



Diversidad de genes bacterianos relacionados con promoción del crecimiento vegetal

TRABAJO FIN DE MÁSTER

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BACTERIAS PROMOTORAS DEL CRECIMIENTO VEGETAL

PLANT GROWTH PROMOTING RHIZOBACTERIA

Capítulo 1. Las Bacterias PGPR. Principales mecanismos de Promoción de crecimiento vegetal.

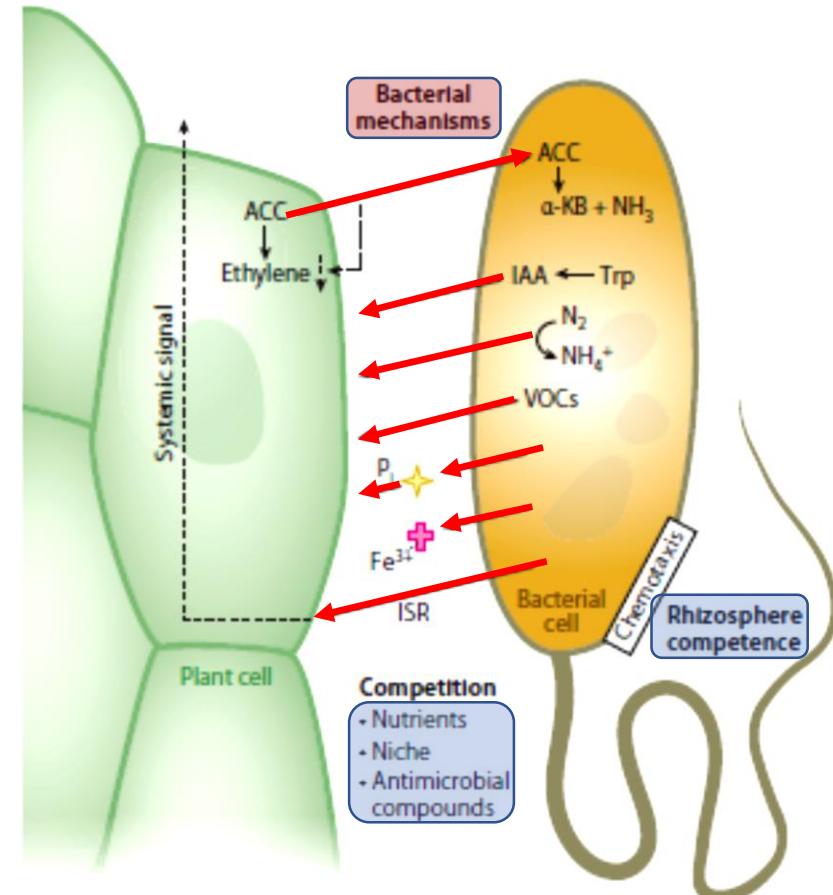
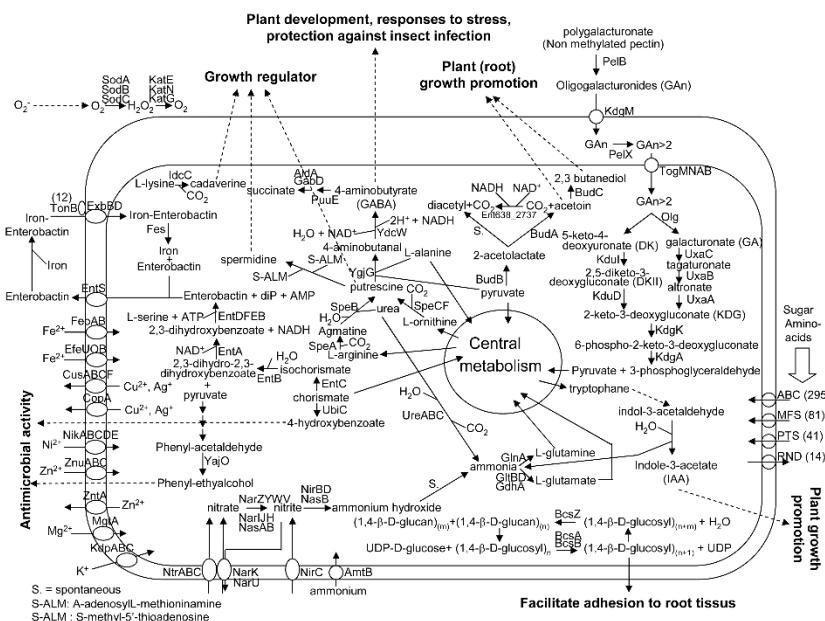
Capítulo 2. Relación filogenética de PGPRs.

Capítulo 3. Estudio combinado de las relaciones entre mecanismos promotores del crecimiento vegetal, diversidad de PGPRs y cultivos.

Bibliografía.

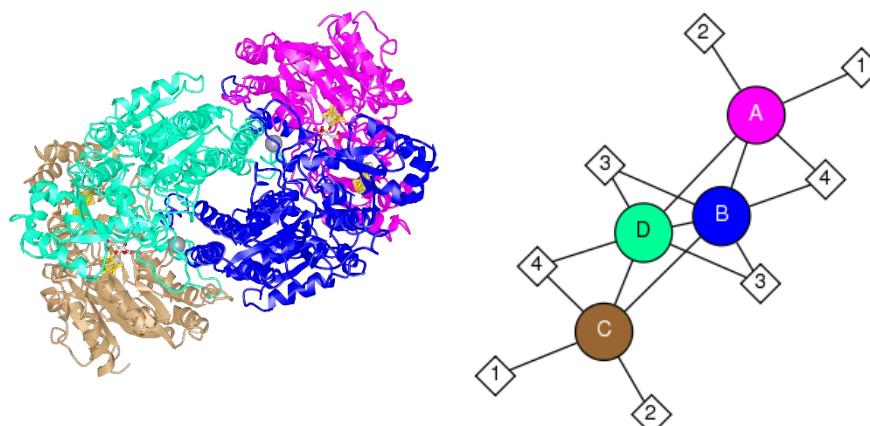
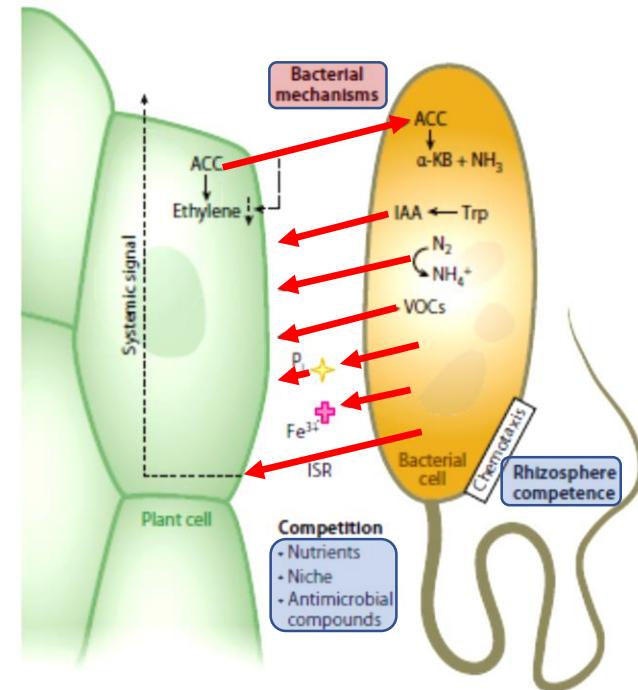
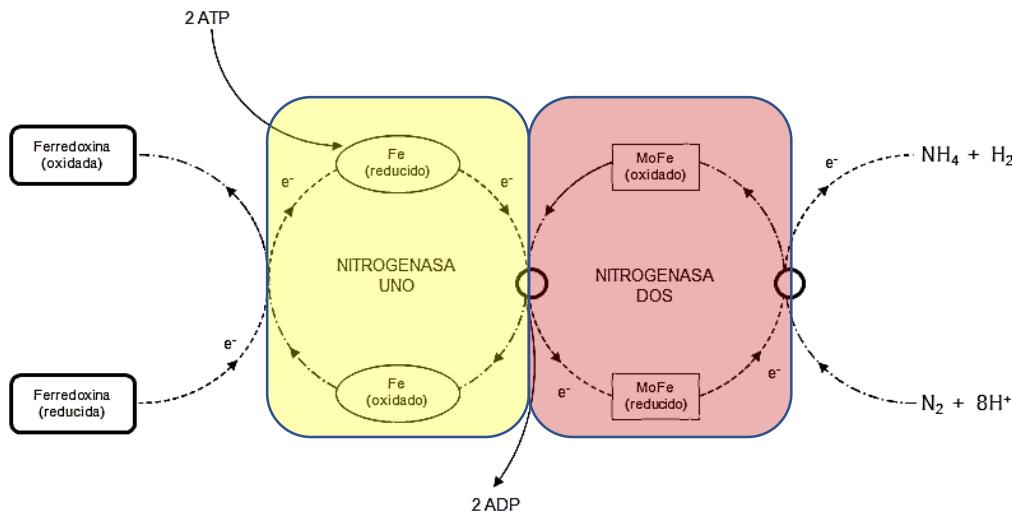
Capítulo 1. Las Bacterias PGPR.

Principales mecanismos de Promoción de crecimiento vegetal



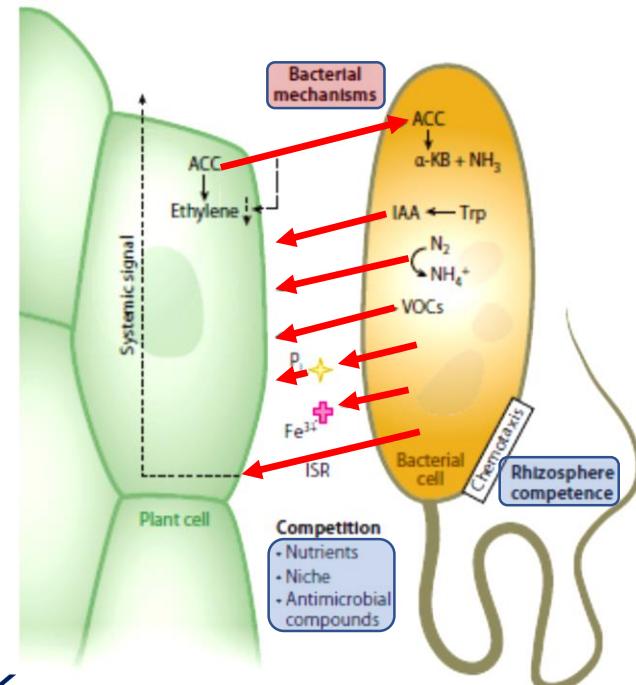
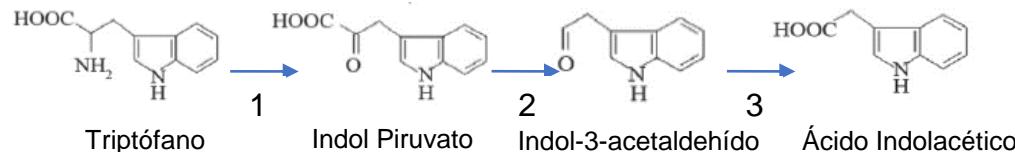
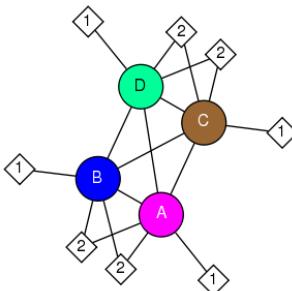
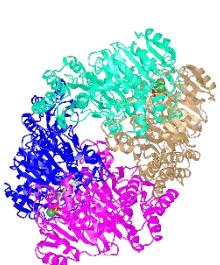
Taghavi S, van der Lelie D, Hoffman A, Zhang Y-B, Walla MD, Vangronsveld J, et al. (2010) Genome Sequence of the Plant Growth Promoting Endophytic Bacterium *Enterobacter* sp. 638. PLoS Genet 6(5): e1000943.
<https://doi.org/10.1371/journal.pgen.1000943>

Nitrogenasa - *nifHDK*

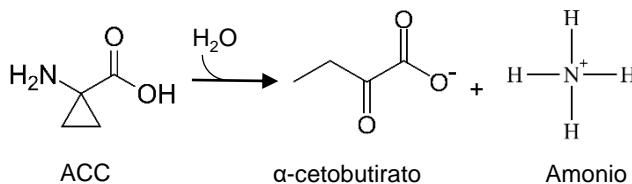
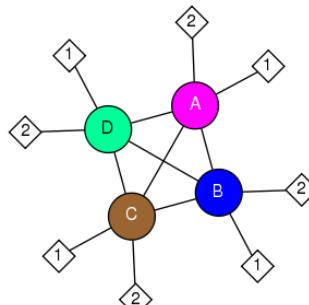
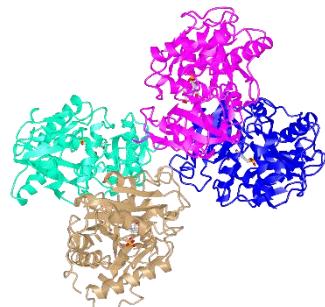


Nitrogenasa Mo-Fe de *Azotobacter vinelandii*, estado oxidado. Compuesta por Fe-prot (A y C) y Fe-Mo prot (B y D). 1: Ácido Homocítrico, 2: Grupo Fe-Mo-S, 3: Ca^{2+} y 4: Grupo Fe-S.

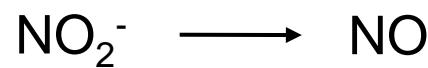
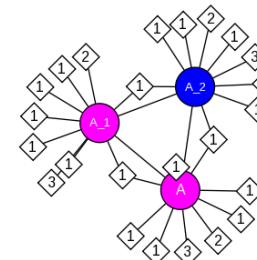
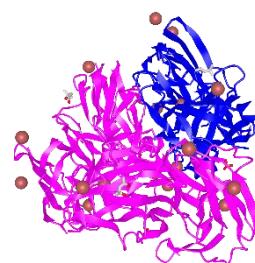
Indolpiruvato Descarboxilasa – *ipdC/ppdC*



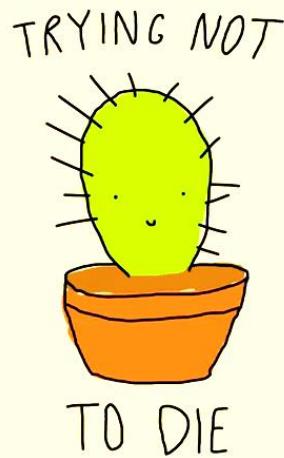
ACC Desaminasa - *acdS*



Nitrito Reductasa - *nirK*



Respuesta Sistémica Adquirida



Ruta 2-3-butanodiol

Piruvato

2-acetolactato

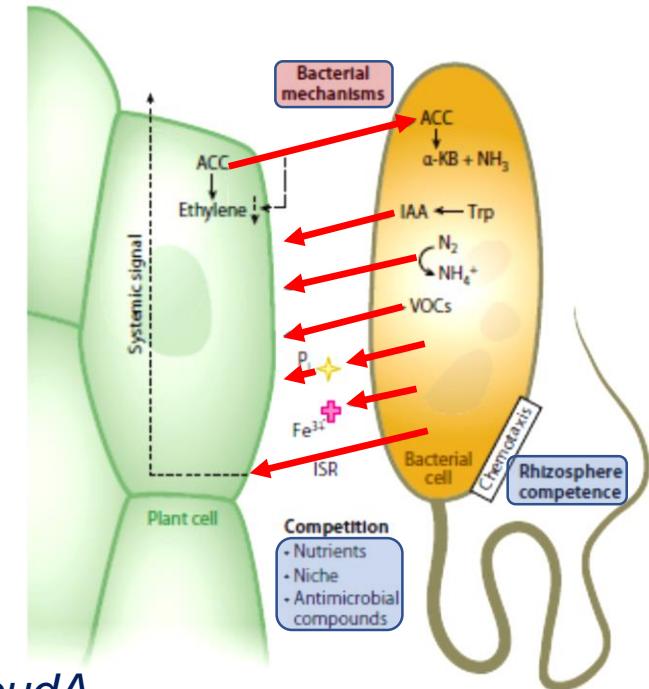
Acetolactato
Sintasa - *budB*

acetoína

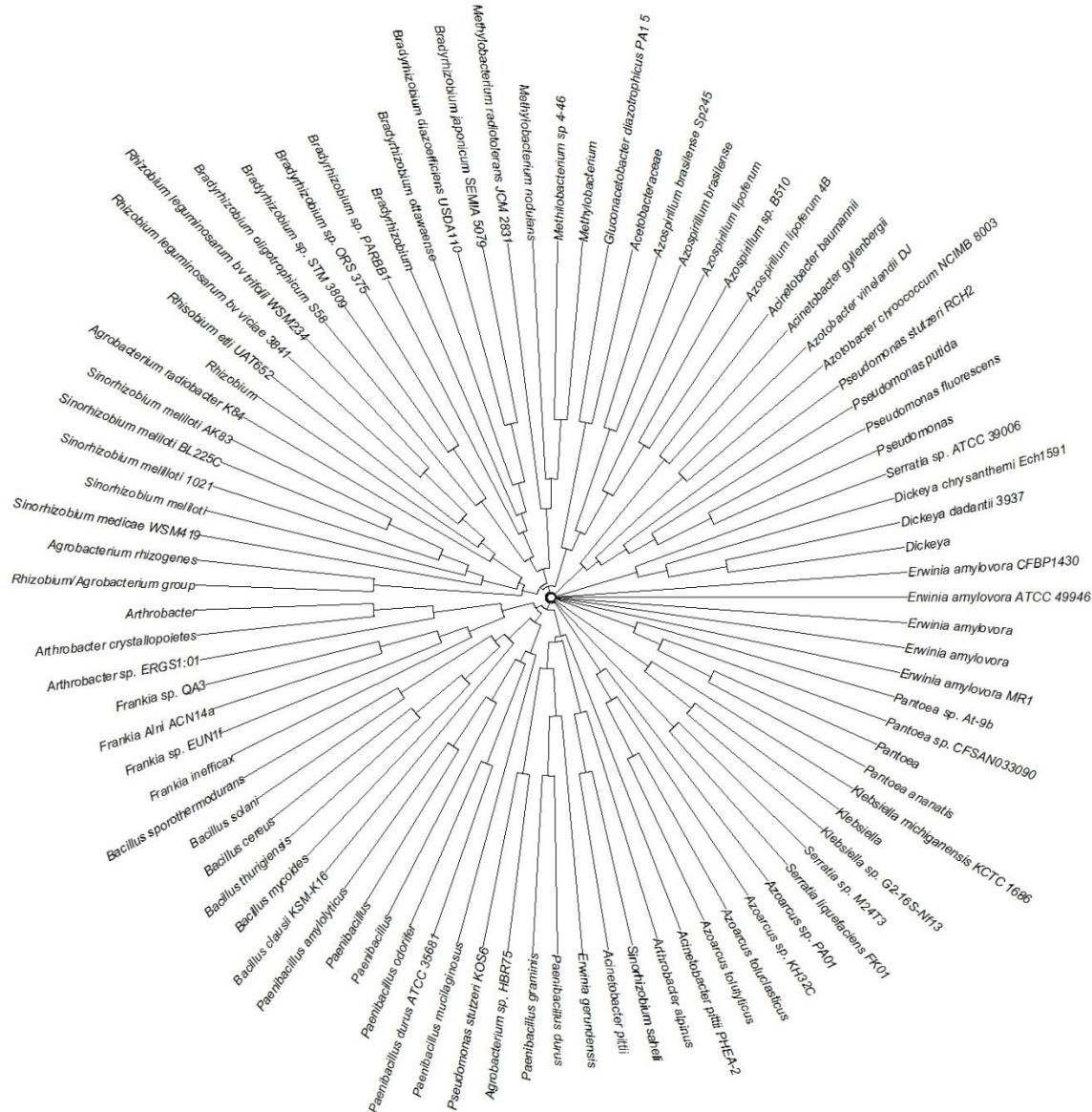
Acetolactato
Descarboxilasa - *budA*

2,3-butanodiol

Diacetil Reductasa - *budC*



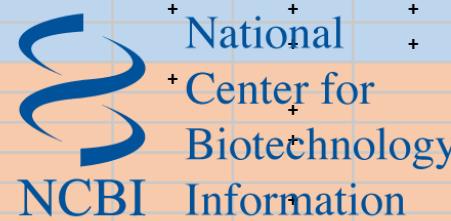
Capítulo 2. Relación filogenética de PGPRs

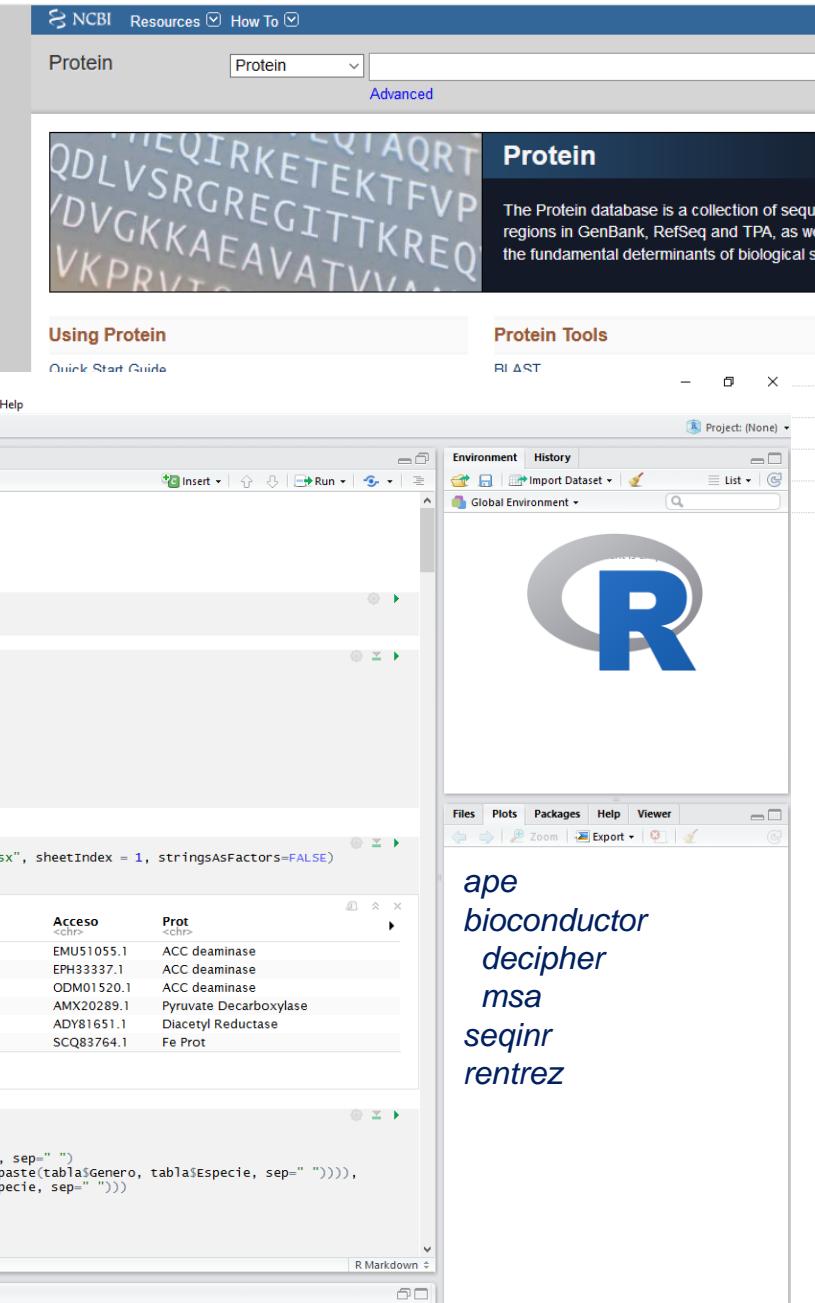


Materiales y métodos

Firmicutes	α Proteobacteria	β Proteobacteria	γ Proteobacteria	Gram + Alto [G+C]
15	34	4	36	11

Cepa	nifH	nifD	nifK	ipdC/ppdC	acdS	nirK	budA	budB	budC	Autor
<i>Acinetobacter baumannii</i> ABNIH24					+					Snitkin,E.S.
<i>Acinetobacter gyllenbergsii</i> MTCC 11365						+				Singh,N.K.
<i>Acinetobacter pittii</i>				+	+					Brasilense,D.M.
<i>Acinetobacter pittii</i> PHEA-2									+	Zhan,Y.
<i>Acinetobacter</i> sp. P7-29	+									Arshad,M.
<i>Acinetobacter</i> sp. P8-1	+									Arshad,M.
<i>Acinetobacter</i> sp. P8-9	+									Arshad,M.
<i>Agrobacterium rhizogenes</i>						+	+			Xiang,T.
<i>Agrobacterium</i> sp.	+									Jha,B.
<i>Agrobacterium</i> sp. P7-7	+									Arshad,M.
<i>Agrobacterium</i> sp. SUL3						+	+			Jones,K.J.
<i>Agrobacterium tumefaciens</i>	+						+			Poret-Peterson,A.T.
<i>Arthrobacter</i> sp. PAMC 25486										Jung,J.-H.
<i>Arthrobacter alpinus</i>										See-Too,W.S.
<i>Arthrobacter crystallopictes</i> BAB-32										Joshi,M.N.
<i>Arthrobacter</i> sp. CCBAU 10948	+									Luo,W.
<i>Arthrobacter</i> sp. ERGS1:01										Kumar,R.
<i>Arthrobacter subterraneus</i>							+			Varghese,N.
<i>Azoarcus</i> sp. KH32C	+	+	+	+			+			Nishizawa,T.
<i>Azoarcus</i> sp. PA01]					+					Junghare,M.
<i>Azoarcus tolulasticus</i>	+				+					NP*
<i>Azoarcus tolulyticus</i>	+	+	+	+						Varghese,N.
<i>Azospirillum brasiliense</i>						+	+		+	NP*
<i>Azospirillum brasiliense</i> Sp245	+	+	+	+			+			Pothier,J.F.
<i>Azospirillum lipoferum</i>						+	+	+		NP*
<i>Azospirillum lipoferum</i> 4B	+	+	+						+	Wisniewski-Dye,F.
<i>Azospirillum</i> sp. B510	+	+	+			+	+			Kaneko,T.
<i>Azotobacter chroococcum</i> NCIMB 8003	+	+	+		+					Robson,R.L.
<i>Azotobacter vinelandii</i> DJ	+	+	+		+					Setubal,J.C.
<i>Bacillus cereus</i>					+	+		+	+	Hall,Neil.
<i>Bacillus mycoides</i>					+		+			Bleich,R.M.





The screenshot shows the RStudio interface running in the background. On the left, the RStudio console displays R code for reading an Excel file, extracting unique genera and species, and creating a matrix of their occurrences. On the right, the NCBI Protein database search results are shown. The search term "Protein" was entered, and the results page displays a protein sequence (QDLVSRGREGITTKREQ...) and information about the Protein database.

Using Protein

Protein Tools

Other Resources

[GenBank Home](#)

[RefSeq Home](#)

[CDD](#)

[Structure](#)

National Center for Biotechnology Information

NCBI

Resources How To

Sign in to NCBI

Help

Protein

Protein Advanced Search

QDLVSRGREGITTKREQ...
/DVGKKAEAVATVVA...

Protein

The Protein database is a collection of sequences from several sources, including translations from annotated coding regions in GenBank, RefSeq and TPA, as well as records from SwissProt, PIR, PRF, and PDB. Protein sequences are the fundamental determinants of biological structure and function.

Using Protein

Quick Start Guide

Protein Tools

Ri AST

Environment History Import Dataset List Global Environment

Files Plots Packages Help Viewer

ape
bioconductor
decipher
msa
seqinr
rentrez

1 ---
2 title: "Semana14Dic"
3 author: "Miguel García Hidalgo"
4 date: "14 de diciembre de 2017"
5 output: html_document
6 ---
7
8 ```{r setup, include=FALSE}
9 knitr::opts_chunk\$set(echo = TRUE)
10```
11
12 + ```{r, eval=FALSE, warning=FALSE}
13 rmi(list = ls())
14
15 require(ape)
16 library(rentrez)
17 library(msa)
18 library(seqinr)
19 library(tools)
20 library(rentrez)
21 library(DECIPIER)
22```
23
24
25 + ```{r, eval=FALSE}
26 nombres<-read.xlsx("Tablas/nombres_completo2.xlsx", sheetIndex = 1, stringsAsFactors=FALSE)
27 head(nombres)
28

Genero	Especie	Acceso	Pro
1 Acinetobacter	baumannii ABNIH24	EMU51055.1	ACC deaminase
2 Acinetobacter	gyllenbergsii MTCC 11365	EPH33337.1	ACC deaminase
3 Acinetobacter	pitti	ODM01520.1	ACC deaminase
4 Acinetobacter	pittii	AMX20289.1	Pyruvate Decarboxylase
5 Acinetobacter	pittii PHEA-2	ADY81651.1	Diacyl. Reductase
6 Acinetobacter	sp. P7-29	SCQ83764.1	Fe Prot

6 rows | 1-5 of 19 columns

29
30 + ```{r}
31 tabla<-nombres[,c(1:2,5)]
32 genes<-unique(nombres\$Gen)
33 tabla\$contr2<-paste(tabla\$Genero, tabla\$Especie, sep=" ")
34 tabla2<-data.frame(matrix(nrow = length(unique(paste(tabla\$Genero, tabla\$Especie, sep=")))),
row.names = unique(paste(tabla\$Genero, tabla\$Especie, sep="))))
35
36 for(i in 1:row(tabla)){
37 + for(j in genes){
38 - if(tabla[i,3]==j){
39 - tabla\$contr2[i]=paste(tabla[i,1], tabla[i,2], tabla\$contr2[i], sep=" ")
40 - }
41 + }
42 + }
43 + tabla\$contr2

54:1 | (Top Level) □ R Markdown □

Console

CLUSTALW

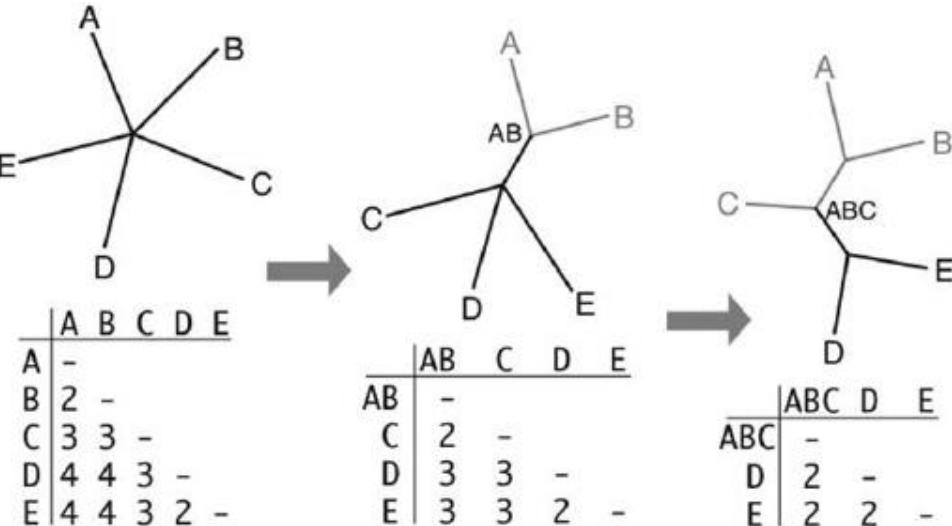
Feng y Doolittle

$$S_{iden(ij)} = \frac{S_{real(ii)} + S_{real(jj)}}{2}$$

$$S_{eff(ij)} = \frac{S_{real(ij)} + S_{rand(ij)}}{S_{iden(ij)} + S_{rand(ij)}} * 100$$

$$D_{ij} = -\ln S_{eff(ij)}$$

Neighbour Joining



$$V_{n,2} = \frac{n!}{2 * (n - 2)!}$$

logo

Agrobacterium rhizogenes
 Agrobacterium tumefaciens
 Agrobacterium sp. SUL3
 Sinorhizobium meliloti BL225C
 Sinorhizobium meliloti 1021
 Sinorhizobium meliloti
 Sinorhizobium sedicae
 Sinorhizobium sedicae WSM419
 Rhizobium etli
 Rhizobium leguminosarum
 Rhizobium gallicum
 Bradyrhizobium japonicum
 Bradyrhizobium sp. SEMIA 5079
 Bradyrhizobium sp. STM 3809
 Bradyrhizobium oligotrophicum S58
 Pseudomonas putida
 Pseudomonas fluorescens

logo
 MTEFHITRNI¹_{AB}
 MTEFHITRNI¹_{AB}
 MTEFHITRNI¹_{AB}
 MSEQFMTRSM¹_{AB}
 MSEQFMTRSM¹_{AB}
 MSEQFMTRSM¹_{AB}
 MSEQFMTRSM¹_{AB}
 MSEQFMTRSM¹_{AB}
 MTTLQHTRTM¹_{AB}
 MTTLQHTRTM¹_{AB}
 MTTLQHTRTM¹_{AB}
 .MLTRTAIS.
 .MLTRTAIS.
 EQEGVSLTRRG¹_{AB}
 AAF GAVAPMIMPSAASAEKKA
 AAF GAVAPMIVPSAASAEKKA
 AAF GAIAVPVIMPSAAGAAEKKKA
 AAI GAVTPLIGVSAAHREE
 AAI GAVTPLIGVSAAHREE
 AAI GAVTPLIGVSAAHREE
 AAI GAVTPLIGVSAAHREE
 AAI GAVTPLIGVSAAHREE
 AAV GALTPIVSSAADNEEVAAA
 AAV GALTPIVGTAADEHAGAA
 AAV GALTPIVGTAADEHAGAA
 AAA ALMLATPTEAG
 AAA ALMLATPTEAG
 AAA AMMLATPVAE
 AAA AMMLATPVAE
 TVLLGVGASALGSGLAKAT
 MGAFQSWLKC.CVVGS
 AAKPLTSAEIAAAPPVVKVDLVRP
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 AVAKTAHINVASPPVVKVDLVRP
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 AVGQITHVDVASPPVVK1DLVRP
 AVGQITHVDVASPPVVK1DLVRP
 EVLKTAQKVVKVDLSTPPREKVEVKP
 DTLKATQRAPVDISEPPREKVEVKP
 ARKLSADIAAAPPREKVEVKP
 DLRPPQKVEVKP
 DLRPPQKVEVKP
 DLRPPQKVEVKP
 AVPGQDPAVGLAKAEVSVEDVAP
 CVSGLVMAAGADCGQIKVQDVAP

Jukes-Cantor

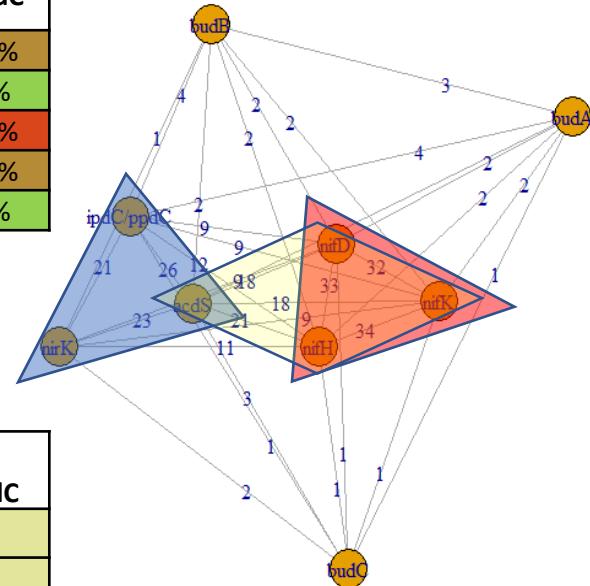
$$p' = \frac{p}{N}$$

$$d = -\frac{s-1}{s} \ln \left(1 - \frac{s}{s-1} p' \right)$$

Resultados

Presencia por gen de estudio

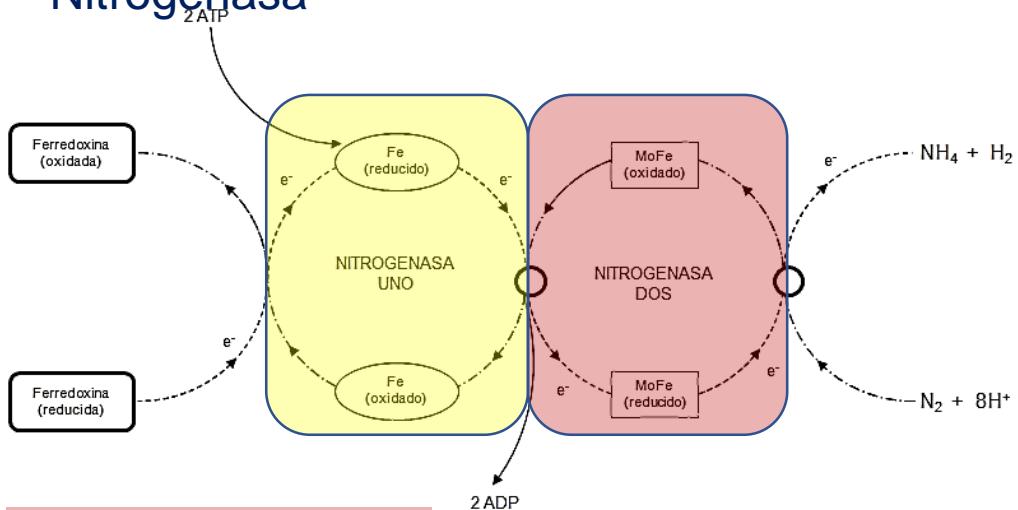
Grupo	nifH	nifD	nifK	ipdC / ppdC	acds	nirK	budA	budB	budC
Alfaproteobacteria	41%	47%	45%	36%	45%	70%	11%	25%	25%
Betaproteobacteria	7%	6%	6%	10%	0%	4%	0%	0%	0%
Gammaproteobacteria	32%	22%	24%	36%	34%	11%	56%	75%	50%
Firmicutes	11%	16%	15%	13%	6%	11%	33%	0%	25%
Gram+alto [G+C]	9%	9%	9%	5%	15%	4%	0%	0%	0%



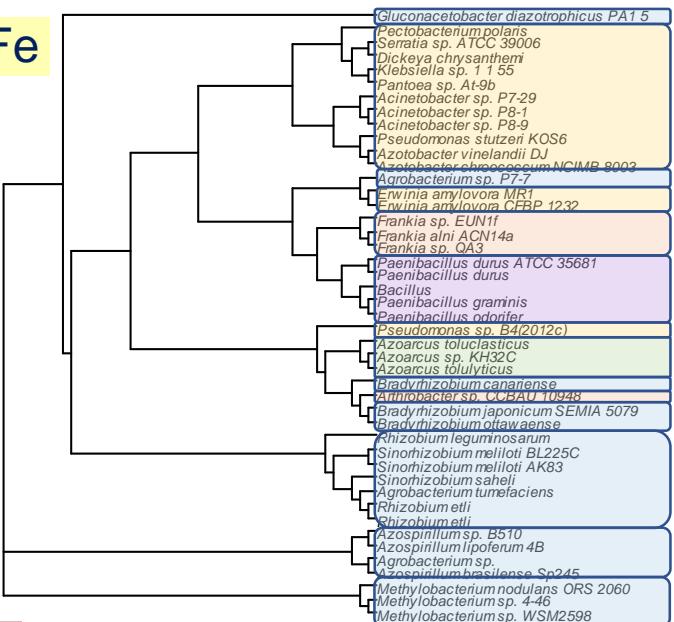
Coocurrencia de genes

Gen	nifH	nifD	nifK	ipdC / ppdC	acds	nirK	budA	budB	budC
nifH	44	33	34	12	21	11	2	2	1
nifD	33	32	32	9	18	9	2	2	1
nifK	34	32	33	9	18	9	2	2	1
ipdC/ppdC	12	9	9	39	26	21	4	4	1
acds	21	18	18	26	47	23	3	2	3
nirK	11	9	9	21	23	27	0	1	2
budA	2	2	2	4	3	0	9	3	1
budB	2	2	2	4	2	1	3	8	0
budC	1	1	1	1	3	2	1	0	8

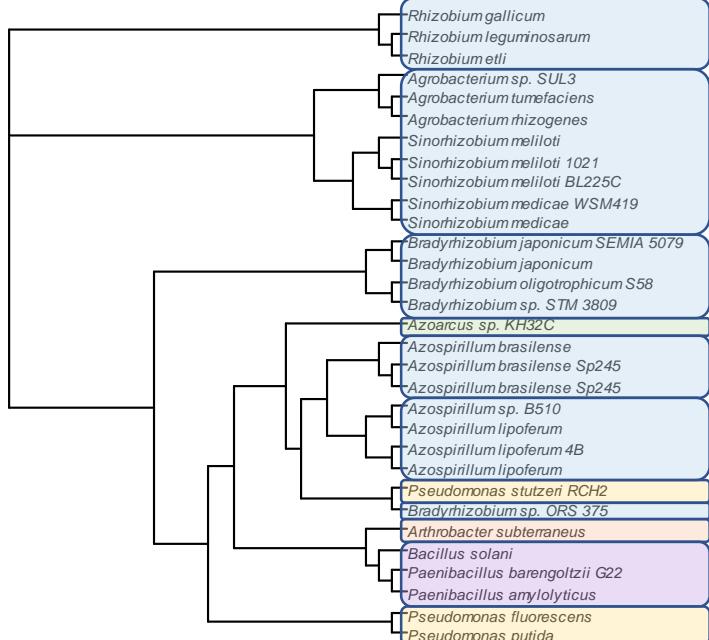
Nitrogenasa



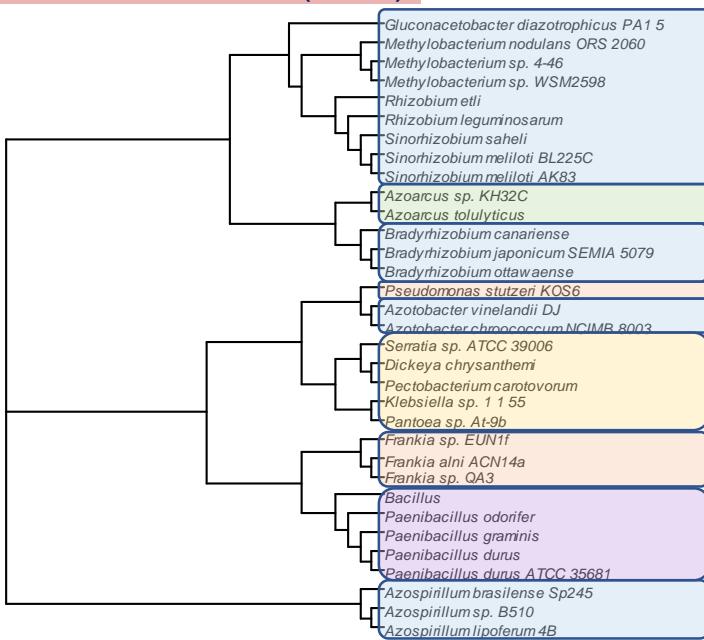
Proteína Fe



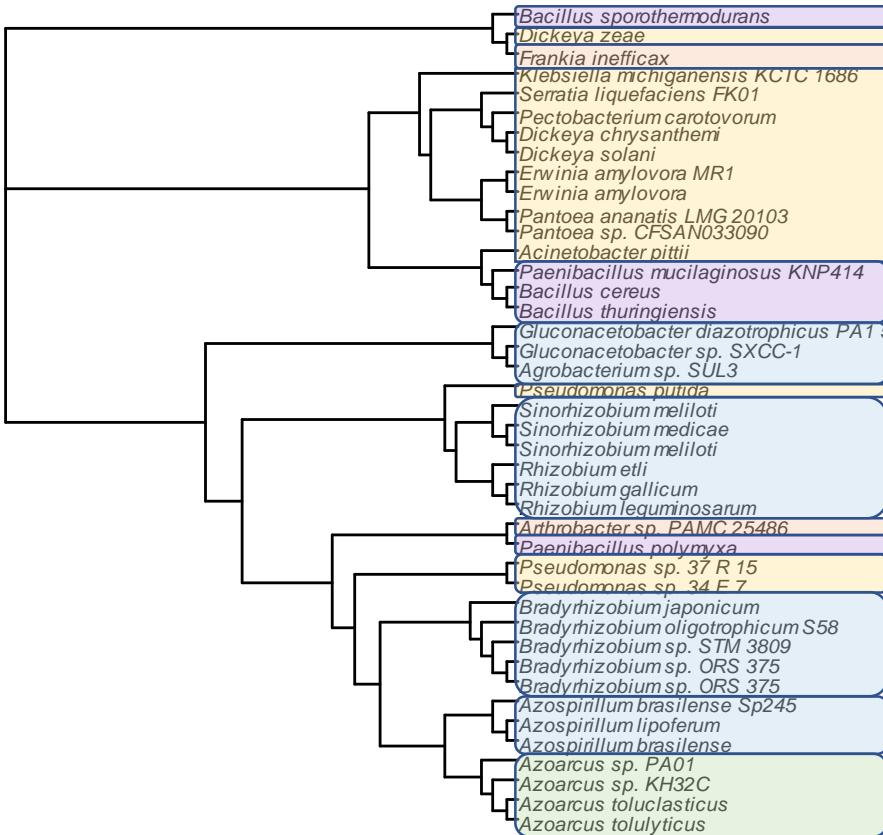
Proteína Fe-Mo (alfa)



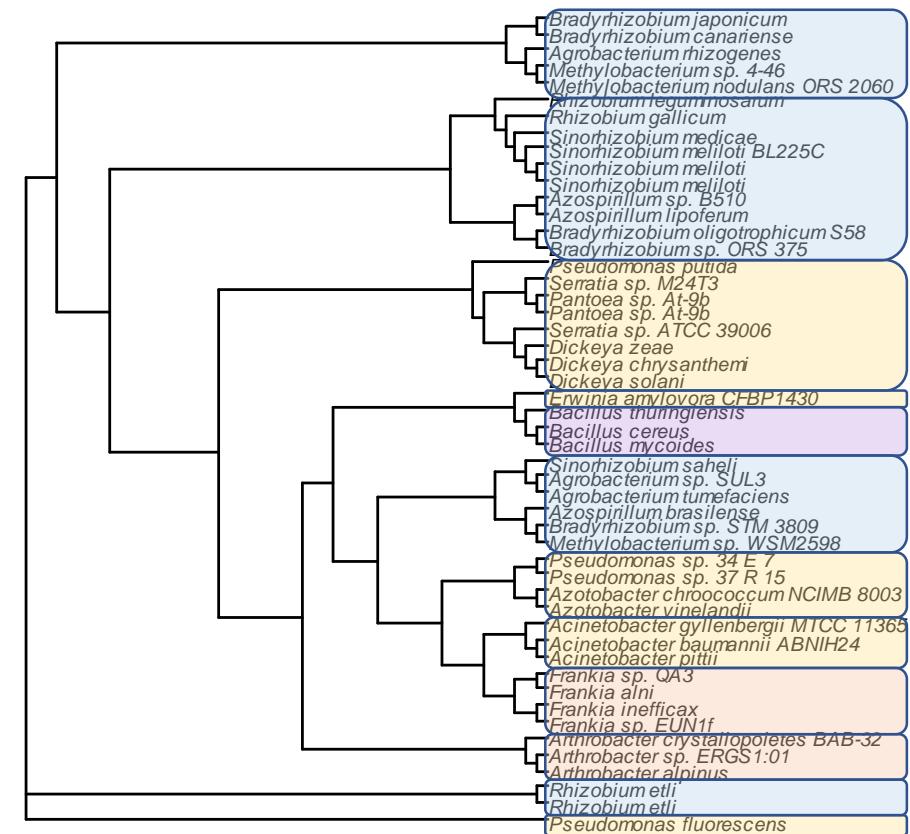
Proteína Fe-Mo (beta)



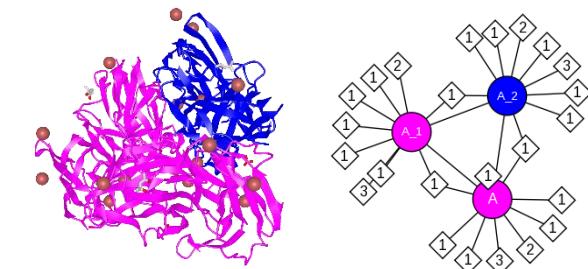
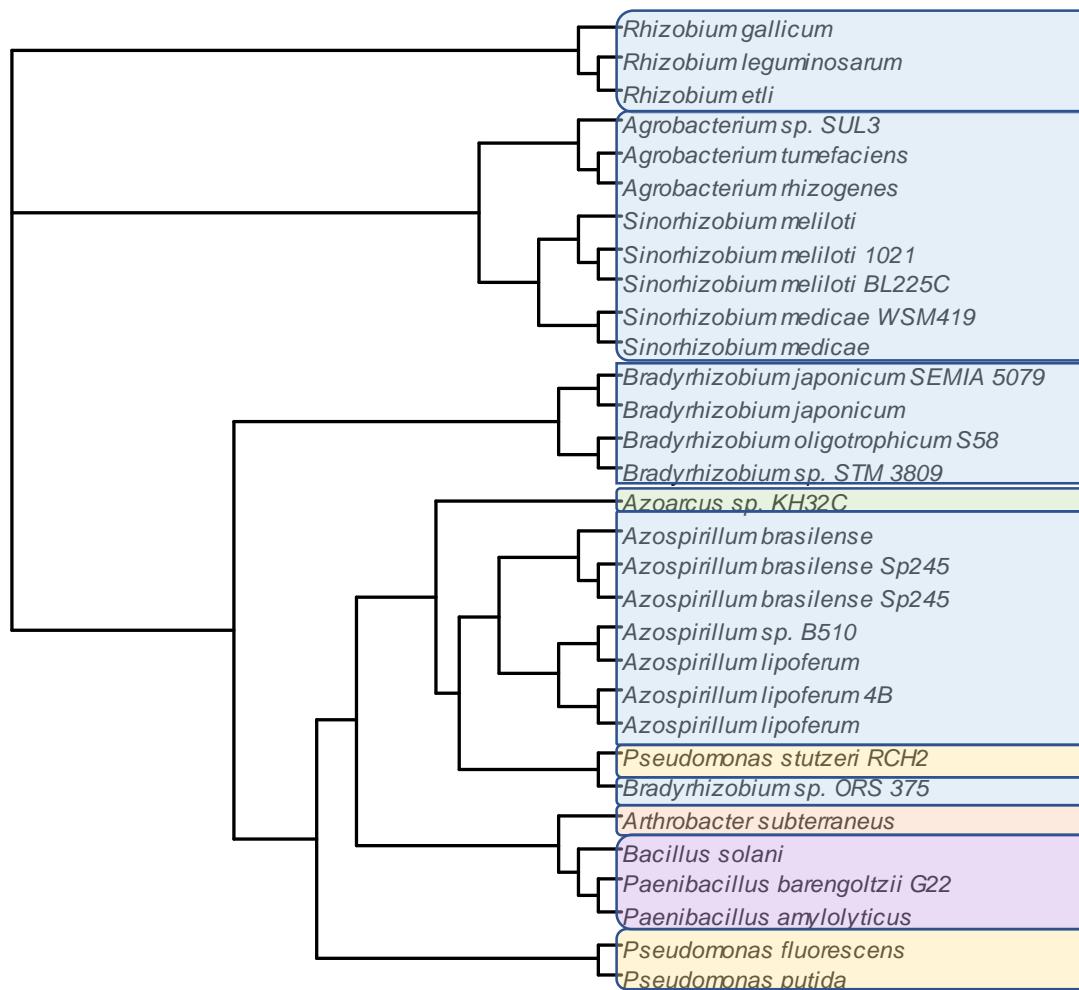
Indolpiruvato Descarboxilasa



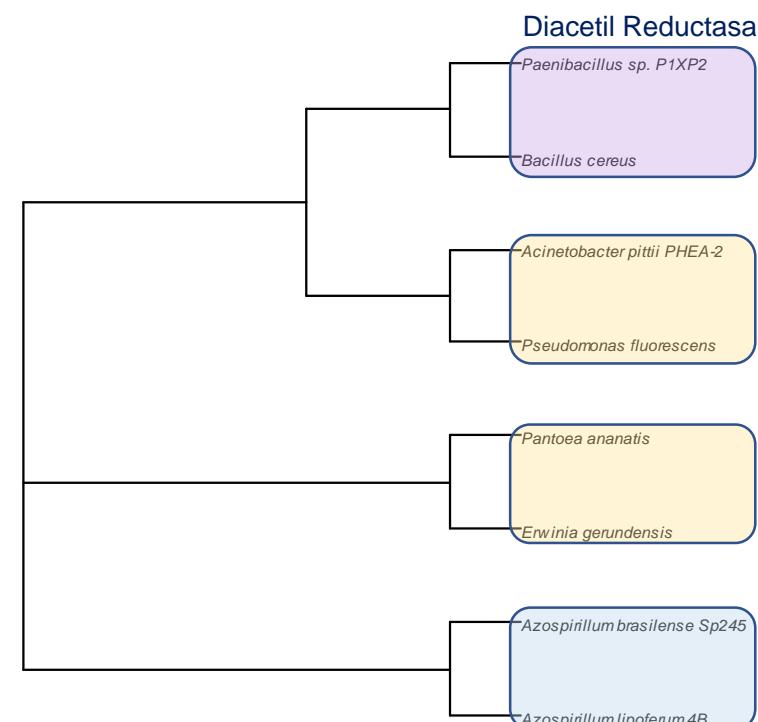
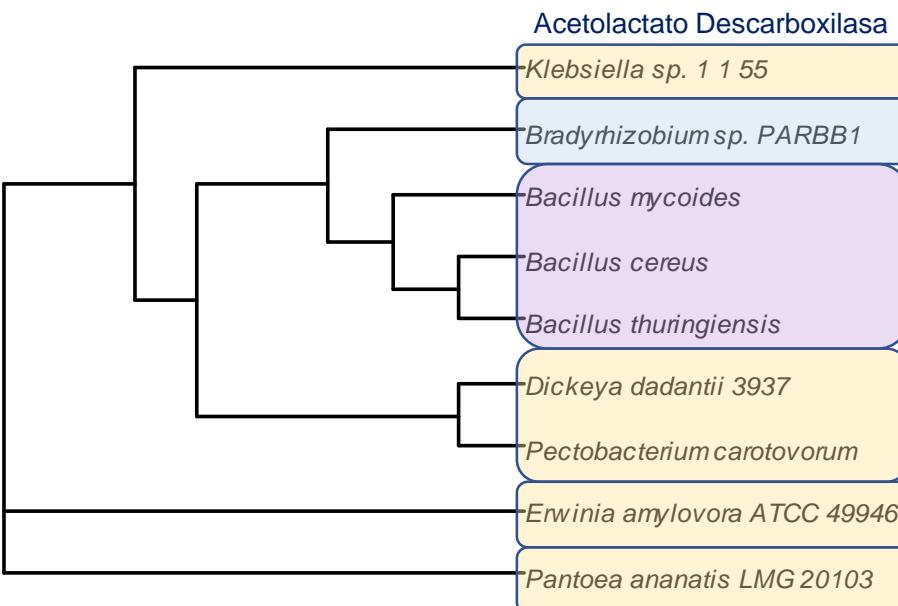
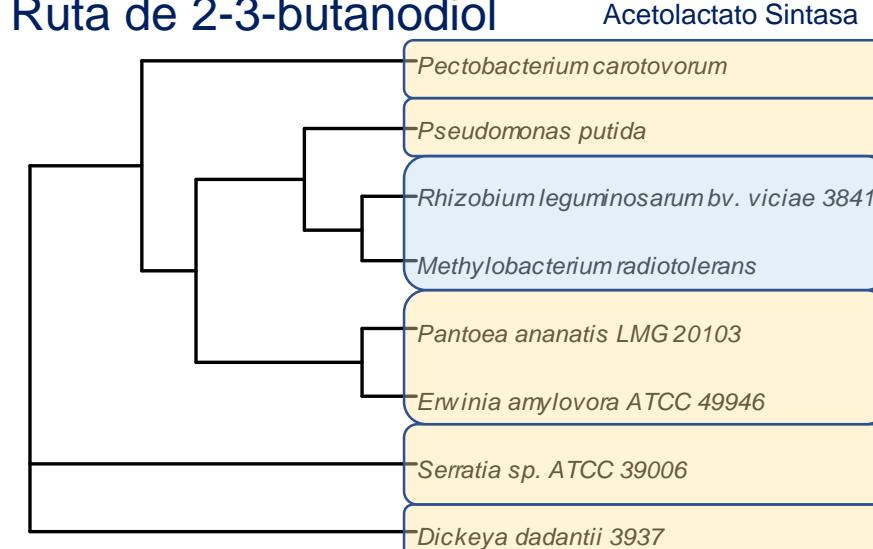
ACC Desaminasa



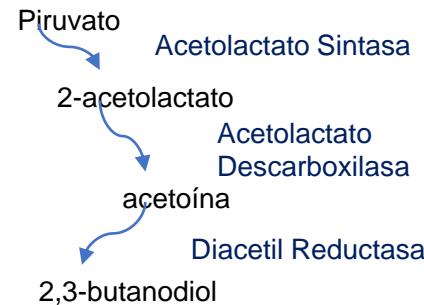
Nitrito Reductasa



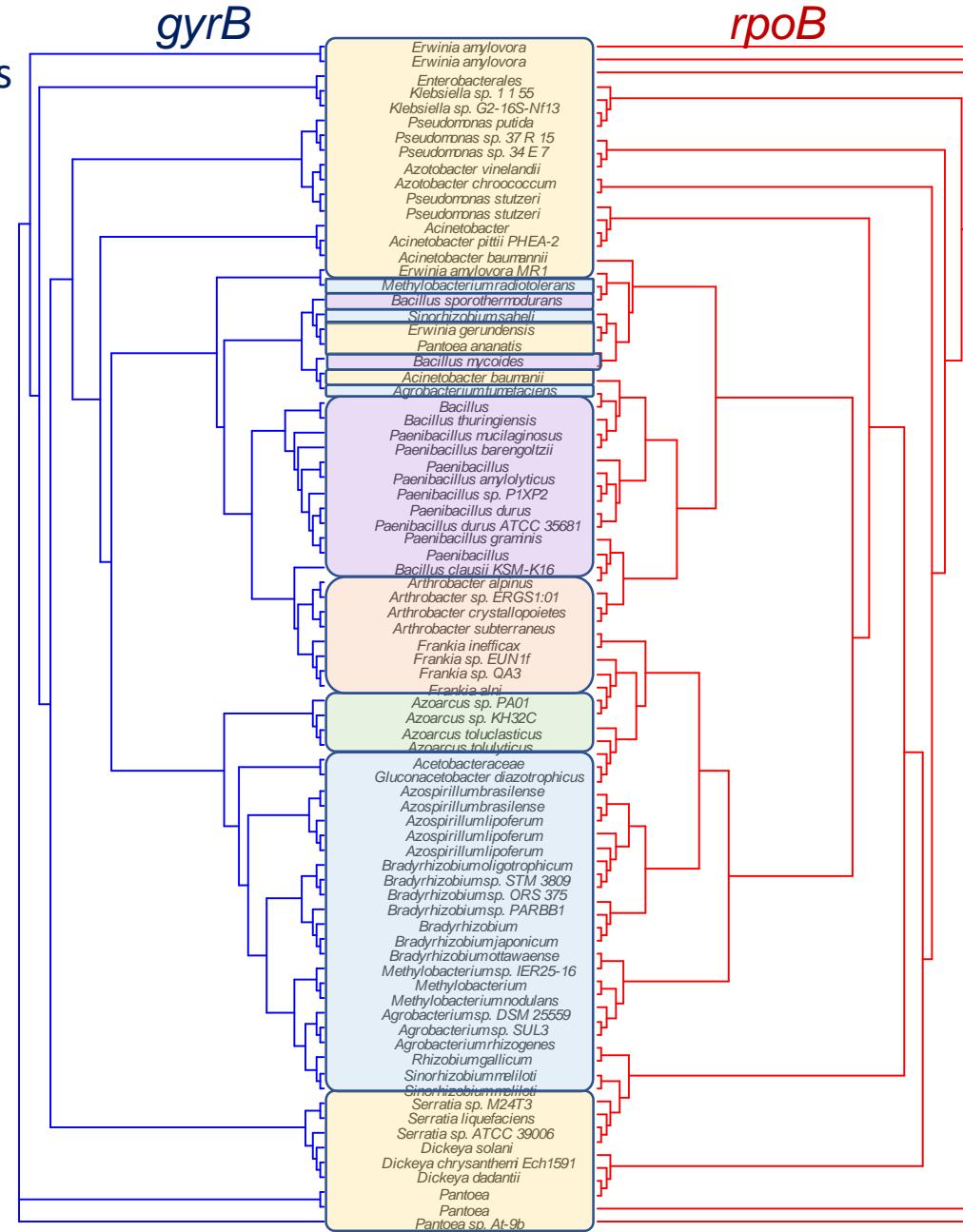
Ruta de 2-3-butanodiol



Ruta 2-3-butanodiol



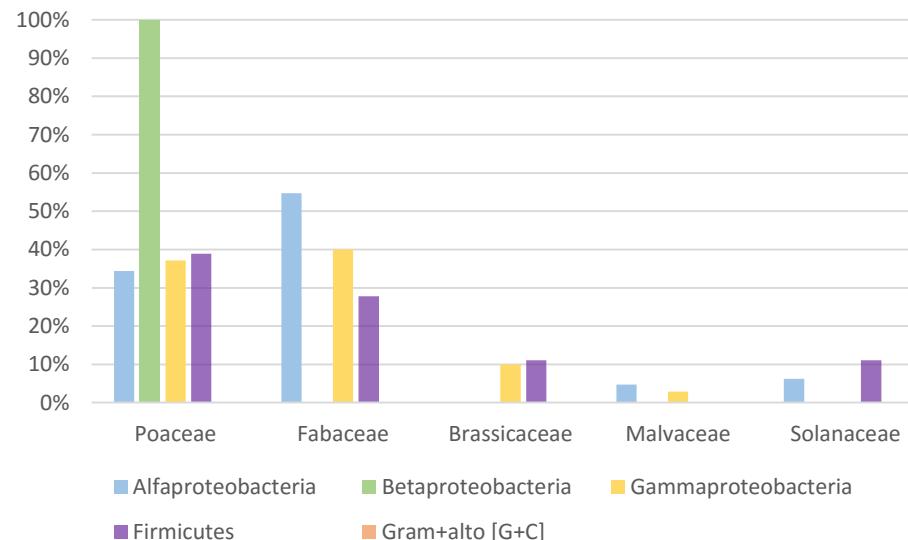
Marcadores filogenéticos



Capítulo 3. Estudio combinado de las relaciones entre mecanismos promotores del crecimiento vegetal, diversidad de PGPRs y cultivos

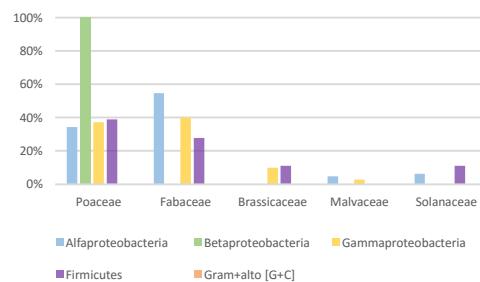
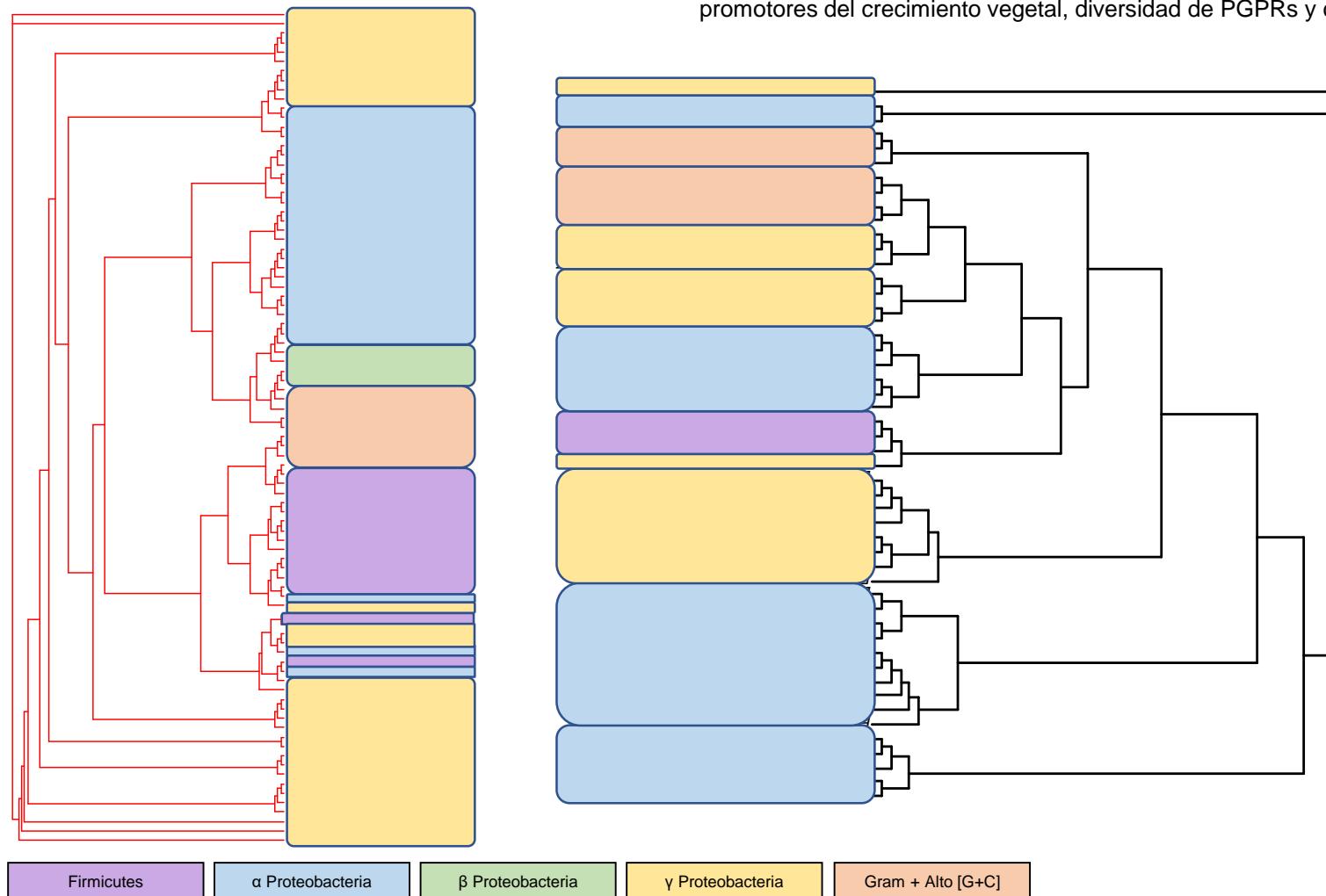
Materiales y métodos

	Arroz	Maíz	Judía Garbanzo	Alcachofa	Brassica	Algodón	Trigo	Cebada	Tomate	Cacahuete	Soja
Alfaproteobacteria	5	13	27	0	0	3	0	4	4	0	8
Betaproteobacteria	4	0	0	0	0	0	0	0	0	0	0
Gammaproteobacteria	7	10	9	0	7	2	9	0	0	7	12
Firmicutes	15	0	0	0	6	0	0	6	6	0	15
Gram+alto [G+C]	0	0	0	0	0	0	0	0	0	0	0



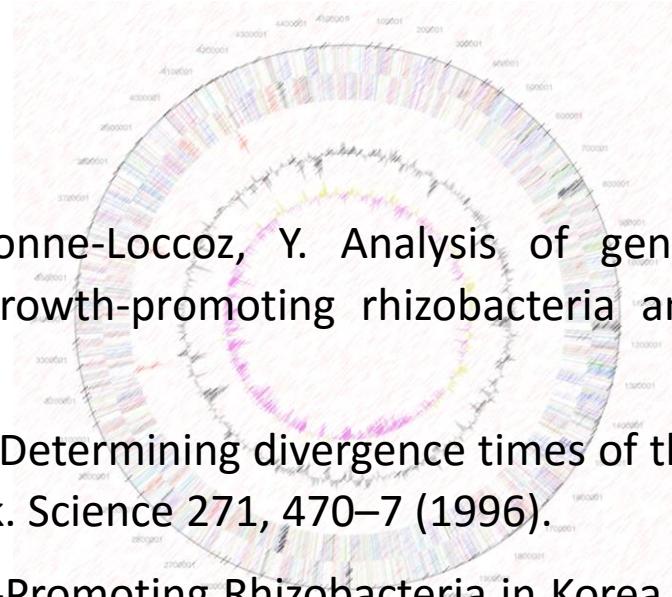
De Souza;Vessey 2003; Ahemad 2014; Pérez-Montaña 2014 y Nadeem 2014

Resultados



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TRABAJO FIN DE MÁSTER

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