

International Conference on

## ENVIRONMENTAL MICROBIOLOGY AND MICROBIAL ECOLOGY

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International Conference on

## ECOLOGY AND ECOSYSTEMS

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**The adaptation of the bacterial plant pathogen *Pseudomonas syringae* onto a novel host through experimental evolution****Andrew Jamnik**

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The bacterial plant pathogen *Pseudomonas syringae* is a highly diverse species complex, with the ability to cause disease on a wide range of hosts, including many economically important crops. Although *P. syringae* as a species has a very large host range, individual strains are highly host specific. The inability of a strain to infect plant species outside of its host range is generally due to its inability to suppress and evade the host's innate immunity. Few studies to date have tested how plant pathogens evolve to overcome novel host immunity, and a further understanding of this could help in uncovering how newly emerging diseases arise. In this study, we are currently experimentally evolving *P. syringae* pv. *phaseolicola* (*Pph*) 1448A, a strain which causes disease on many cultivars of the common bean (*Phaseolus vulgaris*), on the non-host *Arabidopsis thaliana* (*Arabidopsis*) through *in planta* experimental evolution. Although *Pph* 1448A is unable to cause disease on *Arabidopsis*, its ability to grow and persist on *Arabidopsis* has given this strain the potential to adapt within this novel environment. We have constructed 12 uniquely barcoded hyper mutating lineages of *Pph* 1448A for this experiment, to increase the evolvability of the lineages and to allow us to study mutations associated with adaptation towards *Arabidopsis*. By using highly sensitive *in planta* competition assays on *Arabidopsis*, we've shown that after 80 days of *in planta* growth on *Arabidopsis*, two lineages have shown significant gains in fitness on the novel host. Additionally, one of these lineages has shown a gradual increase in fitness throughout the experimental evolution. Population sequencing of these adapted lineages will give us the ability to identify candidate mutations responsible for this novel host adaptation. Overall, this work will provide a further understanding of the early adaptive processes underlying the spread of existing pathogens to new hosts.

**Biography**

Andrew Jamnik is currently a second year MSc candidate at the University of Toronto working under the supervision of Dr. David Guttman. His research has focused on understanding the evolutionary steps a plant pathogen takes to overcome novel host immunity, and to cause disease on a new host. He has specifically been working with the model bacterial plant pathogen *Pseudomonas syringae* and has designed and implemented *in vivo* experimental evolution to uncover the evolutionary steps required for novel host adaptation. Throughout his graduate degree, he has learned both invaluable microbiology skills along with a better understanding of evolutionary genomic analyses.

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