The bacterial glycolipids rhamnolipids trigger Induced Systemic Resistance in Arabidopsis

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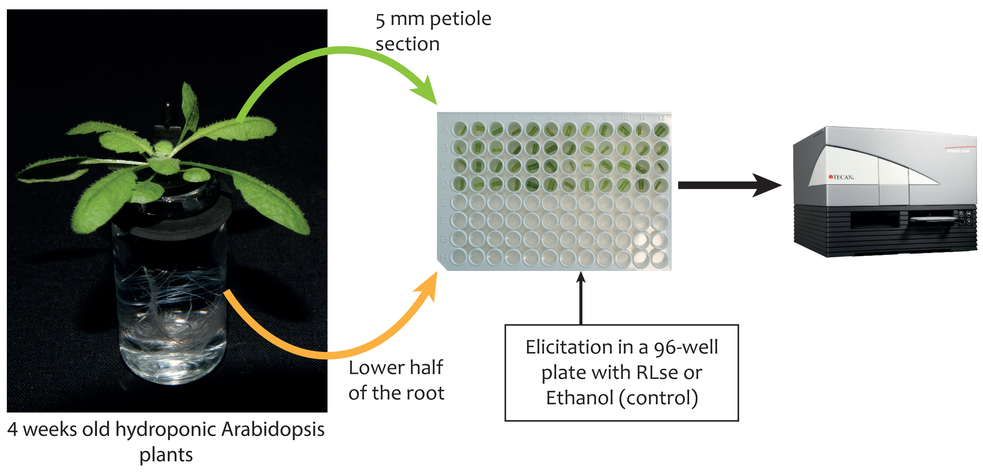
Introduction

In their environment, plants are frequently challenged by pathogenic microorganisms. To deal with these pathogens, plants possess an arsenal of defence mechanisms, quickly activated after microorganism perception. This perception step involve Microbe-Associated Molecular Patterns (MAMPs) that are recognized by plant cells resulting in plant innate immunity. Early events following MAMPs perception, including production of reactive oxygen species, are already well-characterized at the foliar level, but there is a lack of information on the mechanisms involved at the roots level. We previously showed in the laboratory that naturals rhamnolipids secretome (RLse), produced by several bacterial species including some *Pseudomonas sp.* and *Burkholderia sp.*, are highly effective on *Arabidopsis thaliana* leaves to induce local resistance against phytopathogenic microorganisms.

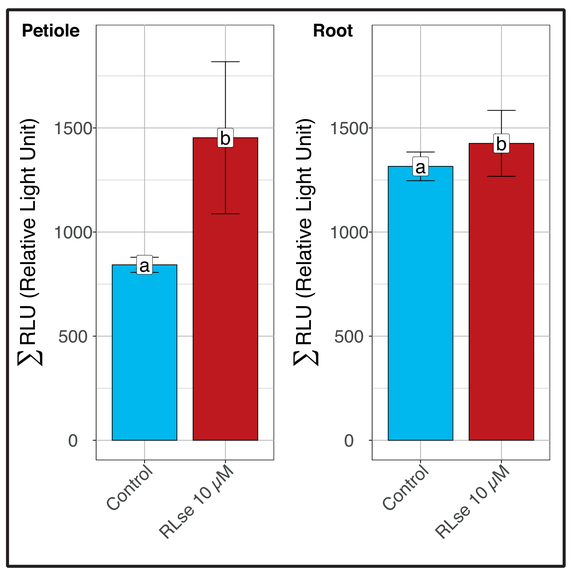
The aim of this study is to determine the ability of *A. thaliana* roots to perceive RLse, and if these molecules can induce a systemic resistance against the necrotrophic fungus *Botrytis cinerea* and against the hemibiotrophic bacteria *Pseudomonas syringae* pv. tomato DC3000 (*Pst* DC3000).

Methods

Production of reactive oxygen species (ROS)

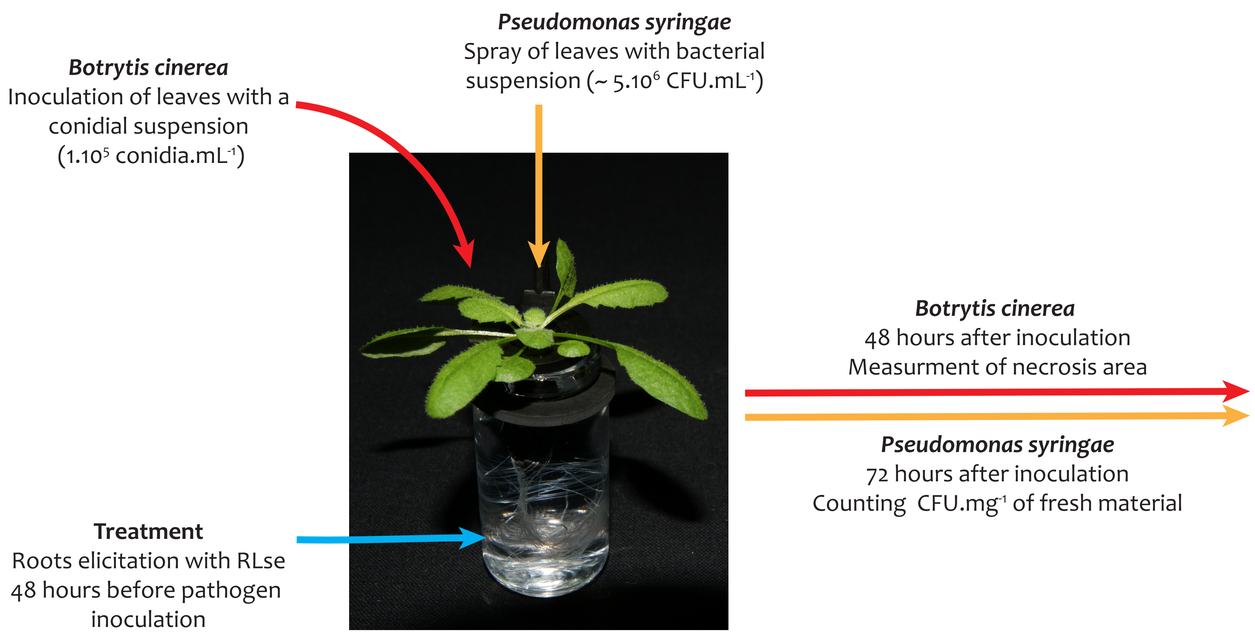


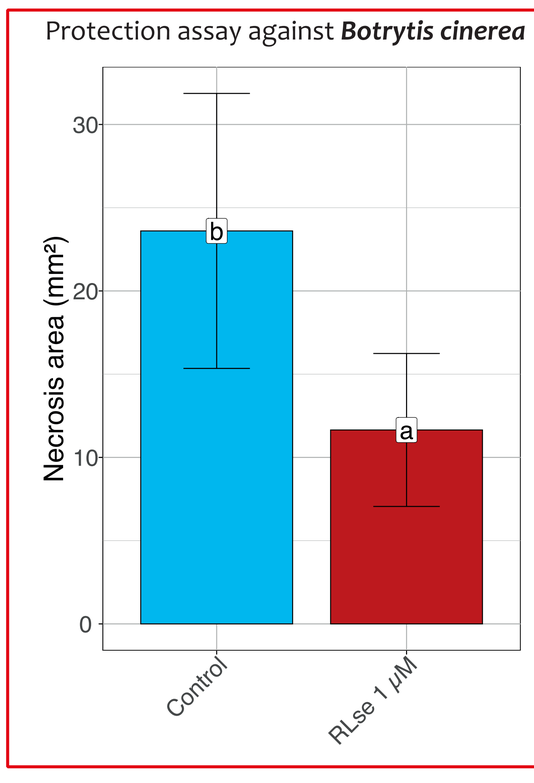
Results

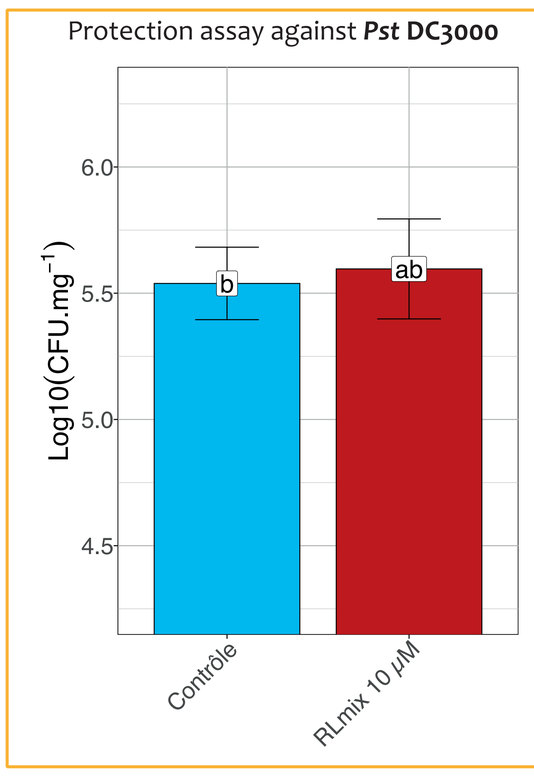


RLse perception stimulate ROS production in leaves but not in roots

Systemic protection assay against *Botrytis cinerea* and *Pst* DC3000







RLse perception trigger a systemic immune response against *B. cinerea*, but not against *Pst* DC3000.

Conclusion

Despite the lack of RLse-triggered ROS production in roots, we found that **RLse trigger a systemic immune response** in *A. thaliana* against the necrotrophic fungus *Botrytis cinerea*. However, we did not observed a similar response against the hemibiotrophic bacteria *Pseudomonas syringae* pv. tomato DC3000. A transcriptomic approach will be further performed to compare the response to a RLse treatment on roots and leaves. The identification of differentially expressed genes should help us to better characterize the local and/or systemic resistance against the pathogen.

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