

A dive into the systemic immune activation induced by surfactin in *Arabidopsis thaliana*

RACE Gaëlle^{1,2}, GENVA Manon¹, DELEU Magali³, FAUCONNIER Marie-Laure¹ and ONGENA Marc²

¹ Laboratory of Chemistry of Natural Molecules, Gembloux Agro-Bio Tech, University of Liège, 5030 Gembloux, Belgium

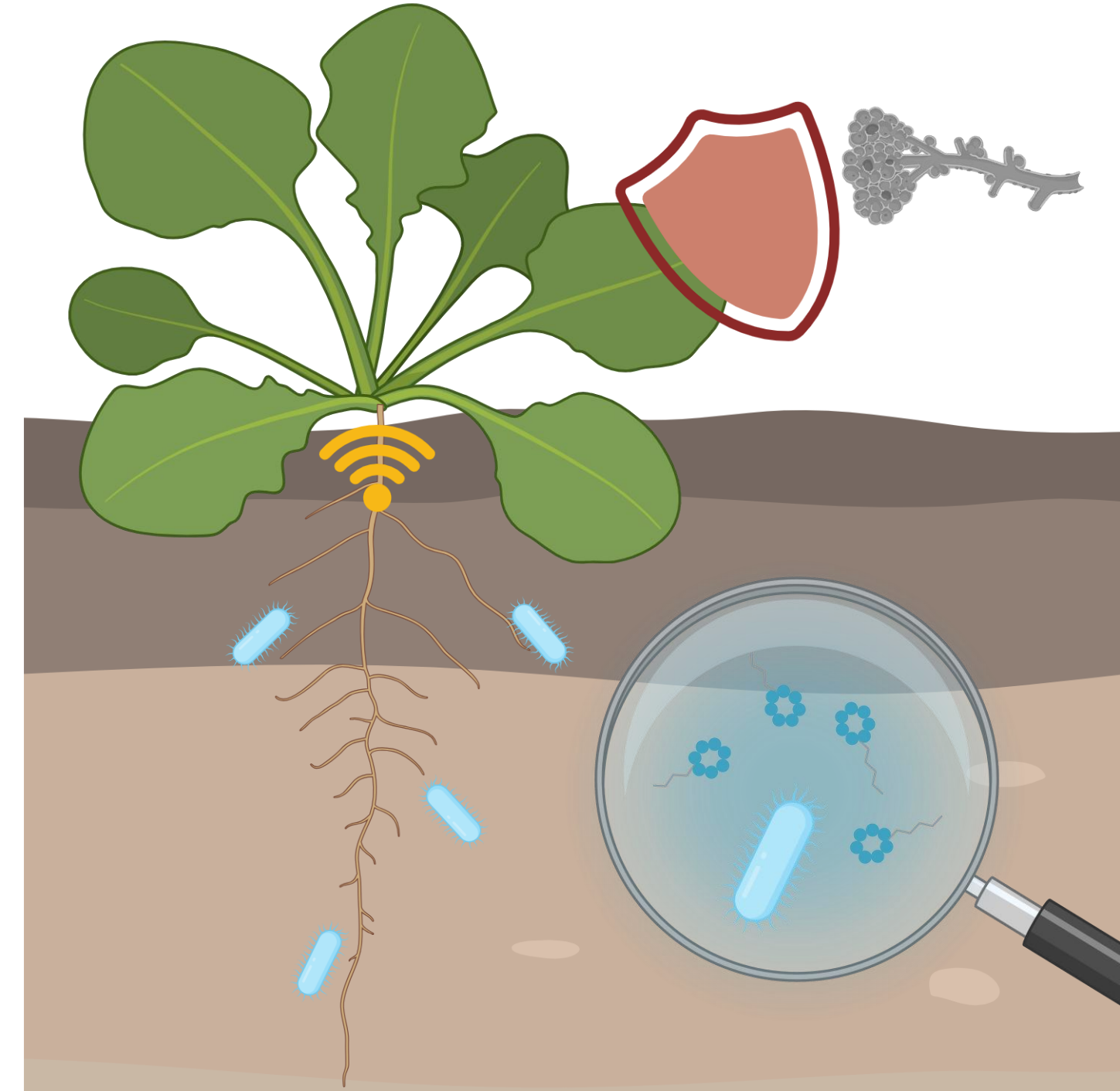
² Microbial Processes and Interactions, TERRA Research centre, Gembloux Agro-Bio Tech, University of Liège, 5030 Gembloux, Belgium

³ Laboratory of Molecular Biophysics at Interfaces, TERRA Research Centre, Gembloux Agro-Bio Tech, University of Liege, Gembloux, Belgium

1. Context

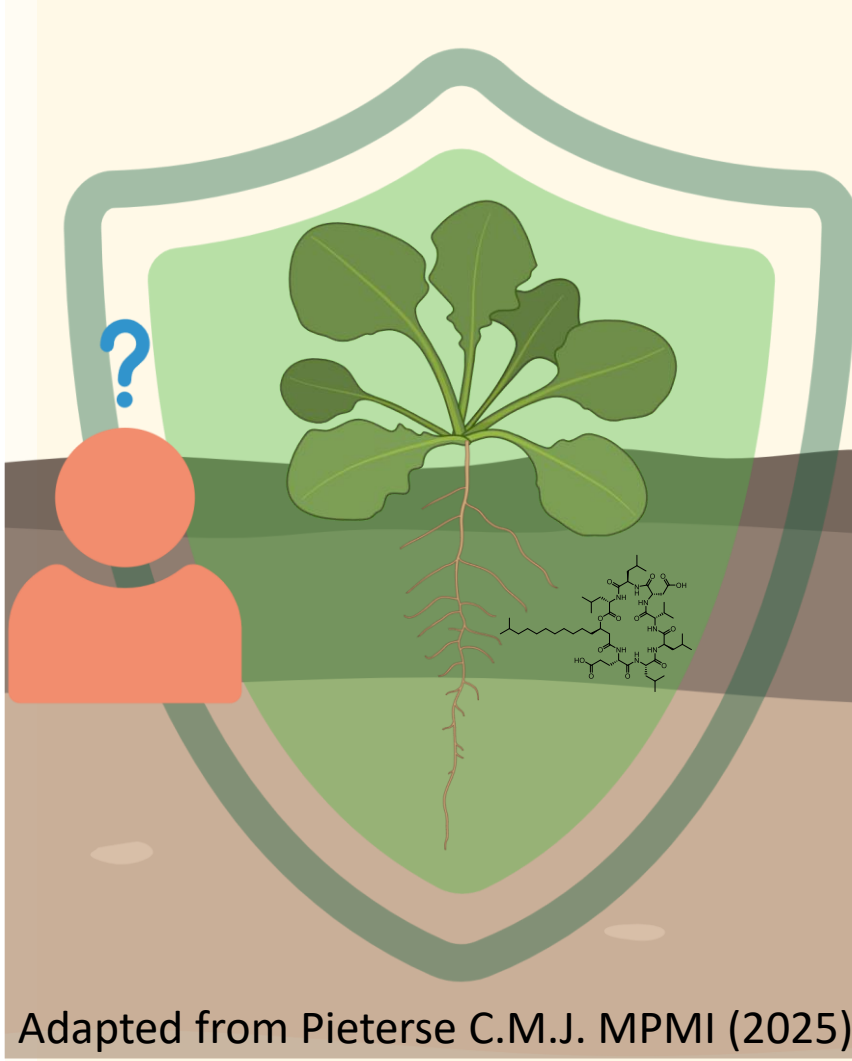
The study of plant-microorganism interactions underscores the crucial role of the plant-associated microbiome, especially within the rhizosphere. This highly diverse microbial community includes both pathogens and beneficial microorganisms, such as PGPRs (*Plant Growth-Promoting Rhizobacteria*). Among PGPRs, *Bacillus spp.* are efficient producers of various secondary metabolites, including lipopeptides with antimicrobial and immunostimulant properties. Among these lipopeptides, surfactins can trigger induced systemic resistance (ISR) in plants, enhancing their immune responses and enabling a faster, stronger reaction to pathogen attack.^{a-d} These responses to pathogenic infections are numerous. The surfactin lipopeptide can include early event in immune activation such as the production of reactive oxygen species (ROS) and cytosolic calcium influx; defense responses as the production of phytoalexins; and systemic signals as the production of phytohormones.^{b-c}

In line with its priming potential, surfactin thus represents a promising biosourced molecule for biocontrol applications. However, the molecular mechanisms related to surfactin-induced ISR remain poorly described, including the identification and the accumulation of defense compounds.



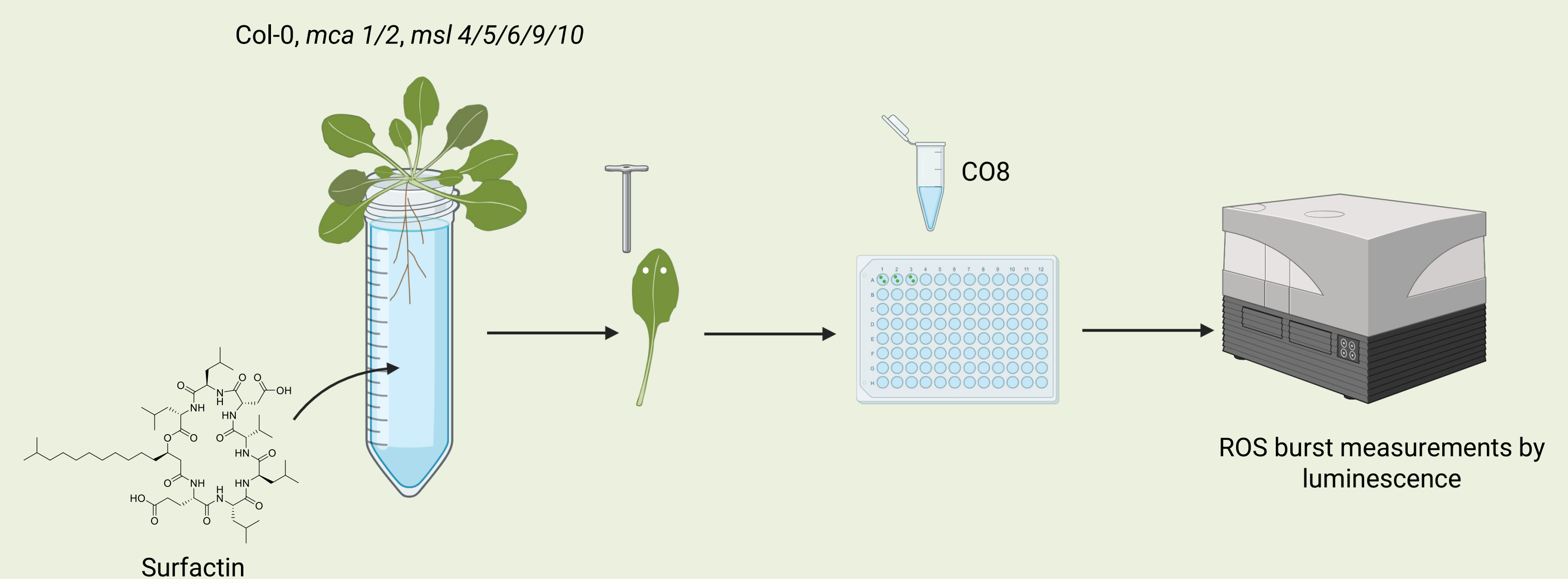
2. Objectives

This work aims to understand the metabolomic modifications induced by the presence of surfactin. First, we demonstrate that surfactin applied as root treatment boosts ROS production in leaves when a *Botrytis*-mimicking MAMP (CO8) is applied thereby showcasing surfactin-mediated induction of the systemic immune activation (SIA). Here, we used in addition to Col-0 two mutants, *mca 1/2* and *msl 4/5/6/9/10*, which are defected in ion channels. This helps to understand the implication of ion channels in the plant response to surfactin elicitation at the root level.



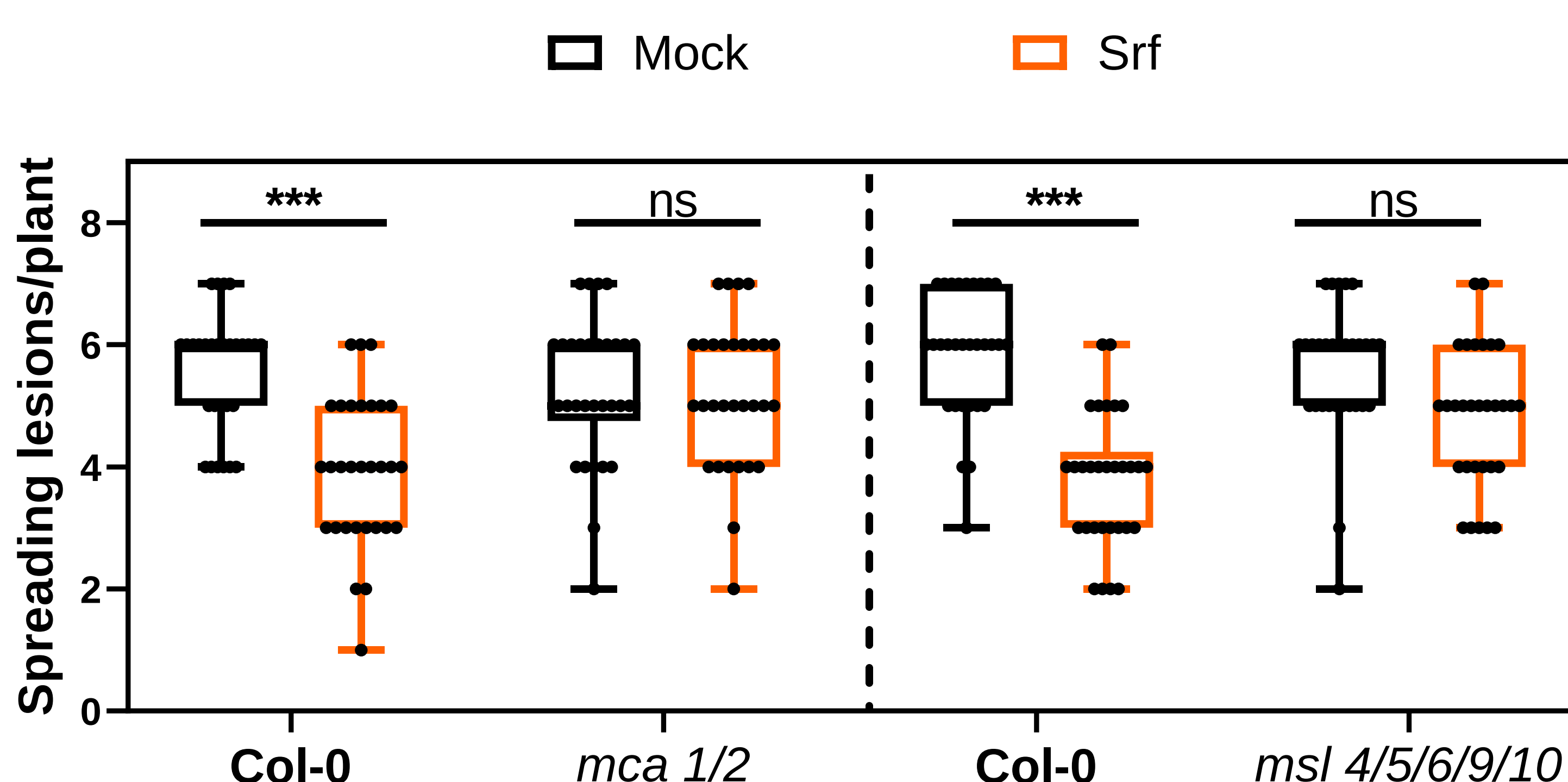
Adapted from Pieterse C.M.J. MPMI (2025)

3. Methods

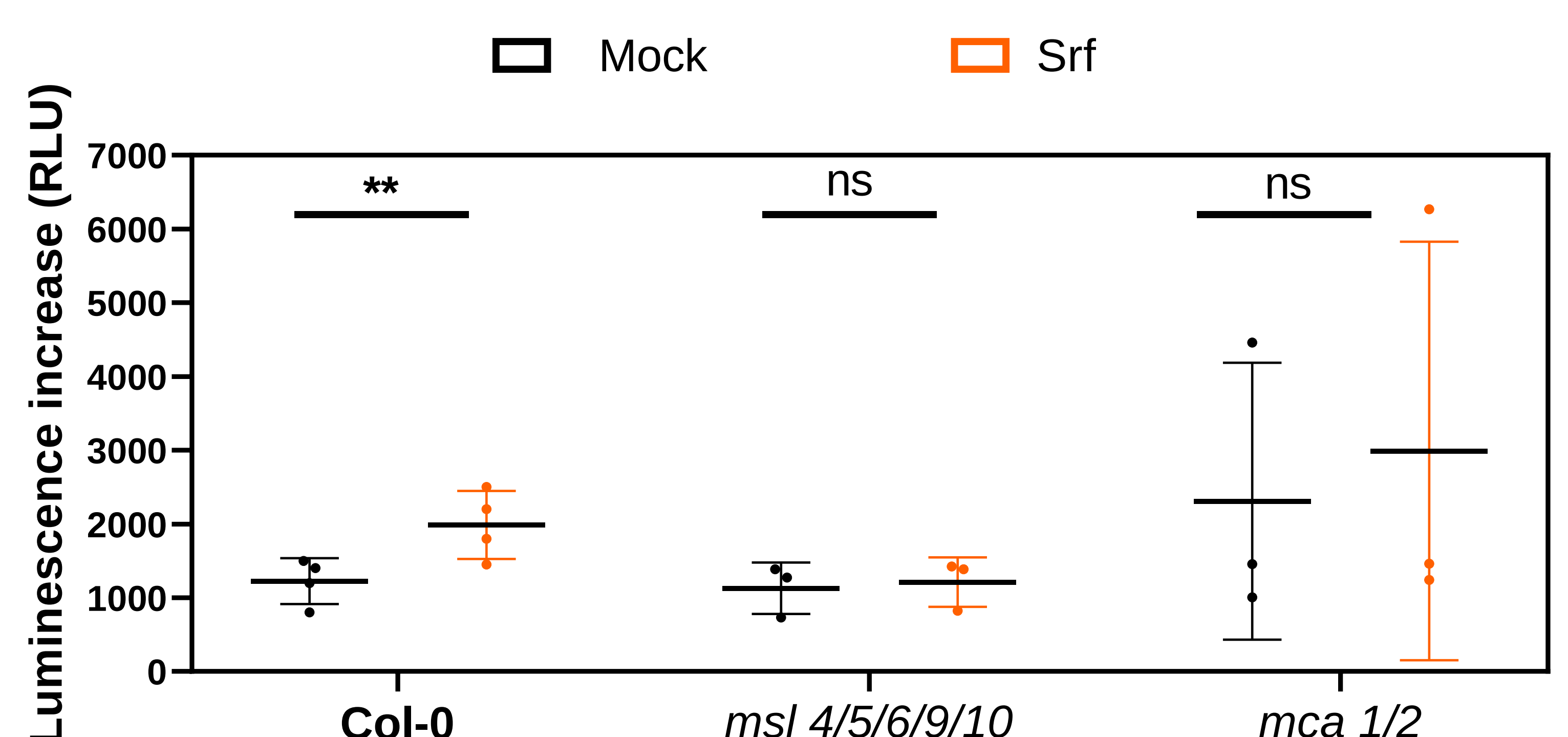


4. Results

Our results highlight a close parallel between SIA and ISR. Pre-treatment with surfactin clearly induces an increase in plant defense responses, using ROS production as a proxy, when CO8 is applied to leaves for *Arabidopsis thaliana* (L.) Heynh Col-0 wild type. Most interestingly, the two mutants with several ion channel defects in the plasma membrane do not display this ROS accumulation when the plant is triggered by a MAMP. This likely implies that those ion channels are necessary to the full responses of the plant when surfactin elicitation at the root level occurs.



Induction of systemic defense responses by surfactin assessed via ISR. Disease incidence was caused by *Botrytis cinerea* in *A. thaliana* Col-0, *mca 1/2*, *msl 4/5/6/9/10* plants pretreated by 10 μ M surfactin or not. *** indicates a *p*-value < 0.001 (two-tailed *t*-test).

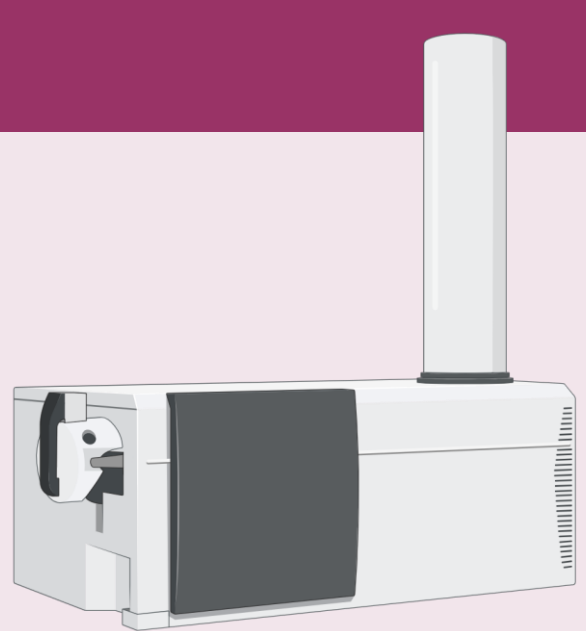


Systemic immune activation (SIA) upon MAMP (CO8) perception assessed in leaves of Col-0, *mca 1/2*, *msl 4/5/6/9/10* plants pre-treated on roots by Srf (10 μ M) or not. The ROS burst response to MAMP was measured on leaf disks via a luminol-based chemiluminescence assay. ** indicates *p*-value < 0.01 (*t*-test).

Gilliard G., et al. Nat. Plants (2026)

5. Conclusion and perspectives

As we observe a clear induction of SIA by surfactin, we intend to investigate the metabolomic modifications induced by the presence of surfactin. In particular, molecules that are locally accumulated in roots and those that are translocated and/or accumulated in the infected tissues will be identified and characterized. Thus, two LC-MS/MS approaches (targeted and non-targeted analysis) will be developed and combined to identify the compounds involved in signaling and in the defense responses, in a time-course context.



References

- Prsic J., & al. Front. Plant Sci. (2020)
- Jeworutzki E., & al. The Plant Journal (2010)
- Mousavi S., & al. Nature (2013)
- Gilliard G., & al. Nat. Plants (2026)
- Pieterse C.M.J. MPMI (2025)



Acknowledgements

M. Ongena and M. Deleu are respectively, research director and senior research associate at the F.R.S.-FNRS.



BioRender was used for some illustrations of this poster



For more information contact Gaëlle Race (gaelle.race@uliege.be)