

EMBO 2025: SATELLITE WORKSHOP
BIODIVERSITY GENOMICS

Genomic and functional study of *Bacillus* endophytes from plants with different lifestyles

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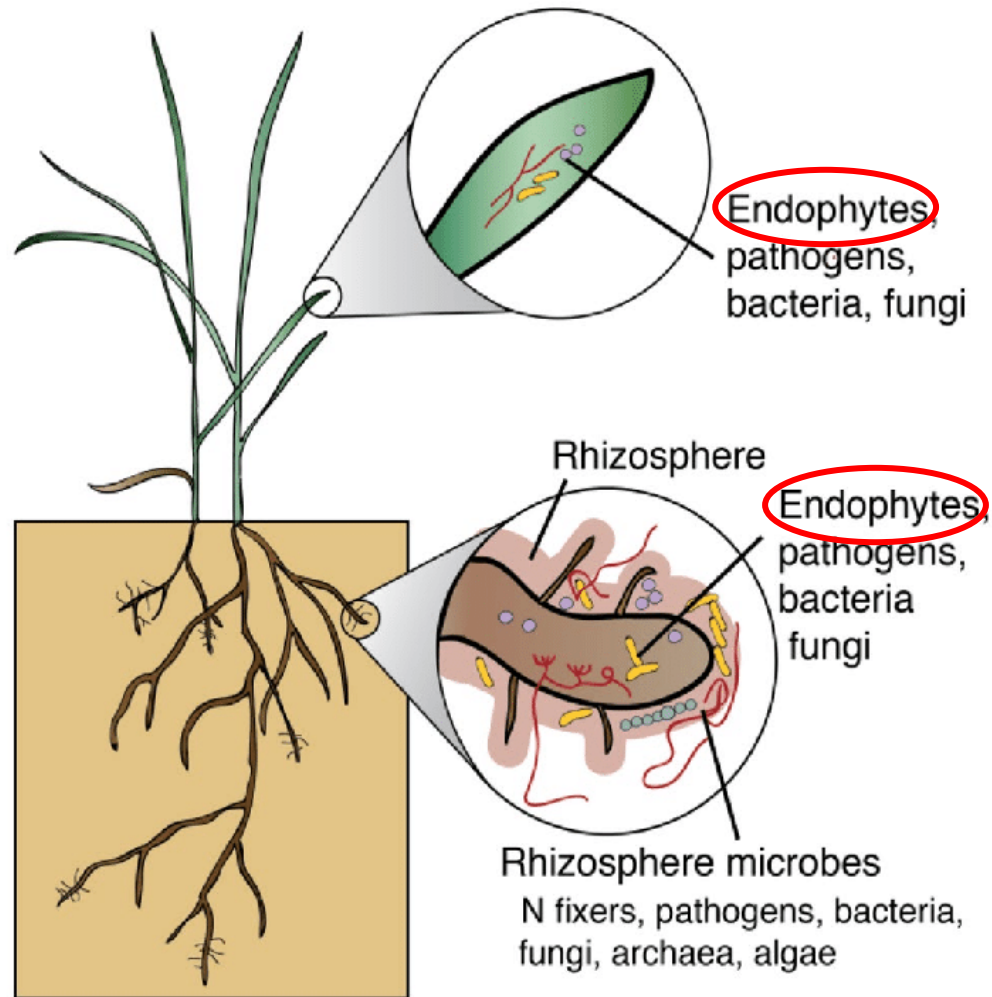
Let's think about something



we give biodiversity most of the times ?



Endophytic Microbes

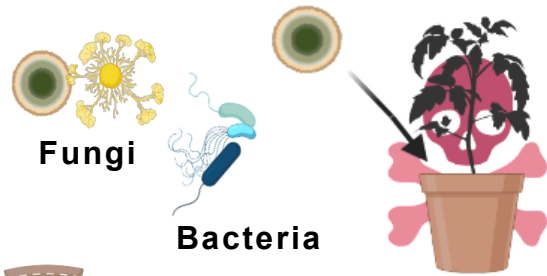


- **Non-pathogenic**
- **Plant growth-promotion**
- Improved **resistance against biotic and abiotic stress** conditions
- Production of **bioactive compounds**

Endophytes as a solution for a sustainable agriculture

1) The challenge of modern agriculture

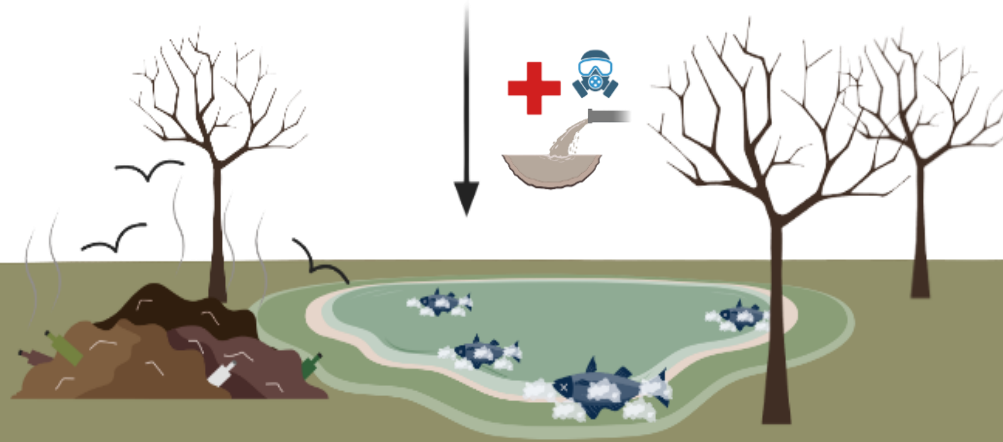
➤ Fight against Pathogens



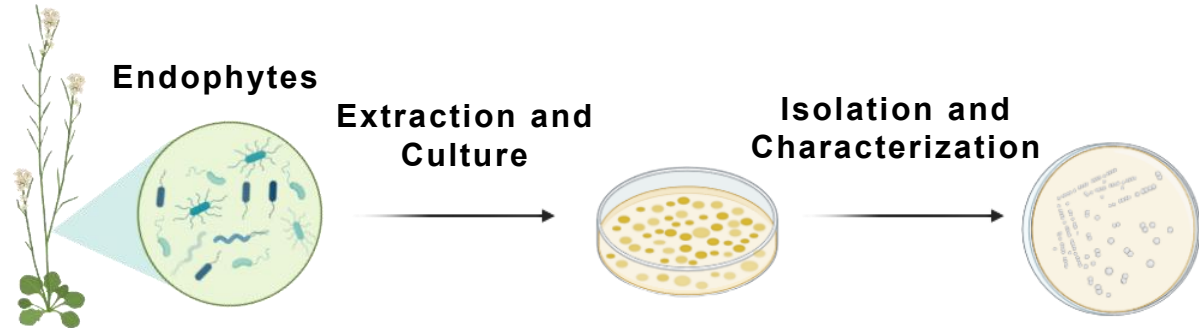
Biopesticides and
Synthetic
Fertilizers



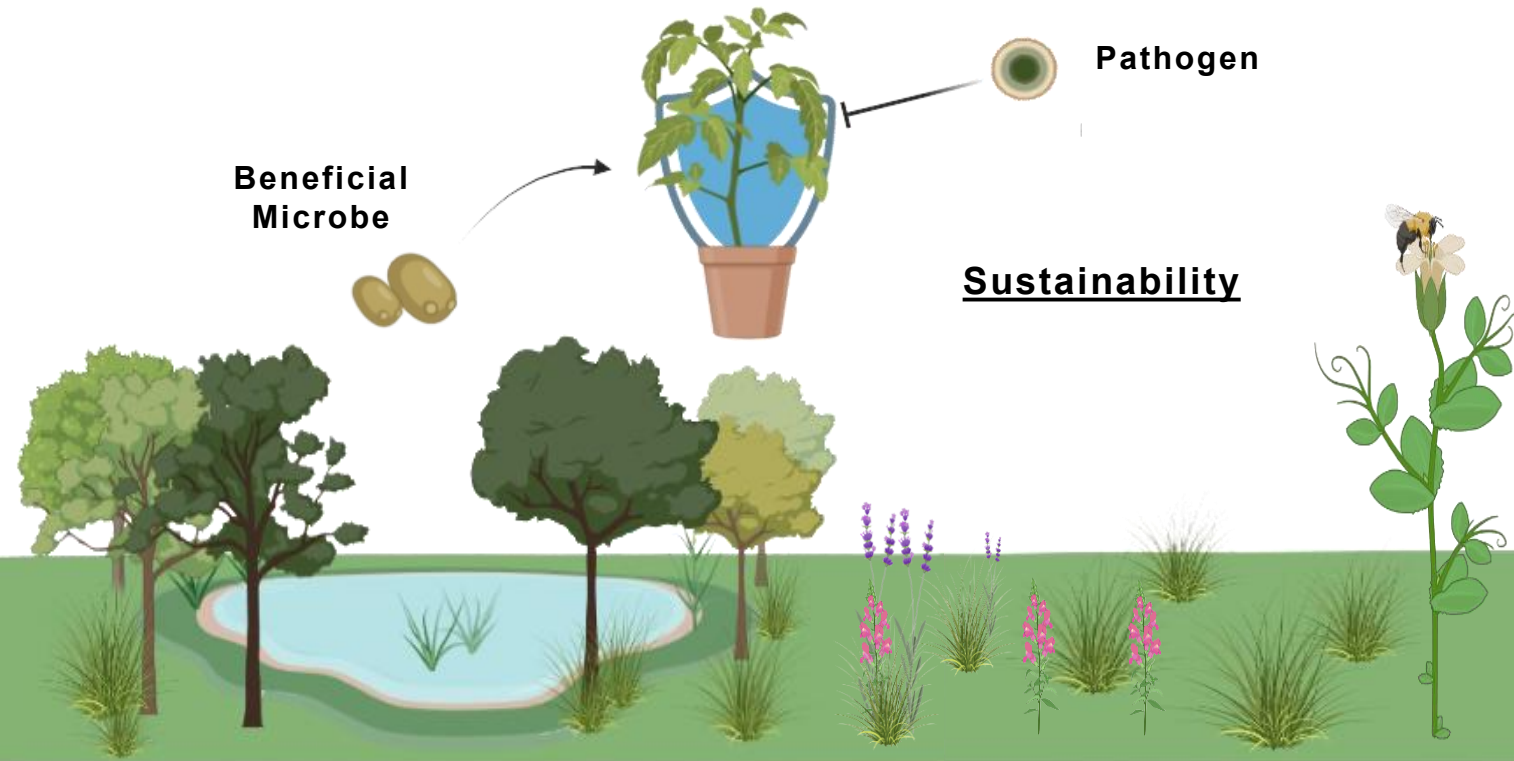
Pollution



2) Exploring the microbial arsenal of plants



➤ Identification of BENEFICIAL MICROBES which protect plants from pathogens



Scientific Questions

- Do the **endophytic microbes** of plants that **live in extreme environments** have a role in **stress tolerance**?
- Could the **endophytic microbes of crop wild relatives (CWRs)** be a good **source of beneficial microbes** for crops contribute to **abiotic** and **biotic stress tolerance**?
- **Approach: Phylogenetics, Comparative Genomics and Functional Analysis** of the endophytes to get unique insights in uncovering **genomic diversity** and identify **novel traits crucial for future applications**

Sampling of halophytes and olive trees in Crete and Chrisi island



Prof. P. Sarris
Group Leader

► Plant species collected from Crete



Cakile maritima



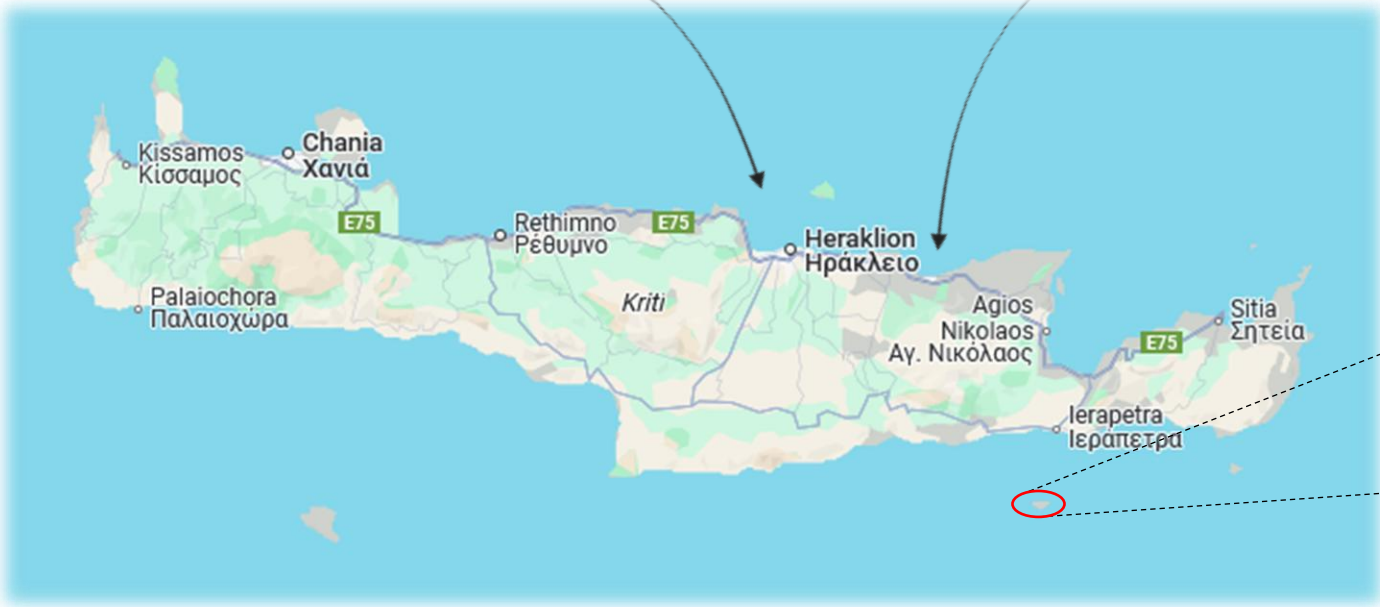
Matthiola tricuspidata



Crithmum maritimum



Olea europaea

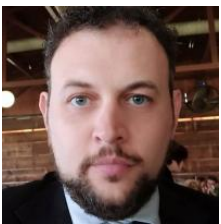


(Christakis, et al., 2021)

(source: Google Maps)



Mr N. Arapitsas
PhD student



Dr Ch. Christakis
former Post-Doc

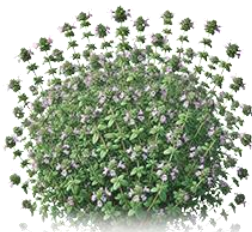


Dr S. Paragkamian
Post-Doc



Mr M. Avramakis
Botanist

► Plant species collected from Chrisi island



Thymus capitatus



Atriplex halimus



Tetraena alba

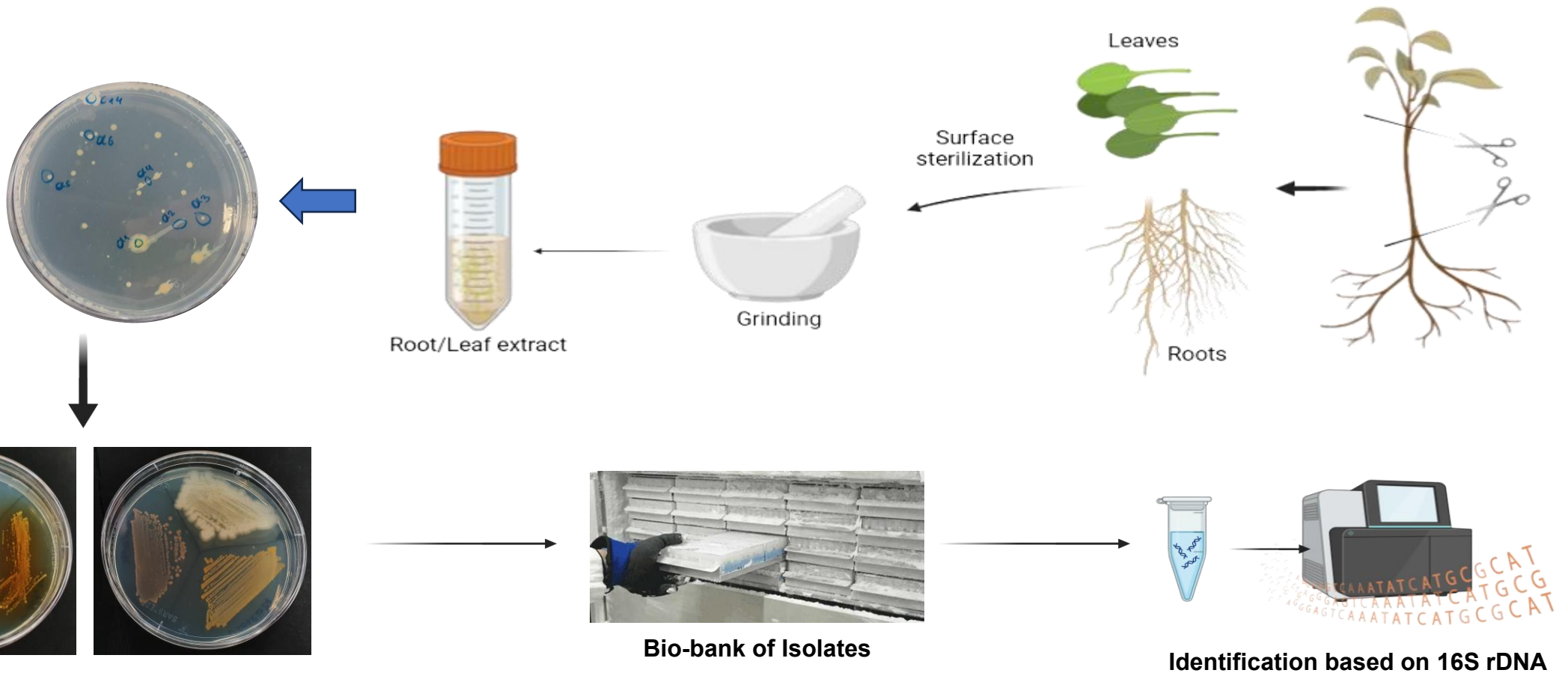


Frankenia sp.

Isolation, identification and characterization of endophytes

Media

- NA
- R2A
- NA1/2



Isolation and characterization of endophytic isolates

Bio-bank of Isolates

Identification based on 16S rDNA

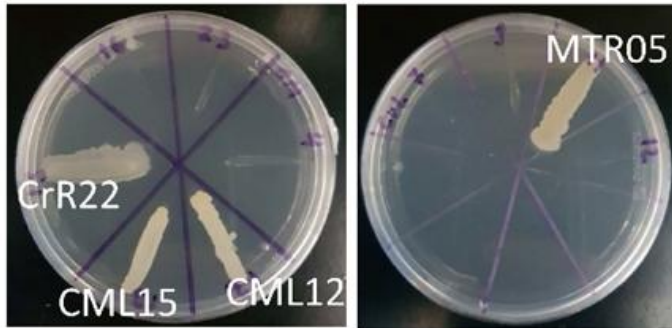
**≈ 500 isolates from halophytes and olive trees from
Crete and halophytes from Chrisi island**

Salt tolerance assays

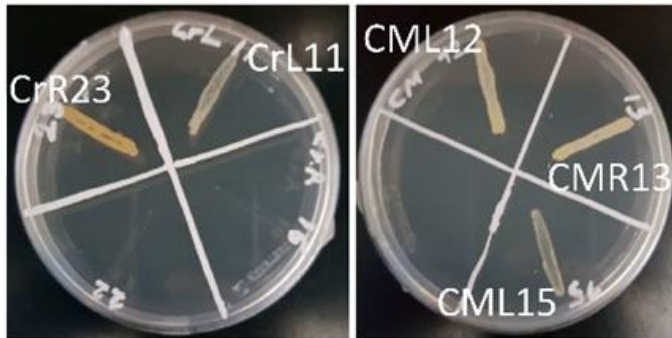
In vitro

Nutrient Agar (NA) medium

15%
NaCl



17.5%
NaCl



*Plants +
Bacterial isolate*

In planta in 250mM NaCl



Control plants

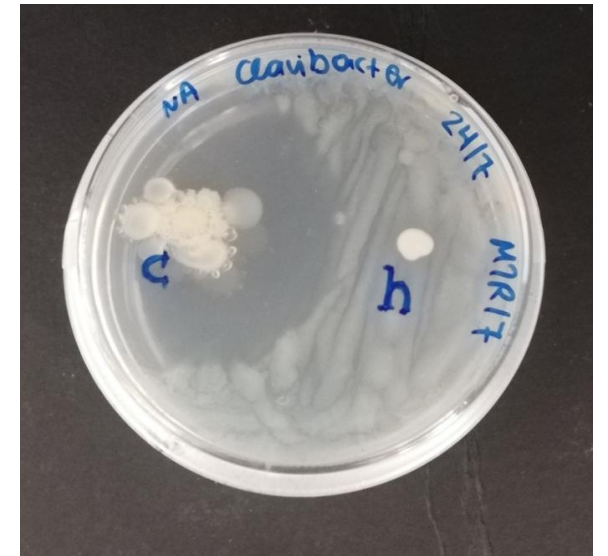
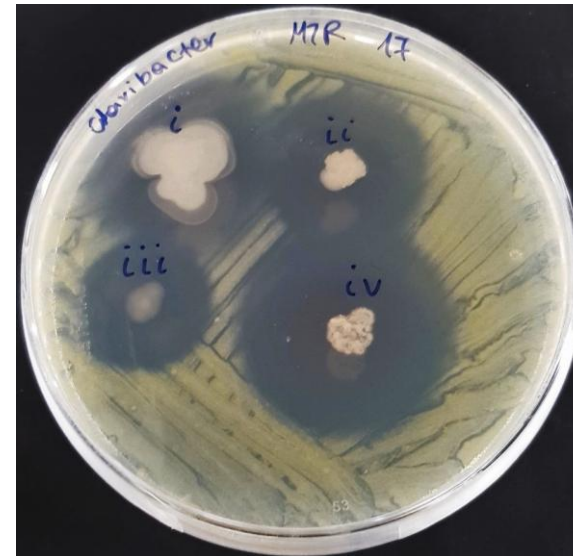


*Control plants
+ E. coli*



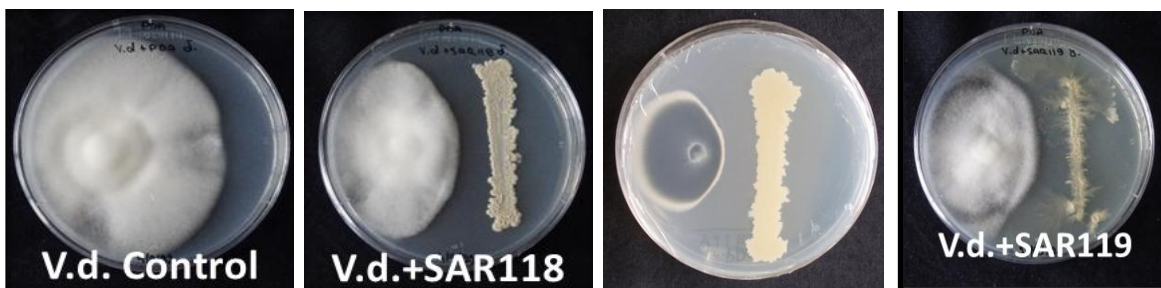
Bioassays against bacterial phytopathogens

- *Clavibacter michiganensis*
- *Paracidovorax citrulli* (former *Acidovorax citrulli*)
- *Ralstonia solanacearum*



Bioassays against phytopathogenic fungi

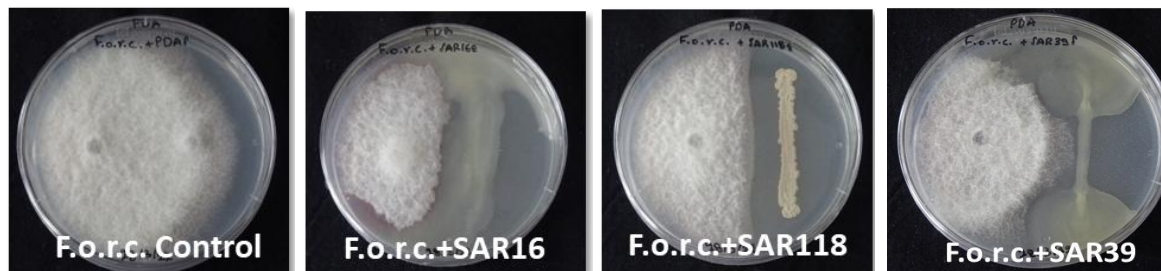
Verticillium



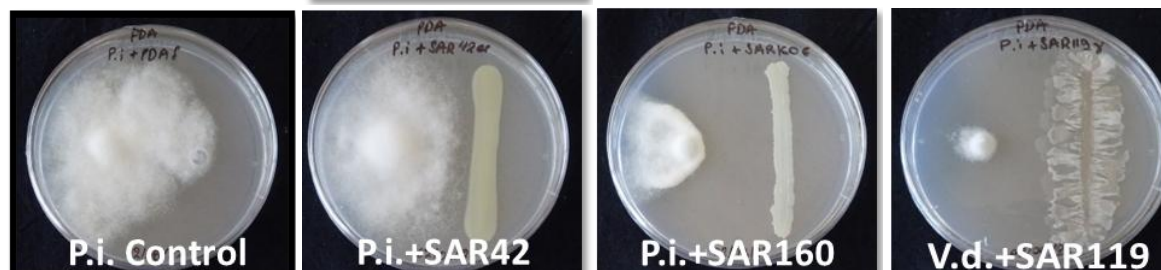
Botrytis



Fusarium



Phytophthora



Mr S. Soultatos
PhD student



Prof. Em. Markakis
Professor

+ *Alternaria*

Bioassays against phytopathogenic fungi

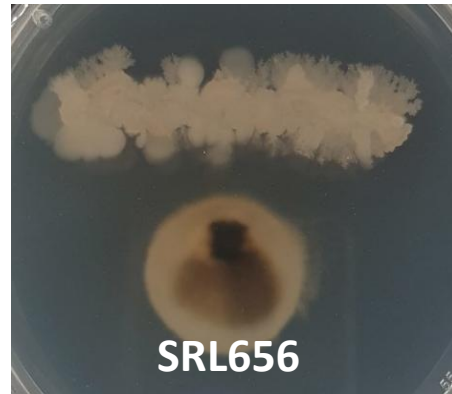


Mr S. Soultatos
PhD student

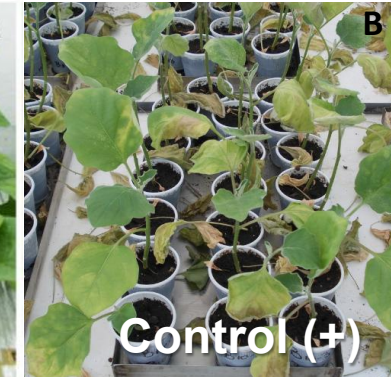
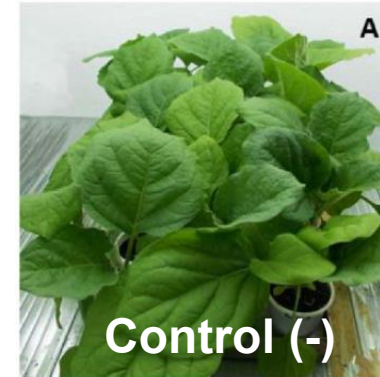


Prof. Em. Markakis
Professor

In vitro



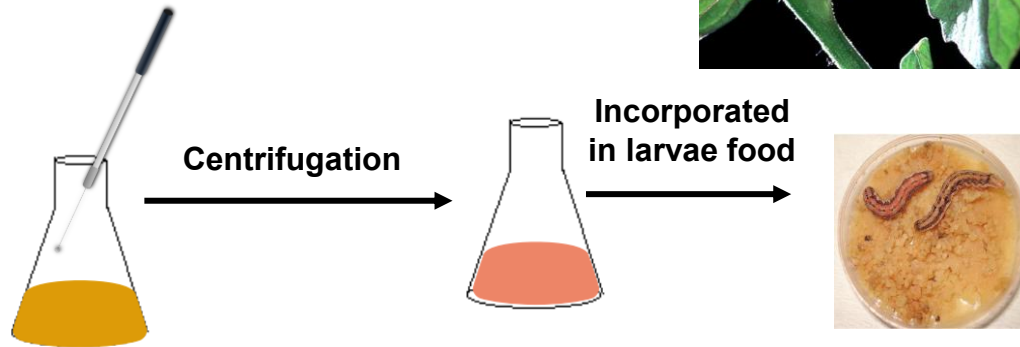
In planta



Symptoms in artificially infected plants
with *Verticillium dahliae*

Bioassays against insect larvae

vs *Helicoverpa* larvae



Control food



Food + bacterial isolate



vs *Culex pipiens* mosquito
(Diptera: Culicidae)



Control (0% mortality in 24hrs)



Bacillus sp. extract (100% mortality in 24hrs)



Dr A. Kampouraki
Postdoc



Mr S. Mastis
PhD student

Selection of isolates for hybrid whole genome sequencing

Isolate ID	Species based on 16S rDNA	Max Salt Tolerance	Inhibition against bacterial pathogens	INH zone against Verticillium dahliae (%)	INH zone against Alternaria sp. (%)	INH zone against Botrytis cinerea (%)	INH zone against Fusarium sp. (%)	Other reasons
SRL152	<i>Bacillus thuringiensis</i>	5% NaCl						interesting phylogenetically
SRL163	<i>Bacillus amyloliquefaciens</i>	7.5% NaCl						interesting phylogenetically
SRL179	<i>Bacillus drentensis</i>	17.5% NaCl						
SRL215	<i>Bacillus thuringiensis</i>	5% NaCl						interesting phylogenetically
SRL218	<i>Bacillus thuringiensis</i>	5% NaCl						interesting phylogenetically
SRL221	<i>Bacillus methylotrophicus</i> synonymous	10% NaCl						interesting phylogenetically
SRL224	<i>Bacillus thuringiensis</i>	5% NaCl						interesting phylogenetically
SRL244	<i>Bacillus siamensis</i>	7.5% NaCl						interesting phylogenetically
SRL266	<i>Peribacillus frigoritolerans</i> strain WS2-1	17.5% NaCl				18.92	24.68	
SRL335	<i>Cytobacillus oceanisediminis</i> 2691			45.45	25.00			
SRL337	<i>Bacillus salacetis</i> strain VS-19	17.5% NaCl						
SRL340	<i>Peribacillus simplex</i> strain BS20				24.24			
SRL342	<i>Paenibacillus xylanexedens</i> strain 3-4T				33.33			
SRL368	<i>Bacillus cereus</i> strain Xuyi_401_1	17.5% NaCl		37.33		35.14	28.57	effective against <i>Culex pipiens</i> and <i>Helicoverpa</i>
SRL369	<i>Bacillus subtilis</i> WN-1	10% NaCl				29.73		
SRL374	<i>Bacillus siamensis</i> strain LB146	10% NaCl		76.00	33.33	45.95	61.04	
SRL379	<i>Bacillus amyloliquefaciens</i> strain PD2	7,5% NaCl	Inhibition against Clavibacter	68.00	30.30	43.24	53.25	
SRL389	<i>Bacillus simplex</i> strain ILQ109	7,5% NaCl		40.00		19.74		
SRL398	<i>Paenibacillus xylanexedens</i> strain 3-4T	5% NaCl	Inhibition against Clavibacter				22.86	
SRL543	<i>Bacillus infantis</i>	10% NaCl		Large				
SRL544	<i>Bacillus haikouensis</i>	15% NaCl						only one other genome and only as a Scaffold
SRL571	<i>Bacillus altitudinis</i>		Inhibition against Clavibacter	Large				
SRL656	<i>Bacillus licheniformis</i>	5% NaCl		Large				
SRL658	<i>Bacillus sonorensis</i>			Large				
SRL662	<i>Bacillus licheniformis</i>			Large				

Selection of isolates for hybrid whole genome sequencing

Selection criteria:

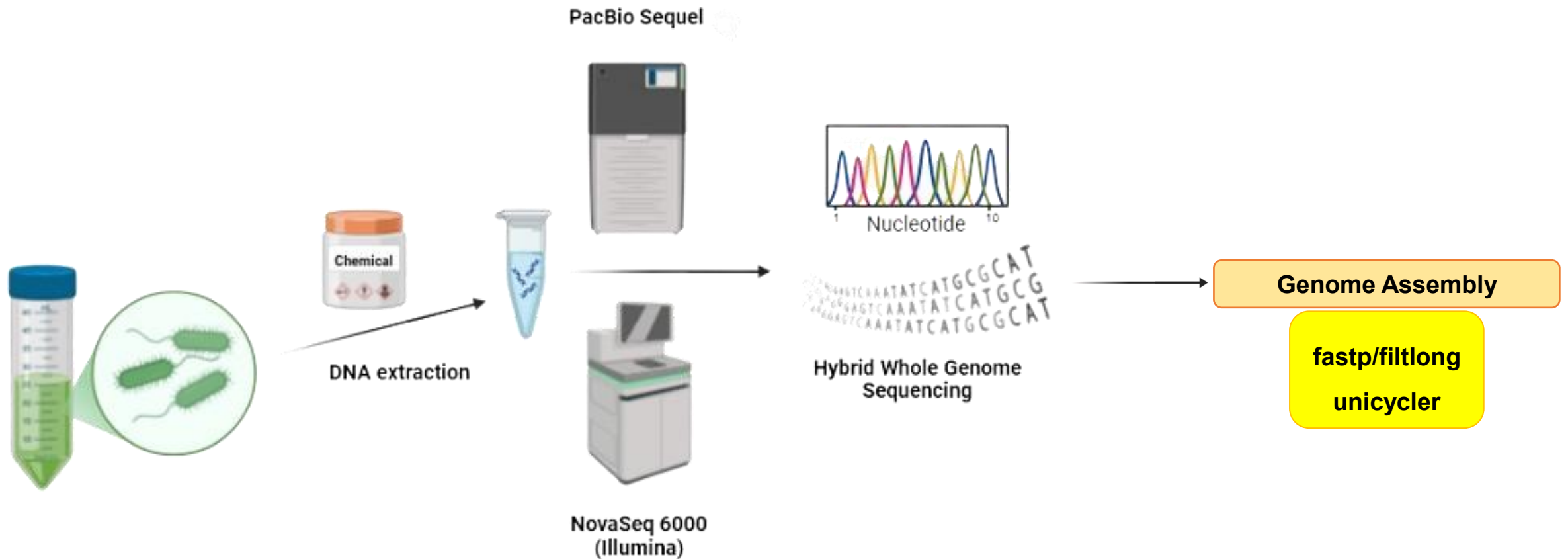
- Salt tolerance
- Inhibition of plant pests and pathogens
- Limited online genome availability



- **25 endophytic isolates** from olive trees and halophytes from
Crete and Chrisi island

Focus on the class Bacilli

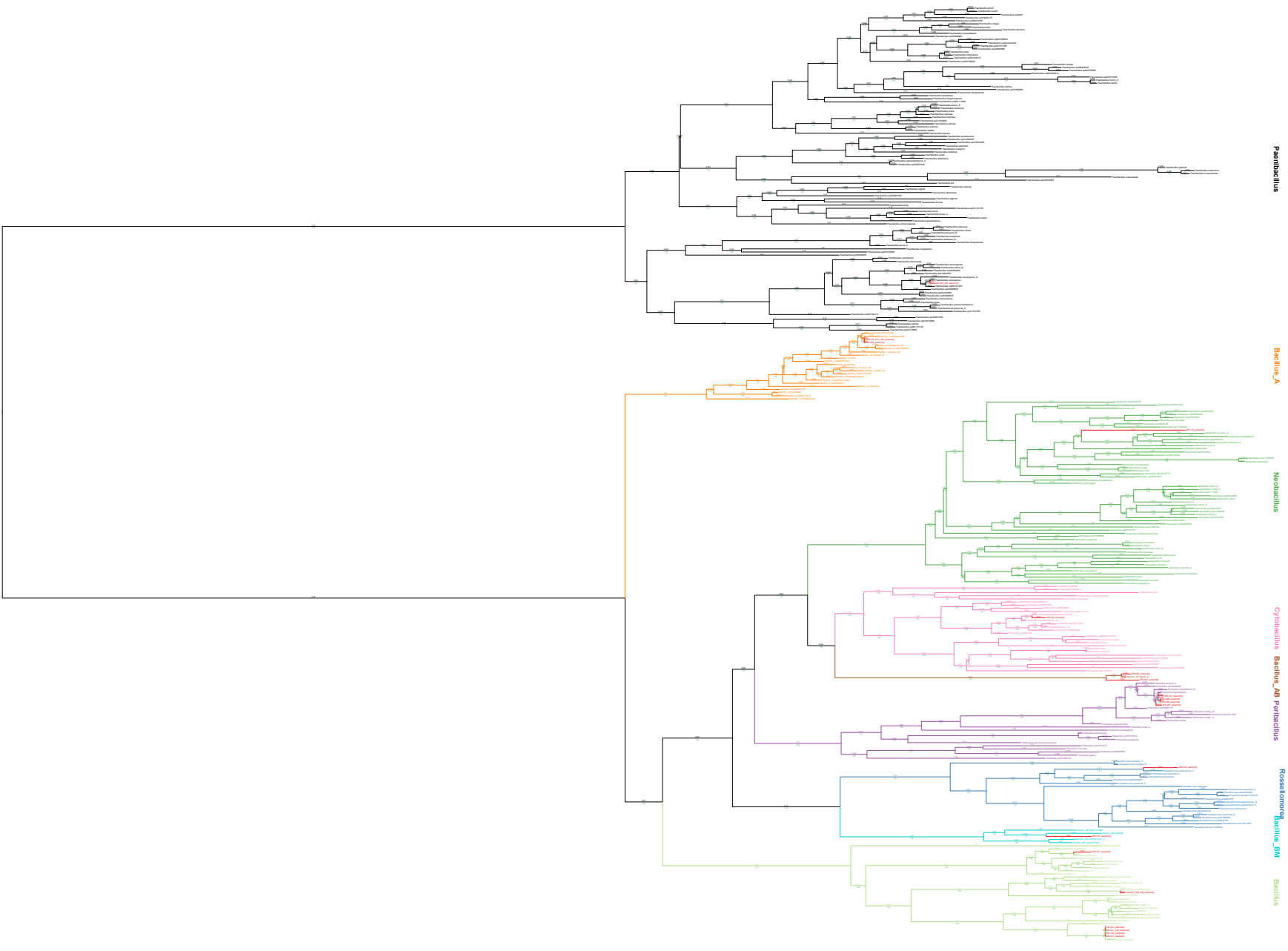
Hybrid whole genome sequencing combining short and long reads

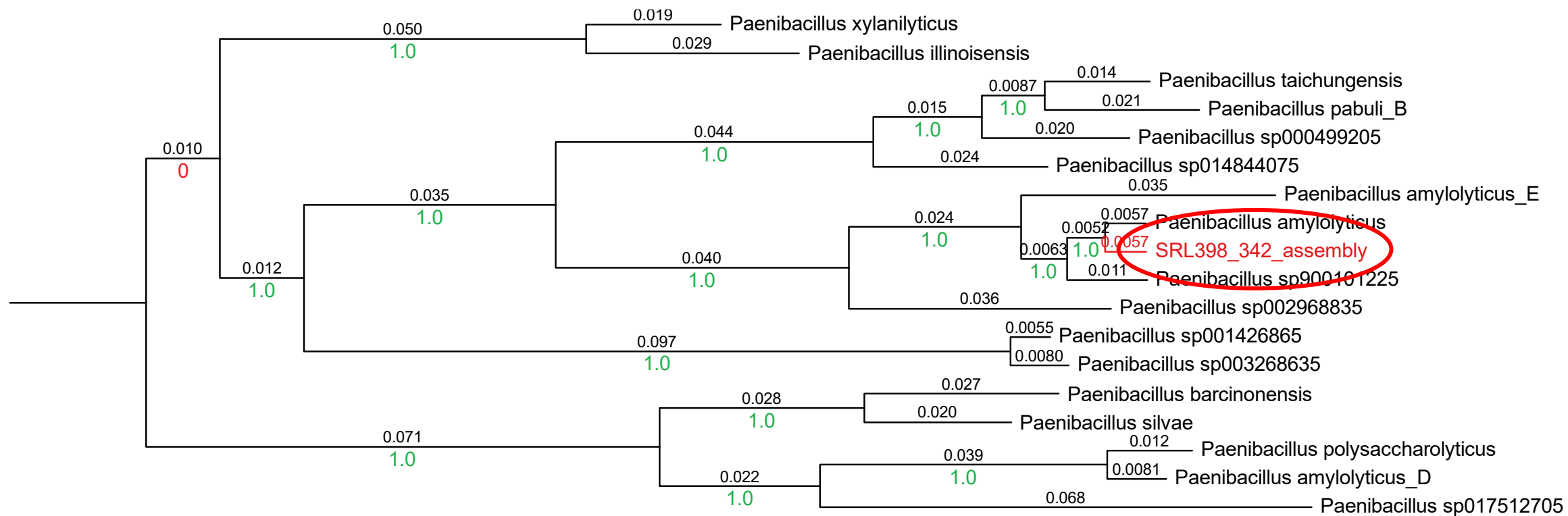


Identification of the isolates using FastANI

Isolate ID	Origin	Species wGTDBk (WGS)	GTDBk FastANI %
SRL152	Olive tree	<i>Peribacillus frigoritolerans</i>	97.47
SRL163	Olive tree	<i>B. velezensis</i>	99.04
SRL179	Olive tree	<i>Neobacillus jeddahensis</i>	80.14
SRL215	Olive tree	<i>Bacillus_A thuringiensis_S</i>	99.21
SRL218	Olive tree	<i>B. thuringiensis</i>	99.07
SRL221	Olive tree	<i>B. velezensis</i>	99.04
SRL224	Olive tree	<i>Bacillus thuringiensis</i>	99.22
SRL244	Olive tree	<i>B. velezensis</i>	99.03
SRL266	Halophyte from Chrysi island	<i>Peribacillus frigoritolerans</i>	96.51
SRL335	Halophyte from Chrysi island	<i>Cytobacillus oceanisediminis</i>	95.33
SRL337	Halophyte from Chrysi island	<i>Bacillus salacetis</i>	83.69
SRL340	Halophyte from Chrysi island	<i>Peribacillus frigoritolerans</i>	95.51
SRL342	Halophyte from Chrysi island	<i>Paenibacillus sp001955855</i>	96.08
SRL368	Halophyte from Chrysi island	<i>Bacillus thuringiensis</i>	99.32
SRL369	Halophyte from Chrysi island	<i>Bacillus infantis</i>	98.95
SRL374	Halophyte from Chrysi island	<i>Bacillus velezensis</i>	99.04
SRL379	Halophyte from Chrysi island	<i>Bacillus velezensis</i>	99.03
SRL389	Halophyte from Chrysi island	<i>Peribacillus frigoritolerans</i>	96.49
SRL398	Halophyte from Chrysi island	<i>Paenibacillus sp001955855</i>	96.08
SRL543	Halophyte from Crete	<i>Bacillus infantis</i>	90.14
SRL544	Halophyte from Crete	<i>Rossellomorea (previously Bacillus) haikouensis</i>	99.99
SRL571	Halophyte from Crete	<i>Bacillus altitudinis</i>	97.98
SRL656	Halophyte from Crete	<i>Bacillus paralicheniformis</i>	98.85
SRL658	Halophyte from Crete	<i>B. paralicheniformis</i>	98.85
SRL662	Halophyte from Crete	<i>Bacillus paralicheniformis</i>	98.85

Four putative novel species





Paenibacillus



Neobacillus

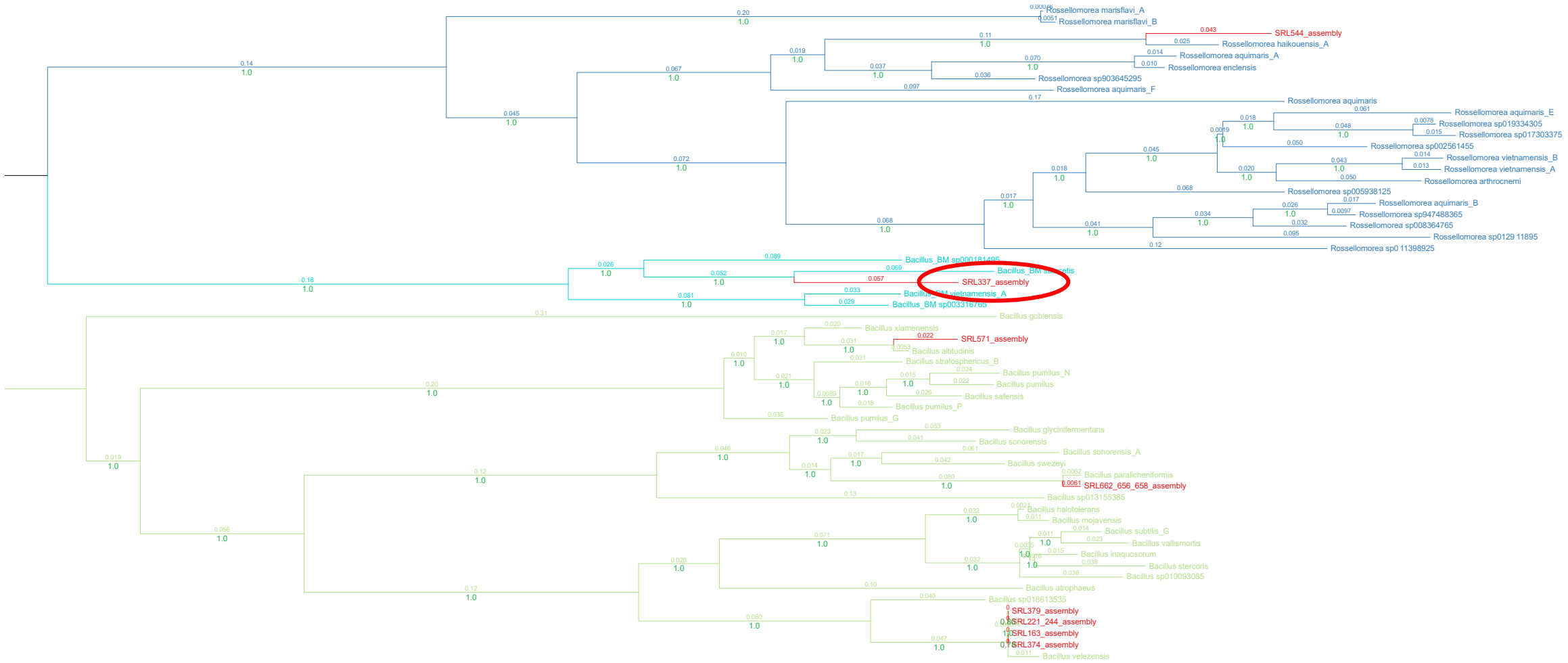
Cytobacillus Bacillus_AB Peribacillus



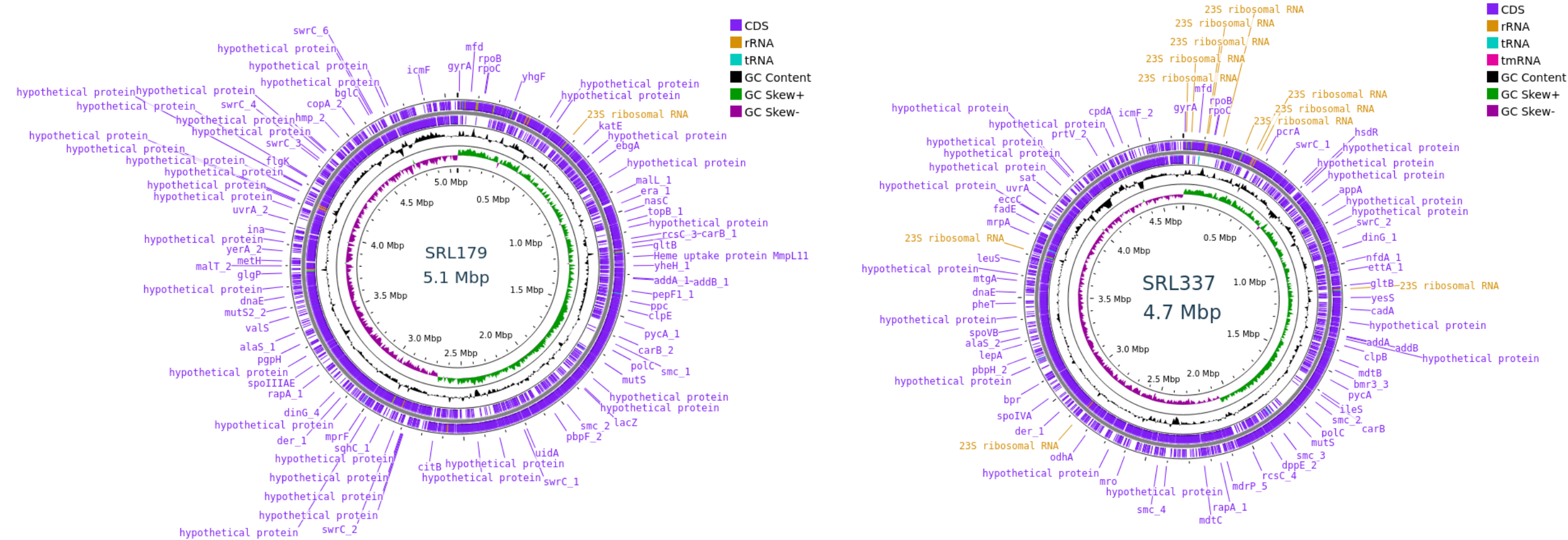
Rossellomorea

Bacillus_BM

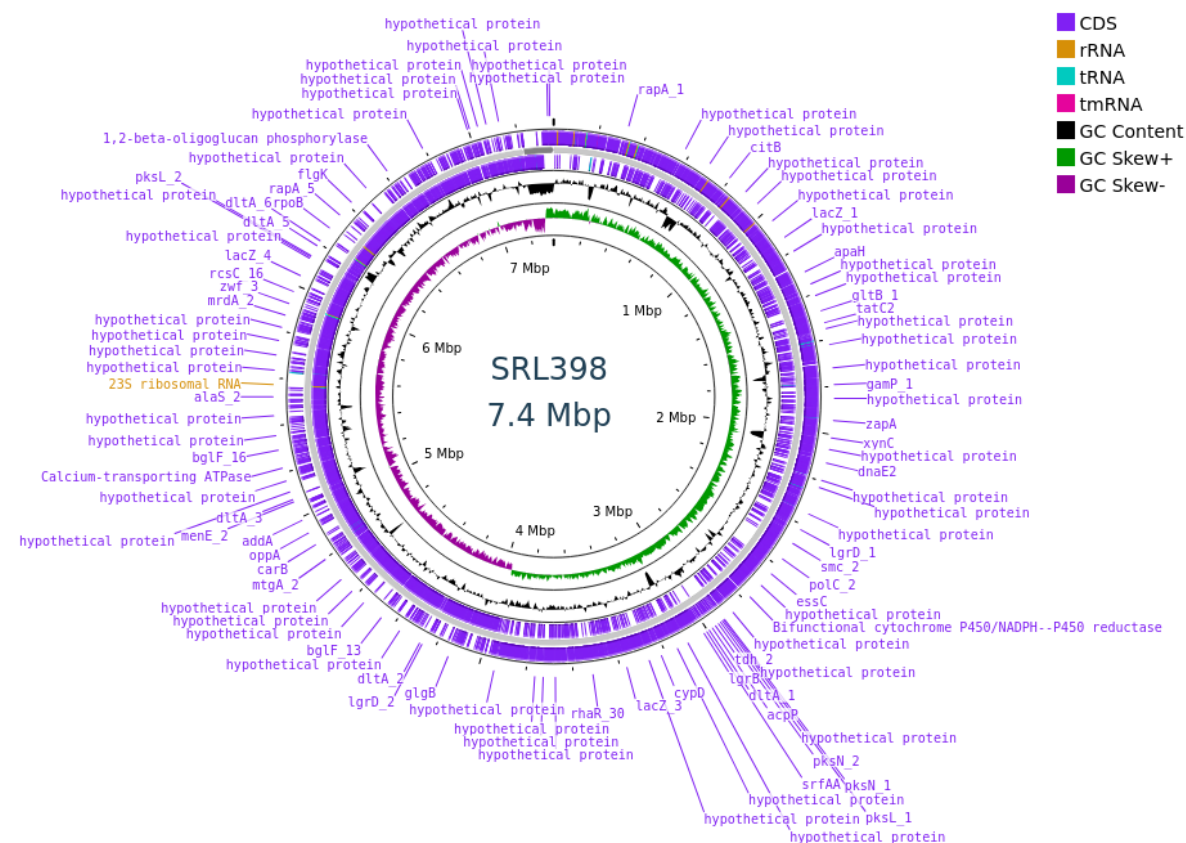
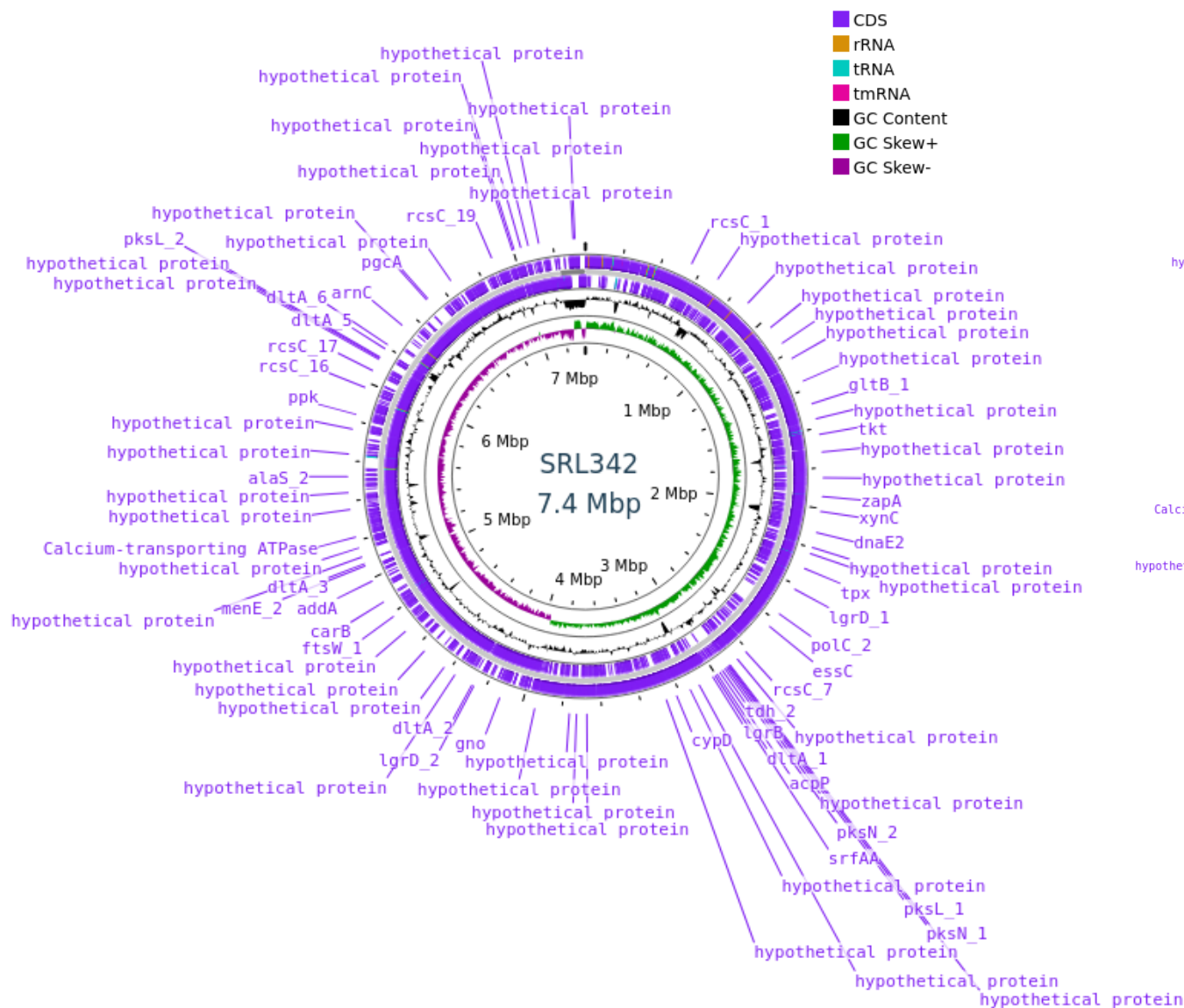
Bacillus



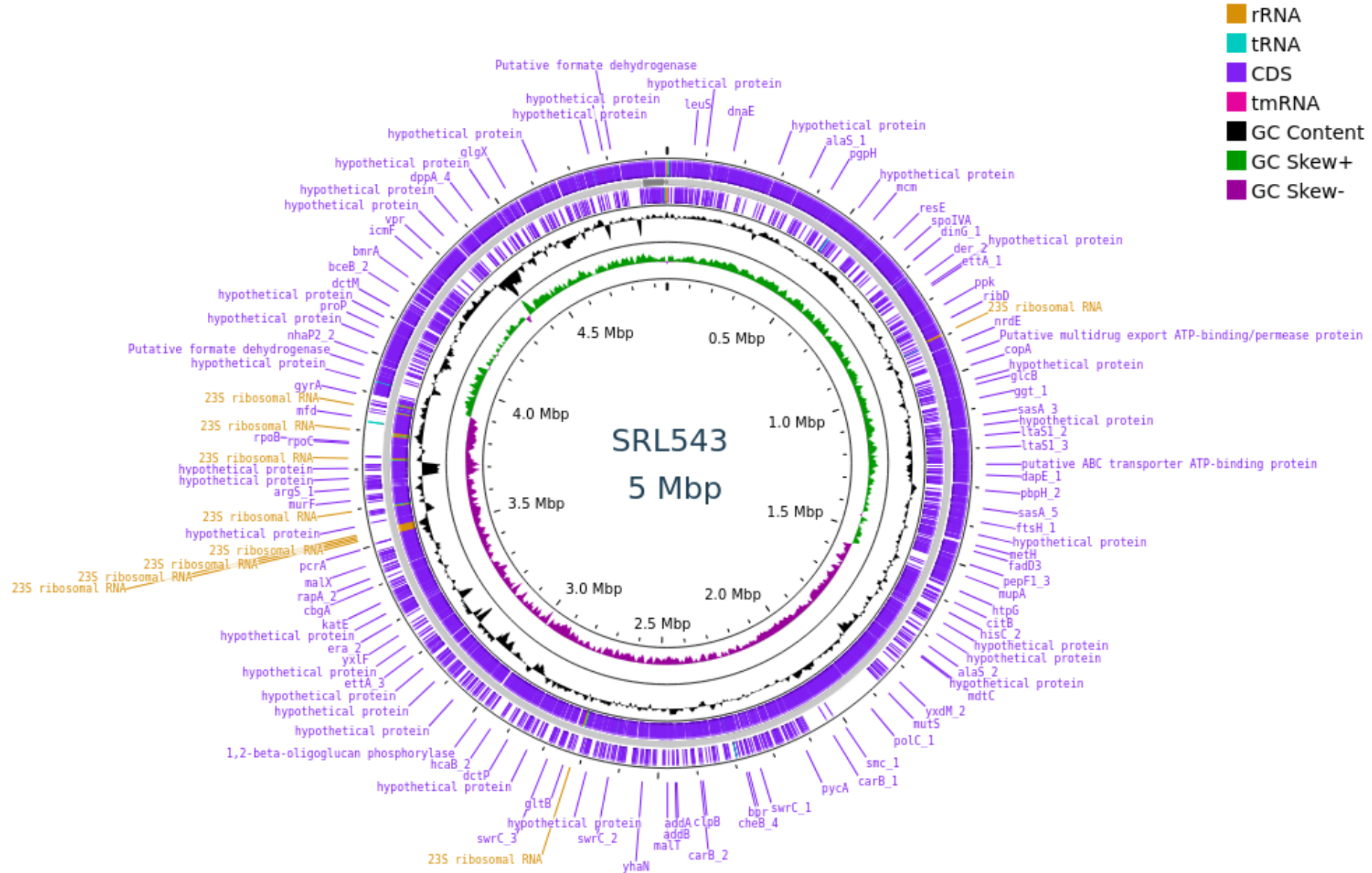
Genome maps of the 4 putative new species



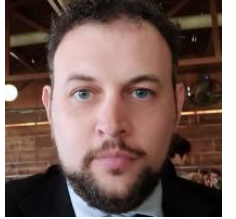
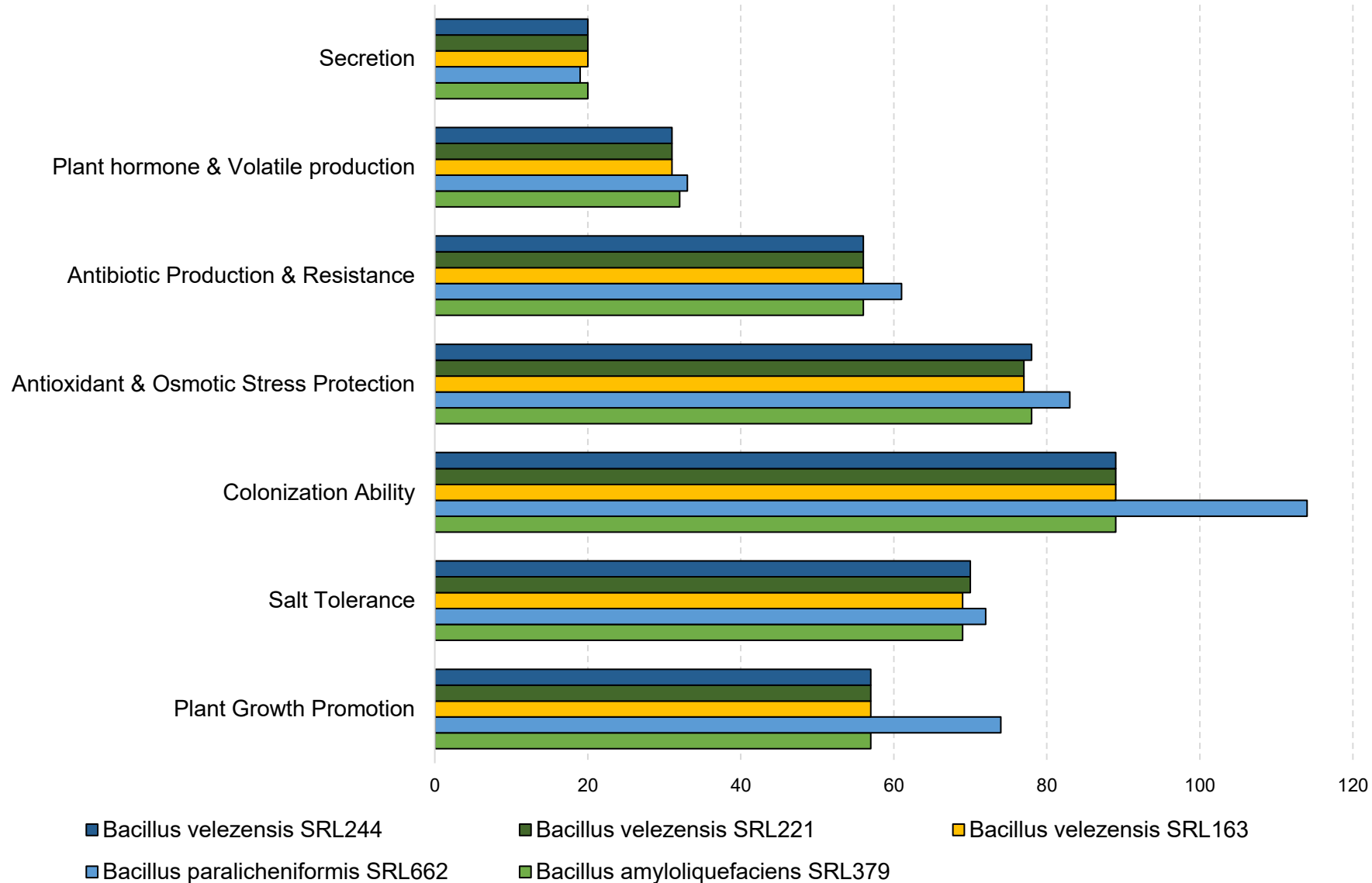
Genome maps of the 4 putative new species



Genome maps of the 4 putative new species



Genome mining for plant-beneficial bacterial genes



Dr Ch. Christakis
former Post-Doc

Comparative Genomics between our 25 isolates using Orthofinder

Orthogroups provide information about:

- The evolution of genes between species.
- The function of gene products (common origin is associated with common function)
- The **Genetic Novelty** within the group of the study

Comparative Genomics between our 25 isolates using Orthofinder

Genetic Novelty

The Genetic Novelty refers to new elements (genes, gene groups, functions etc.) that are present in a new species/lineage but are absent in the ancestral species/lineage.

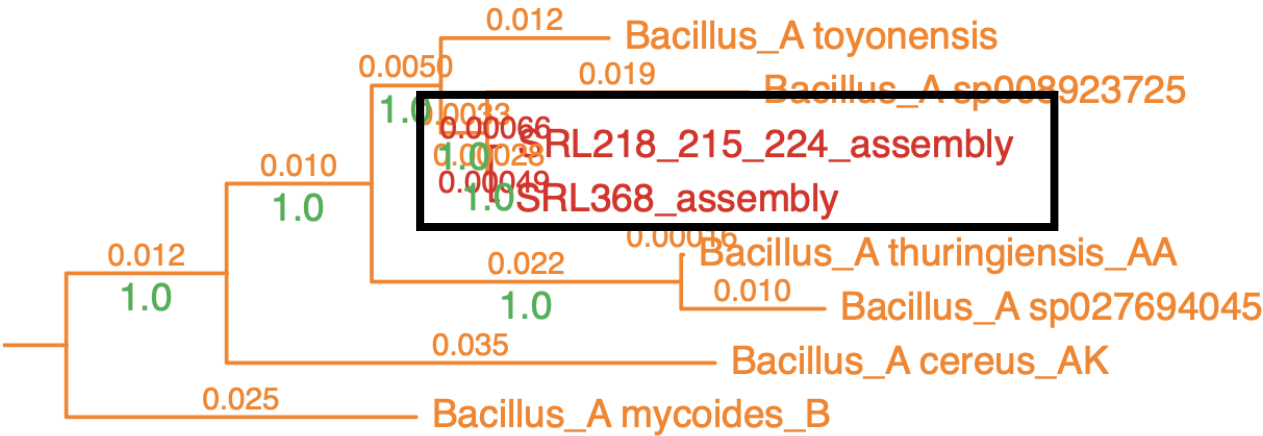
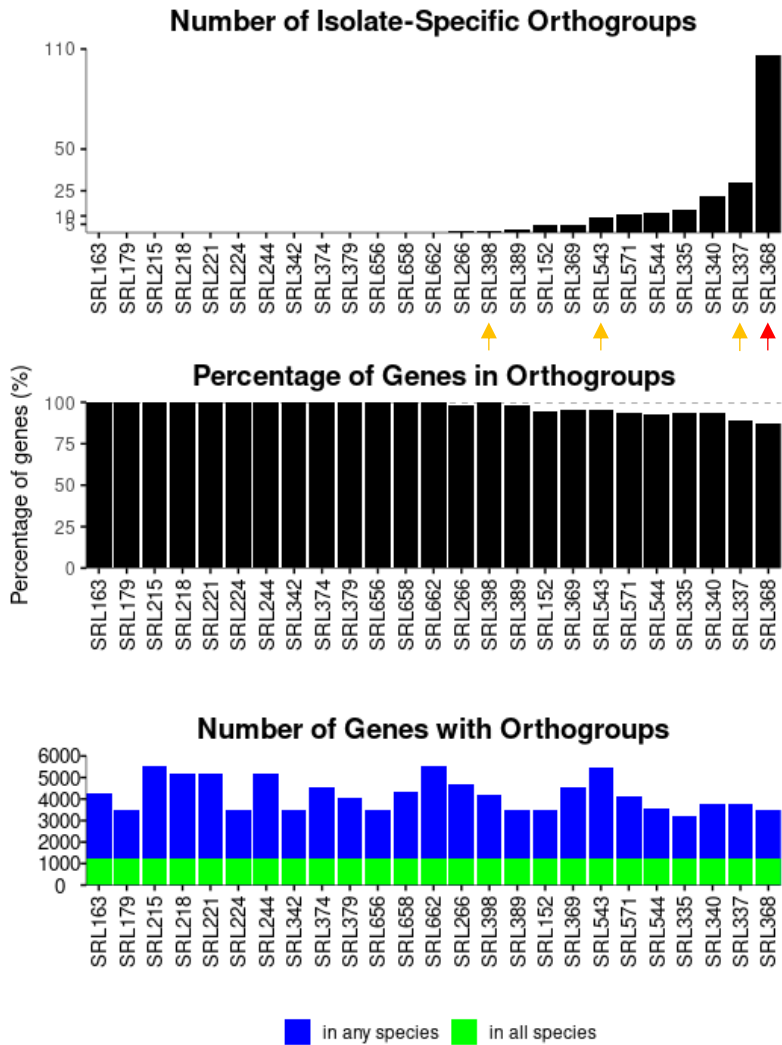
Genetic Novelty can be identified by detecting genes that:

- **Do not belong to an Orthogroup**
- Appear in a **single species or a small number of closely related species** (putatively recent emergence)
- Appear in a **species-specific Orthogroup**

Comparative Genomics between our 25 isolates using Orthofinder

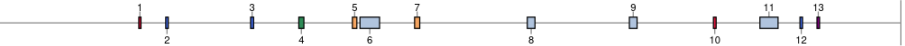
v) OrthoFinder results

Putative novel species: **SRL398, SRL337, SRL342, SRL179, SRL543**



antiSMASH result for the detection of biosynthetic gene clusters (BGCs)

SRL398



Region	Type	From	To	Most similar known cluster	Similarity
Region 1.1	NI-siderophore	1,119,345	1,137,021		
Region 1.2	proteusin	1,335,233	1,355,475		
Region 1.3	lassopeptide	2,014,963	2,038,931	paeninodin	60%
Region 1.4	NRPS-like	2,400,814	2,441,707		
Region 1.5	T3PKS	2,830,061	2,865,828	corynecin III/corynecin I/ corynecin II	13%
Region 1.6	transAT-PKS, NRPS	2,890,875	3,047,662	bacitracin	77%
Region 1.7	T3PKS	3,328,253	3,369,410		
Region 1.8	NRPS, transAT-PKS	4,230,642	4,292,555	paenilipoheptin	23%
Region 1.9	transAT-PKS, T1PKS, NRPS	5,048,087	5,109,944	pellasoren/pellasoren B	33%
Region 1.10	opine-like-metallophore	5,721,144	5,743,296	bacillopaline	100%
Region 1.11	NRPS, transAT-PKS	6,093,583	6,238,902	polymyxin	100%
Region 1.12	cyclic-lactone-autoinducer	6,414,479	6,435,018		
Region 1.13	terpene	6,550,640	6,571,512	carotenoid	33%

SRL337



Region	Type	From	To	Most similar known cluster	Similarity
Region 1	thiopeptide, LAP	431,657	461,376		
Region 2	terpene	2,792,361	2,814,232	longicatenamide B/longicatenamide C/longicatenamide A/longicatenamide D	7%
Region 3	T3PKS	2,928,543	2,969,616		

SRL179



Region	Type	From	To	Most similar known cluster	Similarity
Region 1	LAP	1,076,885	1,100,431	GG exopolysaccharide	12%
Region 2	betalactone	2,350,294	2,382,428	iturin	22%
Region 3	terpene	2,896,647	2,912,796		
Region 4	T3PKS	3,100,439	3,141,527		
Region 5	phosphonate	4,387,028	4,402,411		
Region 6	terpene	4,457,767	4,479,671		

SRL543



Region	Type	From	To	Most similar known cluster	Similarity
Region 1.1	T3PKS	717,773	758,858		
Region 1.2	terpene	1,353,423	1,374,124		
Region 1.3	terpene	2,418,208	2,437,357	carotenoid	50%
Region 1.4	terpene	3,202,382	3,222,871		
Region 1.5	terpene	3,276,417	3,297,313		

Total antiSMASH region counts for the 25 isolates

Isolate ID	Species name	antiSMASH regions	regions with similarity $\leq 60\%$
SRL152	<i>Peribacillus frigoritolerans</i>	9	7
SRL163	<i>Bacillus velezensis</i>	16	7
SRL179	<i>Neobacillus jeddahensis</i>	6	6
SRL215	<i>Bacillus A thuringiensis_S</i>	16	14
SRL218	<i>Bacillus thuringiensis</i>	16	14
SRL221	<i>Bacillus velezensis</i>	16	7
SRL224	<i>Bacillus thuringiensis</i>	16	14
SRL244	<i>Bacillus velezensis</i>	16	7
SRL266	<i>Peribacillus frigoritolerans</i>	9	6
SRL335	<i>Cytobacillus oceanisediminis</i>	5	5
SRL337	<i>Bacillus salacetis</i>	3	3
SRL340	<i>Peribacillus frigoritolerans</i>	8	7
SRL342	<i>Paenibacillus sp001955855</i>	13	10
SRL368	<i>Bacillus thuringiensis</i>	15	12
SRL369	<i>Bacillus infantis</i>	5	5
SRL374	<i>Bacillus velezensis</i>	15	7
SRL379	<i>Bacillus velezensis</i>	15	7
SRL389	<i>Peribacillus frigoritolerans</i>	9	6
SRL398	<i>Paenibacillus sp001955855</i>	13	10
SRL543	<i>Bacillus infantis</i>	5	5
SRL544	<i>Rossellomorea haikouensis</i>	5	5
SRL571	<i>Bacillus altitudinis</i>	12	9
SRL656	<i>Bacillus paralicheniformis</i>	11	8
SRL658	<i>Bacillus paralicheniformis</i>	11	8
SRL662	<i>Bacillus paralicheniformis</i>	18	16

Future plans

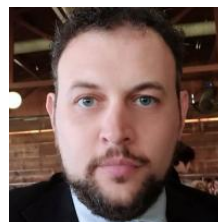
- Study of genes that are not included in Orthogroups
- Comparison of selected isolates with their **closest relatives (pangenome analysis)**.

Conclusions

- 1) The **biodiversity of the endophytic microbiome** is profound and can be used to identify valuable **beneficial microbes**
- 2) **Four putative novel species** of Bacilli endophytes have been isolated and cultivated
- 3) **Increased genetic, functional and taxonomic novelty** among our new species and even in our isolates of already known species
- 4) The **deep exploration of the endophytic microbial diversity** is a key for advances in microbiology, ecology and agriculture



Our team and collaborators!



Dr Ch. Christakis
former Post-Doc



Mr M. Avramakis
Botanist



Institute of Computer Science (ICS)



Prof. A. Stamatakis
Group Leader



Mrs F. Reden
PhD student



Mr S. Soultatos
PhD student



Prof. Em. Markakis
Professor

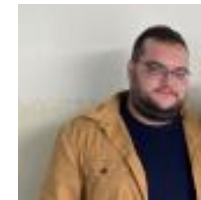


FORTH

INSTITUTE OF MOLECULAR BIOLOGY & BIOTECHNOLOGY



Dr A. Kampouraki
Postdoc



Mr S. Mastis
PhD student



FORTH

INSTITUTE OF MOLECULAR BIOLOGY & BIOTECHNOLOGY



Lab of Microbiology & Molecular Host-Microbe Interactions

Department of Biology, UoC
Institute for Molecular Biology, FORTH

SARRIS-LAB



Thank you!

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- 2) **Four putative novel species** of Bacilli endophytes have been isolated and cultivated
- 3) **Increased genetic, functional and taxonomic novelty** among our new species and even in our isolates of already known species
- 4) The **deep exploration of the endophytic microbial diversity** is a key for advances in microbiology, ecology and agriculture