

Phylogenomics reveals a complex evolutionary history of Fabaceae NLR immune receptors

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1. Background

- Fabaceae is the third largest and one of the most important angiosperm crop families¹
- Biotic stress constrains legume yield²
- Resistance gene breeding is considered the most sustainable disease management method²
- Little is known about legume NLR-encoding genes

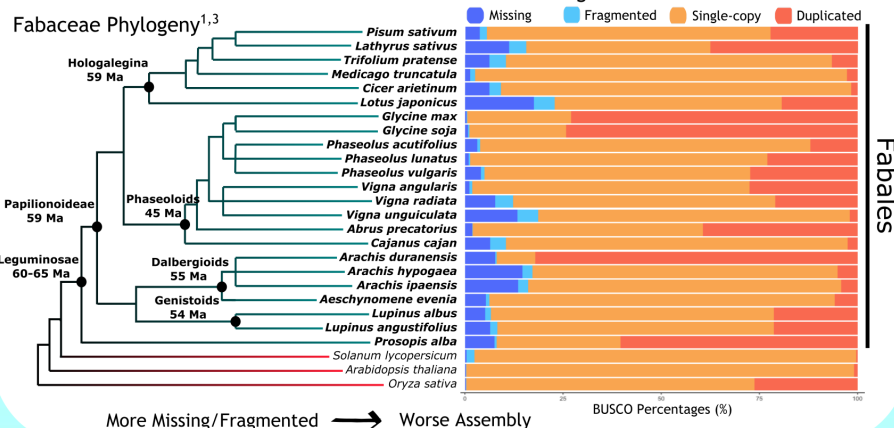


2. Question and Aim

What is the complexity and evolutionary diversity of legume NLRs?

Perform a comparative NLRome study

3. The available proteome predictions could be improved



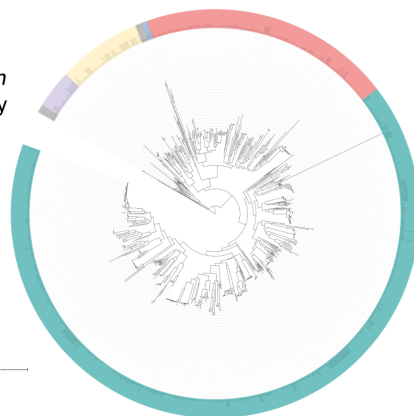
4. We built NLR phylogenies for each species using RefPlantNLR⁴

Example:

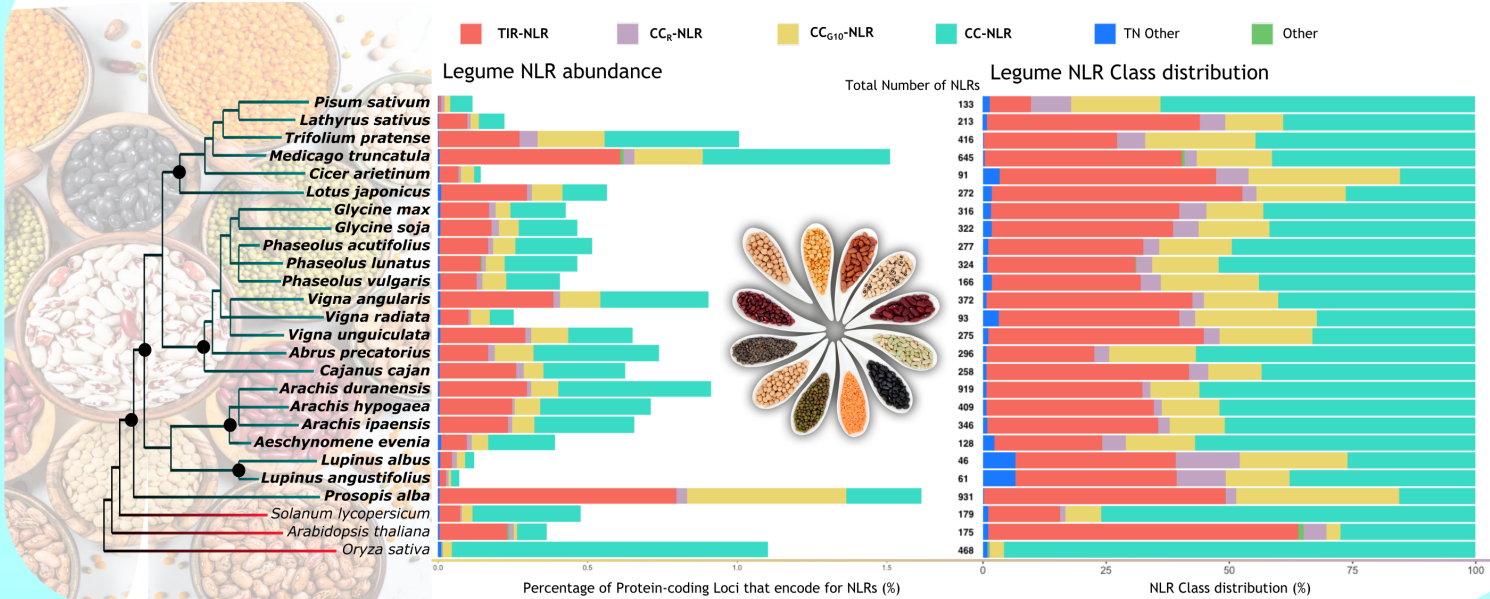
Pisum sativum
NLR Phylogeny

Legend: CC-NLR (Teal), TIR-NLR (Red), CC_R-NLR (Purple), CC_{G10}-NLR (Yellow), TN Other (Blue), Non Plant NLRs (Grey)

Tree Scale: 1



5. The abundance and distribution of NLR classes in the Fabaceae is variable



6. Conclusions and Outlook

- The number and distribution of NLR classes across legume species is variable and mostly reflected legume phylogeny
- Artificial selection and genetic erosion could be playing a role in reducing NLR numbers
- The number of CC_{G10}-NLRs and CC_R-NLRs seems to be more constant
- The ratio between CC-NLRs/TIR-NLRs is constant for most legume species
- The Fabaceae NLR repertoire will be an important tool for comparative resistance mapping studies and for R gene enriched Genome-Wide Association Studies

References

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