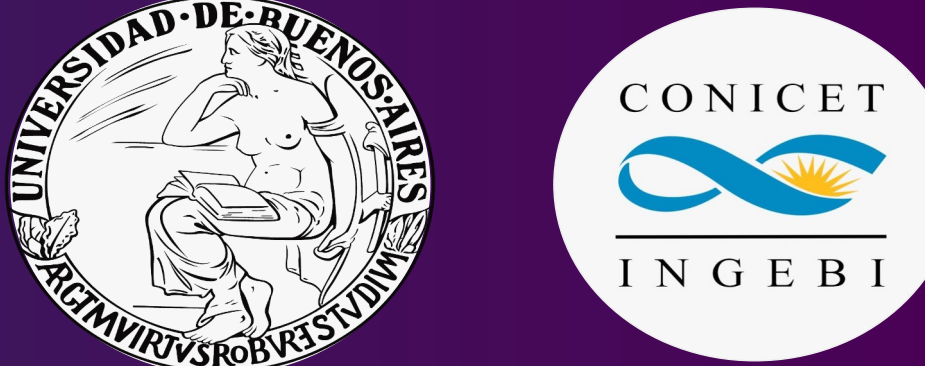


Exploring NRC immune receptor diversity and expression in Spunta potato during *Phytophthora infestans* infection

León, V.^{1,2(*)}; Juárez, M.E.^{1(*)}; Toghani, A.³; Bravo-Almonacid, F.F.¹; Segretin, M.E.^{1,2}

(*) Co-first authors. mariasegretin@gmail.com

1. INGEBI-CONICET – Instituto de Investigaciones en Ingeniería Genética y Biología Molecular “Dr. Héctor N. Torres”, C.A.B.A., Argentina.
2. Departamento de Fisiología, Biología Molecular y Celular, Facultad de Ciencias Exactas y Naturales, Universidad de Buenos Aires, C.A.B.A., Argentina.
3. The Sainsbury Laboratory, Norwich Research Park, United Kingdom.



INTRODUCTION

Late blight, caused by the oomycete *Phytophthora infestans*, remains the most devastating disease affecting potato crops worldwide. Breeding strategies based on the deployment of NLR (nucleotide-binding leucine-rich repeat) genes are critical for sustainable resistance. However, several NLR proteins depend on NRCs (NLR-Required for Cell death), a specialized subclass of NLR immune receptors that act as central signaling hubs. Therefore, understanding the expression profile of plant immunity genes, especially NRCs, under infection conditions is essential to ensure functional resistance.

In this study, we characterized the NRC gene family in *Solanum tuberosum* var. Spunta, a susceptible commercial cultivar, during infection with Argentinean *P. infestans* isolates. Using phylogenomic analysis, transcript quantification, and structural mapping of amino acid variants, we identified and classified NRC homologues, described their expression dynamics during infection, and mapped potential functional divergence within the NRC clade.

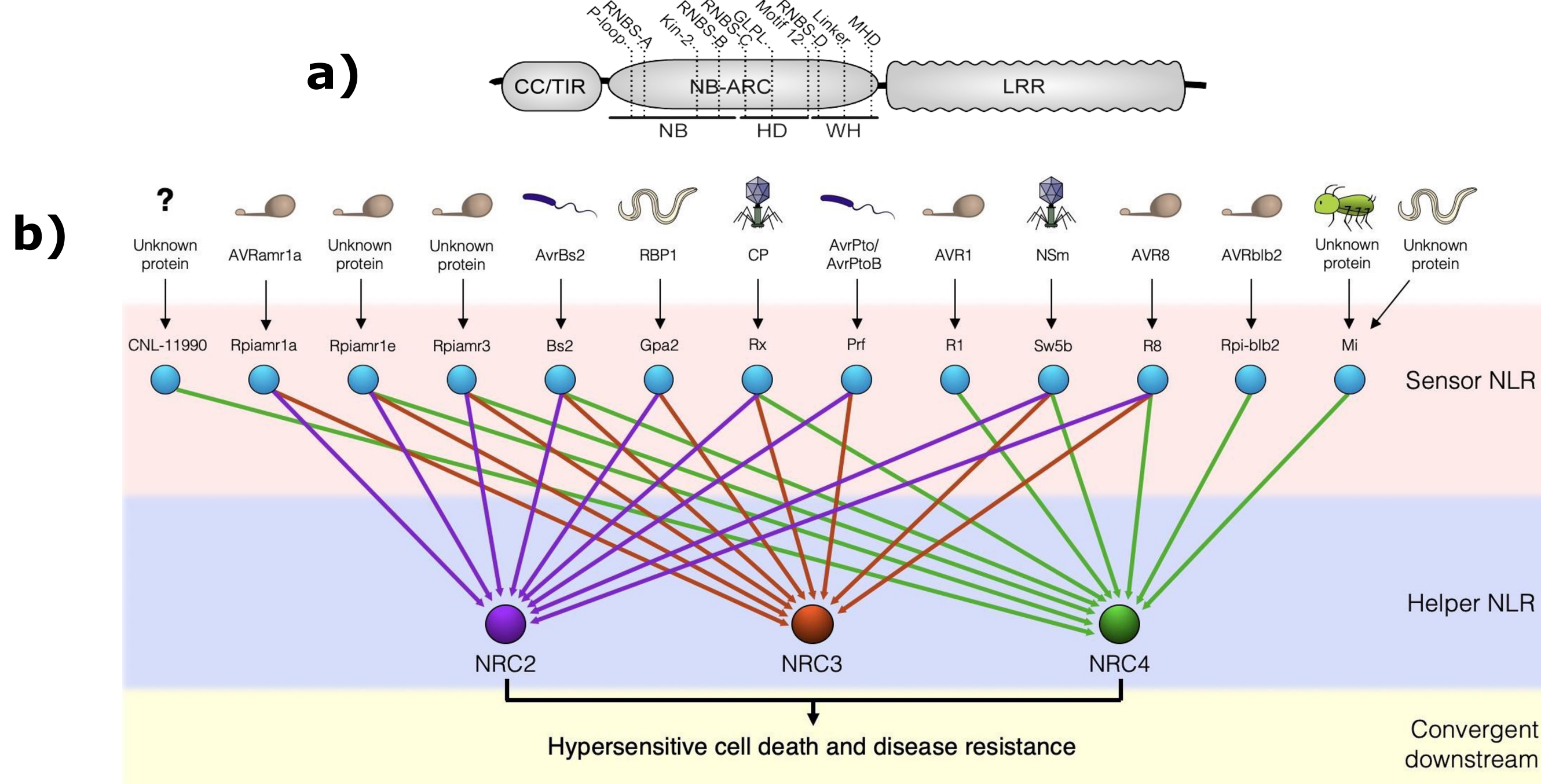
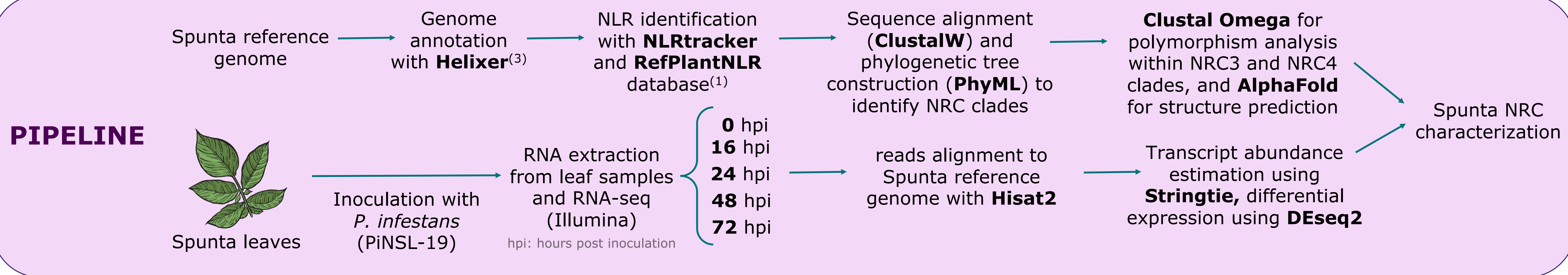
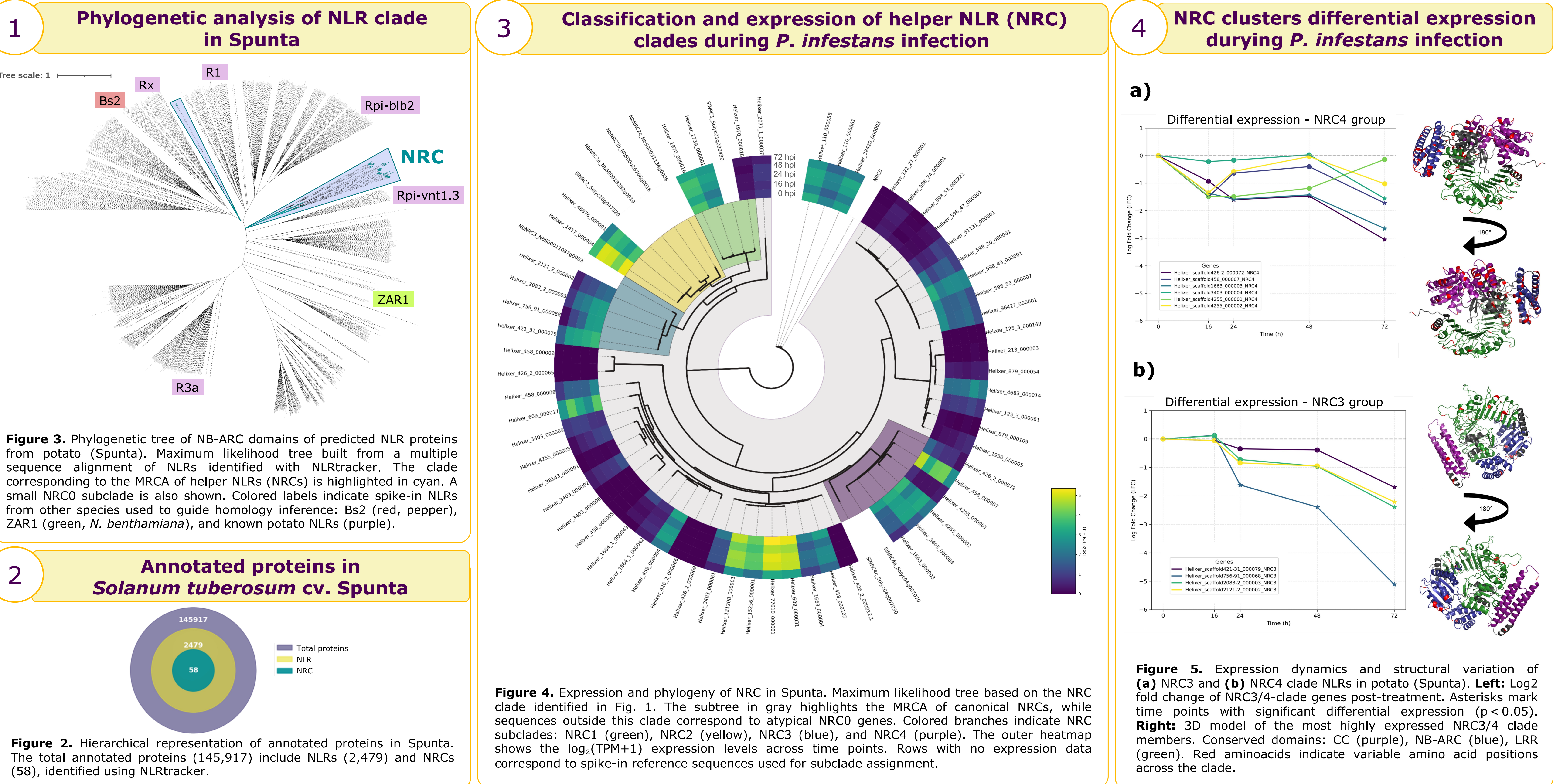


Figure 1. (a) Domain architecture of typical plant NLRs. The structural features and conserved motifs of the NB-ARC are indicated⁽¹⁾. (b) Redundancy in the *Solanaceae* NLR network enables evasion of immune suppression by diverse pathogens⁽²⁾.



RESULTS



CONCLUSIONS

NRC genes from clades NRC0, NRC1, NRC2, NRC3, and NRC4 are present and transcriptionally active in the susceptible potato cultivar Spunta during *P. infestans* infection, with NRC3 and NRC4 showing differential expression at specific post-inoculation time points. Understanding these quantitative expression profiles is crucial, as this knowledge provides a foundation for predicting whether the introduction of resistance genes should be combined with functionally relevant NRC genes in breeding programs aimed at deploying durable resistance to *P. infestans* in potato cultivars. These results support further investigation into functional differences among NRC clades and highlight the need for targeted experiments to test the role of individual NRC paralogues in immune responses.

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