

Diagnosing phylogenetic conflict between genes and proteins: Evidence for the origin of plastids

Blaise Li Peter G. Foster T. Martin Embley Cymon J. Cox

SMBE Meeting - Dublin 2012 - 24/06/2012

The questions

- ▶ Archaeplastida (plants) = **Rhodophyta** (red algae) + **Glaucophyta** + **Viridiplantae** (green plants)

The questions

- ▶ Archaeplastida (plants) = **Rhodophyta** (red algae) + **Glaucophyta** +
Viridiplantae (green plants)
→ Characterised by a plastid, with endosymbiotic origin within
cyanobacteria

¹Notation adapted from Criscuolo and Gribaldo (2011)

The questions

- ▶ Archaeplastida (plants) = **Rhodophyta** (red algae) + **Glaucophyta** + **Viridiplantae** (green plants)
→ Characterised by a plastid, with endosymbiotic origin within **cyanobacteria**
- ▶ Groups of cyanobacteria already identified: **NOST-1**, **OSC-2**, **SPM-3**, **SO-6**, **GBACT**, **UNIT+¹**

¹Notation adapted from Criscuolo and Gribaldo (2011)

The questions

- ▶ Archaeplastida (plants) = **Rhophyta** (red algae) + **Glaucophyta** + **Viridiplantae** (green plants)
→ Characterised by a plastid, with endosymbiotic origin within **cyanobacteria**
- ▶ Groups of cyanobacteria already identified: **NOST-1, OSC-2, SPM-3, SO-6, GBACT, UNIT+¹**
- ▶ What are the relationships between plastids and cyanobacteria?

¹Notation adapted from Criscuolo and Gribaldo (2011)

The questions

- ▶ Archaeplastida (plants) = **Rhophyta** (red algae) + **Glaucophyta** + **Viridiplantae** (green plants)
→ Characterised by a plastid, with endosymbiotic origin within **cyanobacteria**
- ▶ Groups of cyanobacteria already identified: **NOST-1, OSC-2, SPM-3, SO-6, GBACT, UNIT+¹**
- ▶ What are the relationships between plastids and cyanobacteria?
- ▶ Why do the gene tree and the protein tree give a different answer?

¹Notation adapted from Criscuolo and Gribaldo (2011)

Dataset

- ▶ 42 taxa, including 8 outgroup (non-cyano)bacteria, 16 cyanobacteria, and plastids from 1 Glaucophyta, 4 Rhodophyta and 13 Viridiplantae

Dataset

- ▶ 42 taxa, including 8 outgroup (non-cyano)bacteria, 16 cyanobacteria, and plastids from 1 Glauco phyta, 4 Rhodophyta and 13 Viridiplantae
- ▶ 75 protein-coding genes, but 452 missing sequences (i.e. 14% overall, and up to 38 genes missing for one of the outgroup taxa)

Dataset

- ▶ 42 taxa, including 8 outgroup (non-cyano)bacteria, 16 cyanobacteria, and plastids from 1 Glauco phyta, 4 Rhodophyta and 13 Viridiplantae
- ▶ 75 protein-coding genes, but 452 missing sequences (i.e. 14% overall, and up to 38 genes missing for one of the outgroup taxa)
- ▶ Concatenated dataset (cg75)

Analysis method

- ▶ Nucleotide dataset (cg75)

Analysis method

- ▶ Nucleotide dataset (cg75) and amino-acid translation (cp75)

Analysis method

- ▶ Nucleotide dataset (cg75) and amino-acid translation (cp75)
- ▶ Various recodings of cg75 using IUPAC ambiguity codes to remove signal associated with some synonymous substitutions.

Analysis method

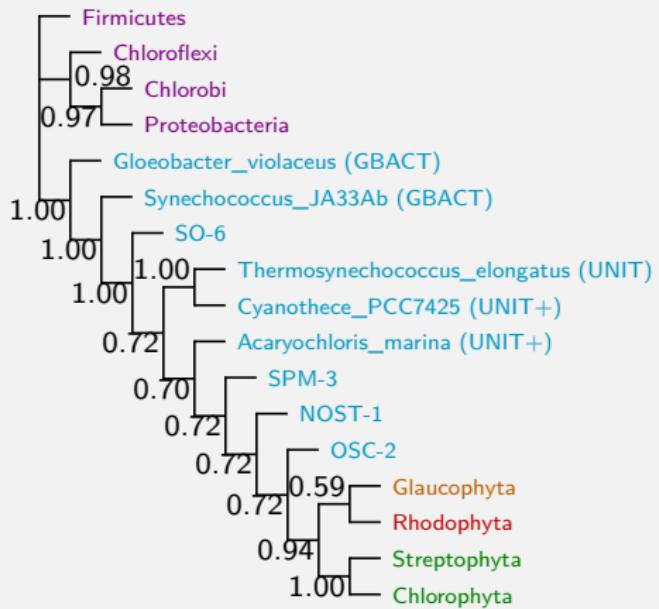
- ▶ Nucleotide dataset (cg75) and amino-acid translation (cp75)
- ▶ Various recodings of cg75 using IUPAC ambiguity codes to remove signal associated with some synonymous substitutions. e.g for His:
 $\text{CAC} \leftrightarrow \text{CAT}$ (synonymous codons) $\rightarrow \text{CAY}$ (degenerate codon)

Analysis method

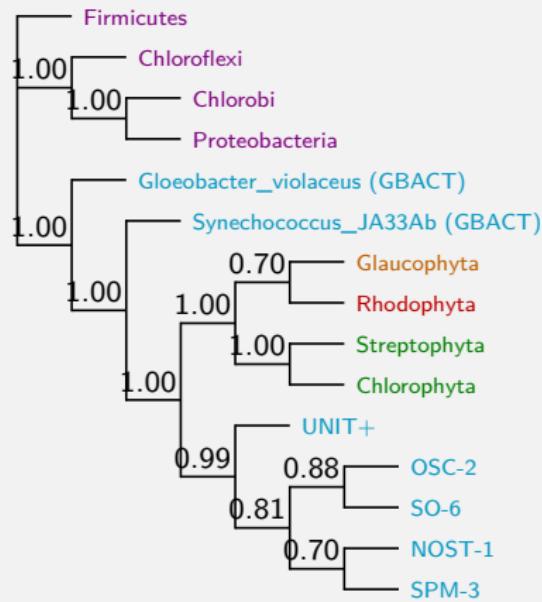
- ▶ Nucleotide dataset (cg75) and amino-acid translation (cp75)
- ▶ Various recodings of cg75 using IUPAC ambiguity codes to remove signal associated with some synonymous substitutions. e.g for His:
 $\text{CAC} \leftrightarrow \text{CAT}$ (synonymous codons) $\rightarrow \text{CAY}$ (degenerate codon)
- ▶ Maximum likelihood bootstrap analyses (200 resamplings) using RAxML, with GTR+I+ Γ (or LG+I+ Γ for cp75, chosen using ProtTest)

Unrecoded ML bootstrap analyses

translation



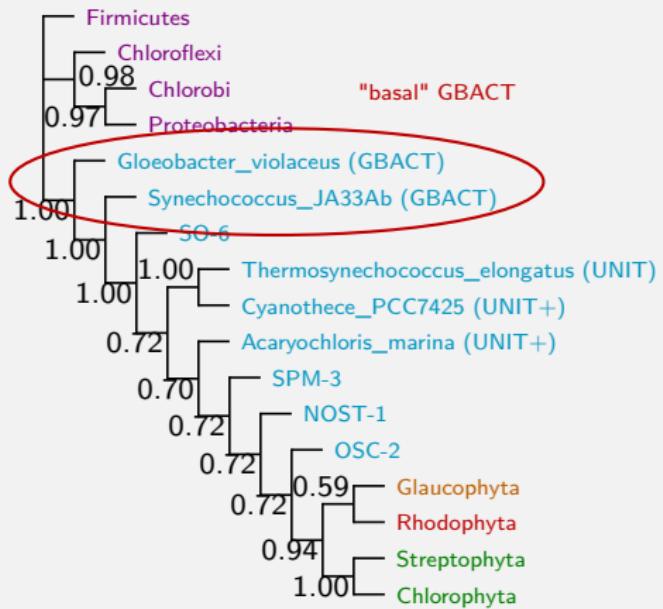
cg75



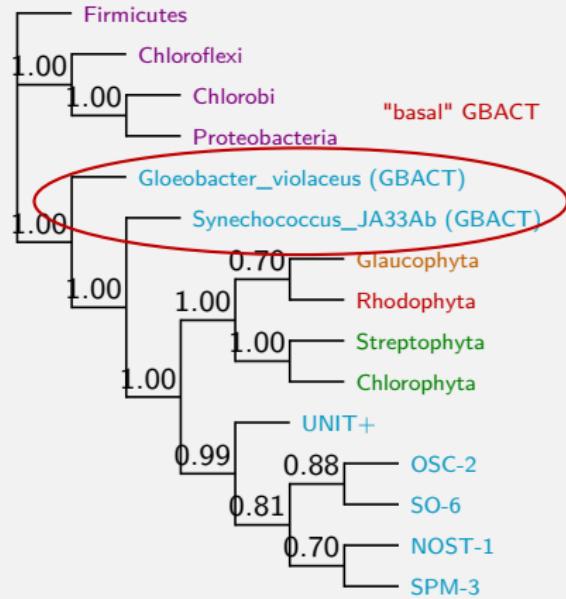
cp75

Unrecoded ML bootstrap analyses

translation



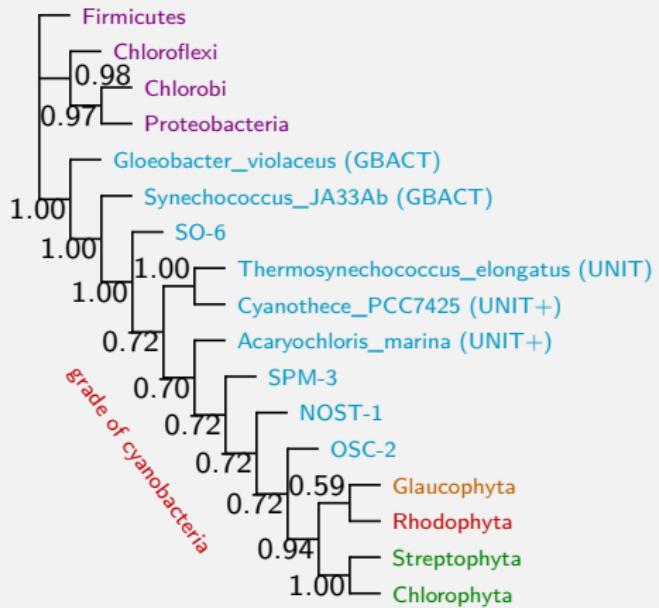
cg75



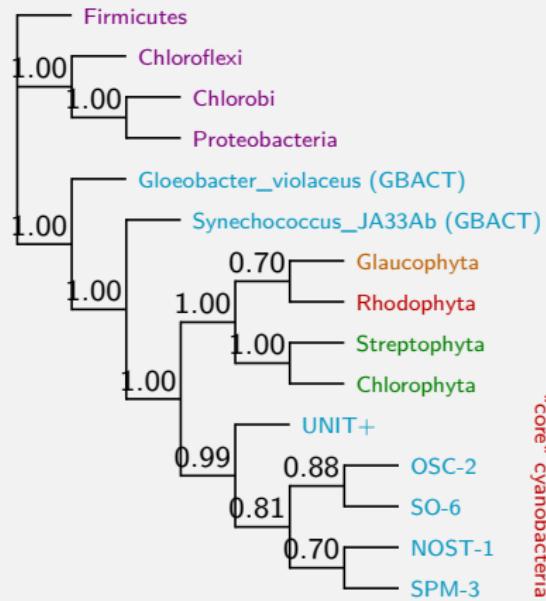
cp75

Unrecoded ML bootstrap analyses

translation



cg75



cp75

Unrecoded ML bootstrap analyses

- ▶ cp75 is a direct translation of cg75

Unrecoded ML bootstrap analyses

- ▶ cp75 is a direct translation of cg75
→ The trees should be the same.

Unrecoded ML bootstrap analyses

- ▶ cp75 is a direct translation of cg75
→ The trees should be the same.
- ▶ But the analyses conflict in the identification of the plastid sister-group.

Unrecoded ML bootstrap analyses

- ▶ cp75 is a direct translation of cg75
 - The trees should be the same.
- ▶ But the analyses conflict in the identification of the plastid sister-group.
 - Something is not well modelled.

Unrecoded ML bootstrap analyses

- ▶ cp75 is a direct translation of cg75
 - The trees should be the same.
- ▶ But the analyses conflict in the identification of the plastid sister-group.
 - Something is not well modelled.
- ▶ Data recoding experiments to identify some causes of model mis-specification.

Degenerating synonymous 3rd codon positions

	T		C		A		G	
T	TTT	Phe	TCT	Ser	TAT	Tyr	TGT	Cys
	TTC		TCC		TAC		TGC	
	TTA	Leu	TCA		TAA	Ter	TGA	Ter
	TTG		TCG		TAG		TGG	Trp
C	CTT	Leu	CCT	Pro	CAT	His	CGT	
	CTC		CCC		CAC		CGC	
	CTA		CCA		CAA	Gln	CGA	Arg
	CTG		CCG		CAG		CGG	
A	ATT	Ile	ACT	Thr	AAT	Asn	AGT	
	ATC		ACC		AAC		AGC	Ser
	ATA		ACA		AAA	Lys	AGA	
	ATG	Met	ACG		AAG		AGG	Arg
G	GTT	Val	GCT	Ala	GAT	Asp	GGT	
	GTC		GCC		GAC		GGC	
	GTA		GCA		GAA	Glu	GGA	Gly
	GTG		GCG		GAG		GGG	

Example:

ATGAAACAGTTGCTGGAAGCCGGTGTTCACCTC
 TTATCAGAACCTTTAGATGCCAGCGCTCACATA
 TTAGAAGATATGATTCAAAGTGAATGCATTTT
 CTCGAACAAATGCTAGATGTAGGTGTTCATTTT
 TTACAGTCAATGCTTGAAGCTGGTGTTCACTTT
 TTAGAACGCACTTTAGAGGCTGGTGTTCATTTT
 TTGGAAGAAATGATGGAAGCAGGGTATTCAATTTC
 TTGGAACAAATGATGGAAGCAGGAGTCCATTTT
 ATTCAAGCAATTATTGGAAGCAGGAGTCCATCTG
 ATTGAAGAATTGTTAGAACGCTGGCGTGCATTTT
 TTAGAACAAATGTTAGATGCAGGTGTACATTTT
 TTACAAAAAAATGATTGAAGCTGGTGTTCATTTT
 CTATCAGAAATGATGGAAGCTGGTGTTCATTTT
 CTGCCGCAAATGCTGGAAGCCGGTGTCCATTTT
 TTAGAAGAAATGATGGAAGCAGGGGTCCATTTT
 TTAGCAGAATTACTAGAACGCGGCGTTCATTTT

Degenerating synonymous 3rd codon positions

	T		C		A		G	
T	TTT	Phe	TCT	Ser	TAT	Tyr	TGT	Cys
	TTG		TCC		TAC	Ter	TGC	
	TTA	Leu	TCA		TAA		TGA	Ter
	TTG		TCG		TAG		TGG	Trp
C	CTT	Leu	CCT	Pro	CAT	His	CGT	
	CTC		CCC		CAC		CGC	Arg
	CTA		CCA		CAA	Gln	CGA	
	CTG		CCG		CAG		CGG	
A	ATT	Ile	ACT	Thr	AAT	Asn	AGT	
	ATC		ACC		AAC		AGC	Ser
	ATA		ACA		AAA	Lys	AGA	Arg
	ATG	Met	ACG		AAG		AGG	
G	GTT	Val	GCT	Ala	GAT	Asp	GGT	
	GTC		GCC		GAC		GGC	Gly
	GTA		GCA		GAA	Glu	GGA	
	GTG		GCG		GAG		GGG	

Example:

ATGAAACAGTTGCTGGAAGCCGGTGTTCACCTTC
 TTATCAGAACCTTTAGATGCCAGCGCTCACATA
 TTAGAACATATGATTCAAAGTGGAAATGCACTTT
 CTCGAACAAATGCTAGATGTAGGTGTTCACTTT
 TTACAGTCATGCTTGAAGCTGGTGTTCACCTTT
 TTAGAACACTTTAGAGGCTGGTGTTCACCTTT
 TTGGAAGAAATGATGGAAGCAGGGTATTCACTTC
 TTGGAACAAATGATGGAAGCAGGAGTCCACCTTT
 ATTCAAGCAATTATTGGAAGCAGGAGTCCACCTTG
 ATTGAAGAATTGTTAGAACGCTGGCGTGCACCTTC
 TTAGAACAAATGTTAGATGCAGGTGTACATTT
 TTACAAAAATGATTGAGCTGGTGTTCACCTTT
 CTATCAGAAATGATGGAAGCTGGTGTTCACCTTC
 CTGCCGCAAATGCTGGAAGCCGGTGTCCACCTTT
 TTAGAACAAATGATGGAAGCAGGGGTCCACCTTT
 TTAGCAGAATTACTAGAACGAGGCGTTCACCTTT

Degenerating synonymous 3rd codon positions

	T		C		A		G	
T	TTY	Phe	TCN	Ser	TAY	Tyr	TGY	Cys
	TTY		TCN		TAY	Ter	TGY	
	TTN	Leu	TCN		TAR		TGR	Ter
	TTN		TCN		TAR		TGG	Trp
C	CTN	Leu	CCN	Pro	CAY	His	CGN	
	CTN		CCN		CAY		CGN	Arg
	CTN		CCN		CAR	Gln	CGN	
	CTN		CCN		CAR		CGN	
A	ATH	Ile	ACN	Thr	AAY	Asn	AGN	Ser
	ATH		ACN		AAY		AGN	
	ATH		ACN		AAR	Lys	AGN	Arg
	ATG	Met	ACN		AAR		AGN	
G	GTN	Val	GCN	Ala	GAY	Asp	GGN	
	GTN		GCN		GAY		GGN	Gly
	GTN		GCN		GAR	Glu	GGN	
	GTN		GCN		GAR		GGN	

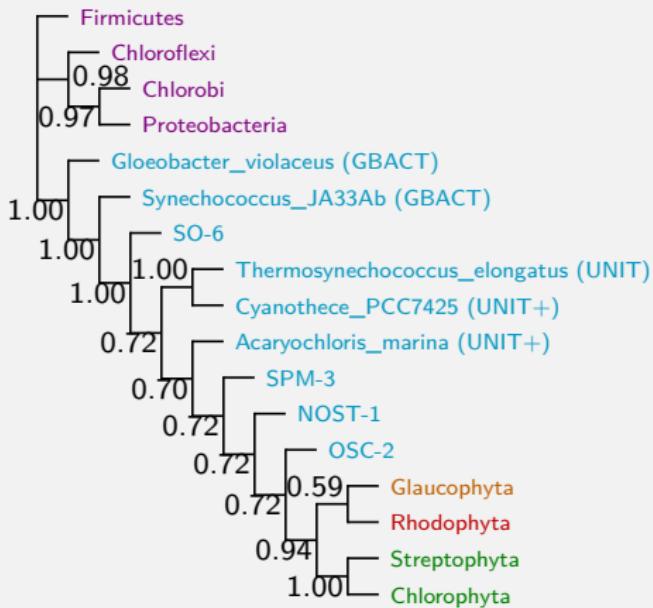
Example:

ATGAARCARTTNCTNGARGCNGGNGTNCAYTTY
 TTNTCNGARCTNTTNGAYGCNAGNGCNCAYATH
 TTNGARGAYATGATHCARAGNGGNATGCAYTTY
 CTNGARCARATGCTNGAYGTNGGNGTNCAYTTY
 TTNCARTCNATGCTNGARGCNGGNGTNCAYTTY
 TTNGARGCNCTNTTNGARGCNGGNGTNCAYTTY
 TTNGARGARATGATGGARGCNGGNATHCAYTTY
 TTNGARCARATGATGGARGCNGGNGTNCAYTTY
 ATHCARCARATTNTTNGARGCNGGNGTNCAYCTN
 ATHGARGARTTNTTNGARGCNGGNGTNCAYTTY
 TTNGARCARATGTTNGAYGCNGGNGTNCAYTTY
 TTNCARAARATGATHGARGCNGGNGTNCAYTTY
 CTNTCNGARATGATGGARGCNGGNGCNCAYTTY
 CTNCCNCARATGCTNGARGCNGGNGTNCAYTTY
 TTNGARGARATGATGGARGCNGGNGTNCAYTTY
 TTNGCNGARTTNCTNGARGCNGGNGTNCAYTTY

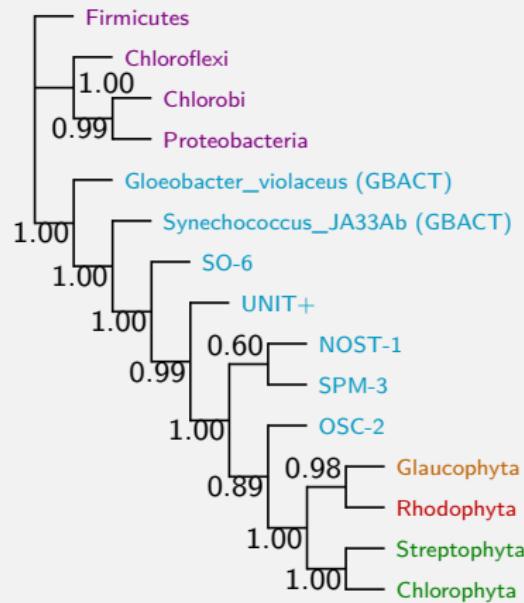
Degenerating synonymous 3rd codon positions

degenerate at 3rd pos.

(27.35% recoded)

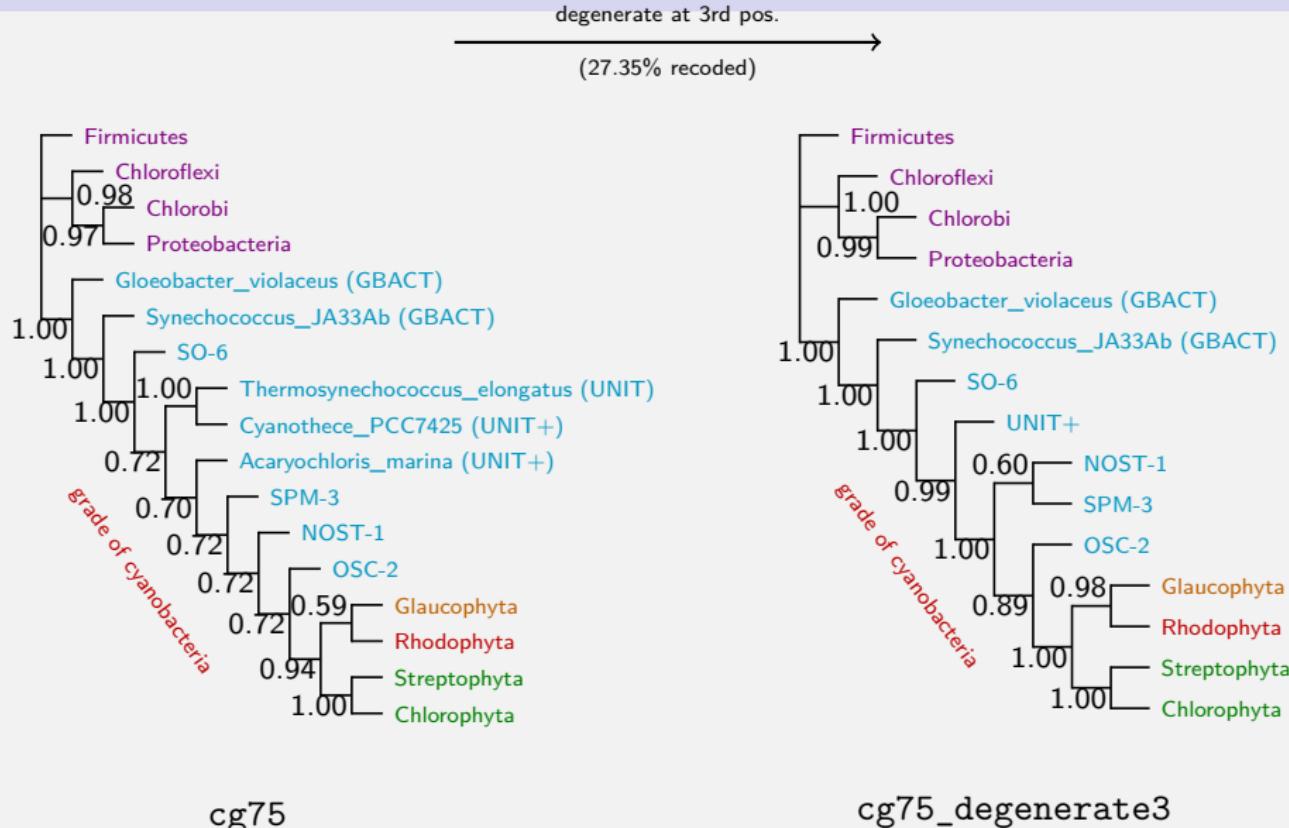


cg75



cg75_degenerate3

Degenerating synonymous 3rd codon positions



Degenerating synonymous 3rd codon positions

- ▶ No "core" cyanobacteria monophyly.

Degenerating synonymous 3rd codon positions

- ▶ No "core" cyanobacteria monophyly.
→ Synonymous substitutions at 3rd codon position are not the only cause of discrepancy between cp75 and cg75.

Degenerating synonymous 3rd codon positions

- ▶ No "core" cyanobacteria monophyly.
→ Synonymous substitutions at 3rd codon position are not the only cause of discrepancy between cp75 and cg75.
- ▶ But there are synonymous substitutions also at 1st and 2nd position:

Degenerating synonymous 3rd codon positions

- ▶ No "core" cyanobacteria monophyly.
→ Synonymous substitutions at 3rd codon position are not the only cause of discrepancy between cp75 and cg75.
- ▶ But there are synonymous substitutions also at 1st and 2nd position:
e.g for Leu: (TTA ↔ CTA) → YTA
e.g for Arg: (CGA ↔ AGA) → MGA
e.g for Ser: (TCT ↔ AGA) → WST

Degenerating synonymous 1st and 2nd codon positions

	T		C		A		G	
T	TTT TTC	Phe	TCT TCC	Ser	TAT TAC	Tyr	TGT TGC	Cys
	TTA TTG	Leu	TCA TCG		TAA TAG	Ter	TGA	Ter
	CTT CTC CTA CTG	Leu	CCT CCC CCA CCG	Pro	CAT CAC	His	CGT CGC	Arg
C					CAA CAG		CGA CGG	
A	ATT ATC ATA	Ile	ACT ACC ACA	Thr	AAT AAC	Asn	AGT AGC	Ser
	ATG		ACG		AAA AAG		AGA AGG	Arg
G	GTT GTC GTA GTG	Val	GCT GCC GCA GCG	Ala	GAT GAC	Asp	GGT GGC	Gly
					GAA GAG		GGA GGG	

Example:

ATGAAACAGTTGCTGGAAGCCGGTGTTCACCTC
 TTATCAGAACTTTAGATGCCAGCGCTCACATA
 TTAGAAGATATGATTCAAAGTGAATGCATTTT
 CTCGAACAAATGCTAGATGTAGGTGTTCATTTT
 TTACAGTCAATGCTTGAAGCTGGTGTTCACTTT
 TTAGAAGCACTTTAGAGGCTGGTGTTCATTTT
 TTGGAAGAAATGATGGAAGCAGGGTATTCAATTTC
 TTGGAACAAATGATGGAAGCAGGAGTCCATTTT
 ATTCAAGCAATTATTGGAAGCAGGAGTCCATCTG
 ATTGAAGAATTGTTAGAACGCTGGCGTGCATTTC
 TTAGAACAAATGTTAGATGCAGGTGTACATTTT
 TTACAAAAAAATGATTGAAGCTGGTGTTCATTTT
 CTATCAGAAATGATGGAAGCTGGTGTTCATTTT
 CTGCCGCAAATGCTGGAAGCCGGTGTCCATTTT
 TTAGAAGAAATGATGGAAGCAGGGGTCCATTTT
 TTAGCAGAATTACTAGAACAGCGGGCGTTCATTTT

Degenerating synonymous 1st and 2nd codon positions

	T		C		A		G	
T	TTT TTC	Phe	TCT TCC	Ser	TAT TAC	Tyr	TGT TGC	Cys
	TTA TTG	Leu	TCA TCG		TAA TAG	Ter	TGA	Ter
					TGG		TGG	Trp
C	CTT CTC CTA CTG	Leu	CCT CCC CCA CCG	Pro	CAT CAC	His	CGT CGC	Arg
					CAA CAG		CGA CGG	
A	ATT ATC ATA	Ile	ACT ACC ACA	Thr	AAT AAC	Asn	AGT AGC	Ser
	ATG		ACG		AAA AAG	Lys	AGA AGG	
G	GTT GTC GTA GTG	Val	GCT GCC GCA GCG	Ala	GAT GAC	Asp	GGT GGC	Gly
					GAA GAG		GGA GGG	

Example:

ATGAAACAGTTGCTGGAAGCCGGTCTTCACTTC
 TTATCAGAACCTTTAGATGCCAGCGCTCACATA
 TTAGAAGATATGATTCAAAGTGGAAATGCATTTT
 CTCGAACAAATGCTAGATGTAGGTGTTCATTTT
 TTACAGTCAATGCTTGAAGCTGGTCTTCACTTT
 TTAGAAGCACCTTTAGAGGCTGGTCTTCACTTT
 TTGGAAGAAATGATGGAAGCAGGGTATTCACTTC
 TTGGAACAAATGATGGAAGCAGGAGTCCATTTT
 ATTCAAGCAAATTATTGGAAGCAGGAGTCCATCTG
 ATTGAAGAAATTGTTAGAACGCTGGCGTGCATTT
 TTAGAACAAATGTTAGATGCAGGTGTACATTTT
 TTACAAAAAAATGATTGAAGCTGGTCTTCACTTT
 CTATCAGAAATGATGGAAGCTGGTCTCATTT
 CTGCCGCAAATGCTGGAAAGCCGGTCTTCACTTT
 TTAGAAGAAATGATGGAAGCAGGGGTCCATTTT
 TTAGCAGAAATTACTAGAACGGCGTTCATTTT

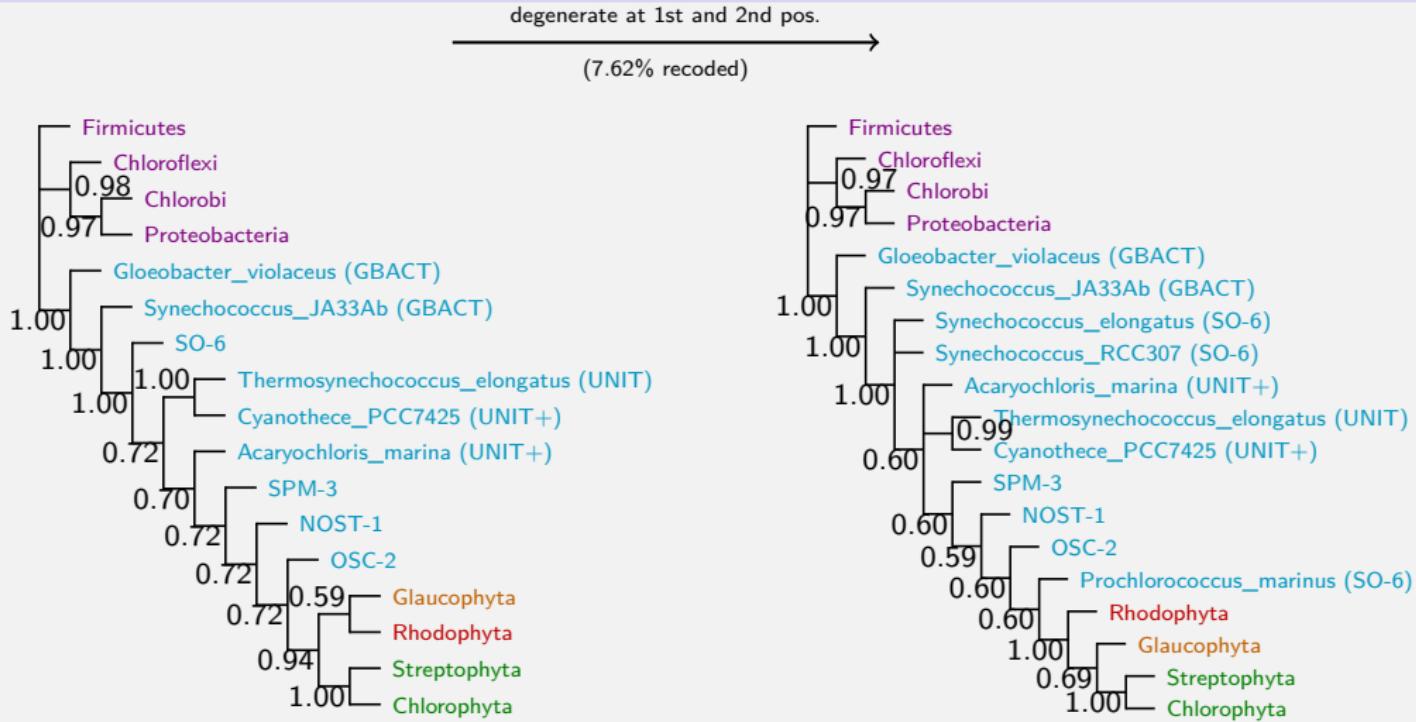
Degenerating synonymous 1st and 2nd codon positions

	T		C		A		G	
T	TTT TTC	Phe	WST WSC	Ser	TAT TAC	Tyr	TGT TGC	Cys
	YTA YTG	Leu	WSA WSG		TAA TAG	Ter	TGA	Ter
	YTG				TGG		TGG	Trp
C	YTT YTC	Leu	CCT CCC	Pro	CAT CAC	His	MGT	Arg
	YTA YTG		CCA CCG		CAA CAG		MGC	
	YTG				Gln		MGA	
	YTG				MGG		MGG	
A	ATT ATC	Ile	ACT ACC	Thr	AAT AAC	Asn	WST WSC	Ser
	ATA		ACA		AAA		MGA	
	ATG	Met	ACG		AAG	Lys	MGG	Arg
G	GTT GTC	Val	GCT GCC	Ala	GAT GAC	Asp	GGT	Gly
	GTA GTG		GCA GCG		GAA GAG		GGC	
	GTG						GGA	
	GTG						GGG	

Example:

ATGAAACAGYTGYTGAAGCCGGTGTTCACCTC
YTAWSAGAAYTTYTAGATGCCWSCGCTCACATA
YTAGAAGATATGATTCAAWSTGGAATGCATTTT
YTCGAACAAATGYTAGATGTAGGTGTTCATTTT
YTACAGWSAATGYTTGAAGCTGGTGTTCACTTT
YTAGAAGCAYTTYTAGAGGCTGGTGTTCATTTT
YTGGAAGAAATGATGGAAGCAGGGTATTCAATTTC
YTGGAACAAATGATGGAAGCAGGAGTCCATTTT
ATTCAAGCAAYTAYTGAAGCAGGAGTCCATYTG
ATTGAAGAAYTGYTAGAACGCTGGCGTGCATTTT
YTAGAACAAATGYTAGATGCAGGTGTACATTTT
YTACAAAAAAATGATTGAAGCTGGTGTTCATTTT
YTAWSAGAAATGATGGAAGCTGGTGTCTCATTTT
YTGCCGCAAATGYTGGAAGCCGGTGTCCATTTT
YTAGAAGAAATGATGGAAGCAGGGGTCCATTTT
YTAGCAGAAYTAYTGAAGCAGGGCGTTCATTTT

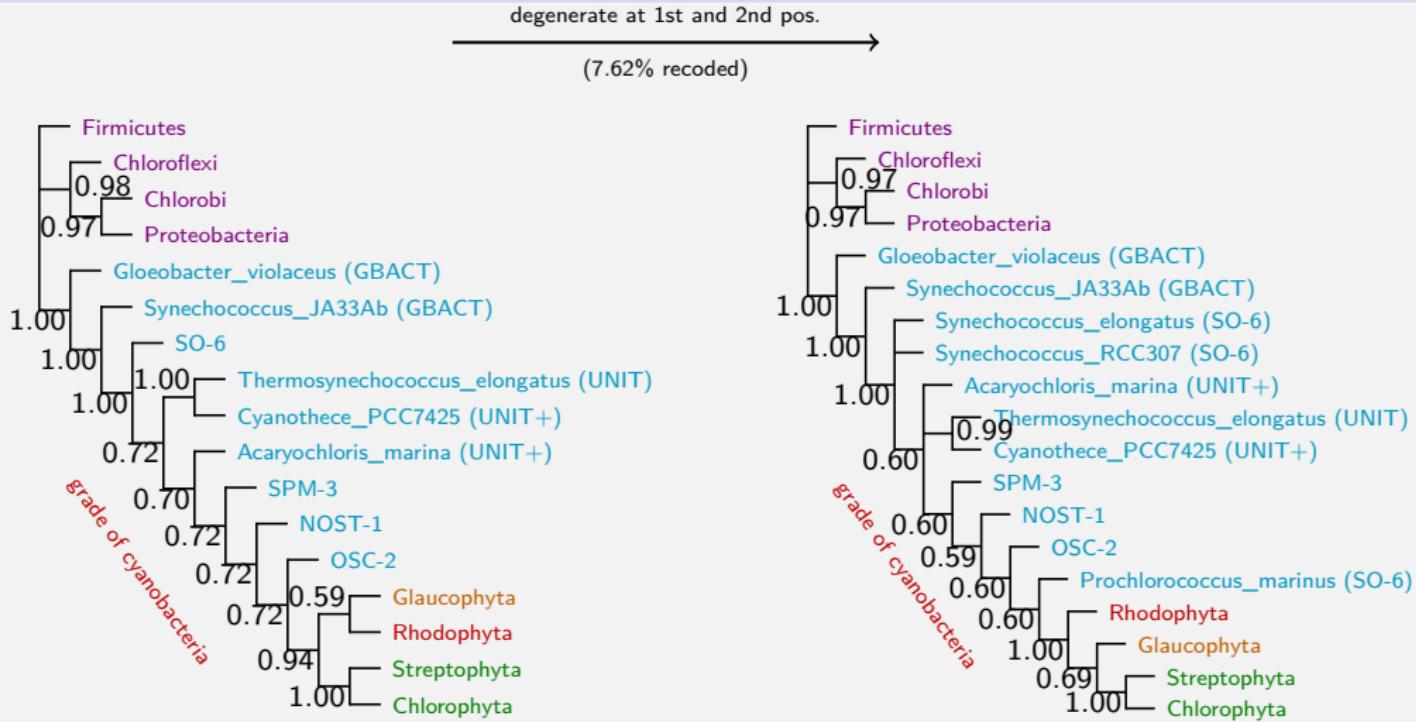
Degenerating synonymous 1st and 2nd codon positions



cg75

cg75_degenerate12

Degenerating synonymous 1st and 2nd codon positions



cg75

cg75_degenerate12

Degenerating synonymous 1st and 2nd codon positions

- ▶ Again no "core" cyanobacteria monophyly.

Degenerating synonymous 1st and 2nd codon positions

- ▶ Again no "core" cyanobacteria monophyly.
→ Synonymous substitutions at 1st and 2nd codon position are not the only cause of discrepancy between cp75 and cg75.

Degenerating synonymous 1st and 2nd codon positions

- ▶ Again no "core" cyanobacteria monophyly.
→ Synonymous substitutions at 1st and 2nd codon position are not the only cause of discrepancy between cp75 and cg75.
- ▶ Let's try to neutralize all synonymous substitutions... .

Degenerating all synonymous codon positions

	T		C		A		G	
T	TTT	Phe	TCT	Ser	TAT	Tyr	TGT	Cys
	TTC		TCC		TAC		TGC	
	TTA	Leu	TCA		TAA	Ter	TGA	Ter
	TTG		TCG		TAG		TGG	Trp
C	CTT	Leu	CCT	Pro	CAT	His	CGT	
	CTC		CCC		CAC		CGC	
	CTA		CCA		CAA	Gln	CGA	Arg
	CTG		CCG		CAG		CGG	
A	ATT	Ile	ACT	Thr	AAT	Asn	AGT	
	ATC		ACC		AAC		AGC	Ser
	ATA		ACA		AAA	Lys	AGA	
	ATG	Met	ACG		AAG		AGG	Arg
G	GTT	Val	GCT	Ala	GAT	Asp	GGT	
	GTC		GCC		GAC		GGC	
	GTA		GCA		GAA	Glu	GGA	Gly
	GTG		GCG		GAG		GGG	

Example:

ATGAAACAGTTGCTGGAAGGCCGGTGTTCACCTC
 TTATCAGAACCTTTAGATGCCAGCGCTCACATA
 TTAGAAGATATGATTCAAAGTGAATGCATTTT
 CTCGAACAAATGCTAGATGTAGGTGTTCATTTT
 TTACAGTCAATGCTTGAAGCTGGTGTTCACTTT
 TTAGAACGCACTTTAGAGGCTGGTGTTCATTTT
 TTGGAAGAAATGATGGAAGCAGGGTATTCAATTTC
 TTGGAACAAATGATGGAAGCAGGAGTCCATTTT
 ATTCAAGCAATTATTGGAAGCAGGAGTCCATCTG
 ATTGAAGAATTGTTAGAACGCTGGCGTGCATTTT
 TTAGAACAAATGTTAGATGCAGGTGTACATTTT
 TTACAAAAAAATGATTGAAGCTGGTGTTCATTTT
 CTATCAGAAATGATGGAAGCTGGTGTTCATTTT
 CTGCCGCAAATGCTGGAAGCCGGTGTCCATTTT
 TTAGAAGAAATGATGGAAGCAGGGGTCCATTTT
 TTAGCAGAATTACTAGAACGCGGCGTTCATTTT

Degenerating all synonymous codon positions

	T		C		A		G	
T	TTT TTC	Phe	TCT TCC	Ser	TAT TAC	Tyr	TGT TGC	Cys
	TTA TTG	Leu	TCA TCG		TAA TAG	Ter	TGA TGG	Ter Trp
C	CTT CTC CTA CTG	Leu	CCT CCC CCA CCG		CAT CAC	His	CGT CGC	Arg
					CAA CAG		CGA CGG	
A	ATT ATC ATA	Ile	ACT ACC ACA	Thr	AAT AAC	Asn	AGT AGC	Ser
	ATG		ACG		AAA AAG	Lys	AGA AGG	
G	GTT GTC GTA GTG	Val	GCT GCC GCA GCG		GAT GAC	Asp	GGT GGC	Gly
					GAA GAG		GGA GGG	

Example:

ATGAAACAGTTGCTGGAAGCCGGTGTTCACCTTC
 TTATCAGAACCTTTAGATGCCAGCGCTCACATA
 TTAGAACATATGATTCAAAAGTGGAAATGCACTTT
 CTCGAACAAATGCTAGATGTAGGTGTTCATTTT
 TTACAGTCAATGCTTGAAGCTGGTGTTCACCTTT
 TTAGAACGCACTTTAGAGGCTGGTGTTCACCTTT
 TTGGAAGAAATGATGGAAGCAGGGTATTTCATTTC
 TTGGAACAAATGATGGAAGCAGGAGTCCATTTT
 ATTCAAGCAATTATTGGAAGCAGGAGTCCATCTG
 ATTGAAGAATTGTTAGAACGCTGGCGTGCATTTC
 TTAGAACAAATGTTAGATGCAGGTGTACATTTT
 TTACAAAAATGATTGAGCTGGTGTTCATTTT
 CTATCAGAAATGATGGAAGCTGGTGCTCATTTC
 CTGCCGCAAATGCTGGAAGCCGGTGTCCATTTT
 TTAGAACAAATGATGGAAGCAGGGGTCCATTTT
 TTAGCAGAATTACTAGAACGAGGGCGTTCATTTT

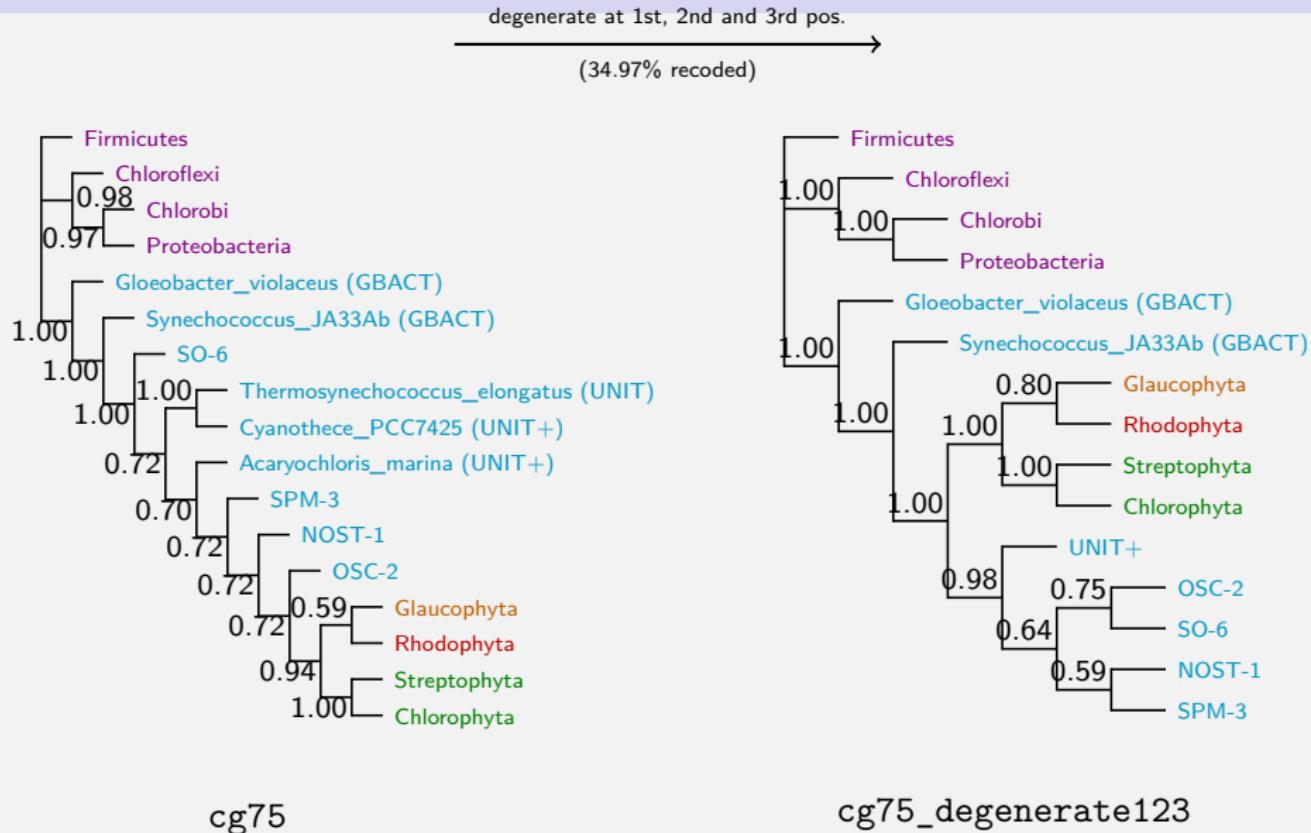
Degenerating all synonymous codon positions

	T		C		A		G	
T	TTY	Phe	WSN	Ser	TAY	Tyr	TGY	Cys
	TTY		WSN		TAY	Ter	TGY	
	YTN	Leu	WSN		TAR		TGR	Ter
	YTN		WSN		TAR		TGG	Trp
C	YTN	Leu	CCN	Pro	CAY	His	MGN	
	YTN		CCN		CAY		MGN	Arg
	YTN		CCN		CAR	Gln	MGN	
	YTN		CCN		CAR		MGN	
A	ATH	Ile	ACN	Thr	AAY	Asn	WSN	Ser
	ATH		ACN		AAY		WSN	
	ATH		ACN		AAR	Lys	MGN	Arg
	ATG	Met	ACN		AAR		MGN	
G	GTN	Val	GCN	Ala	GAY	Asp	GGN	
	GTN		GCN		GAY		GGN	Gly
	GTN		GCN		GAR	Glu	GGN	
	GTN		GCN		GAR		GGN	

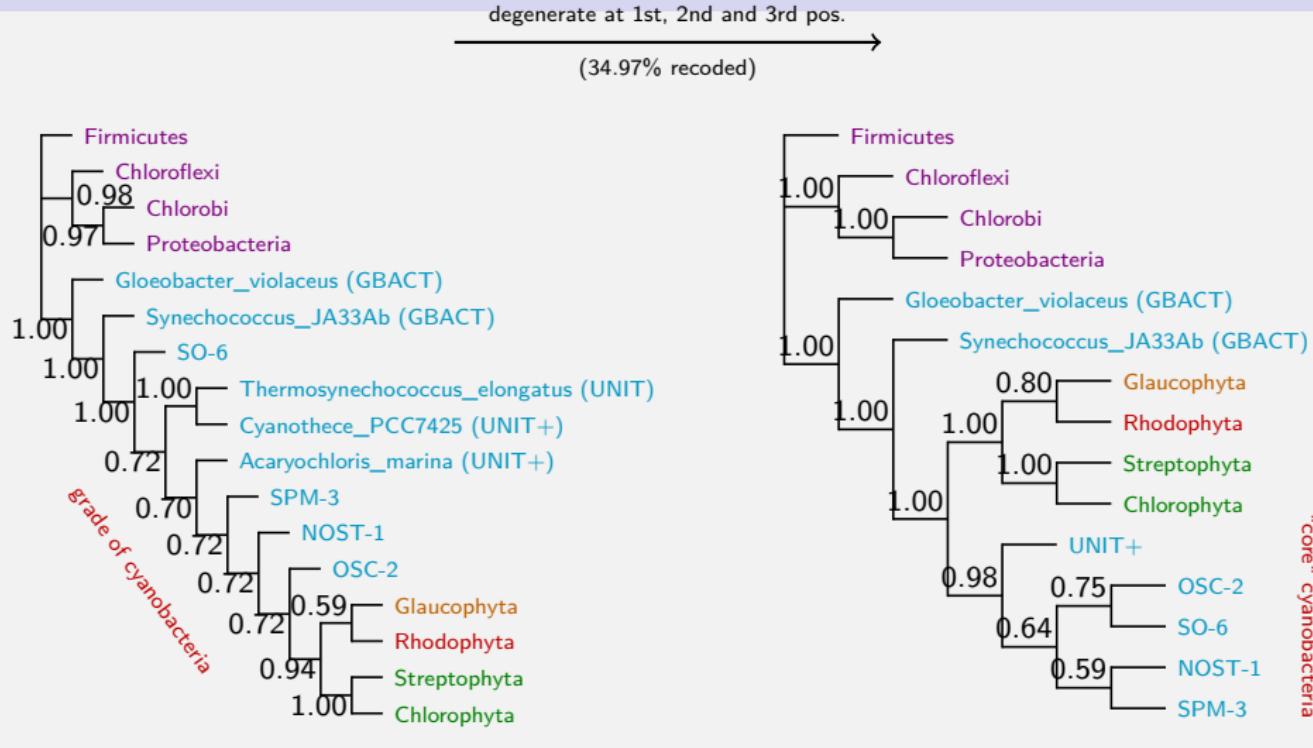
Example:

ATGAARCARYTNYTNGARGCNGGNGTNCAYTTY
 YTNWSNGARAYTNYTNGAYGCNWSNGCNCAYATH
 YTNGARGAYATGATHCARWSNGGNATGCAYTYY
 YTNGARCARATGYTNGAYGTNGGNGTNCAYTTY
 YTNCARWSNATGYTNGARGCNGGNGTNCAYTTY
 YTNGARGCNYTNYTNGARGCNGGNGTNCAYTTY
 YTNGARGARATGATGGARGCNGGNATHCAYTYY
 YTNGARCARATGATGGARGCNGGNGTNCAYTTY
 ATHCARCARAYTNYTNGARGCNGGNGTNCAYTN
 ATHGARGARAYTNYTNGARGCNGGNGTNCAYTTY
 YTNGARCARATGYTNGAYGCNGGNGTNCAYTTY
 YTNCARAARATGATHGARGCNGGNGTNCAYTTY
 YTNWNSNGARATGATGGARGCNGGNGCNCAYTTY
 YTNCNCARATGYTNGARGCNGGNGTNCAYTTY
 YTNGARGARATGATGGARGCNGGNGTNCAYTTY
 YTNGCNGARAYTNYTNGARGCNGGNGTNCAYTTY

Degenerating all synonymous codon positions



Degenerating all synonymous codon positions



cg75

cg75_degenerate123

Degenerating all synonymous codon positions

- ▶ Same topology as with the protein data

Degenerating all synonymous codon positions

- ▶ Same topology as with the protein data
- ▶ Synonymous substitutions are responsible for the incongruence between nucleotide and amino-acid data.

Degenerating all synonymous codon positions

- ▶ Same topology as with the protein data
- ▶ Synonymous substitutions are responsible for the incongruence between nucleotide and amino-acid data.
- ▶ This could be explained by effects of biases in codon usage and DNA composition:

Degenerating all synonymous codon positions

- ▶ Same topology as with the protein data
- ▶ Synonymous substitutions are responsible for the incongruence between nucleotide and amino-acid data.
- ▶ This could be explained by effects of biases in codon usage and DNA composition:
 - ▶ Codon preference / composition biases: "allowed" within a synonymy class (neutral at the protein level and above)

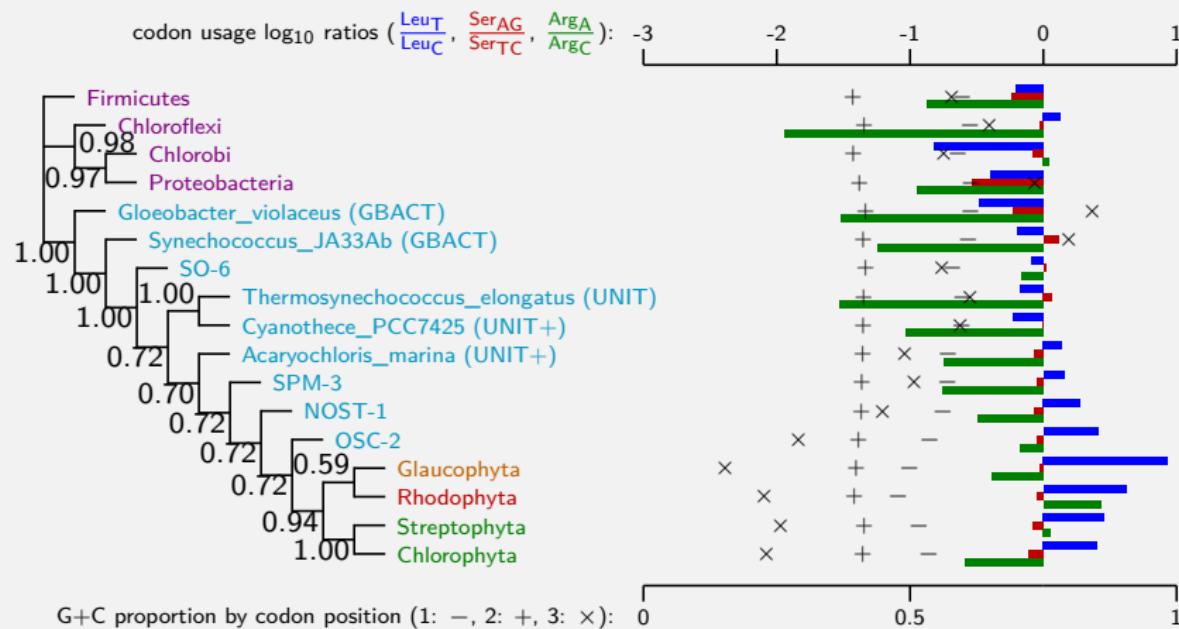
Degenerating all synonymous codon positions

- ▶ Same topology as with the protein data
- ▶ Synonymous substitutions are responsible for the incongruence between nucleotide and amino-acid data.
- ▶ This could be explained by effects of biases in codon usage and DNA composition:
 - ▶ Codon preference / composition biases: "allowed" within a synonymy class (neutral at the protein level and above)
→ Convergence between taxa sharing the same biases

Degenerating all synonymous codon positions

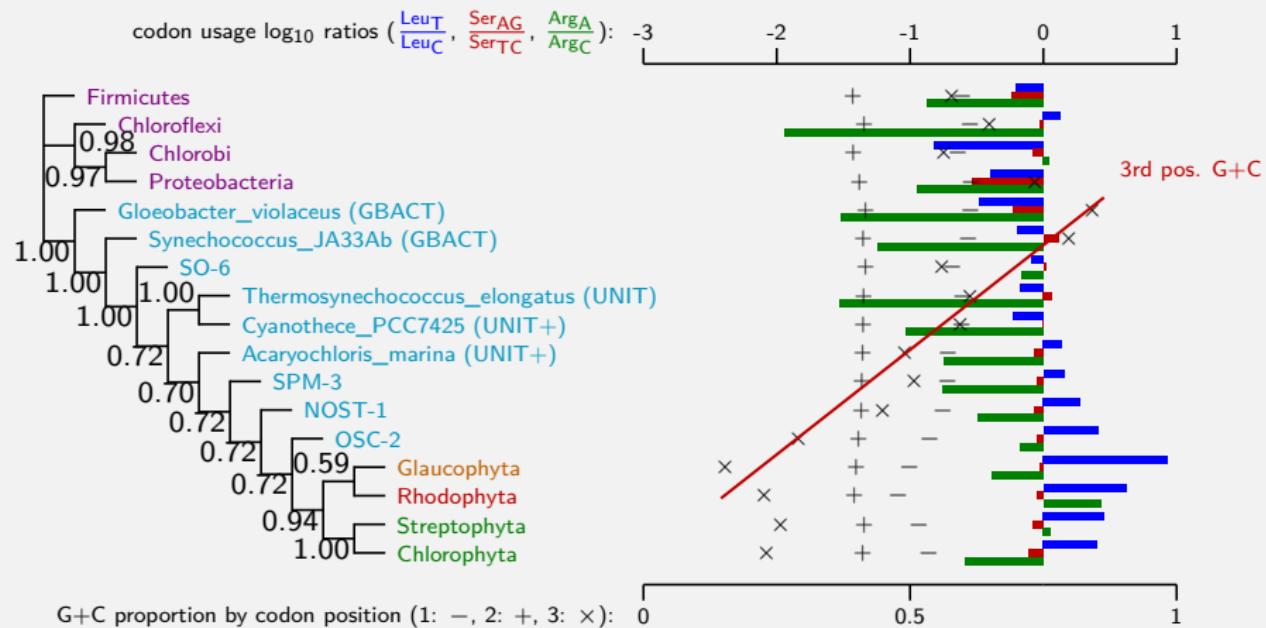
- ▶ Same topology as with the protein data
- ▶ Synonymous substitutions are responsible for the incongruence between nucleotide and amino-acid data.
- ▶ This could be explained by effects of biases in codon usage and DNA composition:
 - ▶ Codon preference / composition biases: "allowed" within a synonymy class (neutral at the protein level and above)
→ Convergence between taxa sharing the same biases
 - ▶ Let's visualize this...

Effects of composition and codon usage



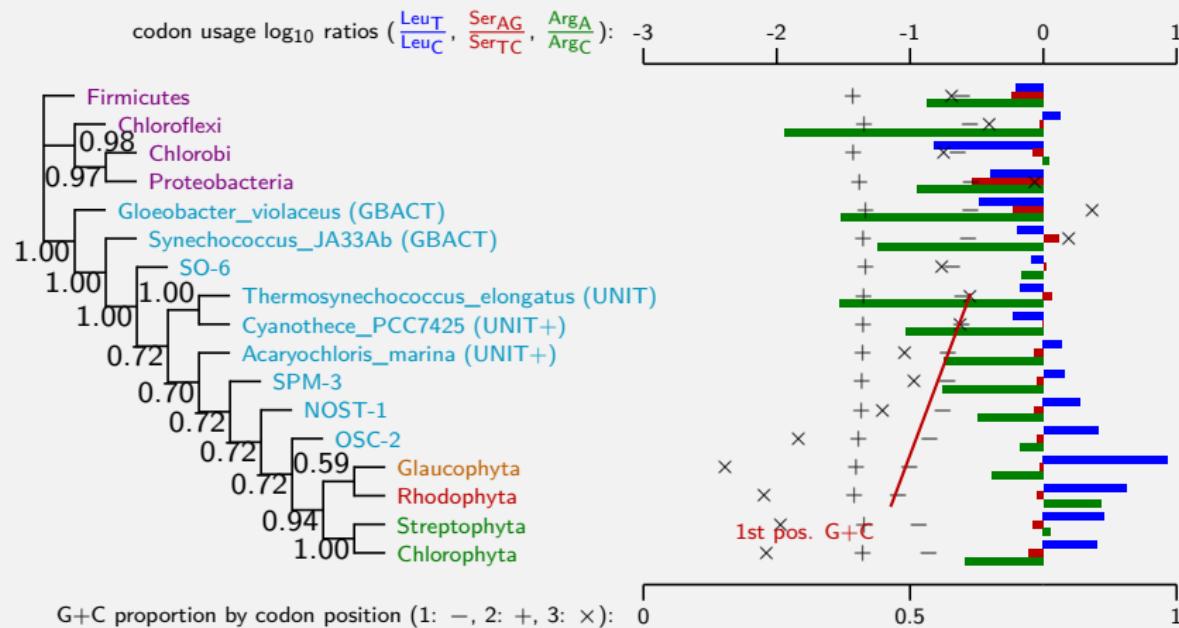
cg75

Effects of composition and codon usage



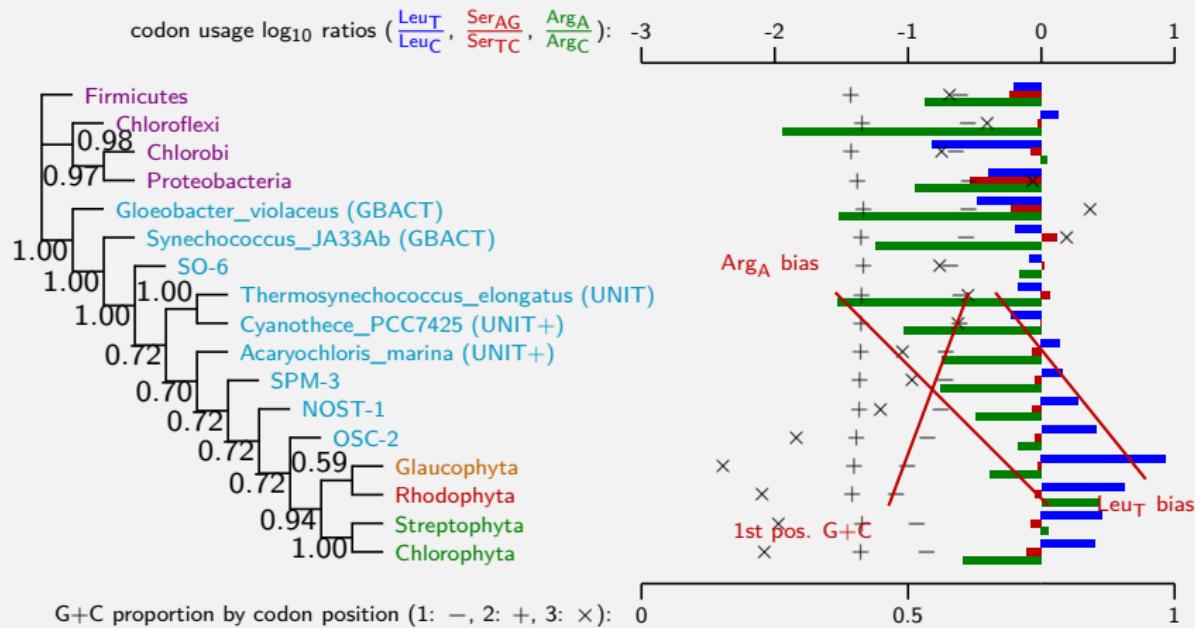
cg75

Effects of composition and codon usage



cg75

Effects of composition and codon usage



cg75

The conclusions

- ▶ Synonymous substitutions enable convergence in codon usage and composition biases.

The conclusions

- ▶ Synonymous substitutions enable convergence in codon usage and composition biases.
 - Nucleotide data are prone to reconstruction errors for large scale relationships (more time for convergence).

The conclusions

- ▶ Synonymous substitutions enable convergence in codon usage and composition biases.
 - Nucleotide data are prone to reconstruction errors for large scale relationships (more time for convergence).
 - We favour the hypothesis of a monophyletic "core" cyanobacteria clade sister to plastids (protein topology).

The conclusions

- ▶ Synonymous substitutions enable convergence in codon usage and composition biases.
 - Nucleotide data are prone to reconstruction errors for large scale relationships (more time for convergence).
 - We favour the hypothesis of a monophyletic "core" cyanobacteria clade sister to plastids (protein topology).
- ▶ But information potentially useful for small scale resolution is lost in translated / recoded data

The conclusions

- ▶ Synonymous substitutions enable convergence in codon usage and composition biases.
 - Nucleotide data are prone to reconstruction errors for large scale relationships (more time for convergence).
 - We favour the hypothesis of a monophyletic "core" cyanobacteria clade sister to plastids (protein topology).
- ▶ But information potentially useful for small scale resolution is lost in translated / recoded data
- ▶ The use of more advanced models could turn misleading signal into useful signal.

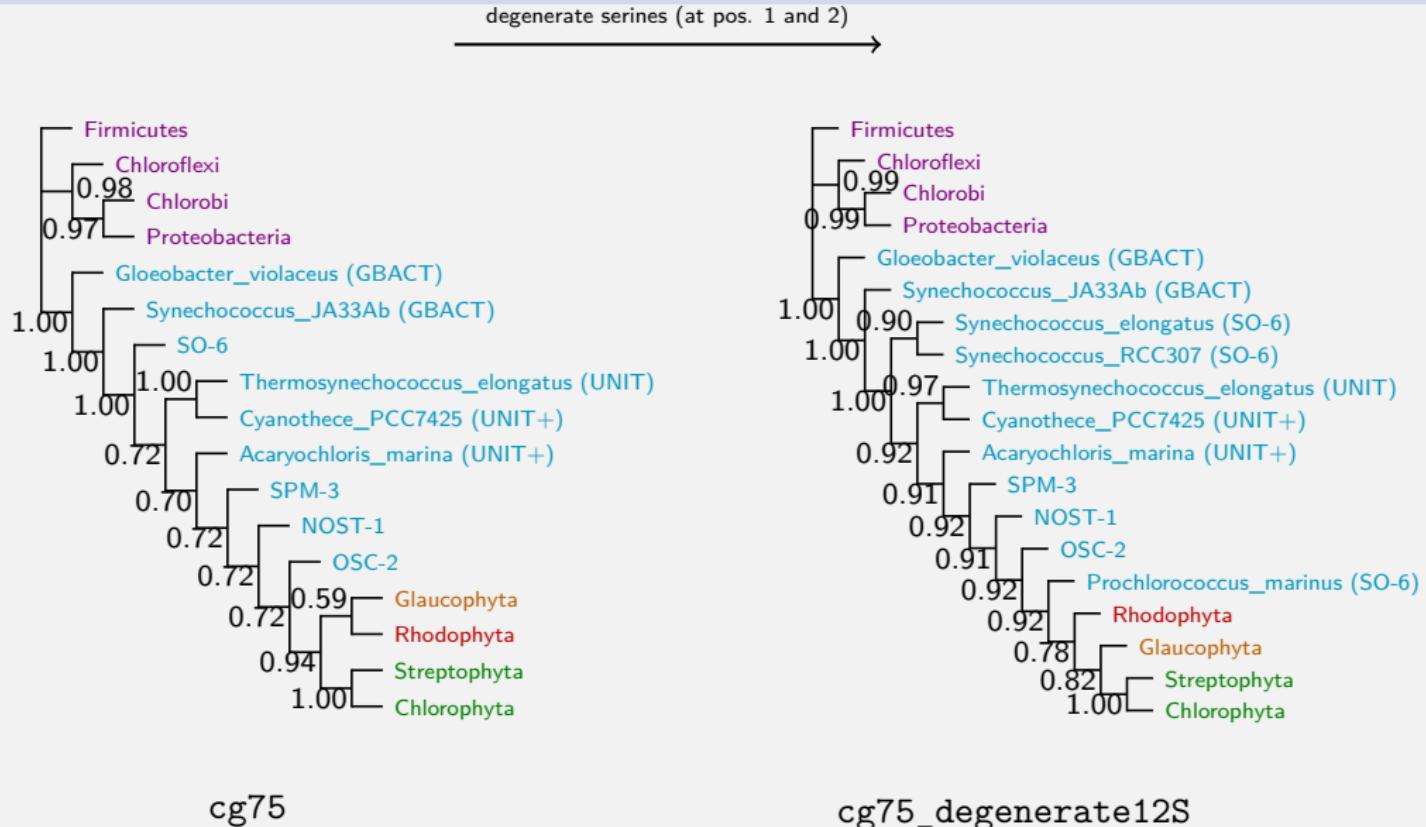
The conclusions

- ▶ Synonymous substitutions enable convergence in codon usage and composition biases.
 - Nucleotide data are prone to reconstruction errors for large scale relationships (more time for convergence).
 - We favour the hypothesis of a monophyletic "core" cyanobacteria clade sister to plastids (protein topology).
- ▶ But information potentially useful for small scale resolution is lost in translated / recoded data
- ▶ The use of more advanced models could turn misleading signal into useful signal.
 - Could we then get both large and small scale resolution using un-recoded nucleotide data?

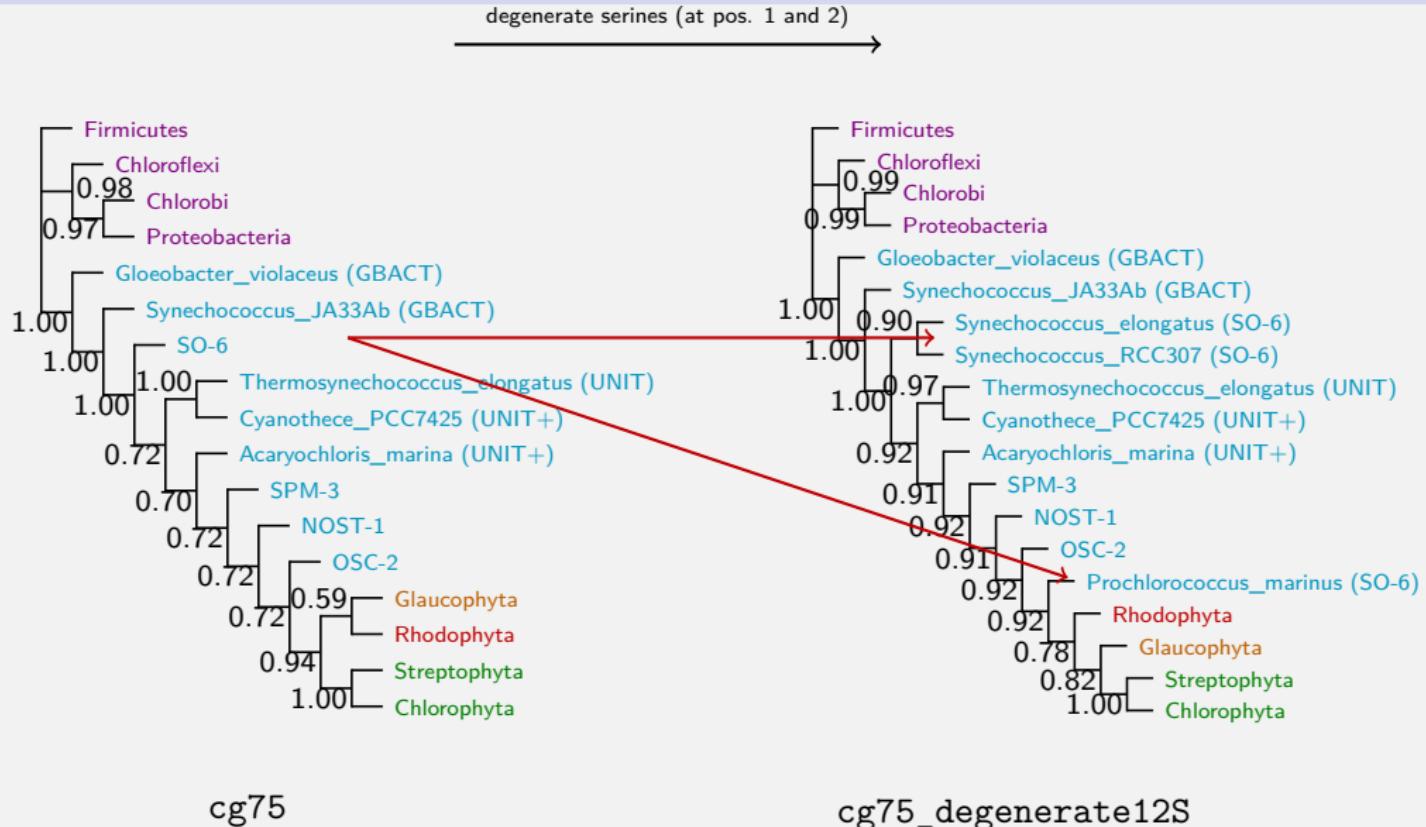
Thanks for your attention

- ▶ This work was supported by a Fundação para a Ciência e a Tecnologia (FCT, Portugal) grant to Cymon J. Cox, Centro de Ciencias do Mar (CCMAR) - CIMAR-Lab. Assoc., (PTDC/BIA-BCM/099565/2008).
- ▶ Contact: blaise.li@normalesup.org

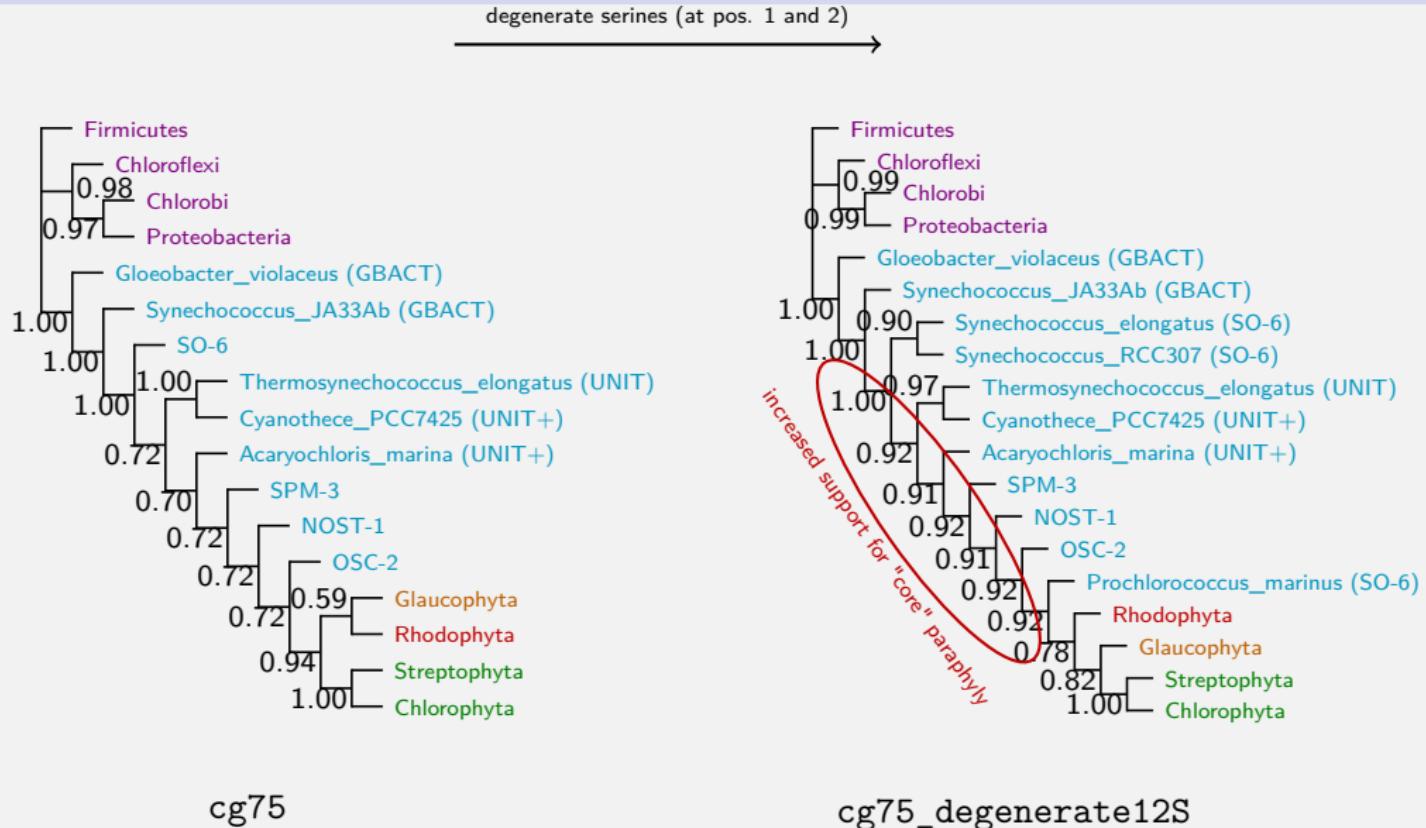
Effects of serine synonymous substitutions



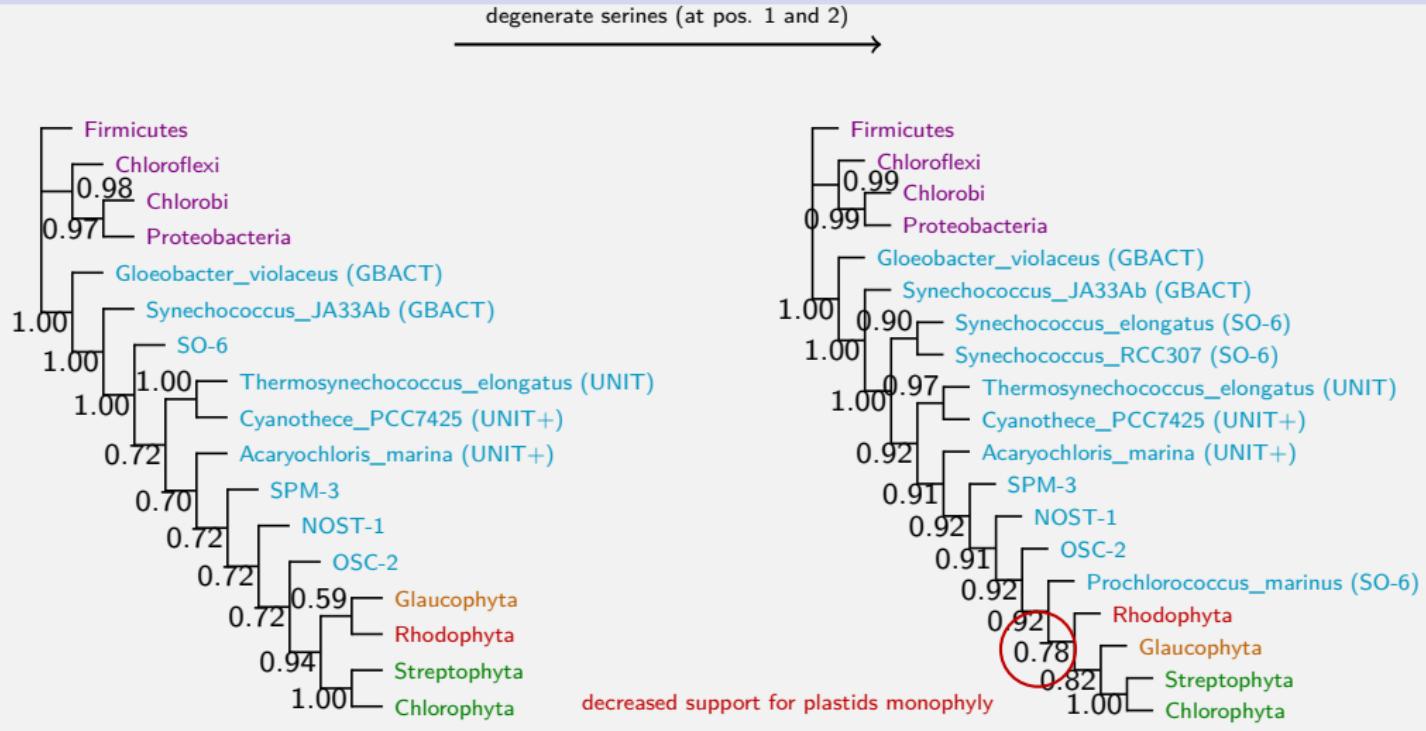
Effects of serine synonymous substitutions



Effects of serine synonymous substitutions



Effects of serine synonymous substitutions



cg75

cg75_degenerate12S

Effects of serine synonymous substitutions

- ▶ Serine signal:

Effects of serine synonymous substitutions

- ▶ Serine signal:
 - ▶ contributes to SO-6 and plastid monophyly

Effects of serine synonymous substitutions

- ▶ Serine signal:
 - ▶ contributes to SO-6 and plastid monophyly
 - ▶ decreases the support of "core" cyanobacteria paraphyly

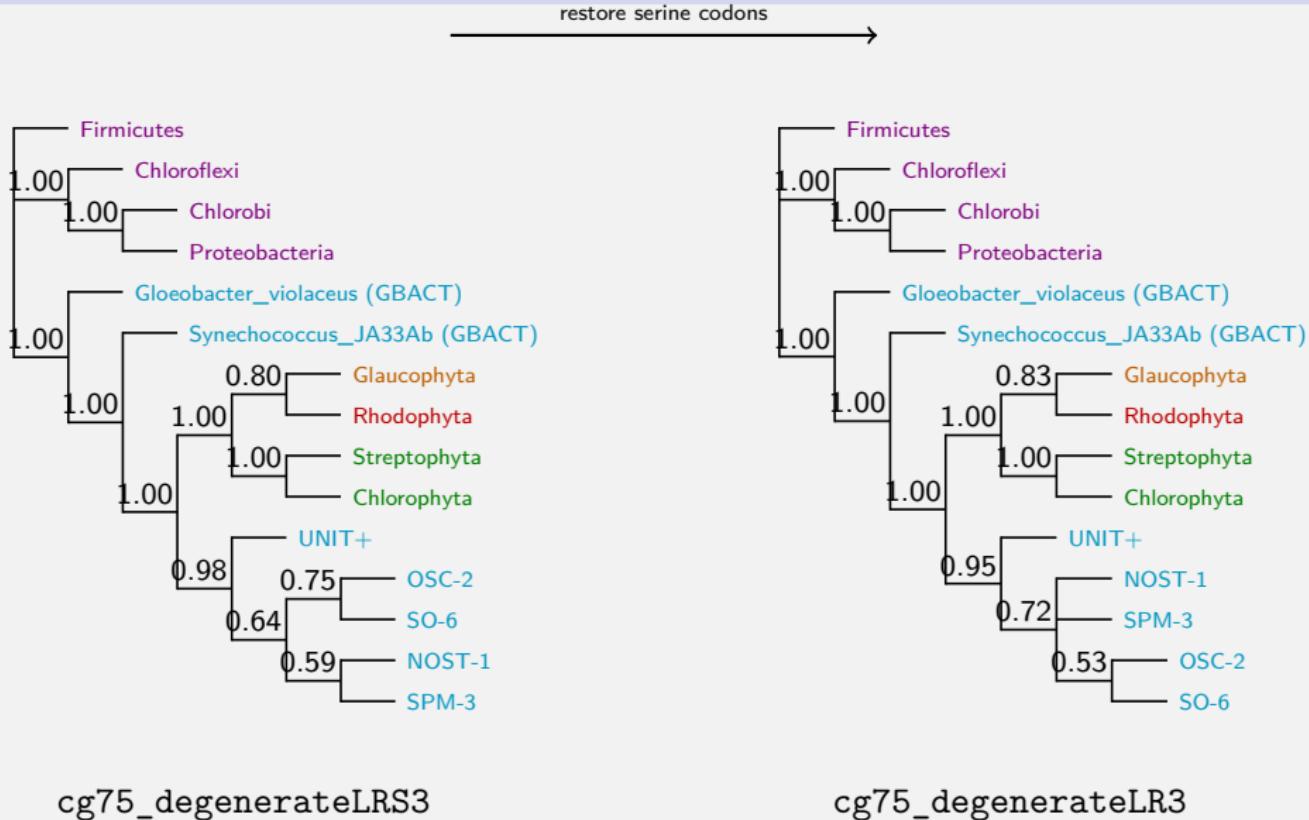
Effects of serine synonymous substitutions

- ▶ Serine signal:
 - ▶ contributes to SO-6 and plastid monophyly
 - ▶ decreases the support of "core" cyanobacteria paraphyly
- ▶ Serine signal is not present in translated datasets

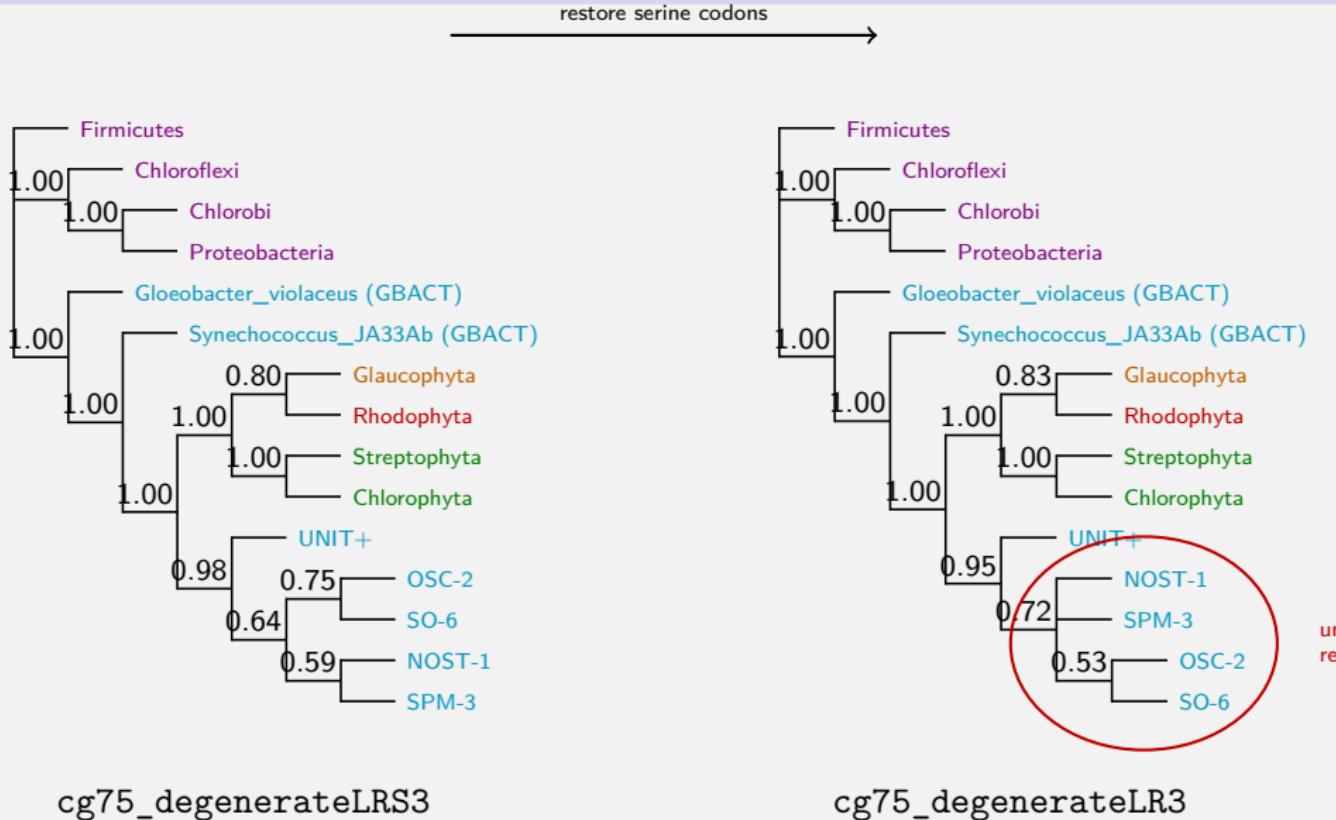
Effects of serine synonymous substitutions

- ▶ Serine signal:
 - ▶ contributes to SO-6 and plastid monophyly
 - ▶ decreases the support of "core" cyanobacteria paraphyly
- ▶ Serine signal is not present in translated datasets
- ▶ Maybe we should keep this signal in the nucleotide dataset?

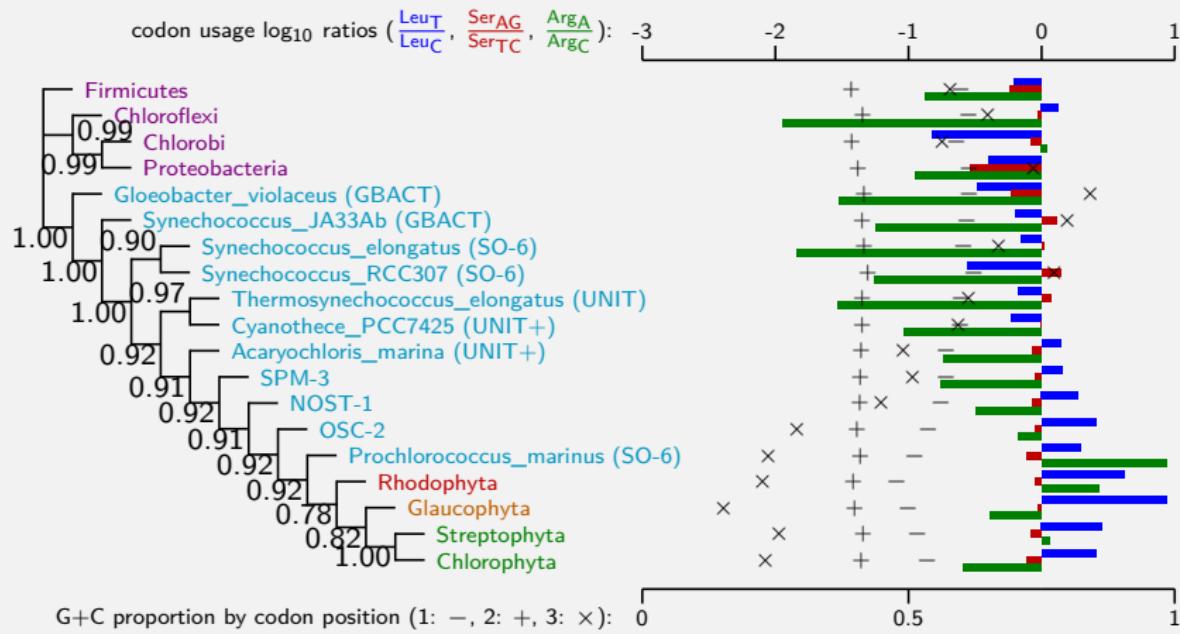
Effects of serine synonymous substitutions



Effects of serine synonymous substitutions

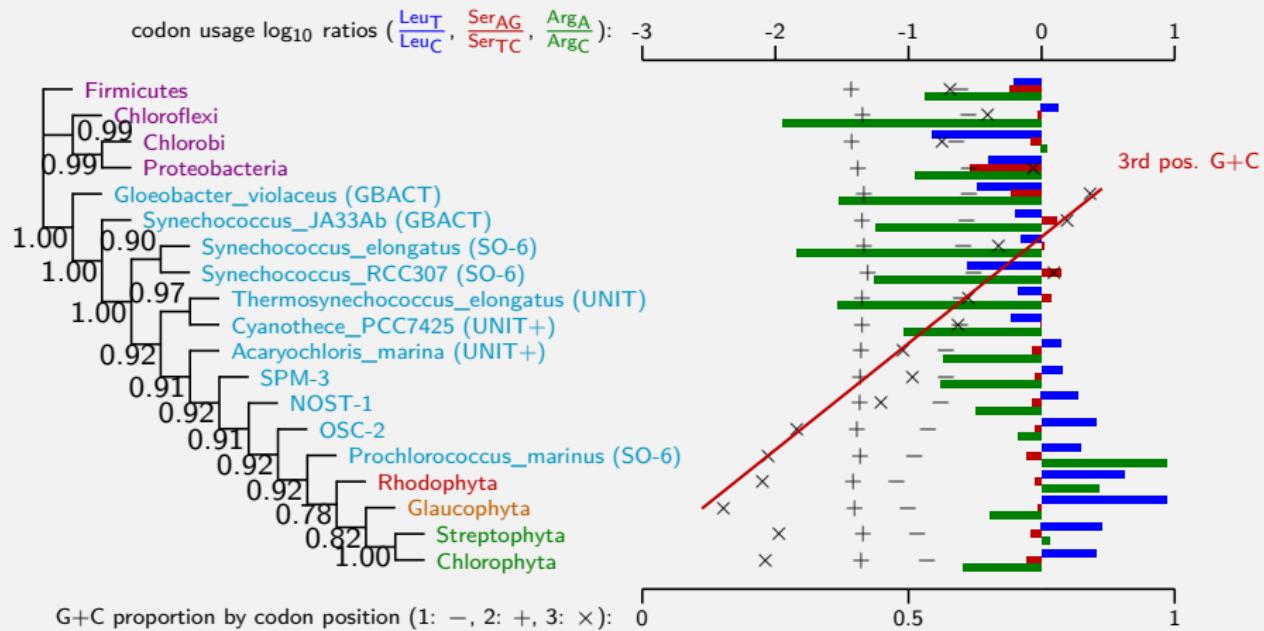


Effects of composition and codon usage

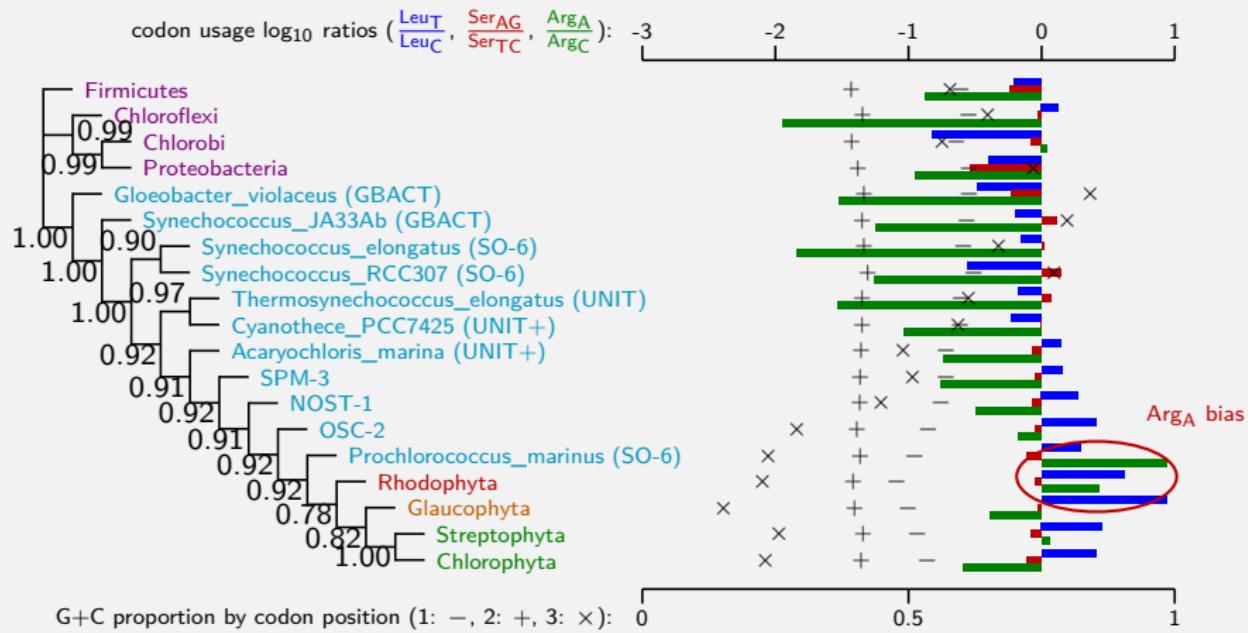


cg75_degenerate12S

Effects of composition and codon usage

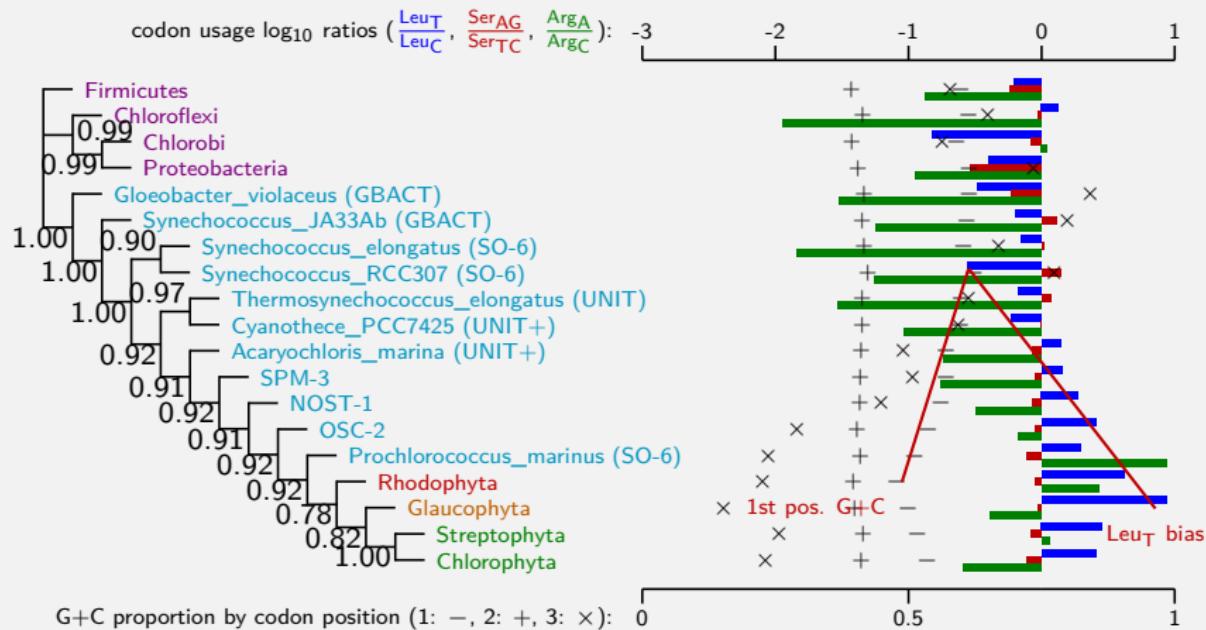


Effects of composition and codon usage



cg75_degenerate12S

Effects of composition and codon usage



cg75_degenerate12S