

Defence-related pathways, phytohormones and primary metabolism are key players in the distinct tolerance of *Actinidia* spp. to *Pseudomonas syringae* pv. *actinidiae*

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INTRODUCTION

- ❖ The kiwifruit bacterial canker (KBC), caused by *Pseudomonas syringae* pv. *actinidiae* (Psa), is a quarantine disease that leads to decreased yield and often to plant death.
- ❖ So far, no curative methods have been developed.
- ❖ Although *Actinidia arguta* (kiwi berry) is more tolerant than *A. chinensis* (green-fleshed kiwifruit) to Psa, the molecular mechanisms underpinning plant tolerance are not fully understood.

METHODS



A. chinensis - susceptible
A. arguta - tolerant



Plant inoculation

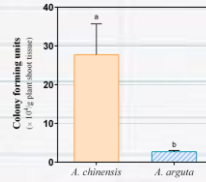
48 hours



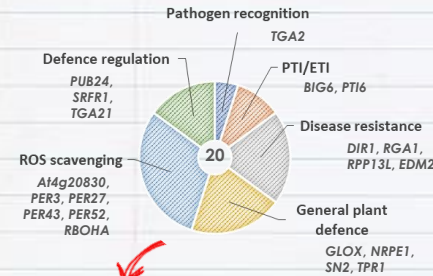
Sampling

- ✓ Bacterial endophytic density
- ✓ Whole-transcriptome sequencing

RESULTS AND DISCUSSION



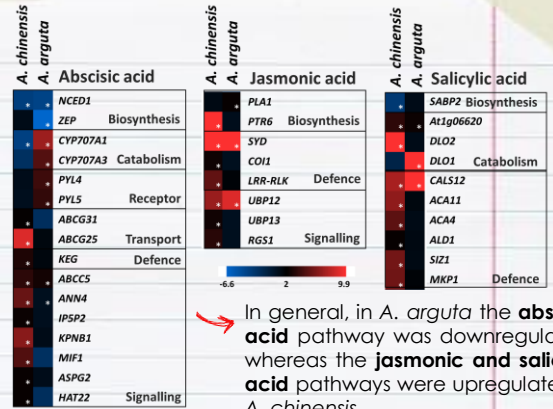
Psa endophytic density was 10-fold higher in *A. chinensis* than in *A. arguta*.



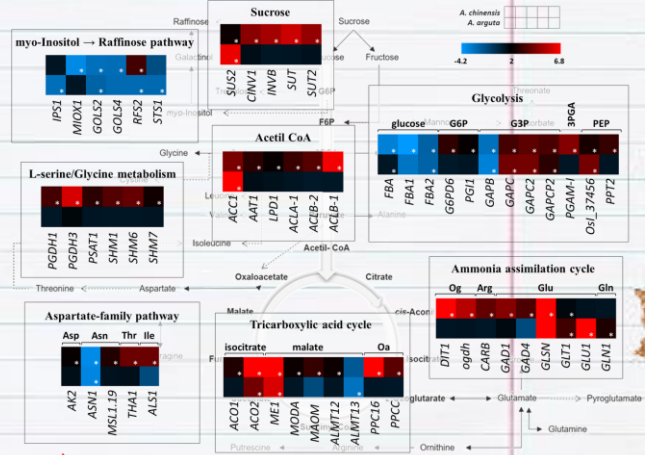
Twenty genes related to **plant defences** were only differentially regulated in *A. arguta*, potentially contributing to its tolerance.

CONCLUSION

- ❖ *A. chinensis*' susceptibility to Psa results from an inefficient activation of plant defences, with impairments in primary metabolism.
- ❖ *A. arguta*'s tolerance may result from the downregulation of the abscisic acid pathway and the expression of specific genes involved in plant defence.



In general, in *A. arguta* the **abscisic acid** pathway was downregulated, whereas the **jasmonic acid** and **salicylic acid** pathways were upregulated in *A. chinensis*.



Infection impaired plant **primary metabolism**, including **glycolysis**, the **tricarboxylic acid cycle** and the **ammonia assimilation cycle**.