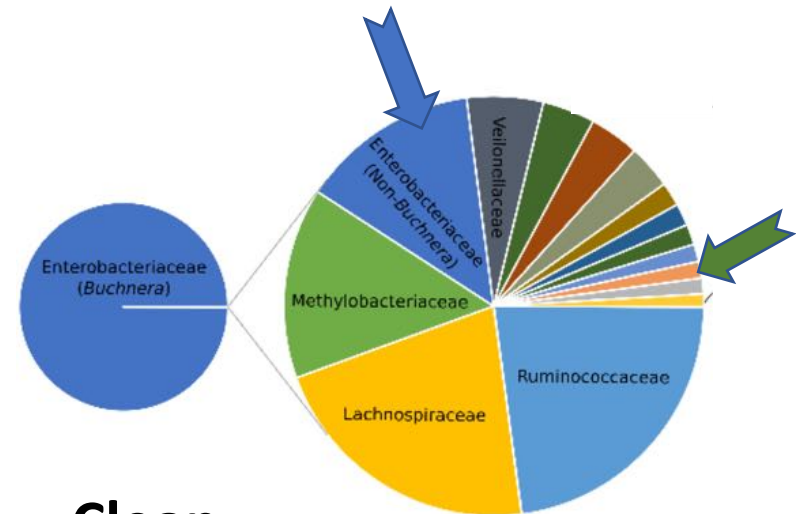


# Dirty aphid microbiome: more diverse and more Enterobacteriaceae and Moraxellaceae



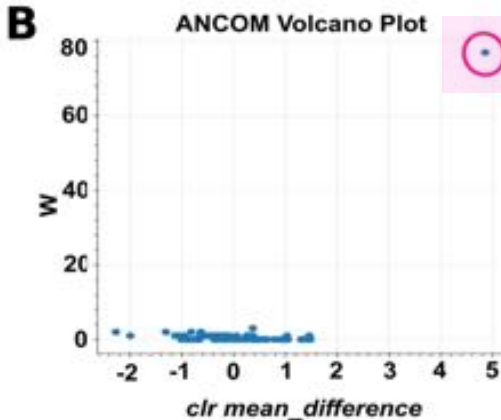
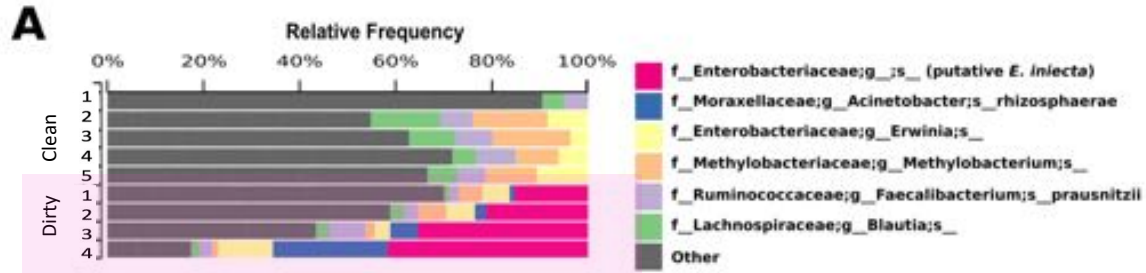
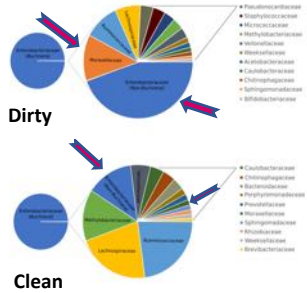
**Dirty**

- *Buchnera* dominates
- Dirty aphid microbiome more diverse & enriched in *Enterobacteriaceae* and *Moraxellaceae*



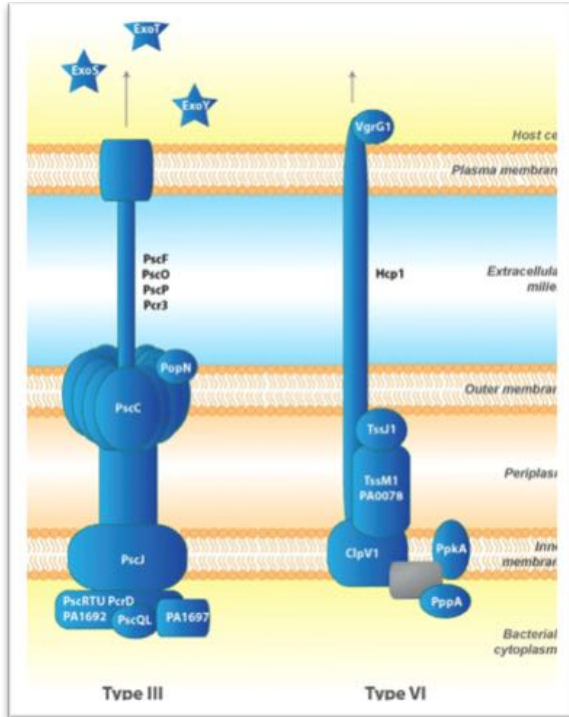
**Clean**

Dirty aphid microbiome: more diverse and more *Enterobacteriaceae* and *Moraxellaceae*





# Pacbio SMRT genome sequencing

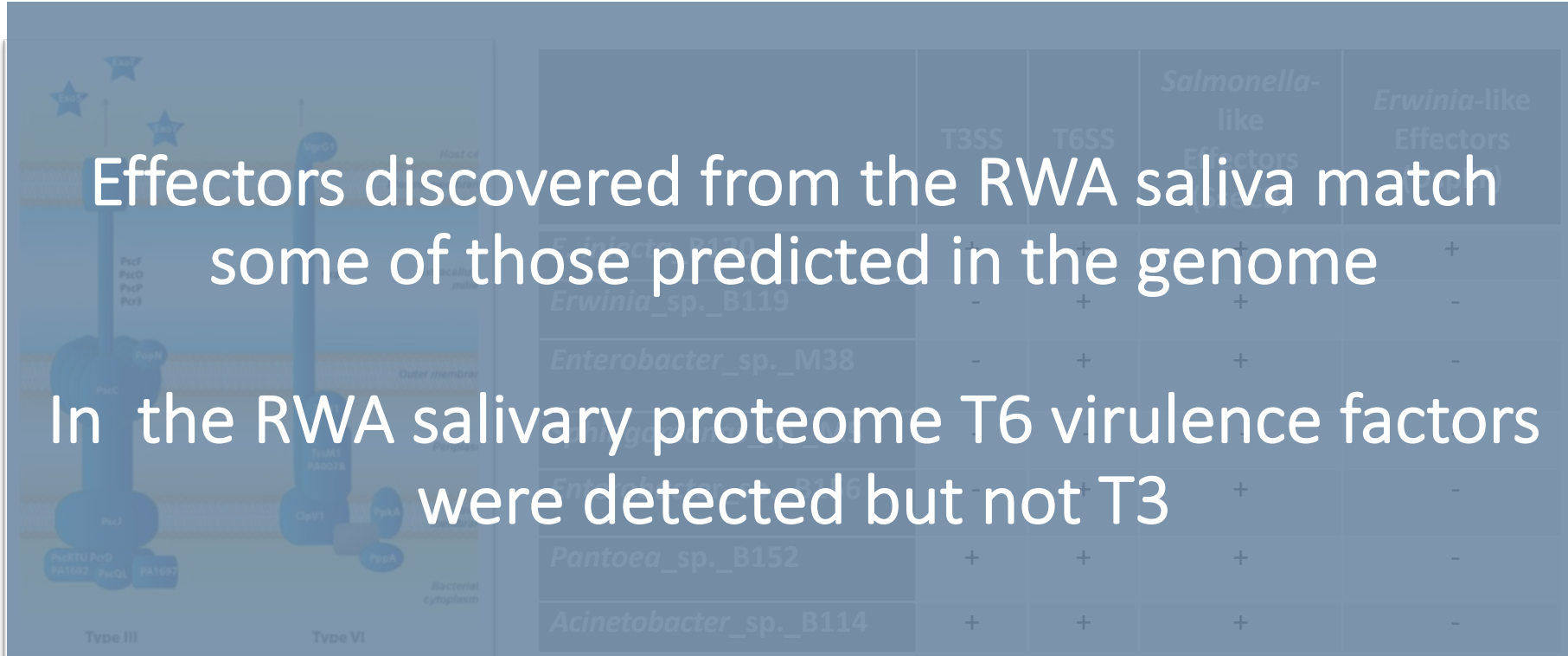


	T3SS	T6SS	<i>Salmonella</i> -like Effectors (SseCB)	<i>Erwinia</i> -like Effectors (DspEF)
<i>E. inei</i> cta_B120	+	+	+	+
<i>Erwinia</i> _sp._B119	-	+	+	-
<i>Enterobacter</i> _sp._M38	-	+	+	-
<i>Sphingomonas</i> _sp._M5	-	-	-	-
<i>Enterobacter</i> _sp._B156	-	+	+	-
<i>Pantoea</i> _sp._B152	+	+	+	-
<i>Acinetobacter</i> _sp._B114	+	+	+	-

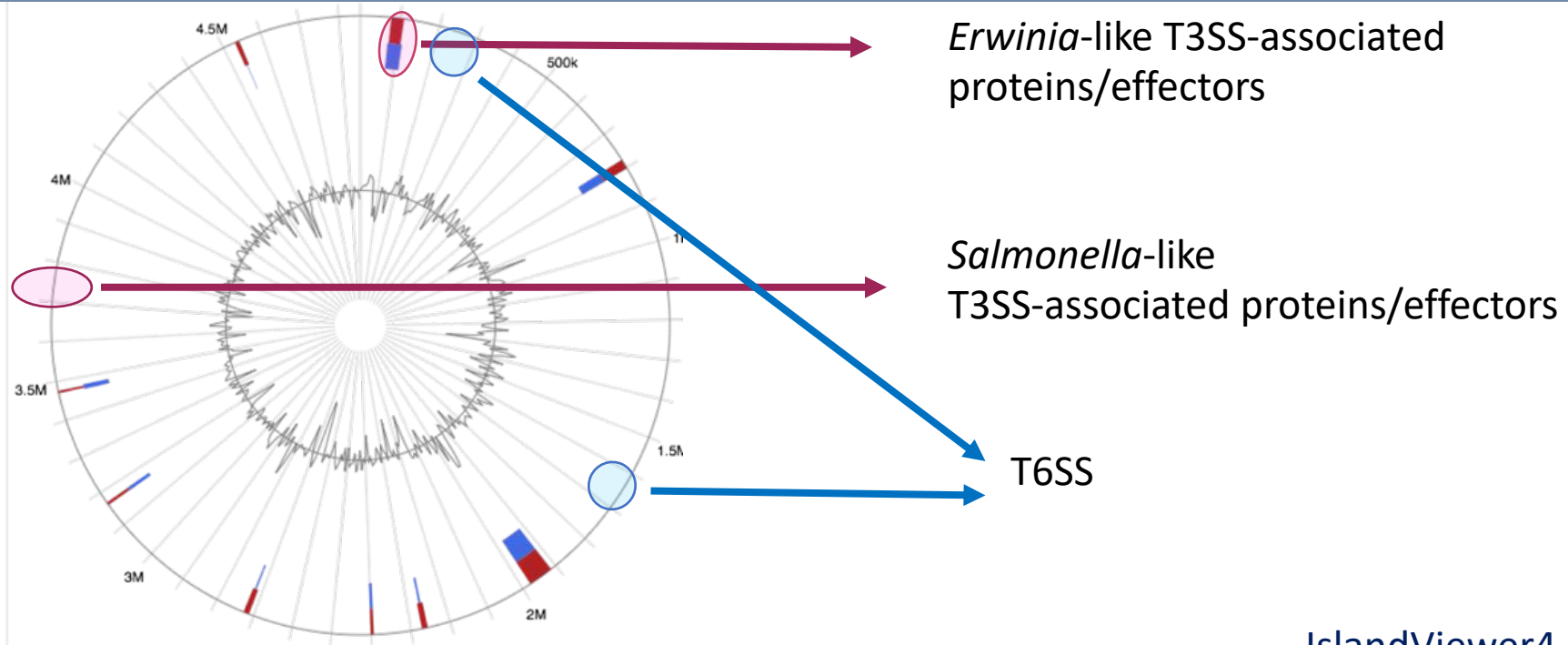
# Pacbio SMRT genome sequencing

Effectors discovered from the RWA saliva match some of those predicted in the genome

In the RWA salivary proteome T6 virulence factors were detected but not T3

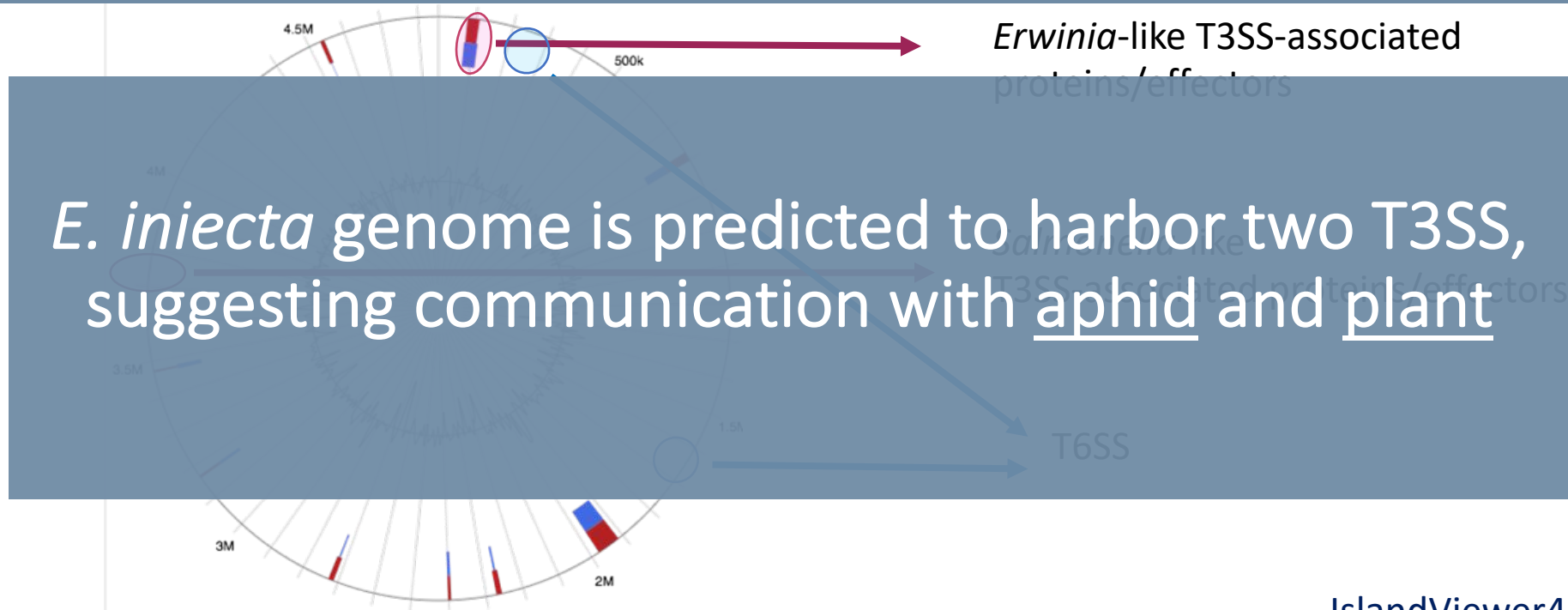


# T3SS-associated genes are clustered in GI of *E. iniecta* genome



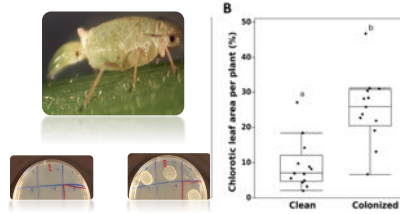


T3SS-associated genes are clustered in GI of *E. iniecta* genome

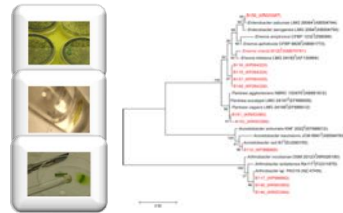




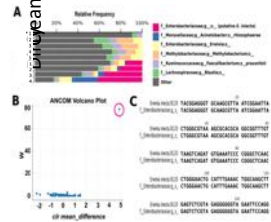
## RWA salivary proteome is mostly comprised of bacterial proteins



## RWA-associated bacteria contribute to aphid virulence



## Isolated bacteria are the same genera as detected in proteome

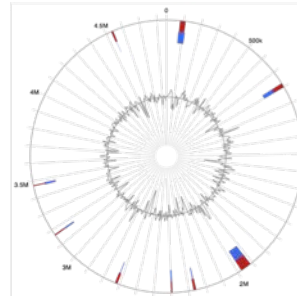


## RWA MB is enriched in Enterobacteriaceae and Moraxellaceae

**In the clean aphid MB there is an absence of Ei suggesting it is important**

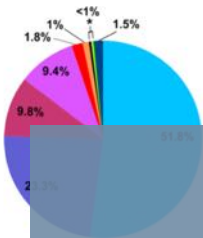


## Bacteria are present on the aphid stylet



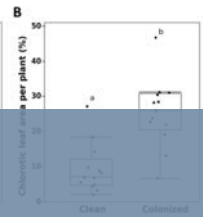
### E. iniecta genome shows evidence of T3 and T6 secretion systems.

## Two T3 suggesting capable of communicating with plant and animal



- Erwinia* spp.
- Pantoea* spp.
- Acinetobacter* spp.
- Enterobacter* spp.
- Photorhabdus* spp.
- Aphididae
- Regiella insecticola*
- Arsenophonus* spp.
- Hamiltonella defensa*
- Serratia symbiotica*

**RWA salivary proteome is mostly comprised of bacterial proteins**



**RWA-associated bacteria contribute to aphid virulence**

Can we use information gained from phytobiome-related studies to guide breeding programs?



**Bacteria are present on the aphid stylet**

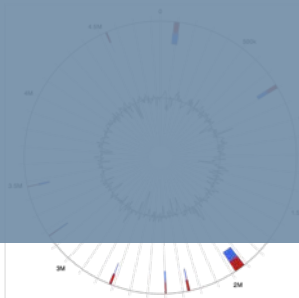


**RWA MB is enriched in Enterobacteriaceae**

**In the clean aphid MB there is an absence of Enterobacteriaceae**

***E. iniecta* genome shows evidence of T3 and T6 secretion systems.**

**Two T3 suggesting capable of communicating with plant and animal**



# Collaborators

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## Pacific Biosciences

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Christine Chang



# Acknowledgements



## CSU Insectary

Jeff Rudolph

Terri Randolph

Darren Cockrell

Frank Peairs

## Electron Microscopy

Kim Vanderpool

