

Uncovering the repertoire of legume NLR immune receptors

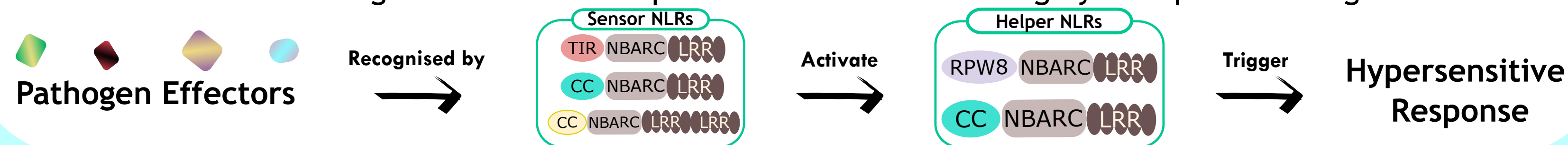
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1. Background

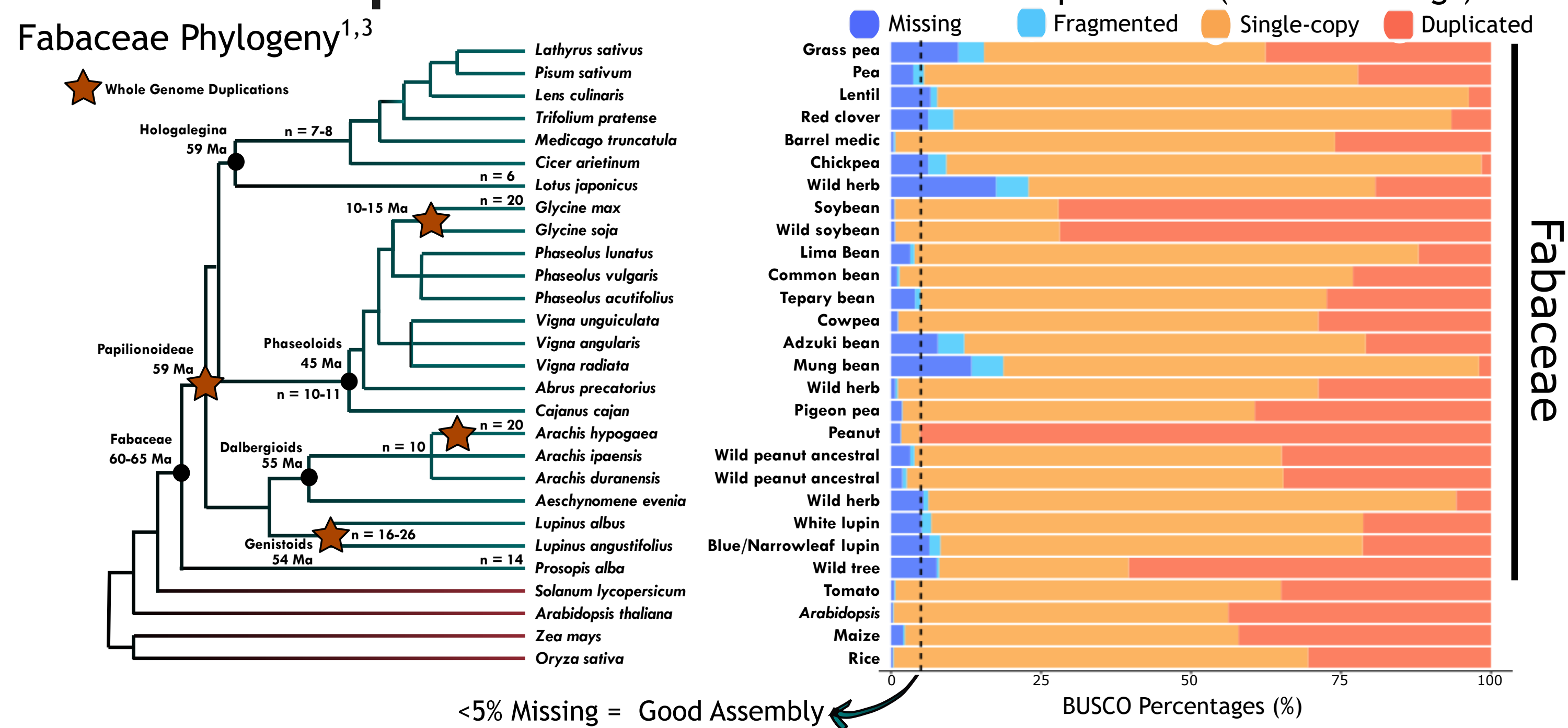
- Fabaceae, the legume family, is a large and diverse angiosperm crop family, with much ecological and economic importance.^{1,3} However, biotic stress continues to seriously constrain legume yield²
- Resistance breeding is considered the most sustainable plant disease management method²
- Nucleotide-binding Leucine Rich genes (NLRs) are intracellular receptors that detect pathogen effectors, triggering a powerful defensive mechanism known as Hypersensitive Response⁴
- The NLR resistance genes and their respective classes remain largely unexplored in legumes



Genome Quality Control

Proteome + NLR tracker

3. The completeness of legume proteomes could be improved



2. Question and Aim

What is the nature and diversity of Legume NLRs?

Perform a comparative NLRome study

4. We built NLR phylogenies for each species using RefPlantNLR⁴

Max. likelihood trees
- Clustal Omega Alignment
- FastTree algorithm

Example:

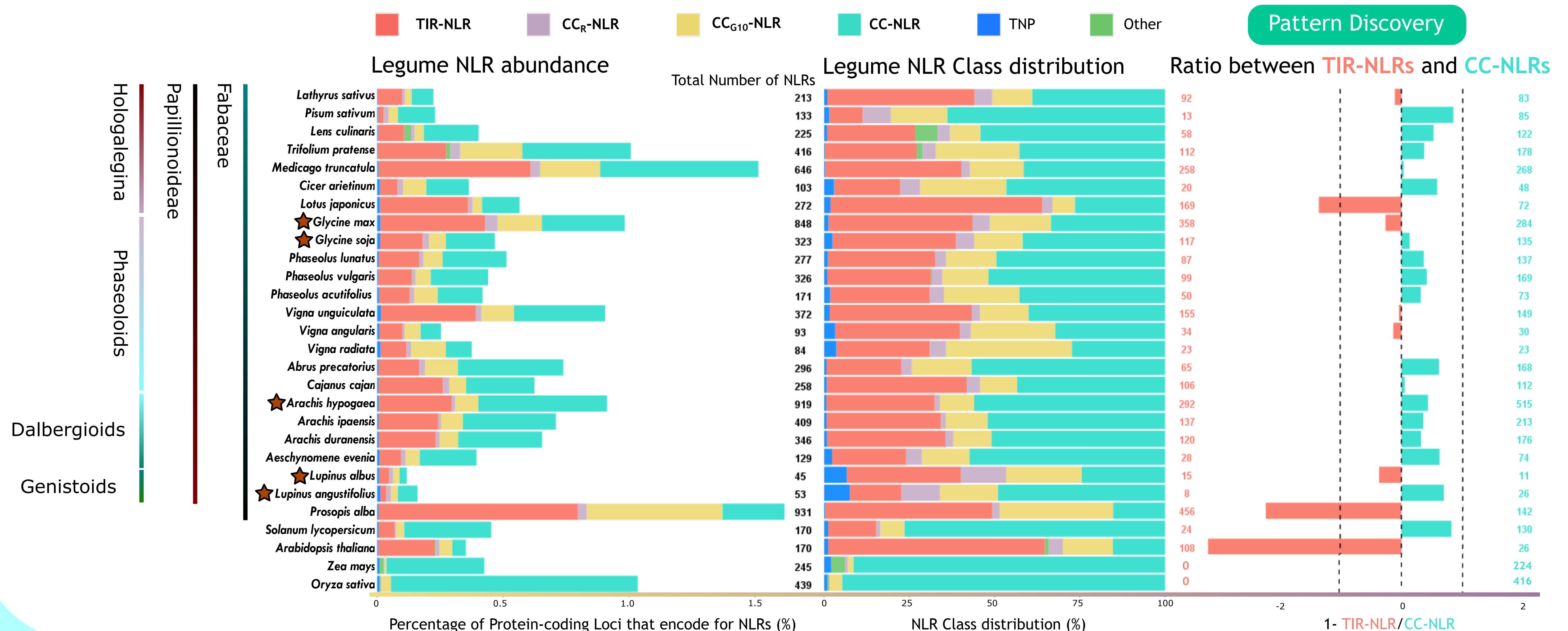
Phaseolus vulgaris
NLR Phylogeny

CC-NLR
TIR-NLR
CC_R-NLR
CC_{G10}-NLR
TNP
Non Plant NLRs

Tree Scale: 1

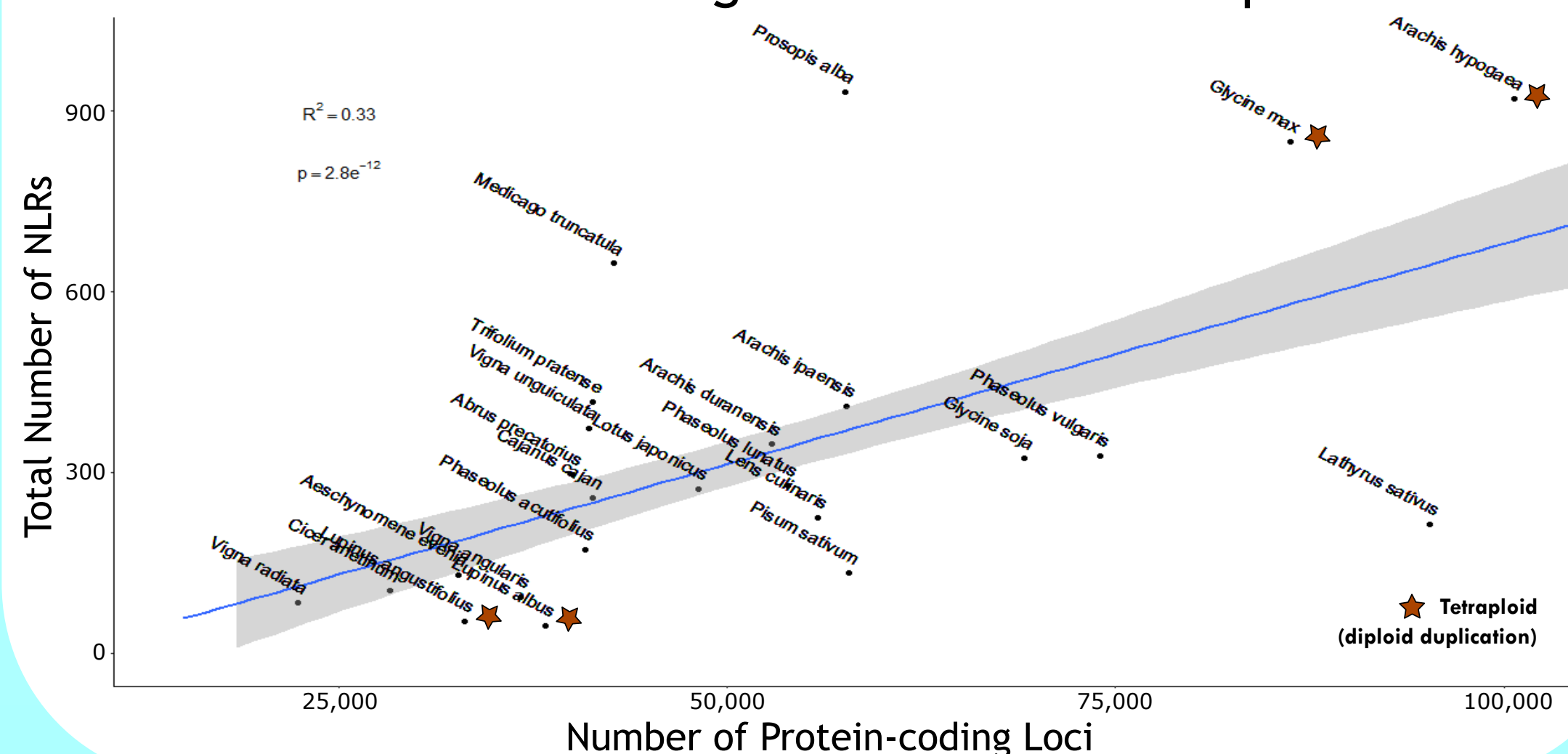
Characterization of Legume NLRomes

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



6. Legumes display expansions and contractions in NLR numbers

NLR number according to total number of proteins



7. Conclusions and Outlook

- The number and distribution of NLR classes across legume species is variable and mostly reflects legume phylogeny
- Most legume species tend to have more CC-NLRs than TIR-NLRs
- The number of CC_{G10}-NLRs and CC_R-NLRs appears less variable
- Whole genome duplications and genetic erosion could be altering NLR numbers
- The Fabaceae NLR repertoire will be an important tool for comparative resistance mapping studies and for R gene enriched Genome-Wide Association Studies

1. Cardoso, D. B. O. S. *et al.* (2013). Reconstructing the deep-branching relationships of the papilionoid legumes. *SA Journal of Botany*, 89, 58-75.
2. Mundt, C. C. (2014). Durable resistance: a key to sustainable management of pathogens and pests. *Infection, Genetics and Evolution*, 27, 446-455.
3. de Queiroz, L. P. *et al.* (2015). A multilocus phylogenetic analysis reveals the monophyly of a recircumscribed papilionoid legume tribe Diocleae with well-supported generic relationships. *Molecular Phylogenetics and Evolution*, 90, 1-19.
4. Kourelis J *et al.* (2021) RefPlantNLR is a comprehensive collection of experimentally validated plant disease resistance proteins from the NLR family. *PLOS Biology* 19(10): e3001124. <https://doi.org/10.1371/journal.pbio.3001124>.