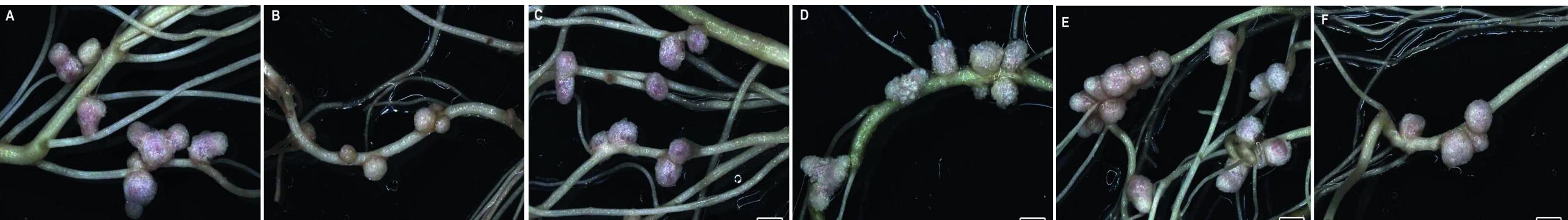




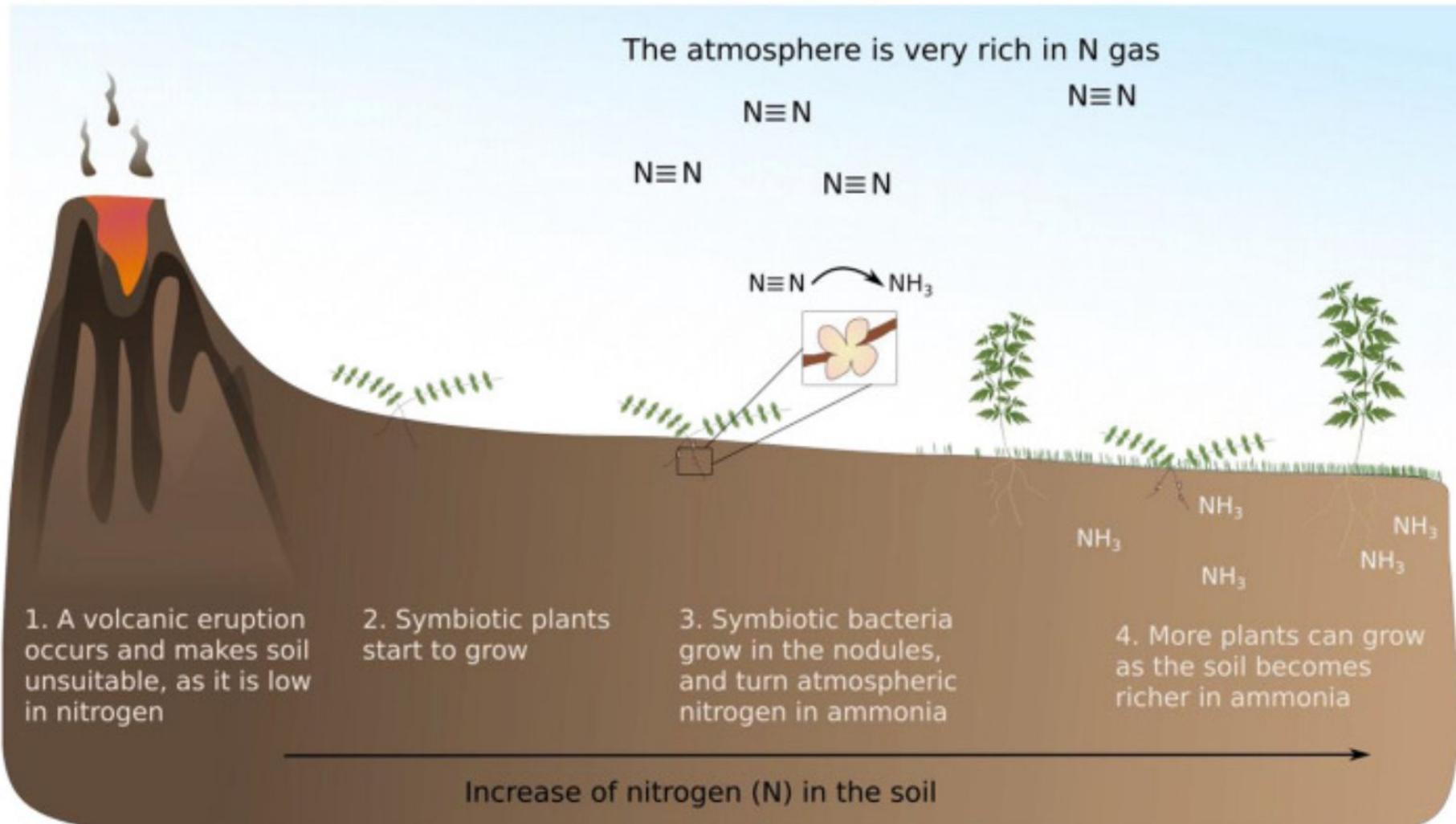
# Investigating biogeographic patterns of *Rhizobium leguminosarum* symbiovar *viciae* within the tribe Fabeae

Rafaela J. Trad, Sarah Roberts, Matías Morales, Peter J. Young, Euan K. James &  
Gregory Kenicer



# Introduction - Nodulation

## - What is nodulation and why is it important?



Plant growth

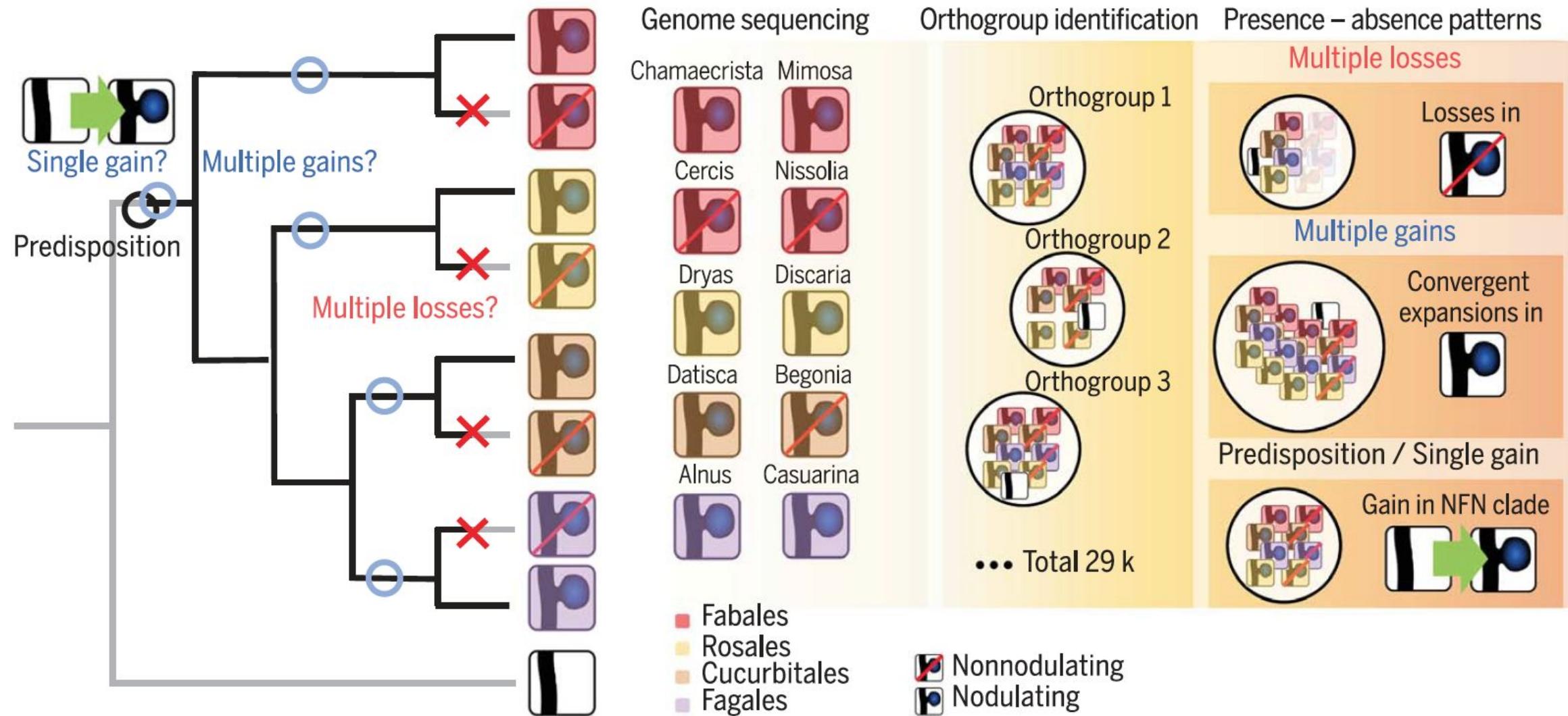
N cycling

Agriculture

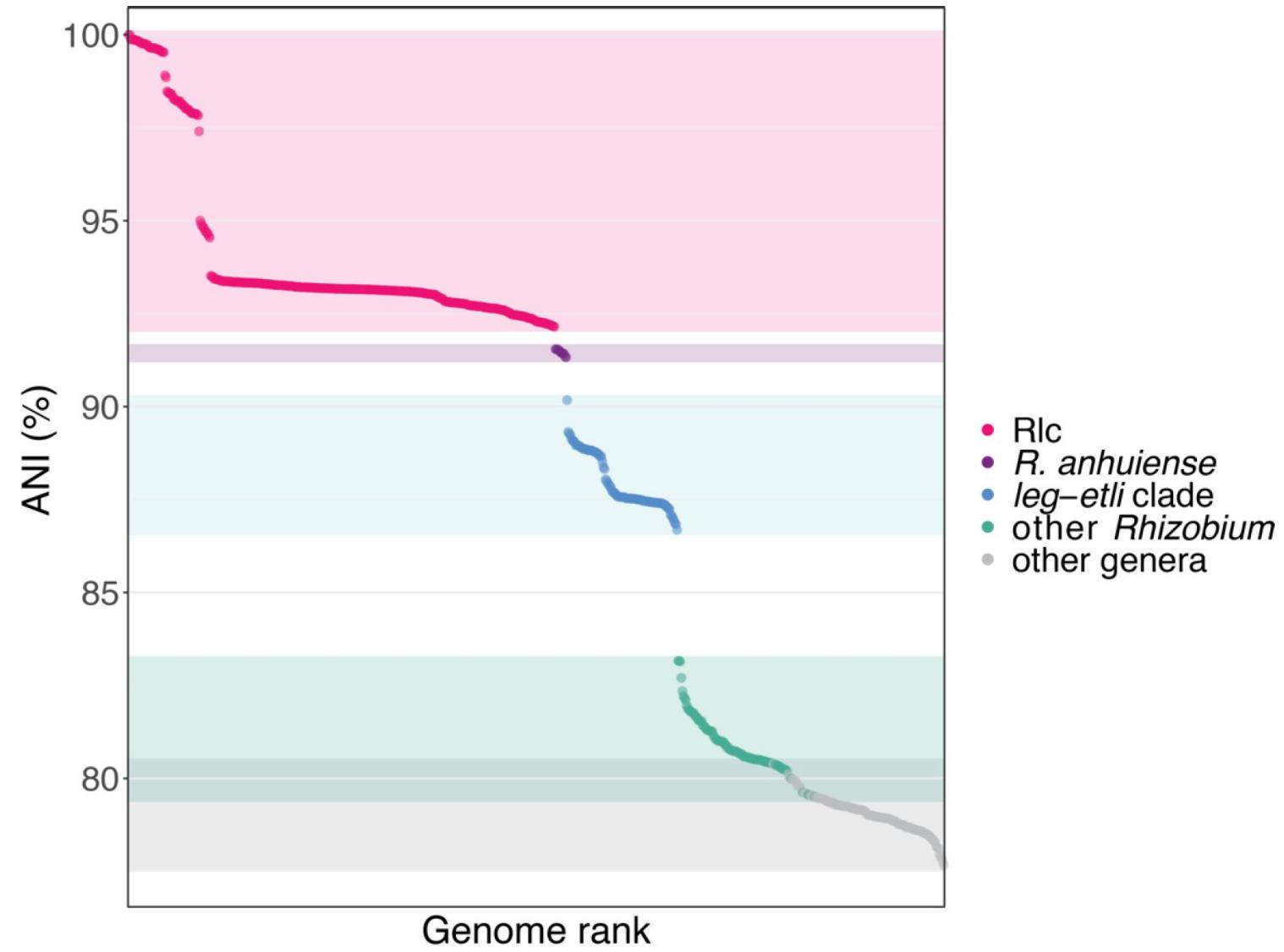
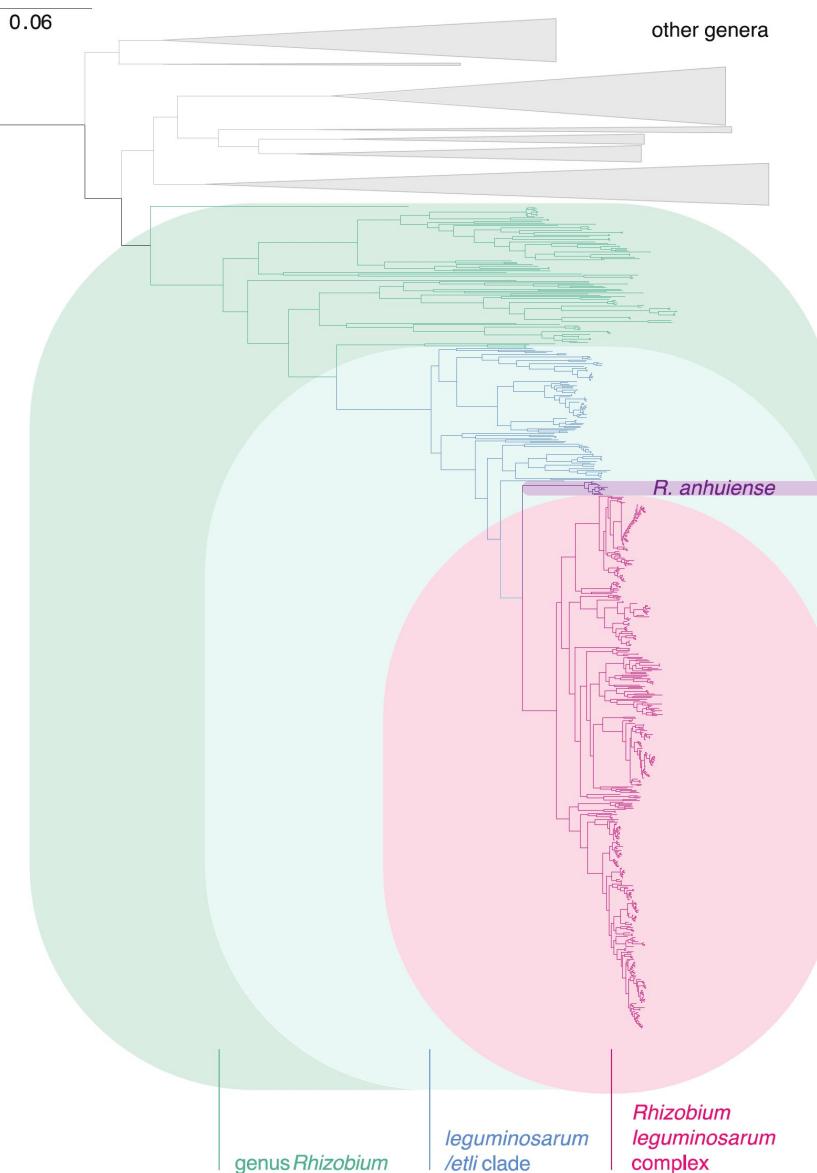
# Introduction – Nodule diversity



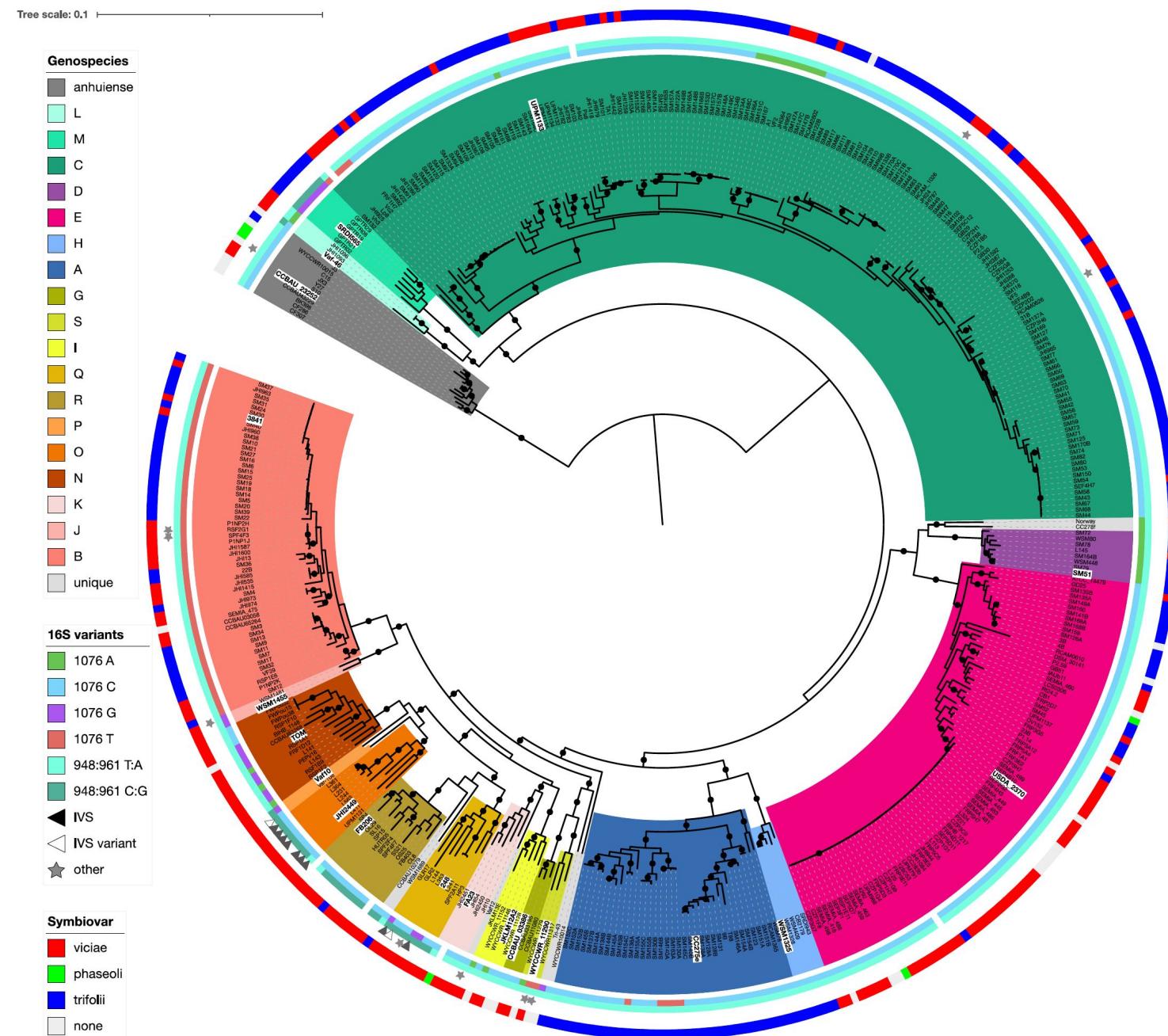
# Introduction – Origins of nodulation



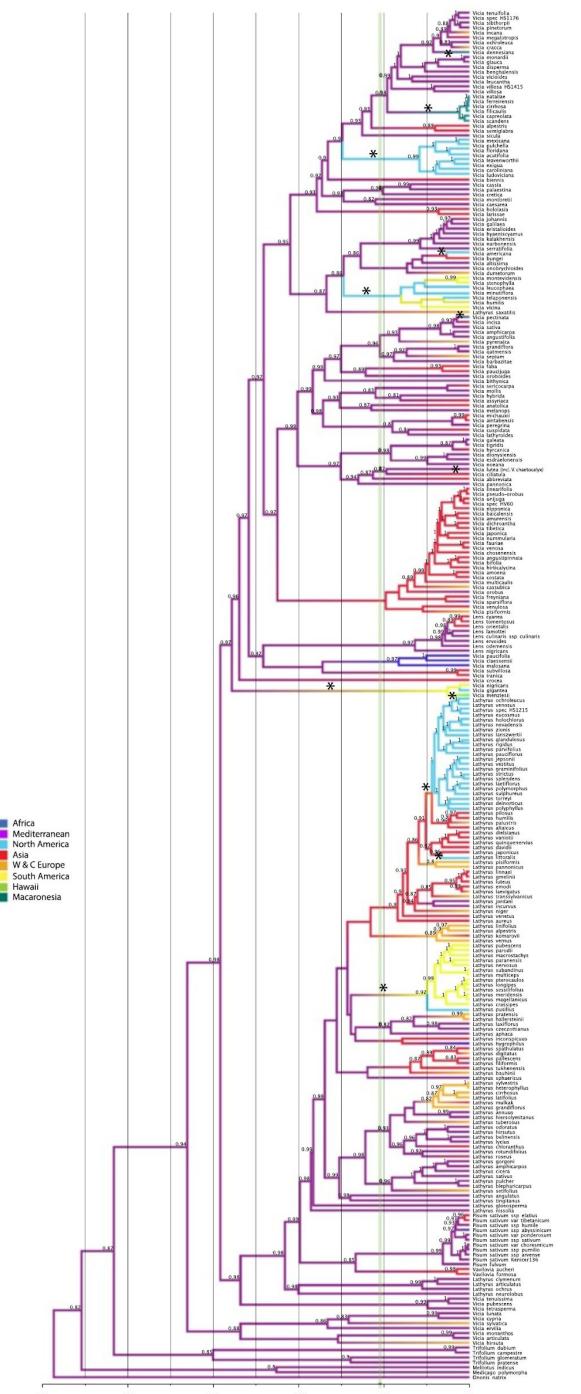
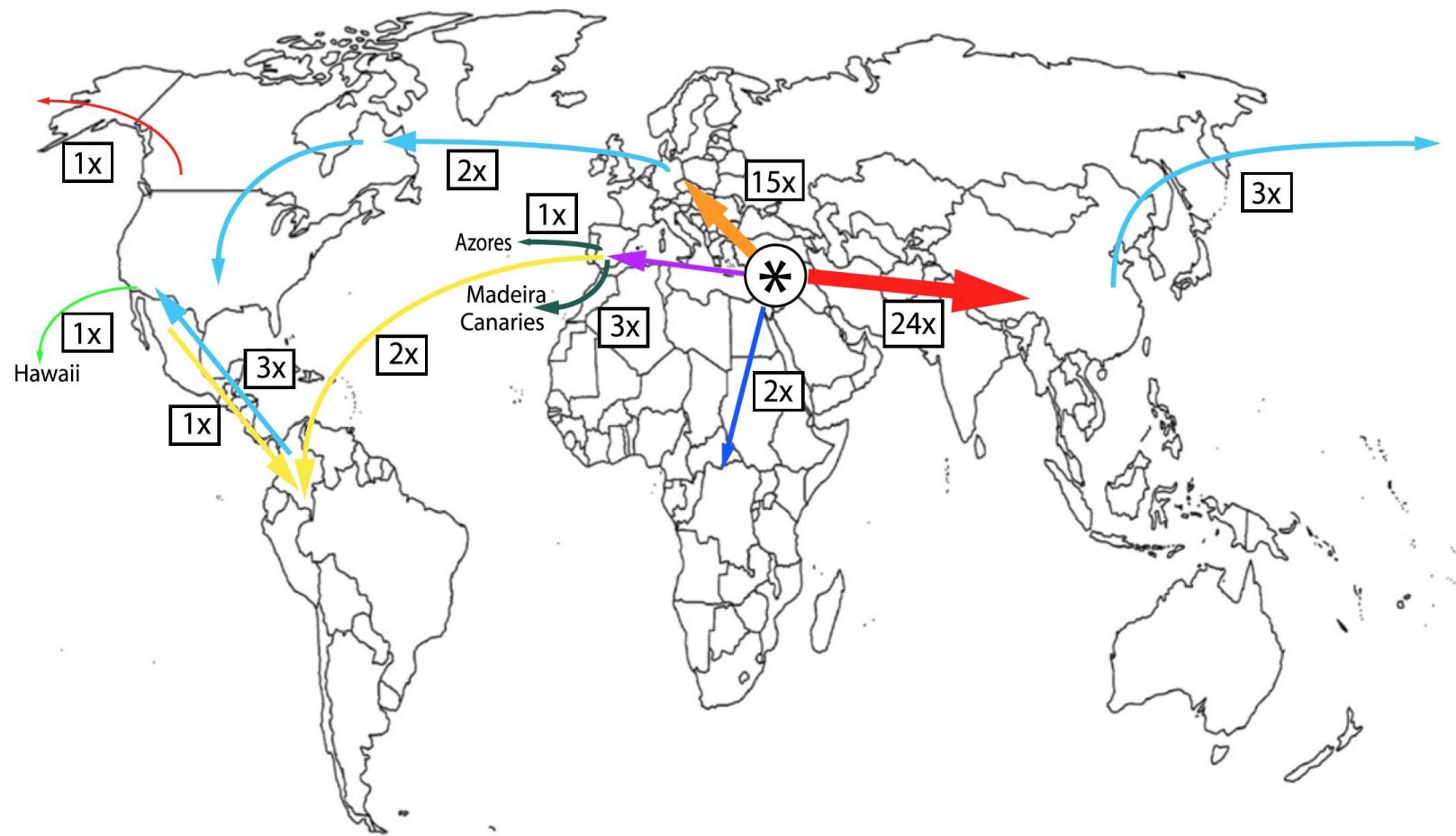
# Introduction



# Introduction



# Introduction - Fabeae



# Introduction - Fabeae

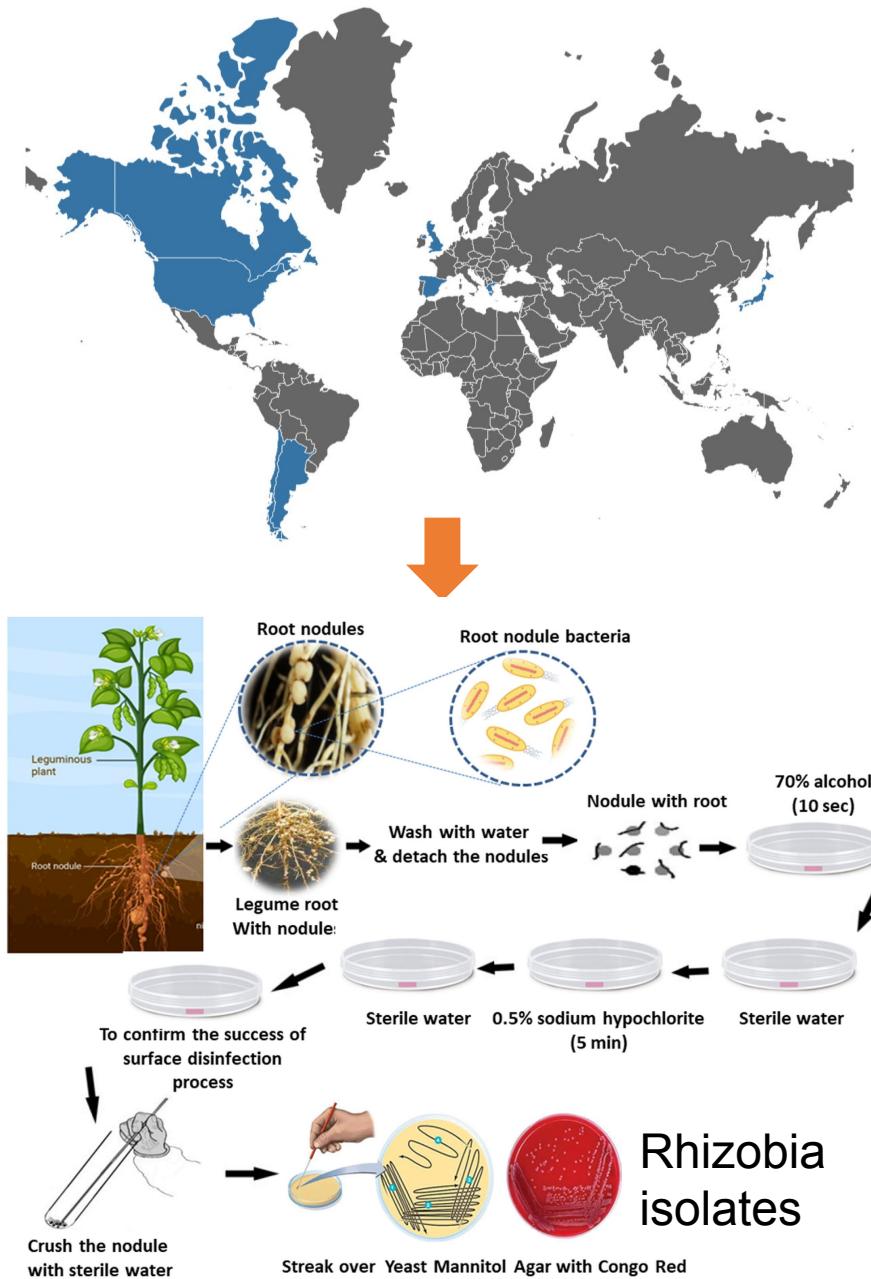
- The tribe includes four genera: *Ervilia* Link, *Ervum* L., *Lathyrus* L., and *Vicia* L.



# Methods

Source: Visme  
(<https://dashboard.visme.co/v2/login>)

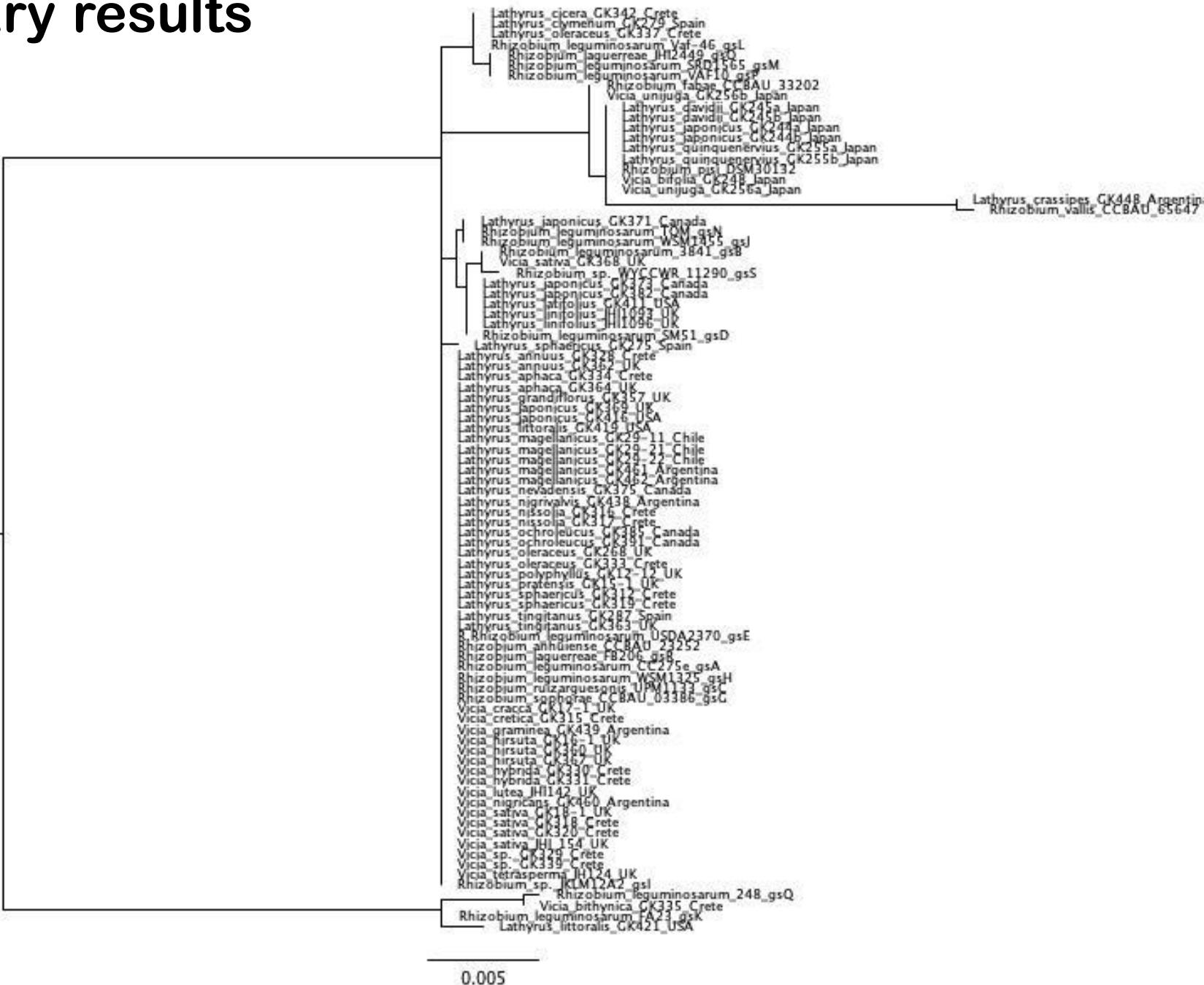
Etesami, H. 2022. CRBIOT 4: 78–86.



- Three sets of genes:**
- 16S rRNA
  - 120 core-genes
  - Nodulation genes

# Preliminary results

16S



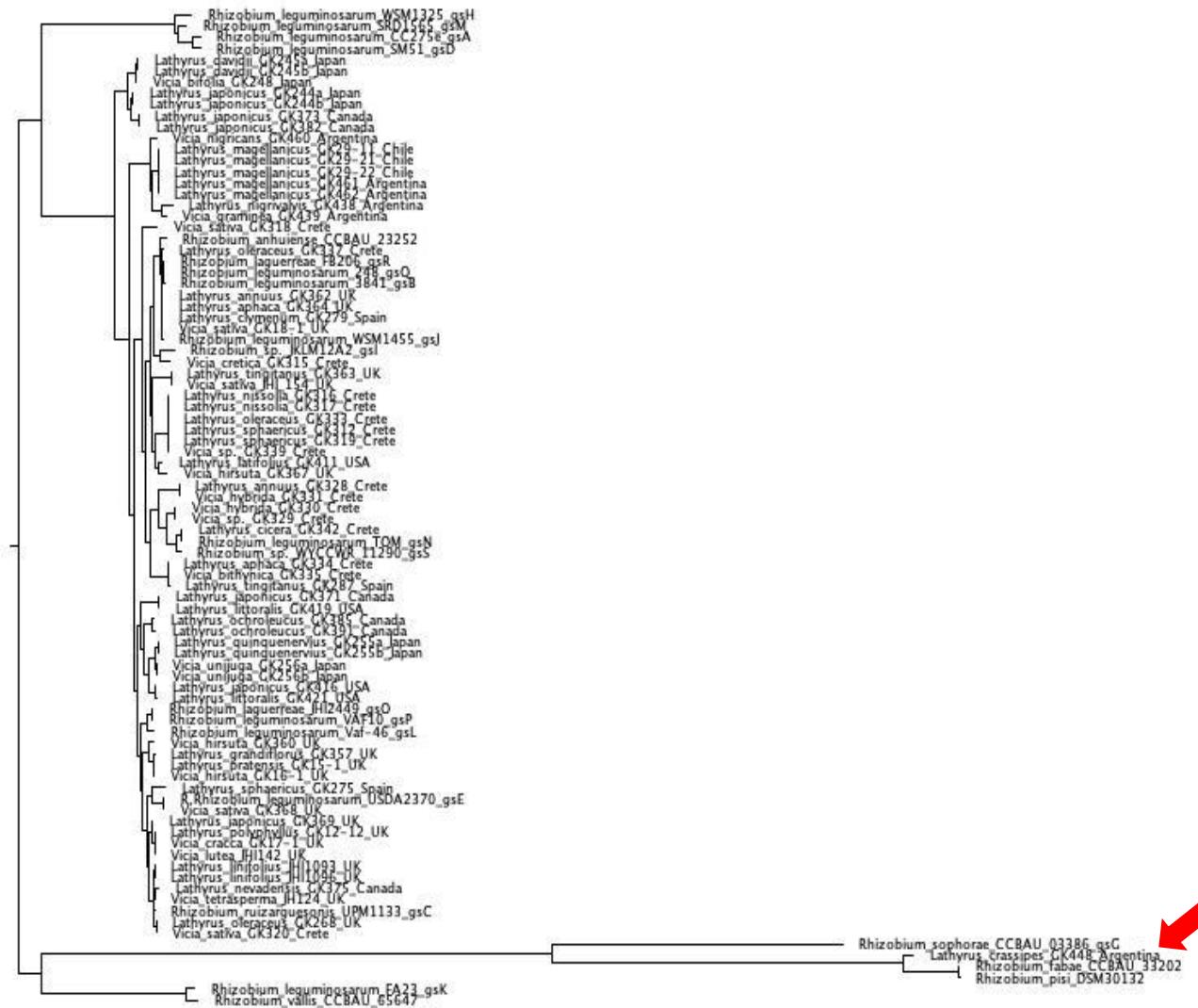
# Preliminary results

*nodA*



0.06

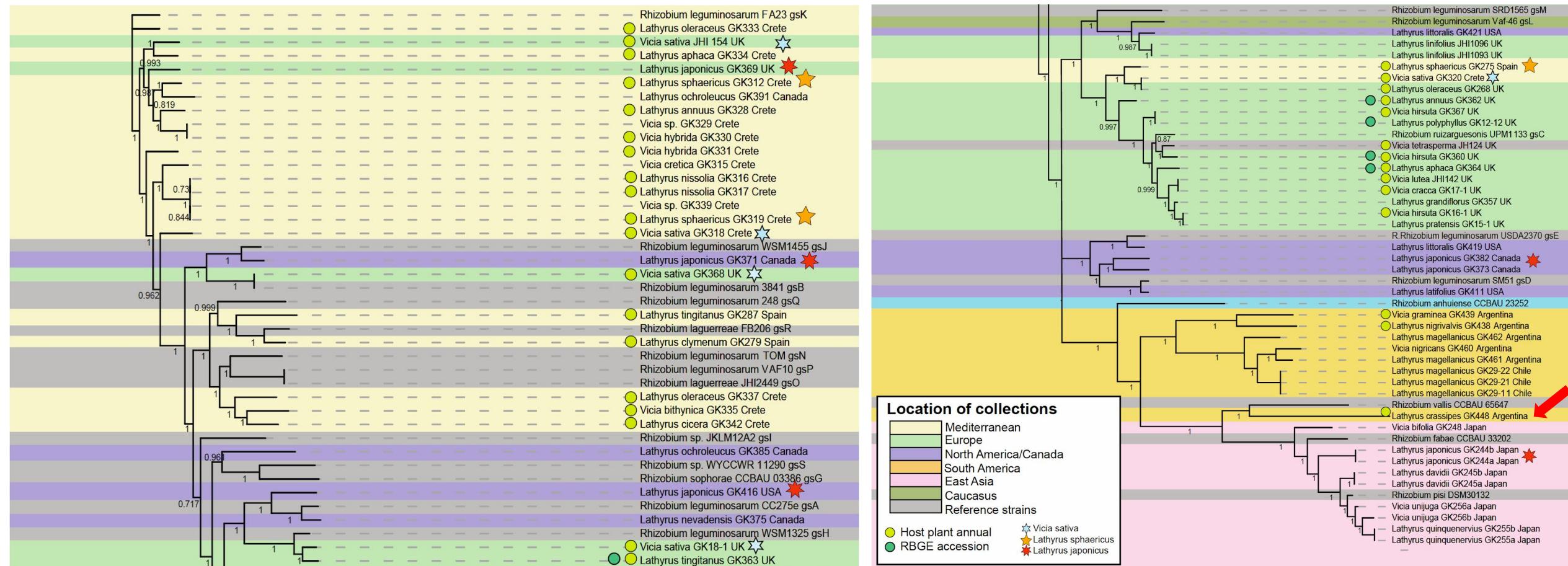
*nodC*



0.2



# Preliminary results



# Next steps

Sample	Best_kmer	N_contigs	Dead_ends	Length	N50	Longest_contig		N_contigs	L50	N50	Longest_contig
17648	127	144	14	6,460,695	322,886	938,375		171	9	299,796	622,587
17649	127	1,281	67	7,677,786	103,842	426,828		469	20	98,805	426,954
17650	119	1,368	24	7,687,887	144,122	363,751		461	17	143,81	364,124
17651	119	1,964	53	7,018,180	72,678	215,999		885	30	75,479	216,725
17652	119	357	12	7,016,213	377,100	677,198		133	9	252,123	752,978
17653	127	623	28	7,246,404	181,637	534,086		216	15	152,259	419,216
22766	127	328	18	7,098,350	282,838	568,456		189	9	292,07	626,005
22767	127	335	29	7,096,549	215,547	489,205		189	12	226,803	546,690
22768	127	512	9	6,923,260	259,844	532,406		192	10	226,335	535,277
22769	127	352	14	7,011,273	263,162	567,874		129	9	263,429	631,435
22770	127	306	45	8,055,376	363,150	680,101		411	21	145,654	603,831
22771	127	278	16	7,567,465	253,488	642,125		120	11	244,377	571,185
22772	127	290	34	7,745,187	208,536	642,984		204	11	247,455	642,344

# Next steps

- 1) Try to improve the assemblies (Jigome);
- 2) Extract the genes again (Rlc);
- 3) Rerun the analysis and use other tree estimations methods.



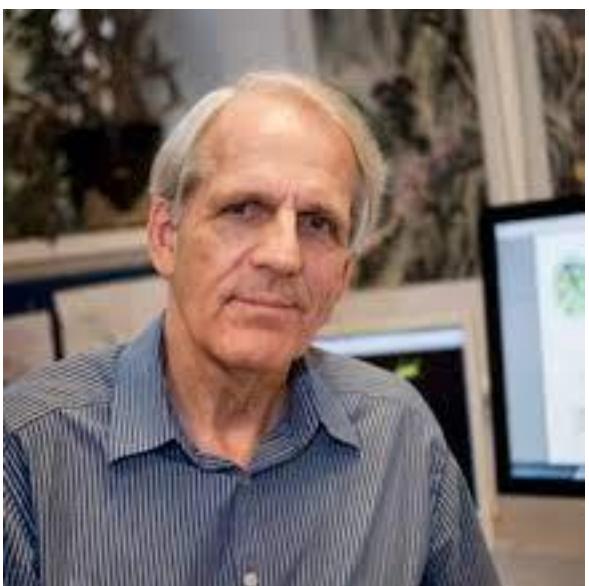
# Acknowledgements



Royal  
Botanic Garden  
Edinburgh



The James  
**Hutton**  
Institute



Instituto Nacional  
de Tecnología Agropecuaria



UNIVERSITY  
*of York*

Coming next...



**IBC  
2024**

July, 21st - 27th, 2024

**XX International  
Botanical  
Congress  
Madrid Spain**



**RECENT ADVANCES IN THE MEGADIVERSE LEGUME SUBFAMILY PAPILIONOIDEAE - PART I**

**RECENT ADVANCES IN THE MEGADIVERSE LEGUME SUBFAMILY PAPILIONOIDEAE - PART II**

**LEGUME SYSTEMATICS: FROM COLLABORATIVE NETWORKS TO GENOME SEQUENCING**

- 1) Rafaela Jorge Trad and Gregory Kenicer – Tentative title: Papilionoid legumes phylogeny: what do we know and what is still left to do?
- 2) Ana Paula Fortuna and Bente Bang Klitgård – Tentative title: Advances in legume systematics: insights from the Dalbergiod clade (from rosewoods to fodder plants and peanuts).
- 3) Ozan Şentürk, Gregory Kenicer, and Zeki Aytaç – Tentative title: Revisiting *Ebenus* L. (Leguminosae): A molecular perspective.
- 4) Flávia Fonseca Pezzini, Moabe Ferreira Fernandes and Toby Pennington – Tentative title: Combining legacy Sanger with new phylogenomic DNA sequence data to produce a densely sampled papilionoid phylogeny for comparative biology.
- 5) Annah Moteeetee, Tlou Manyelo, and Abdulwakeel Ayokun-nun Ajao – Tentative title: Developments in the phylogenetic and taxonomic studies of southern African genera of the tribe Phaseoleae.
- 6) James Clugston – Tentative title: Phylogenetic resolution of the Australian Bush Peas in the tribe Mirbelieae (Fabaceae).