

Chemotaxonomy of *Arthrobacter* - possibilities and limits

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Genus *Arthrobacter*

described by Conn & Dimmick (1947)

including the type species *Arthrobacter globiformis*.

Genus description based on physiological and
morphological traits.

It is not surprising that *Arthrobacter* is very heterogeneous. Indeed, for decades this genus has been a dumping ground for a variety of strains as long as they were Gram-positive, aerobic, non-sporeforming organisms with a rod-coccus growth cycle and L-lysine as the characteristic diamino acid of the peptidoglycan; and more recently if just one recognized *Arthrobacter* species (but not the type species) was identified as the next relative.

***Arthrobacter* species described until 1995**

Arthrobacter aurescens

Arthrobacter citreus

Arthrobacter crystallopoietes

Arthrobacter histidinolovorans

Arthrobacter ilicis

Arthrobacter mysorens

Arthrobacter nicotianae

Arthrobacter oxydans

Arthrobacter pascens

Arthrobacter protophormiae

Arthrobacter polychromogenes

Arthrobacter ramosus

Arthrobacter sulfureus

Arthrobacter uratoxydans

Arthrobacter ureafaciens

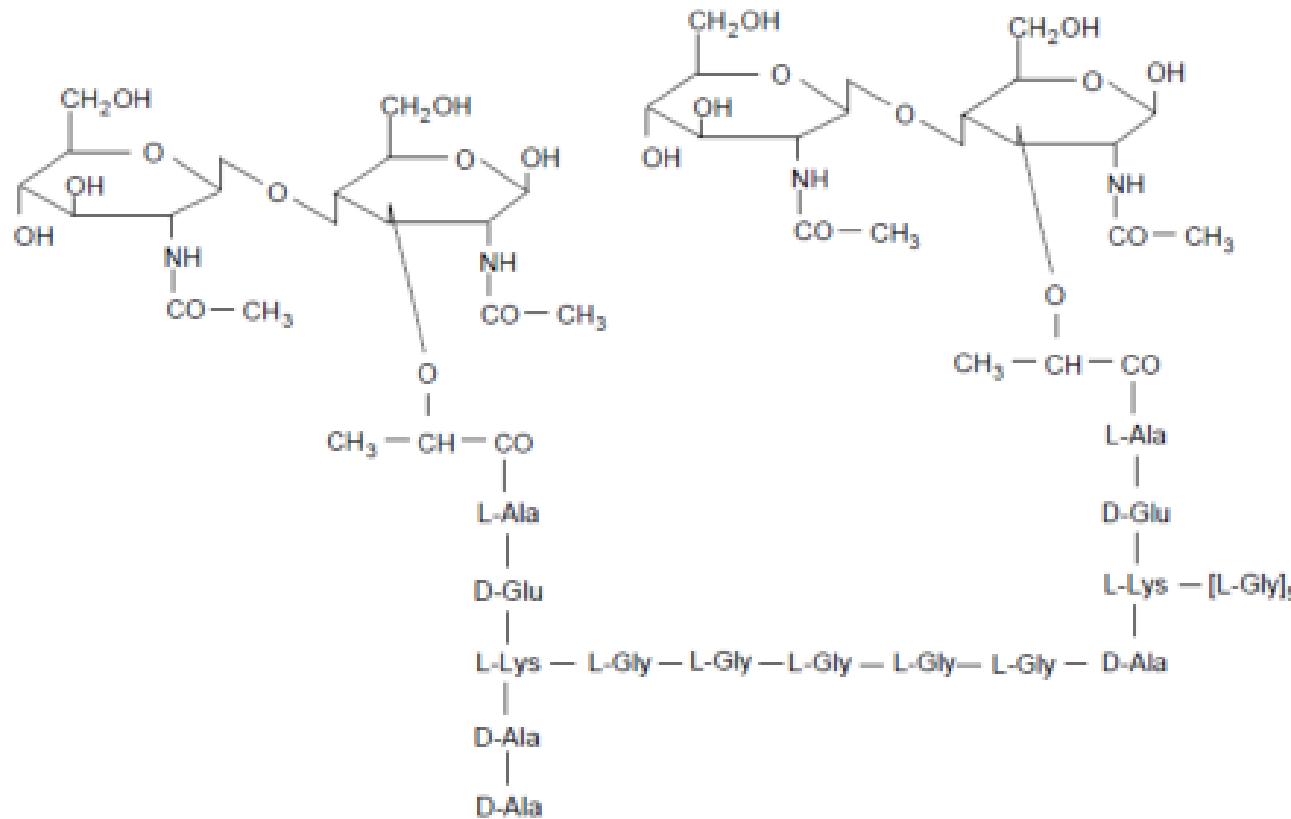
Classification of *Arthrobacter* species based on the quinone system and peptidoglycan type and presence of phosphatidylinositol (PI)

Stackebrandt *et al.* (1983), *Syst. Appl. Microbiol.* 4, 470–486. Keddie *et al.* (1986), Bergey's Manual 618-625

Group	Peptidoglycan type	Quinone system	PI	Species
“globiformis” group or <i>Arthrobacter globiformis/citreus</i> group	A3 α (Lys-Ala ₁₋₄ , Lys-Ser-Thr-Ala, Lys-Ala-Thr-Ala, Lys-Thr-Ala ₂ or Lys-Ser-Ala ₂₋₃)	Monosaturated menaquinone MK-9(H₂)	present	<i>A. histidinolovorans</i> , <i>A. aurescens</i> , <i>A. crystallopoietes</i> , <i>A. globiformis</i> , <i>A. oxydans</i> , <i>A. polychromogenes</i> , <i>A. pascens</i> , <i>A. ureafaciens</i> , <i>A. citreus</i> , <i>A. ramosus</i> , <i>A. ilicis</i> , <i>A. atrocyaneus</i>
“nicotianae” group or <i>Arthrobacter nicotianae</i> group	A4 α (Lys-Ala-Glu or Lys-Glu)	Completely unsaturated menaquinones MK-8 and/or 9	absent	<i>A. nicotianae</i> , <i>A. protophormiae</i> , <i>A. uratoxydans</i> , <i>A. sulfureus</i> , <i>A. mysorens</i>

Peptidoglycan Structure

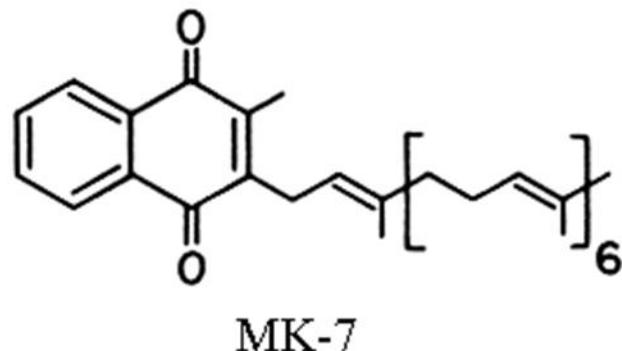
Staphylococcus aureus



Chemical structure of a menaquinone MK-7

Naphthalene ring system

Side chain (composed of 7 isoprenoic subunits



Menaquinone 7

Phylogeny of *Arthrobacter* species and their relationship to species of other genera based on 16S rRNA cataloguing

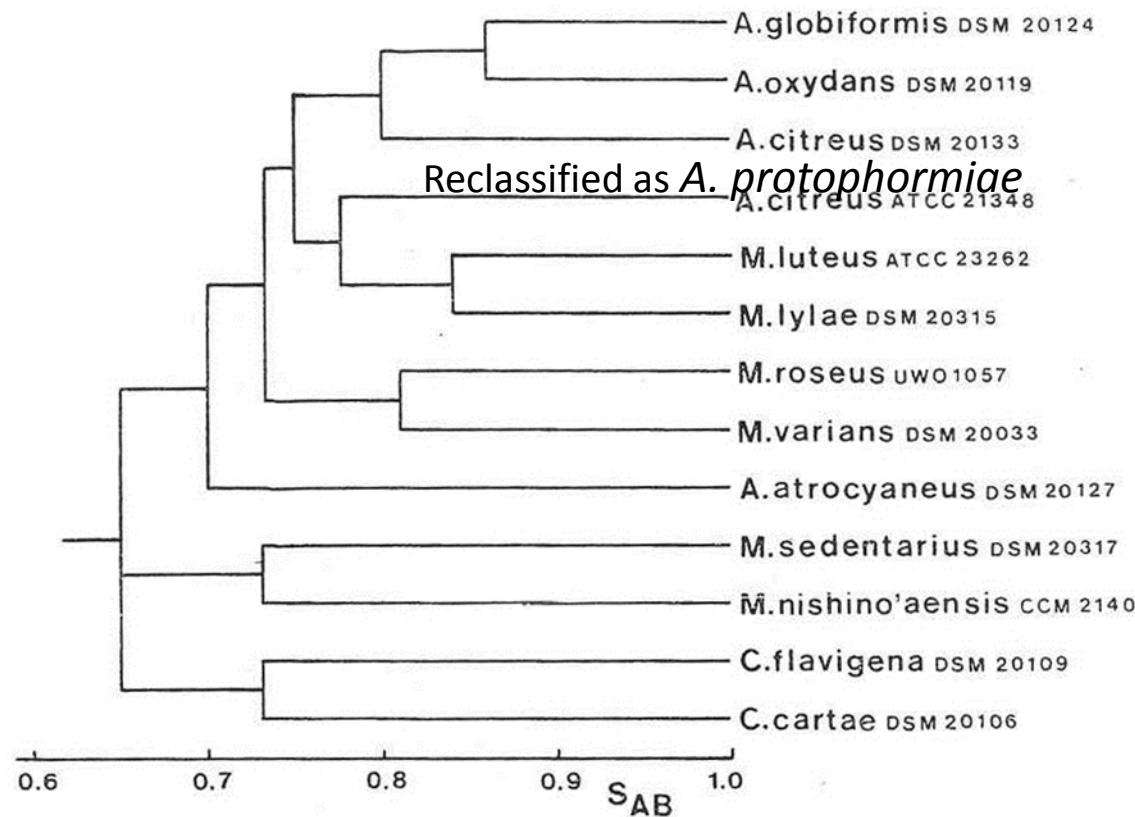


Fig. 1. Dendrogram of relationships, showing the phylogenetic position of *A. citreus* DSM 20133 and ATCC 21348.

Phylogeny of *Arthrobacter* species and their relationship to species of other genera based on 16S rRNA cataloguing

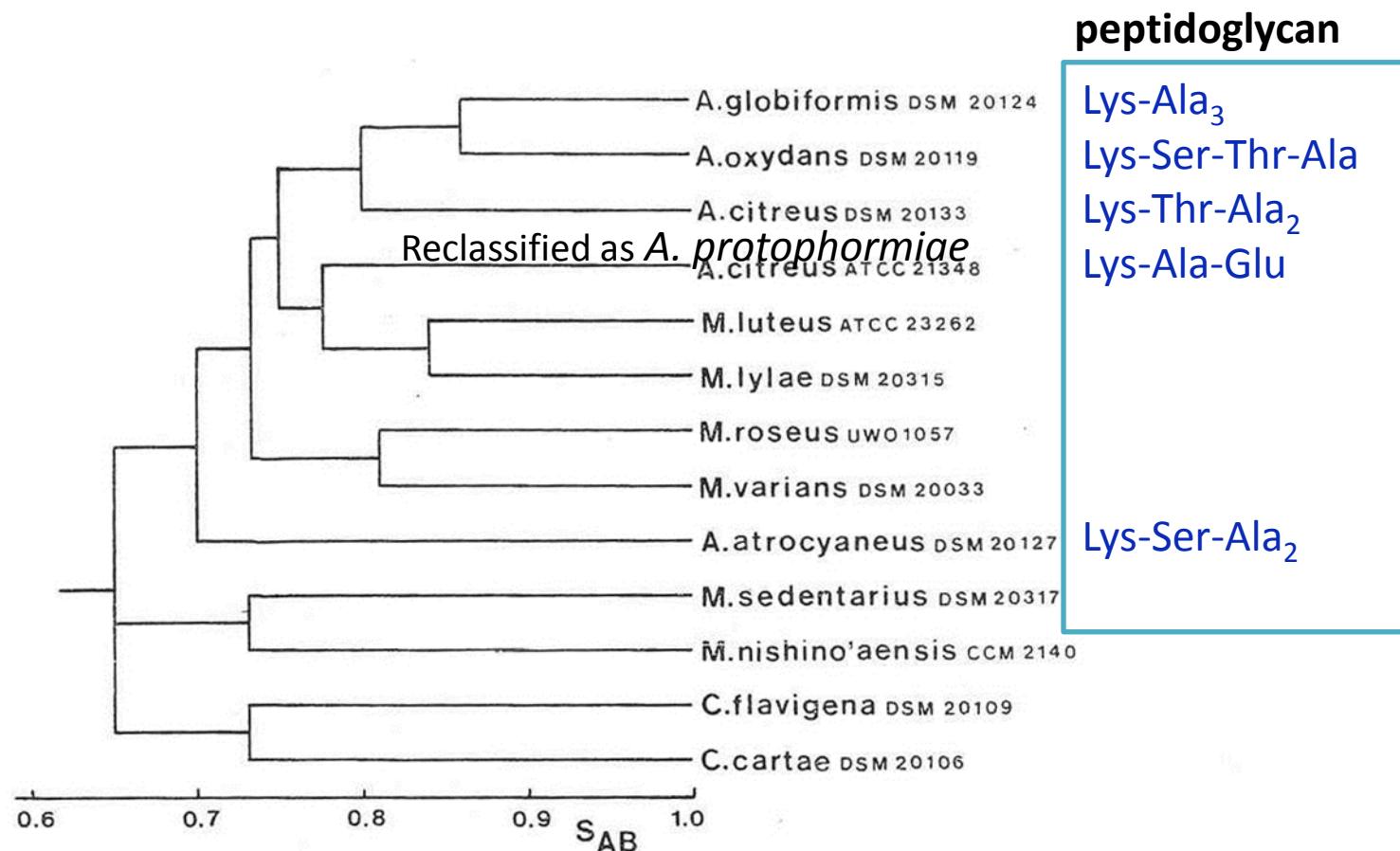


Fig. 1. Dendrogram of relationships, showing the phylogenetic position of *A. citreus* DSM 20133 and ATCC 21348.

Phylogeny of *Arthrobacter* species and their relationship to species of other genera based on 16S rRNA cataloguing

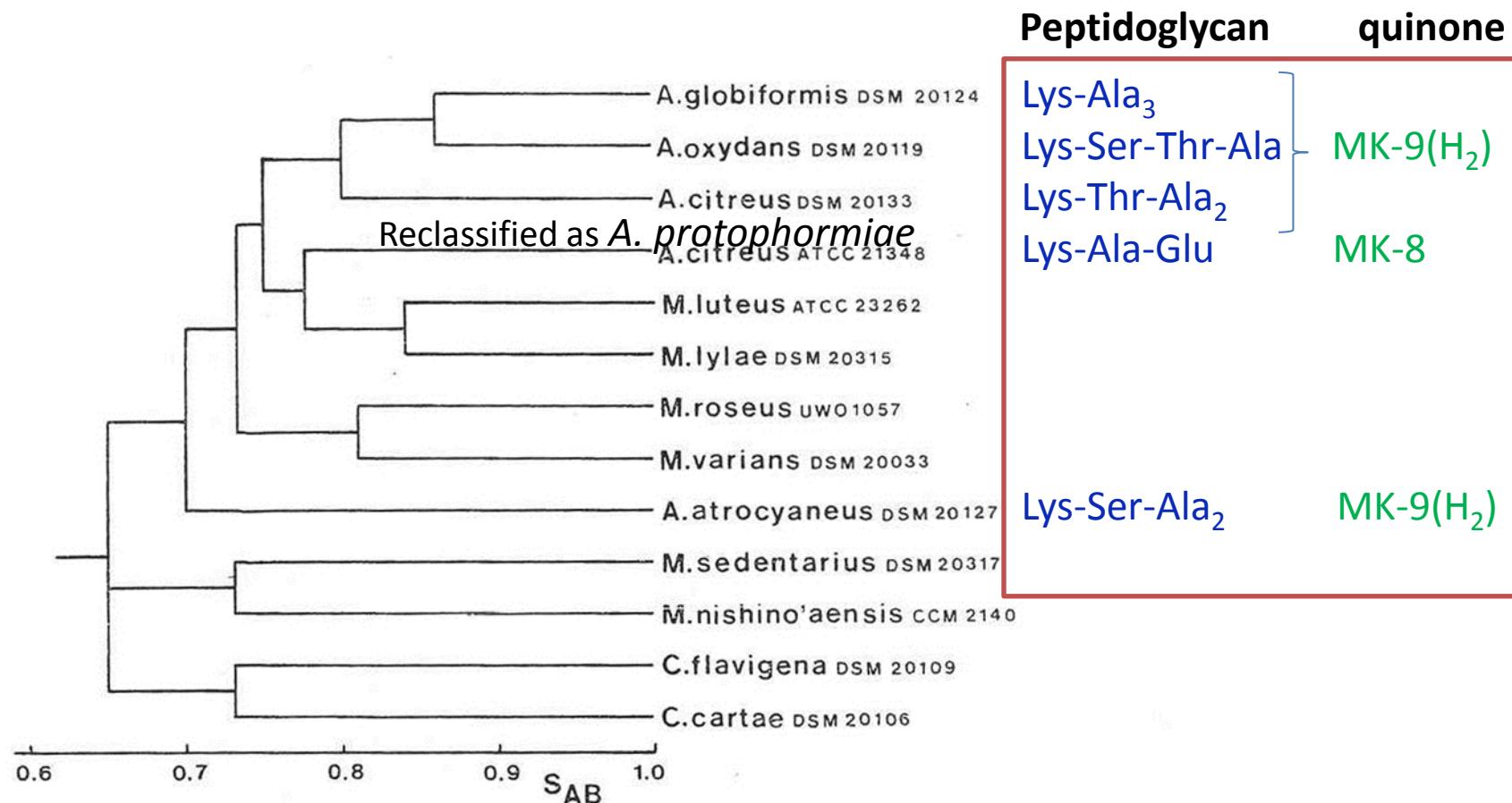
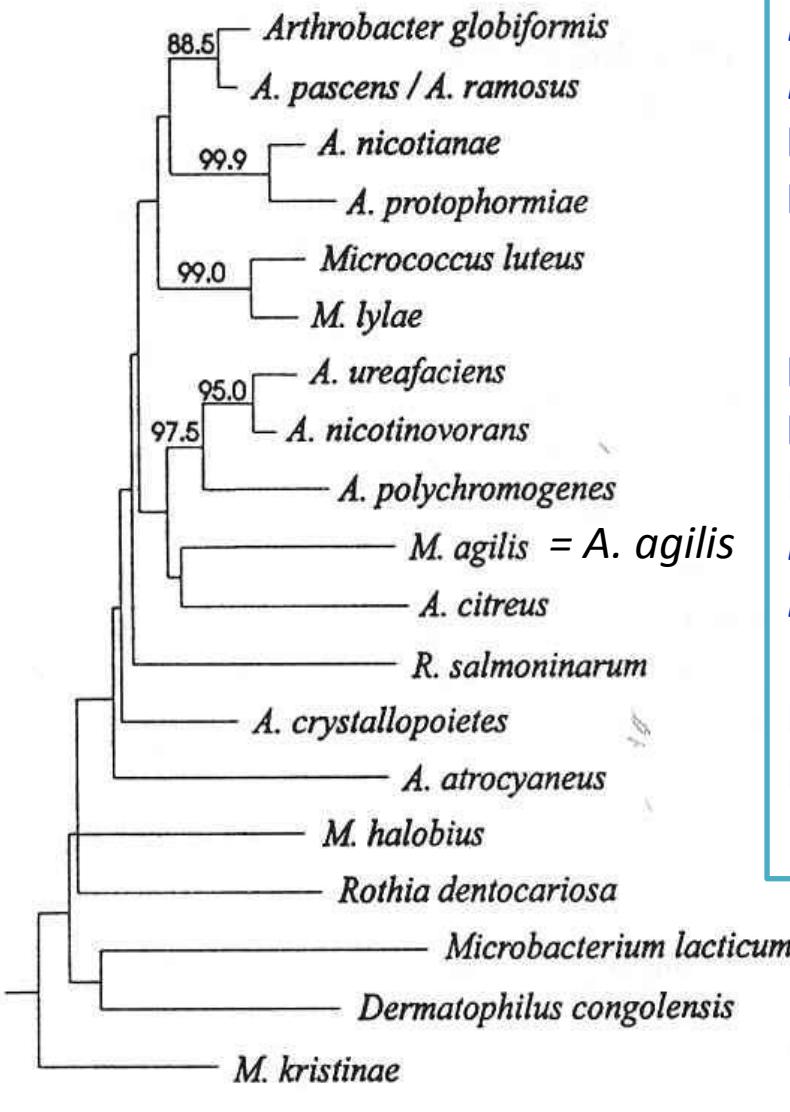


Fig. 1. Dendrogram of relationships, showing the phylogenetic position of *A. citreus* DSM 20133 and ATCC 21348.

Phylogeny of *Arthrobacter* species and their relationship to species of other genera based on 16S rRNA gene sequences



Lys-Ala₃
Lys-Ala₂
Lys-Ala-Glu
Lys-Ala-Glu

Lys-Ala-Thr-Ala
Lys-Ala-Thr-Ala
Lys-Ser-Thr-Ala
Lys-Thr-Ala₃
Lys-Thr-Ala₂

Lys-Ala
Lys-Ser-Ala₂

Peptidoglycan types of *Arthrobacter* species

Interpeptide bridge	Species
Lys-Ser-Thr-Ala	<i>A. oxydans</i> , <i>A. polychromogenes</i>
Lys-Ala-Thr-Ala	<i>A. aurescens</i> , <i>A. histidinolovorans</i> , <i>A. ilicis</i> , <i>A. nicotinovorans</i> , <i>A. ureafaciens</i>
Lys-Ala ₁₋₄	<i>A. crystallopoietes</i> , <i>A. globiformis</i> , <i>A.</i> <i>pascens</i> , <i>A. ramosus</i>
Lys-Ser-Ala ₂₋₃	<i>A. atrocyaneus</i>
Lys-Thr-Ala ₂	<i>A. citreus</i>
Lys-Ala-Glu	<i>A. nicotianae</i> , <i>A. creatinolyticus</i> , <i>A.</i> <i>uratoxydans</i> , <i>A. protophormiae</i>
Lys-Glu	<i>A. sulfureus</i>

Peptidoglycan types of *Arthrobacter* species and quinone systems

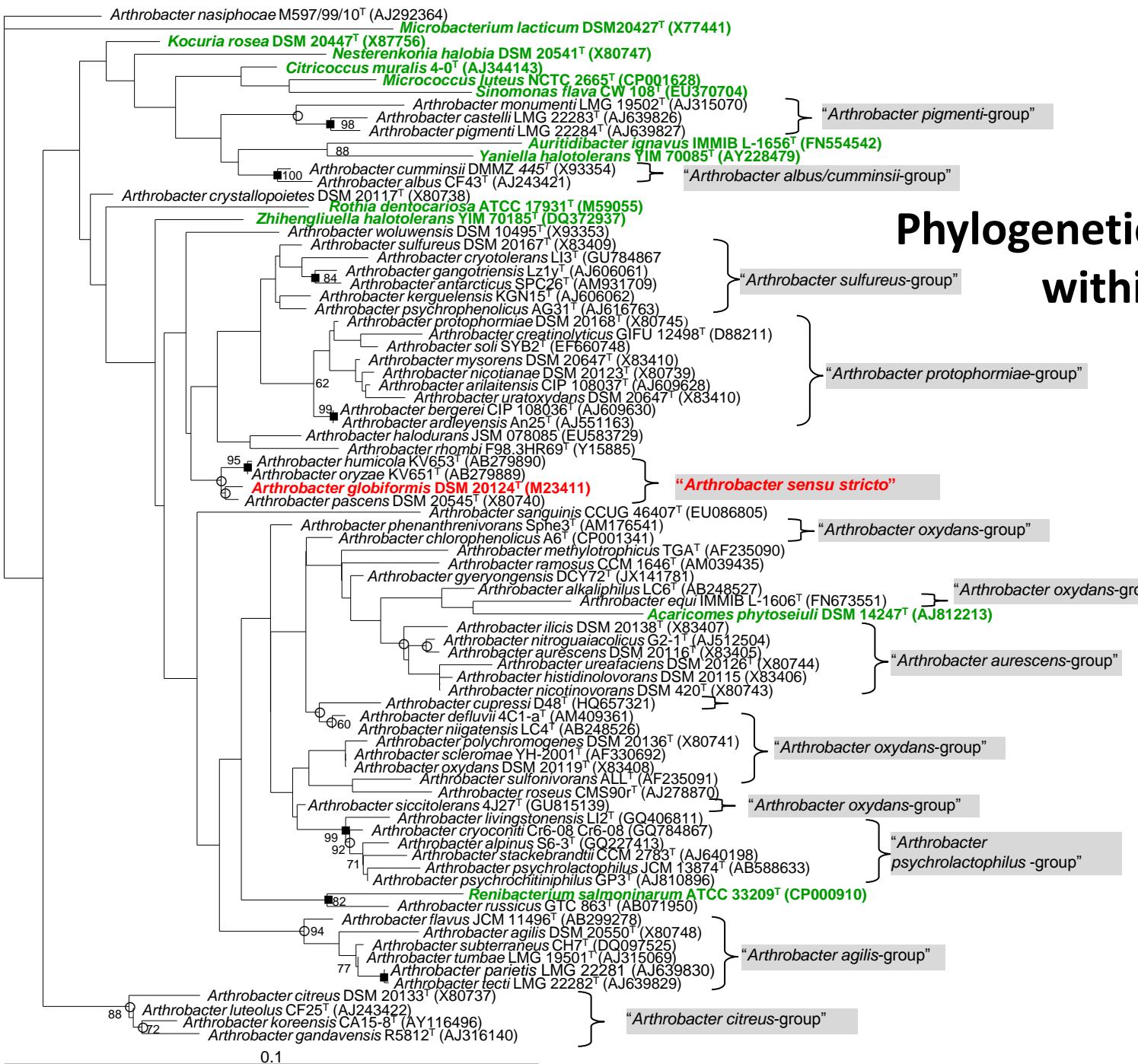
Interpeptide bridge	Species	Quinone system
Lys-Ser-Thr-Ala	<i>A. oxydans</i> , <i>A. polychromogenes</i>	MK-9(H ₂)
Lys-Ala-Thr-Ala	<i>A. aurescens</i> , <i>A. histidinolovorans</i> , <i>A. ilicis</i> , <i>A. nicotinovorans</i> , <i>A. ureafaciens</i>	MK-9(H ₂)
Lys-Ala ₁₋₄	<i>A. crystallopoietes</i> , <i>A. globiformis</i> , <i>A. pascens</i> , <i>A. ramosus</i>	MK-9(H ₂)
Lys-Ser-Ala ₂₋₃	<i>A. atrocyaneus</i>	MK-9(H ₂)
Lys-Thr-Ala ₂	<i>A. citreus</i>	MK-9(H ₂)
Lys-Ala-Glu	<i>A. nicotianae</i> , <i>A. creatinolyticus</i> , <i>A. uratoxydans</i> , <i>A. protophormiae</i>	MK-8
Lys-Glu	<i>A. sulfureus</i>	MK-9

Peptidoglycan types of *Arthrobacter* species and quinone systems and presence of phosphatidylinositol (PI)

Interpeptide bridge	Species	Quinone system	PI present
Lys-Ser-Thr-Ala	<i>A. oxydans</i> , <i>A. polychromogenes</i>	MK-9(H ₂)	+
Lys-Ala-Thr-Ala	<i>A. aurescens</i> , <i>A. histidinolovorans</i> , <i>A. ilicis</i> , <i>A. nicotinovorans</i> , <i>A. ureafaciens</i>	MK-9(H ₂)	+
Lys-Ala ₁₋₄	<i>A. crystallopoietes</i> , <i>A. globiformis</i> , <i>A. pascens</i> , <i>A. ramosus</i>	MK-9(H ₂)	+
Lys-Ser-Ala ₂₋₃	<i>A. atrocyaneus</i>	MK-9(H ₂)	+
Lys-Thr-Ala ₂	<i>A. citreus</i>	MK-9(H ₂)	+
Lys-Ala-Glu	<i>A. nicotianae</i> , <i>A. creatinolyticus</i> , <i>A. uratoxydans</i> , <i>A. protophormiae</i>	MK-8	-
Lys-Glu	<i>A. sulfureus</i>	MK-9	-

Phylogenetic relationships within the genus *Arthrobacter*

(Busse et al. 2012)



Peptidoglycan types and Quinone systems within *Arthrobacter* species (2015)

Lys-Ser-Thr-Ala

Lys-Ala-Thr-Ala Lys-Ala₁₋₄

Lys-Ser-Ala₂₋₃

Lys-Thr-Ala₂

Lys-Ala₂-Gly₂₋₃-Ala(Gly)

Lys-Ala-Gly

Lys-Ala-Glu

Lys-Glu

Lys-Ser-Glu

Lys-Asp

MK-8(H₂)

MK-9(H₂)

MK-8(H₂), MK-9(H₂)

MK-8

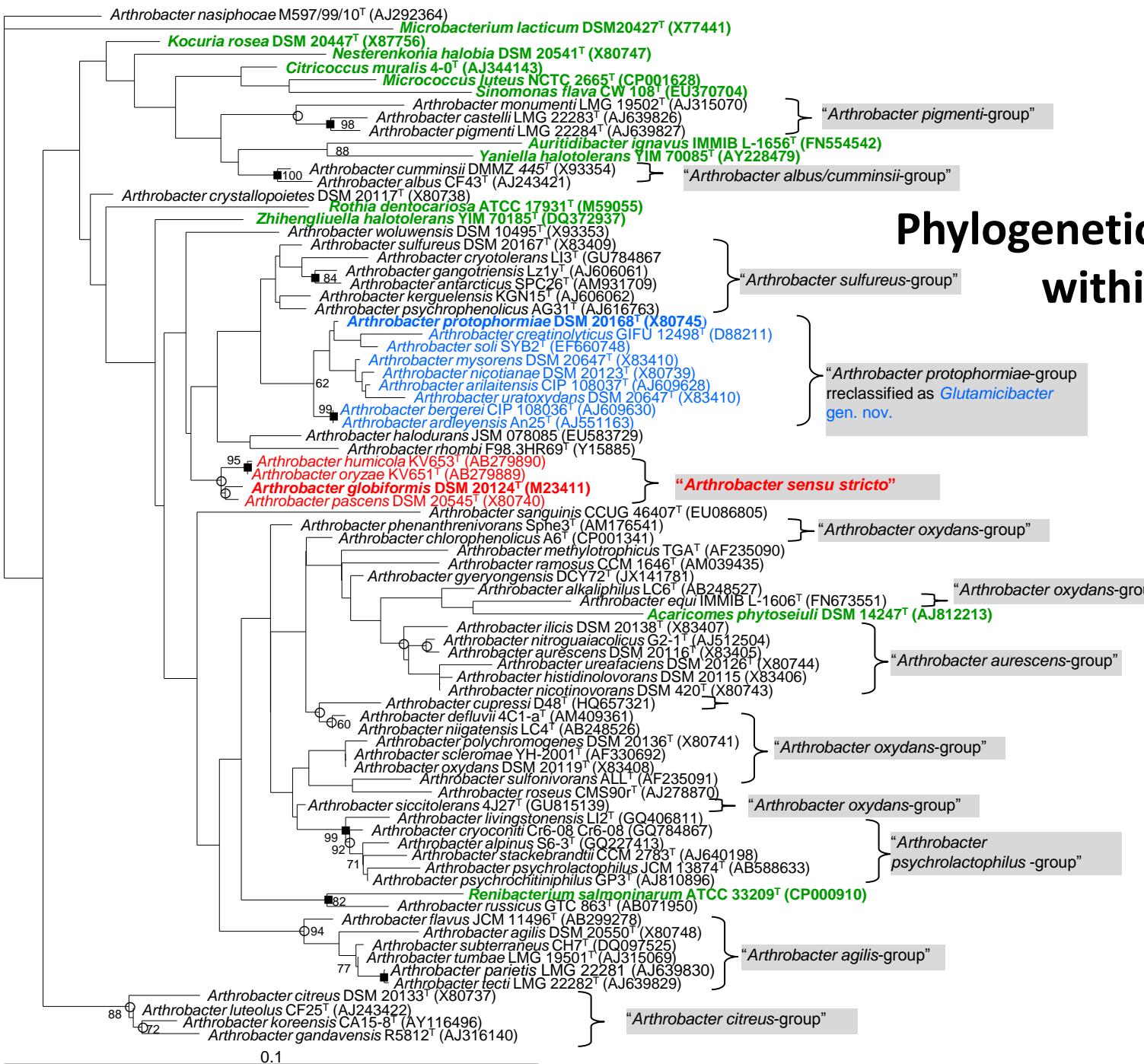
MK-9

Reclassification of *Arthrobacter* species

Based on phylogenetic evidence, **absence of phosphatidylinositol** and **presence of dimannosylglyceride** in the polar lipid profile, quinone system **MK-8 and/or MK-9** and peptidoglycan type **Lys-Ala-Glu** nine species namely *A. protophormiae*, *A. creatinolyticus*, *A. soli*, *A. mysorens*, *A. nicotianae*, *A. arilaitensis*, *A. uratoxidans*, *A. bergerei* and *A. ardleyensis* were reclassified in the genus ***Glutamicibacter***.

Phylogenetic relationships within the genus *Arthrobacter*

(Busse et al. 2012)

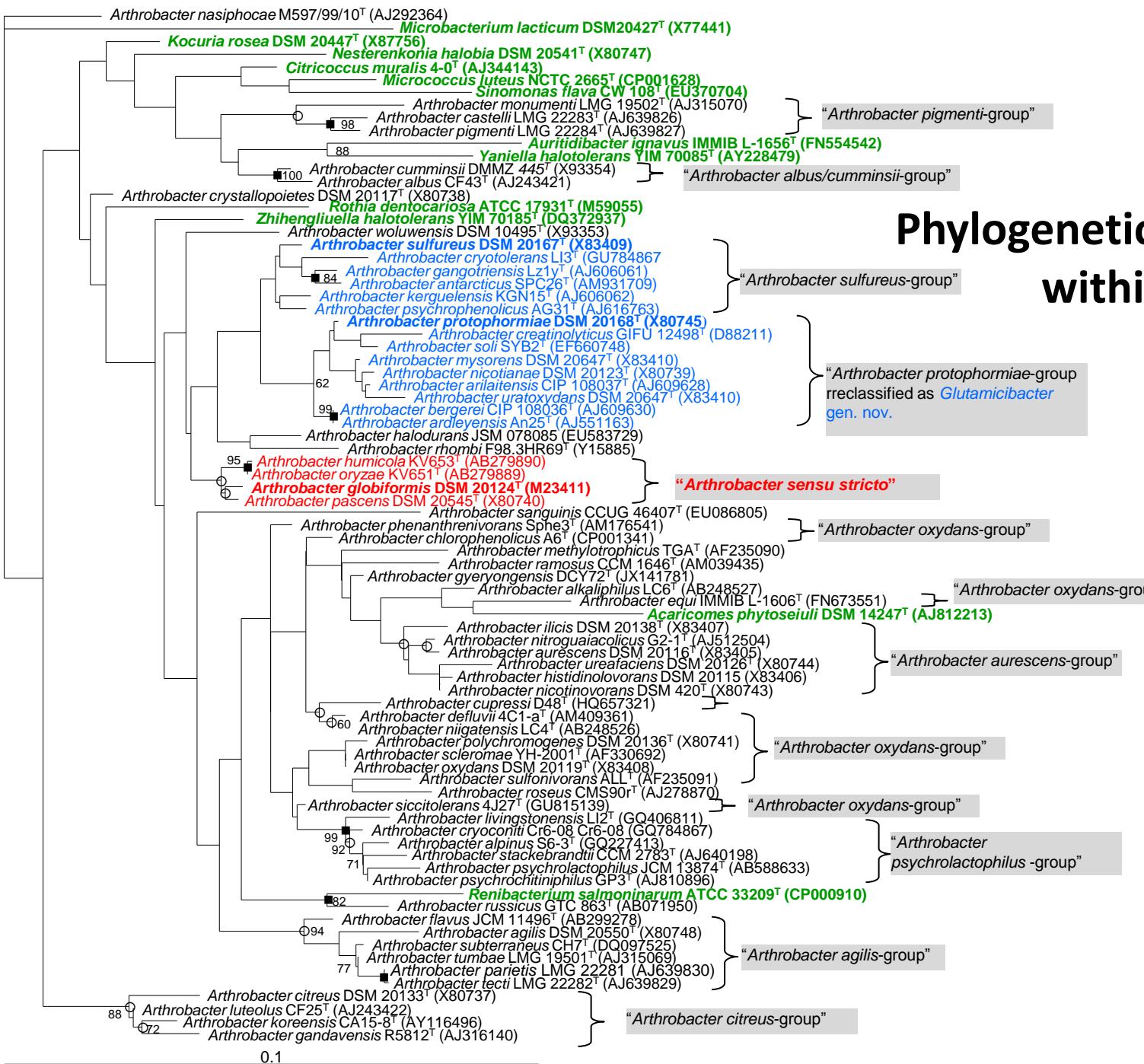


Reclassification of *Arthrobacter* species

Based on phylogenetic evidence, **absence of phosphatidylinositol** and **presence of digalactosyldiacylglycerol** in the polar lipid profile, quinone system **MK-9 and/or MK-10** and peptidoglycan type **Lys-Glu** six species namely *A. sulfureus*, *A. cryotolerans*, *A. gangotriensis*, *A. antarcticus*, *A. kerguelensis* and *A. psychrophenolicus* were reclassified in the genus ***Paeniglutamicibacter***.

Phylogenetic relationships within the genus *Arthrobacter*

(Busse et al. 2012)



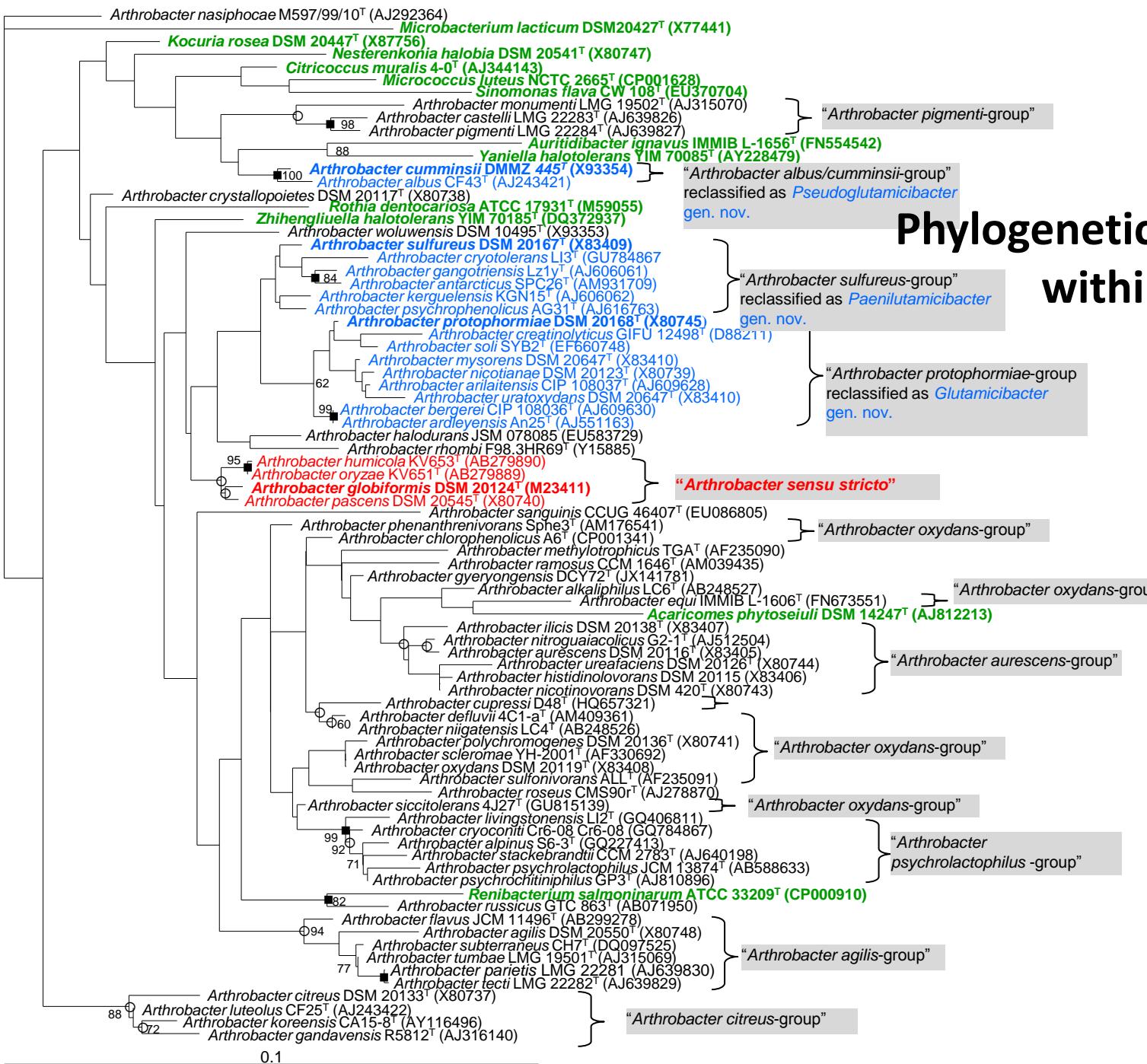
Reclassification of *Arthrobacter* species

Based on phylogenetic evidence, **complex polar lipid profile**, quinone system **MK-8(H₂)** and similar peptidoglycan type (**Lys-Ala-Glu** or **Lys-Ser-Glu**) two species namely *A. cumminsii* and *A. albus* were reclassified in the genus

***Pseudoglutamicibacter*.**

Phylogenetic relationships within the genus *Arthrobacter*

(Busse et al. 2012)

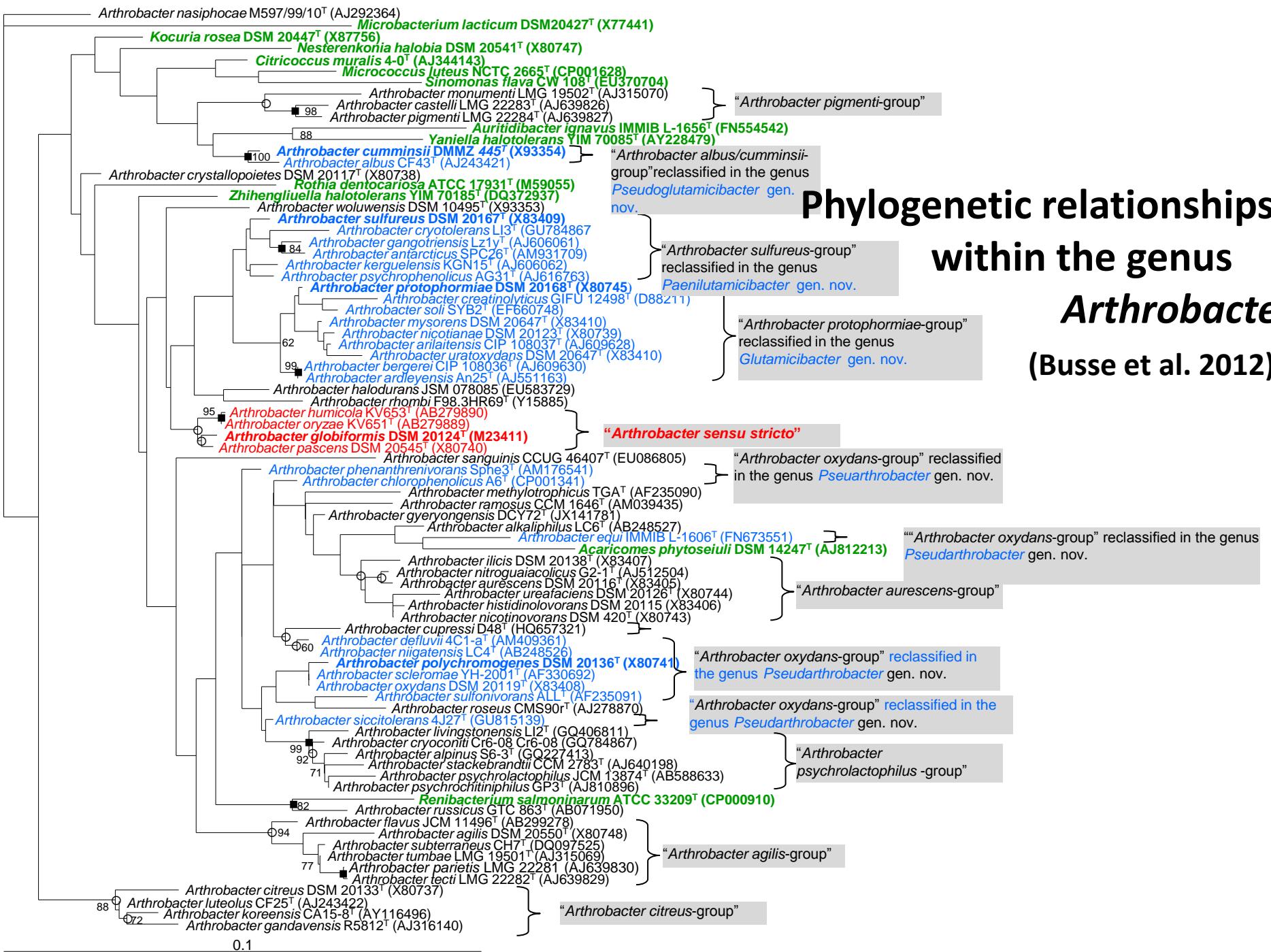


Reclassification of *Arthrobacter* species

Based on 16S rRNA gene sequence similarities and unique peptidoglycan type **Lys-Ser-Thr-Ala** ten species namely *A. polychromogenes*, *A. chlorophenolicus*, *A. defluvii*, *A. equi*, *A. niigatensis*, *A. oxydans*, *A. phenantrenivorans*, *A. scleromae*, *A. siccitolerans* and *A. sulfonivorans* were reclassified in the genus ***Pseudarthrobacter***.

Phylogenetic relationships within the genus *Arthrobacter*

(Busse et al. 2012)



Reclassification of *Arthrobacter* species

Based on phylogenetic evidence and unique peptidoglycan type **Lys-Ala-Thr-Ala** six species namely *A. aurescens*, *A. histinolovorans*, *A. ilicis*, *A. nicotinovorans*, *A. nitroguajacolicus* and *A. ureafaciens* were reclassified in the genus ***Paenarthrobacter***.

Arthrobacter nasiphocae M597/99/10^T (AJ292364)

Microbacterium lacticum DSM20427^T (X77441)

Kocuria rosea DSM 20447^T (X87756)

Nesterenkonia halobia DSM 20541^T (X80747)

Citricoccus muralis 4-0^T (AJ344143)

Micrococcus luteus NCTC 2665^T (CP001628)

Sinomonas flava CW 108^T (EU370704)

Arthrobacter monumenti LMG 19502^T (AJ315070)

Arthrobacter castelli LMG 22283^T (AJ639826)

Arthrobacter pigmenti LMG 22284^T (AJ639827)

Auritidibacter ignavus IMMB L-1656^T (FN554542)

Yanilla halotolerans YIM 70085^T (AY228479)

Arthrobacter cumminsii DMMZ 445^T (X93354)

Arthrobacter albus CF43^T (AJ243421)

Arthrobacter crystallopoietes DSM 20117^T (X80738)

Rothia dentocariosa ATCC 17931^T (M59055)

Zhihengliuella halotolerans YIM 70185^T (DQ372937)

Arthrobacter woluwensis DSM 10495^T (X93353)

Arthrobacter sulfureus DSM 20167^T (X83409)

Arthrobacter cryotolerans LJ3^T (GU784867)

Arthrobacter gangotriensis Lz1^T (AJ606061)

Arthrobacter antarcticus SPC26^T (AM931709)

Arthrobacter keruguenensis KGN15^T (AJ606062)

Arthrobacter psychrophenolicus AG31^T (AJ616763)

Arthrobacter protophormiae DSM 20168^T (X80745)

Arthrobacter creatinolyticus Gifu 12498^T (D88211)

Arthrobacter soli SYB2^T (EF660748)

Arthrobacter mysorensis DSM 20647^T (X83410)

Arthrobacter nicotianae DSM 20123^T (X80739)

Arthrobacter arilaitensis CIP 108037^T (AJ609628)

Arthrobacter uratoxydans DSM 20647^T (X83410)

Arthrobacter bergeriei CIP 108036^T (AJ609630)

Arthrobacter ardleyensis An25^T (AJ551163)

Arthrobacter halodurans JSM 078085 (EU583729)

Arthrobacter rhombi F98.3HR69^T (Y15885)

Arthrobacter humicola KV653^T (AB279890)

Arthrobacter oryzae KV651^T (AB279889)

Arthrobacter globiformis DSM 20124^T (M23411)

Arthrobacter pascens DSM 20545^T (X80740)

Arthrobacter sanguinis CCUG 46407^T (EU086805)

Arthrobacter phenanthrenivorans Sphe3^T (AM176541)

Arthrobacter chlorophenolicus A6^T (CP001341)

Arthrobacter methylotrophicus TGAT (AF235090)

Arthrobacter ramosus CCM 1646^T (AM039435)

Arthrobacter gyerongensis DCY72^T (JX141781)

Arthrobacter alkaliphilus LC6^T (AB248527)

Arthrobacter equi IMMB L-1606^T (FN673551)

Acaricomes phytoseiuli DSM 14247^T (AJ812213)

Arthrobacter ilicis DSM 20381^T (X83407)

Arthrobacter nitroguaiacolicus G2-1^T (AJ512504)

Arthrobacter aurescens DSM 20116^T (X83405)

Arthrobacter ureafaciens DSM 20126^T (X80744)

Arthrobacter histidinolovorans DSM 20115 (X83406)

Arthrobacter nicotinovorans DSM 420^T (X80743)

Arthrobacter cupressi D48^T (HQ657321)

Arthrobacter defluvii 4C1-a^T (AM409361)

Arthrobacter niigatensis LC4^T (AB248526)

Arthrobacter polychromogenes DSM 20136^T (X80741)

Arthrobacter scleromae YH-2001^T (AF330692)

Arthrobacter oxydans DSM 20119^T (X83408)

Arthrobacter sulfonivorans ALL^T (AF235091)

Arthrobacter roseus CMS90^T (AJ278870)

Arthrobacter siccitolerans 4J2^T (GU815139)

Arthrobacter livingstonensis Li2^T (GQ406811)

Arthrobacter cryocornis Cr6-08 Cr6-08 (GQ784867)

Arthrobacter alpinus S6-3^T (GQ227413)

Arthrobacter stackebrandtii CCM 2783^T (AJ640198)

Arthrobacter psychrolactophilus JCM 13874^T (AB588633)

Arthrobacter psychrochitiniphilus GP3^T (AJ810896)

Renibacterium salmoninarum ATCC 33209^T (CP000910)

Arthrobacter russicus GTC 863^T (AB071950)

Arthrobacter flavus JCM 11496^T (AB299278)

Arthrobacter agilis DSM 20550^T (X80748)

Arthrobacter subterraneus CH7^T (DQ097525)

Arthrobacter umbrae LMG 19501^T (AJ315069)

Arthrobacter parietis LMG 22281 (AJ639830)

Arthrobacter tecti LMG 22282^T (AJ639829)

Arthrobacter citreus DSM 20133^T (X80737)

Arthrobacter luteolus CF25^T (AJ243422)

Arthrobacter koreensis CA15-8^T (AY116496)

Arthrobacter gandavensis R5812^T (AJ316140)

"Arthrobacter citreus-group"

"Arthrobacter agilis-group"

"Arthrobacter parietis-group"

"Arthrobacter tecti-group"

"Arthrobacter russicus-group"

"Arthrobacter livingstonensis-group"

"Arthrobacter cryocornis-group"

"Arthrobacter alpinus-group"

"Arthrobacter stackebrandtii-group"

"Arthrobacter psychrolactophilus-group"

"Arthrobacter histidinolovorans-group"

"Arthrobacter oxydans-group"

"Arthrobacter protophormiae-group"

"Arthrobacter sulfureus-group"

"Arthrobacter albus/cumminsii-group"

"Arthrobacter pigmenti-group"

Phylogenetic relationships within the genus *Arthrobacter*

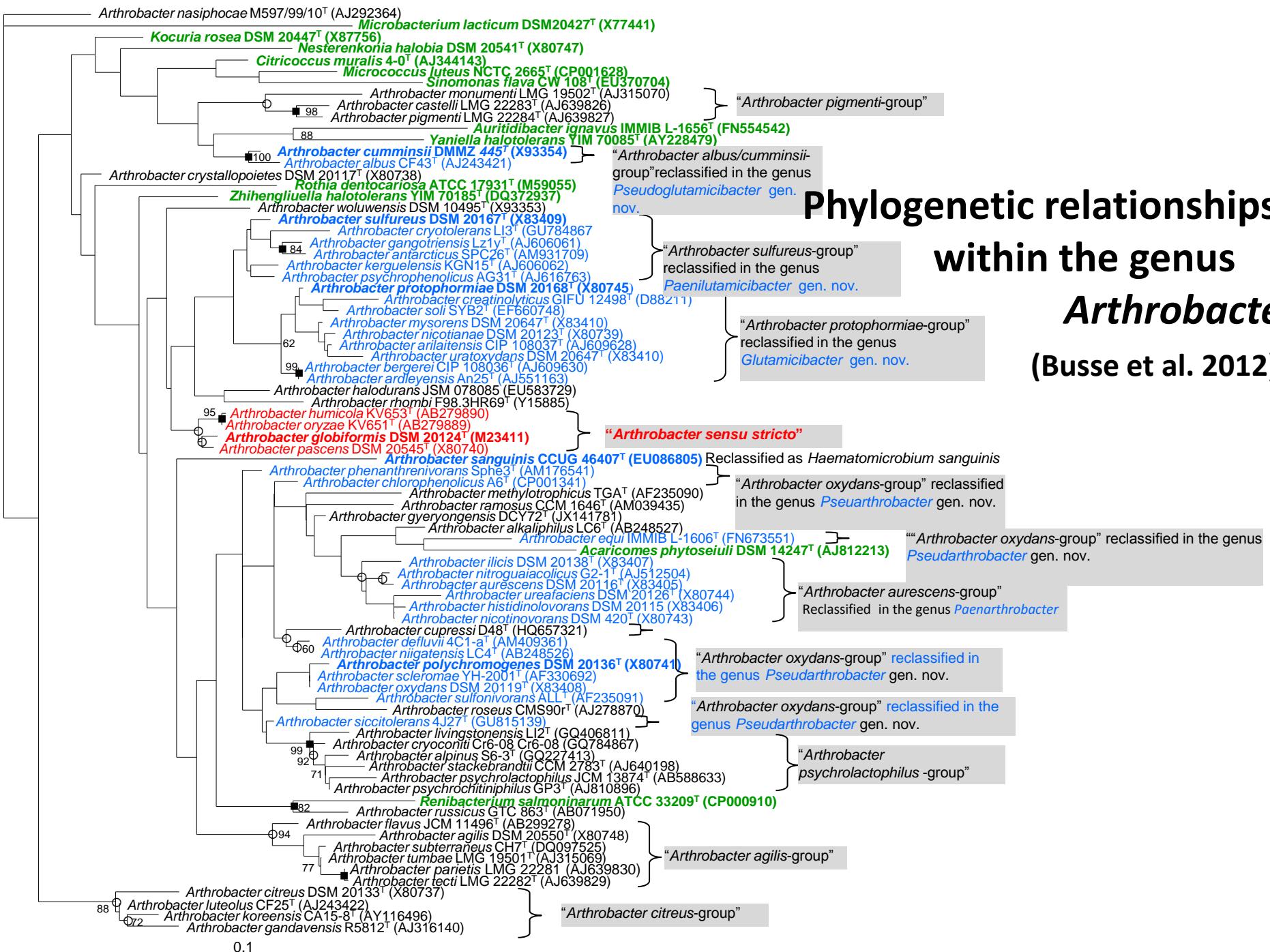
(Busse et al. 2012)

Reclassification of *Arthrobacter* species

Based on phylogenetic evidence and unique peptidoglycan type **Lys-Ala-Gly** the species *A. sanguinis* was reclassified in the genus ***Haematomicbium***.

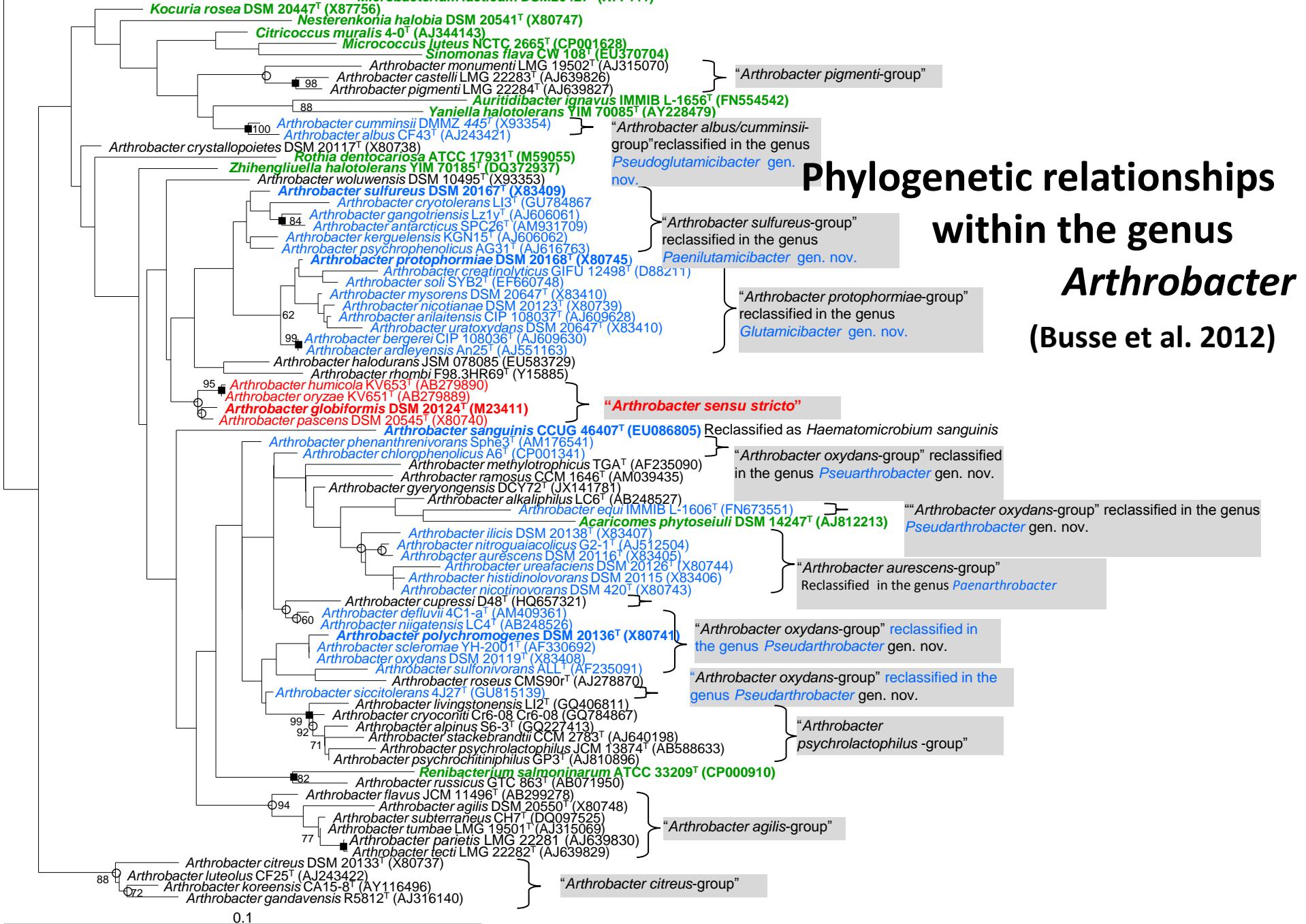
Phylogenetic relationships within the genus *Arthrobacter*

(Busse et al. 2012)



Based on phylogenetic evidence, unique peptidoglycan type **Lys-Ala₂-Gly₂₋₃-Ala (Gly)** and quinone system **MK-8(H₂) and MK-9(H₂)** a manuscript has been submitted proposing

***Falsarthrobacter nasiphoeiae* gen. nov., sp. nov.**

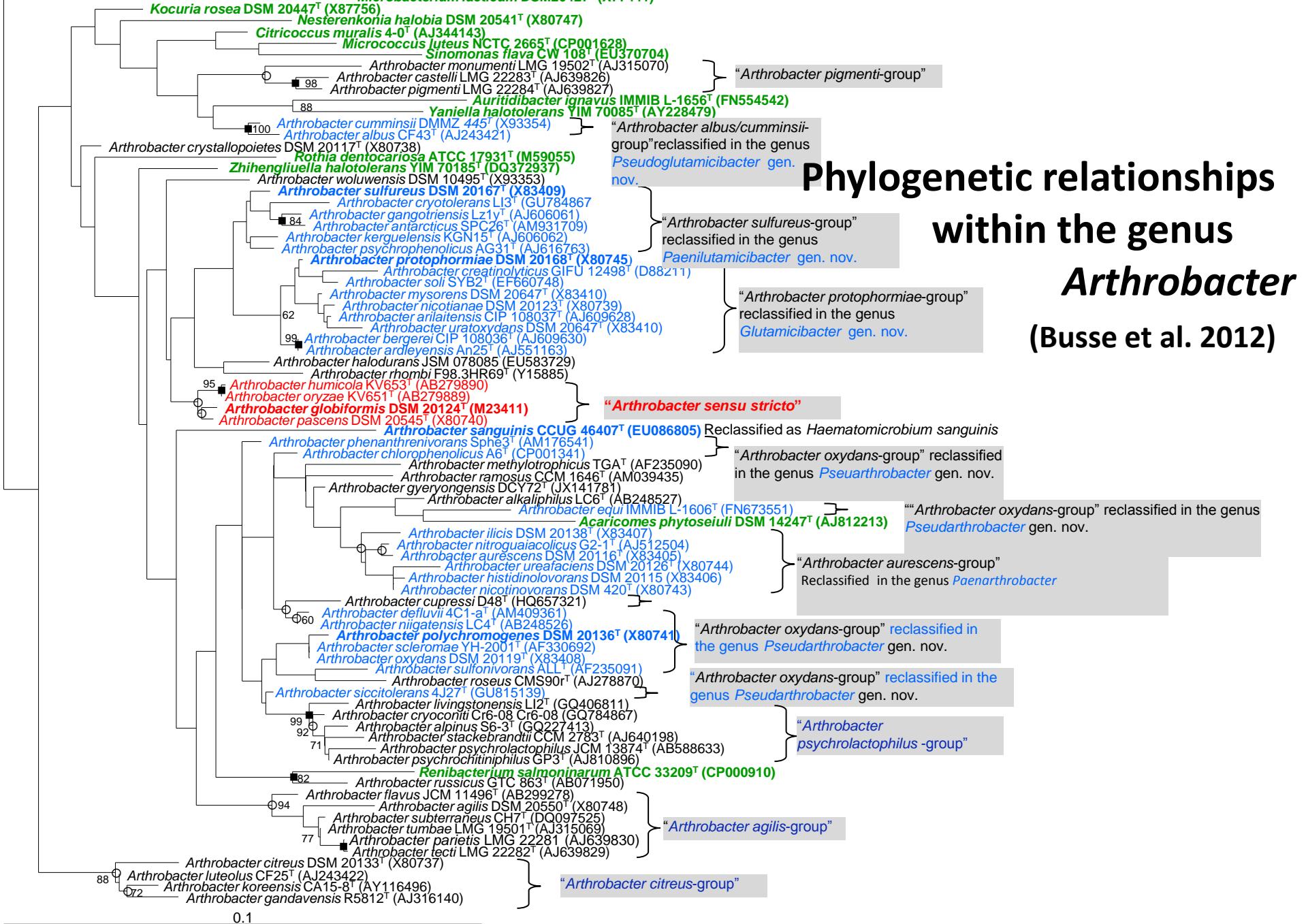


Phylogenetic relationships within the genus *Arthrobacter* (Busse et al. 2012)

Limitations

Species of “*Arthrobacter agilis* group” and “*Arthrobacter citreus* group” and some species of “*Arthrobacter psychrolactophilus* group” share the same peptidoglycan type Lys-Thr-Ala₂₋₃ quinone system.

→ phenotypic differentiation between the three groups is not possible



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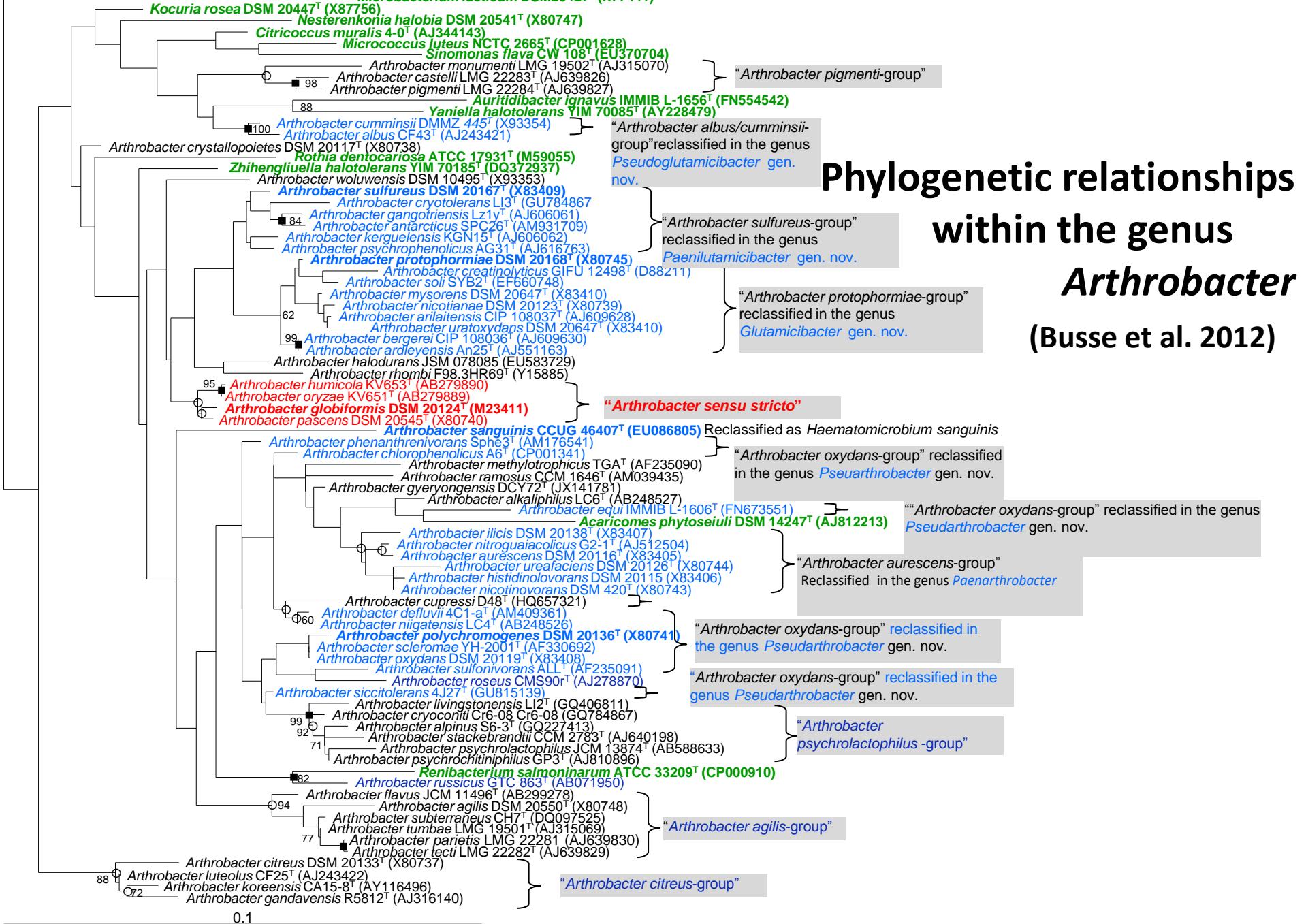
Species of the robust clade “*Arthrobacter psychrolactophilus* group” share the same quinone system but show different peptidoglycan types Lys-Thr-Ala₁, Lys-Thr-Ala₂, Lys-Thr-Ala₃ or Lys-Ala₂
→ a genus proposed for the species of this group would be heterogeneous.

Limitations

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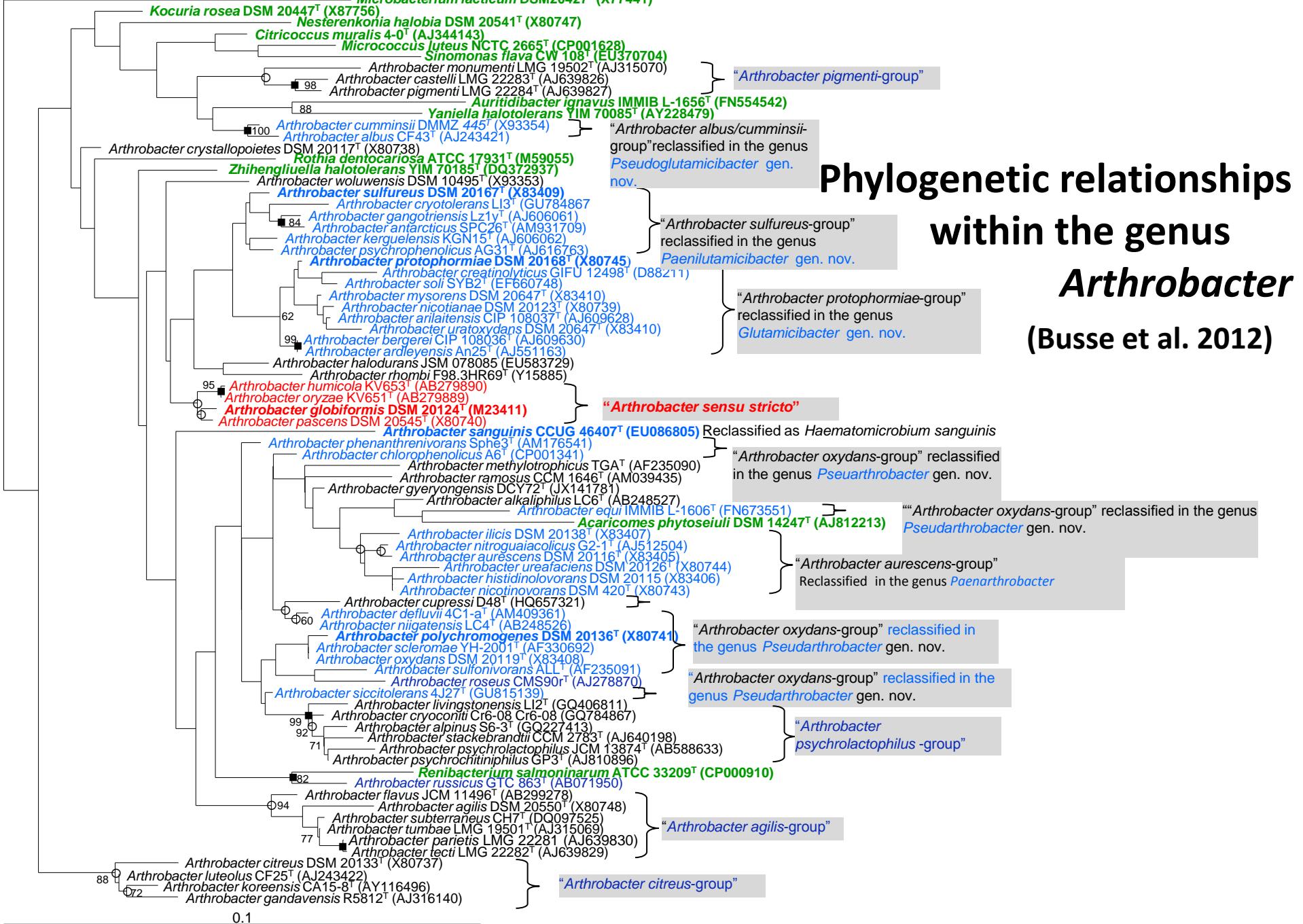
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→ a genus proposed for the species of this group would be heterogeneous.



Phylogenetic relationships within the genus *Arthrobacter* (Busse et al. 2012)

Limitations

Species of “*Arthrobacter pigmenti* group” differ in respect to the peptidoglycan type, either Lys-Ala₄ or Lys-Ala-Ser-Ala₃.
→ ???



Phylogenetic relationships within the genus *Arthrobacter*

(Busse et al. 2012)

What can we do to solve the remaining taxonomic problems
within the genus *Arthrobacter*?

Are housekeeping genes and/or the genomes the solution of
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Hopefully!