

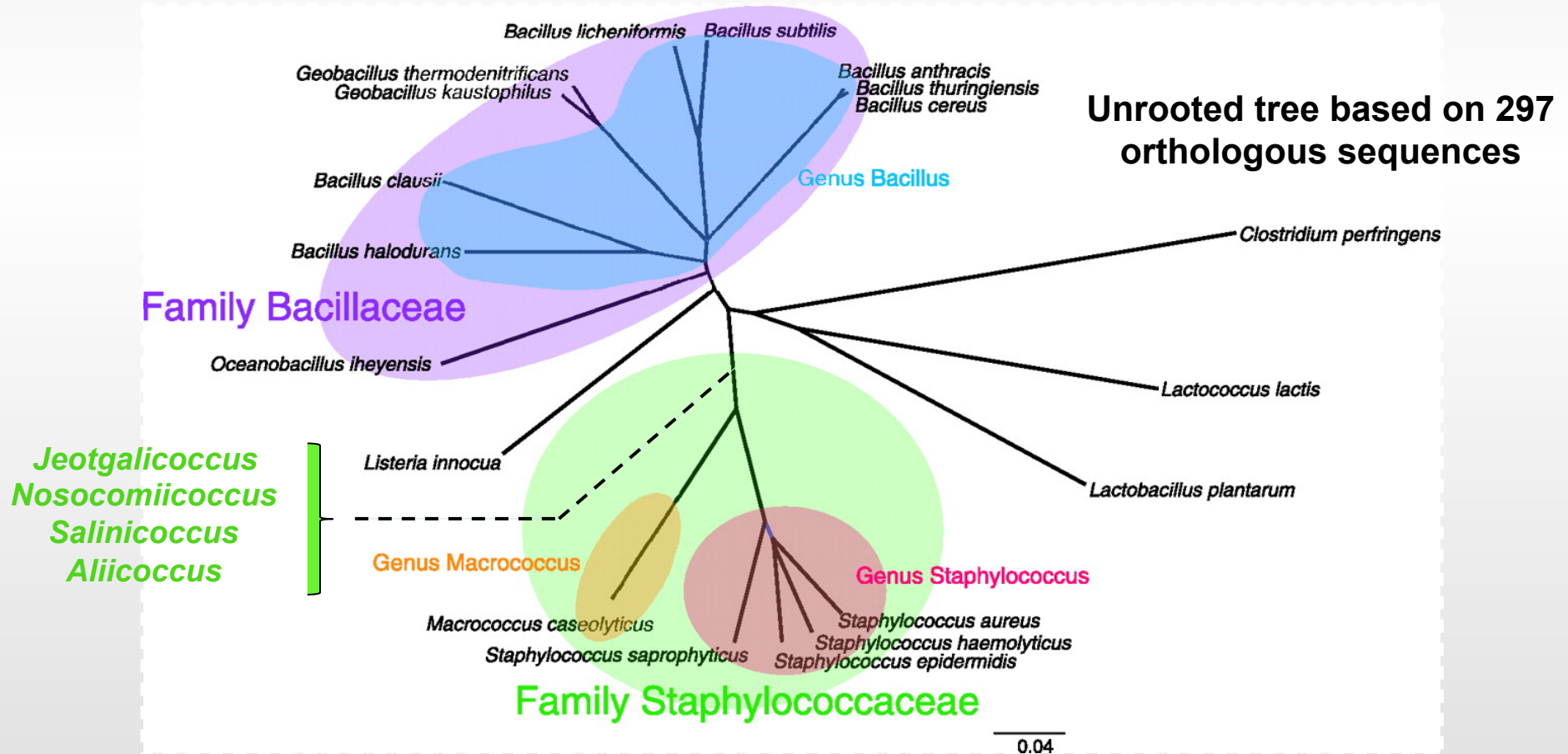
**Genome sequence of *Staphylococcus sciuri*  
as a milestone in the understanding of the  
evolution of the *Staphylococcaceae* family**

Olivier Chesneau, Institut Pasteur  
Microbiology department

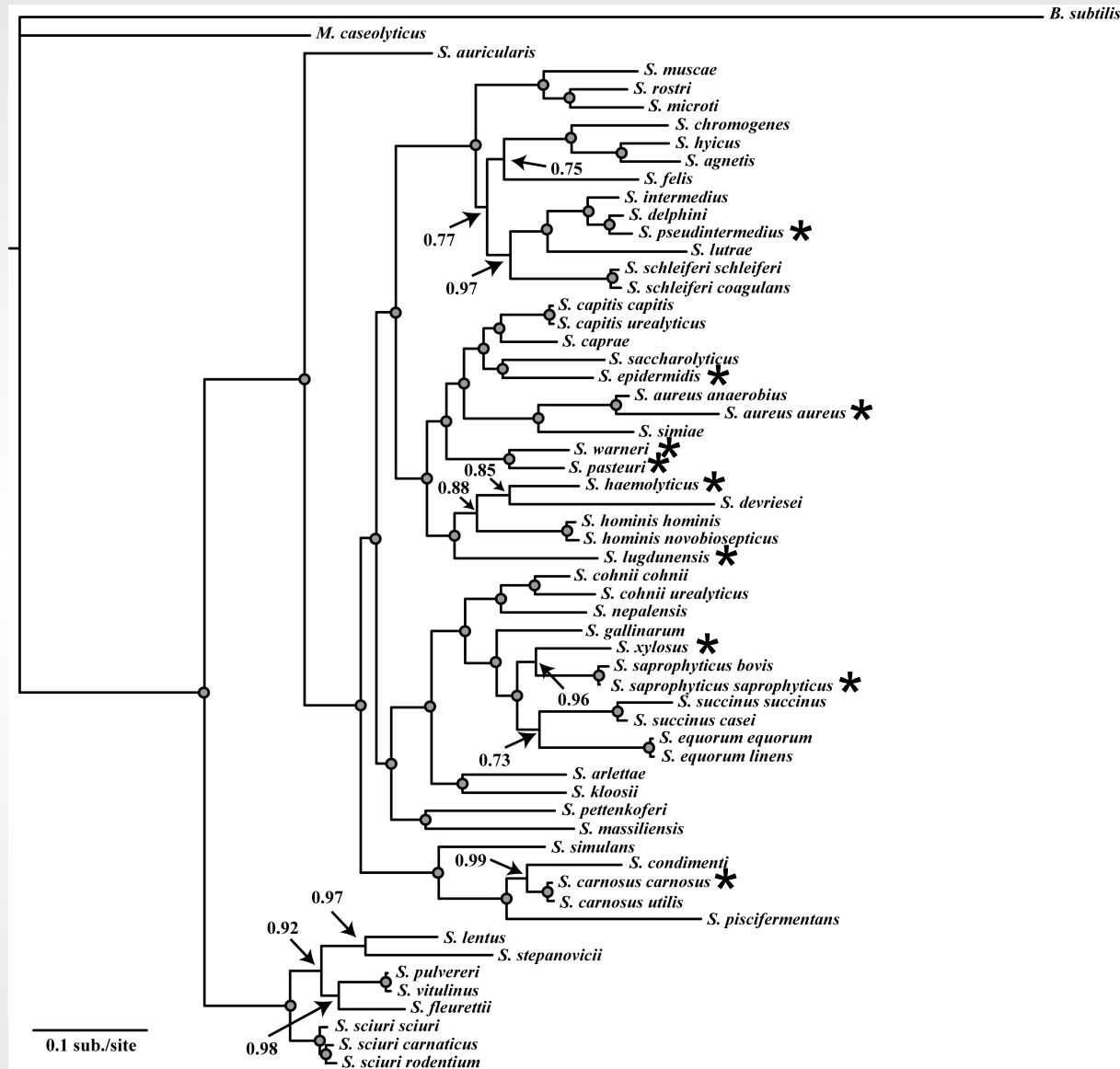
## Complete Genome Sequence of *Macrococcus caseolyticus* Strain JSCS5402, Reflecting the Ancestral Genome of the Human-Pathogenic Staphylococci<sup>7</sup>

Tadashi Baba,<sup>1\*</sup> Kyoko Kuwahara-Arai,<sup>1</sup> Ikuo Uchiyama,<sup>2</sup> Fumihiko Takeuchi,<sup>3</sup>  
Teruyo Ito,<sup>1</sup> and Keiichi Hiramatsu<sup>1</sup>

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*Japan<sup>2</sup>; and Wellcome Trust Sanger Institute, Hinxton, Cambridge CB10 1SA, United Kingdom<sup>3</sup>*



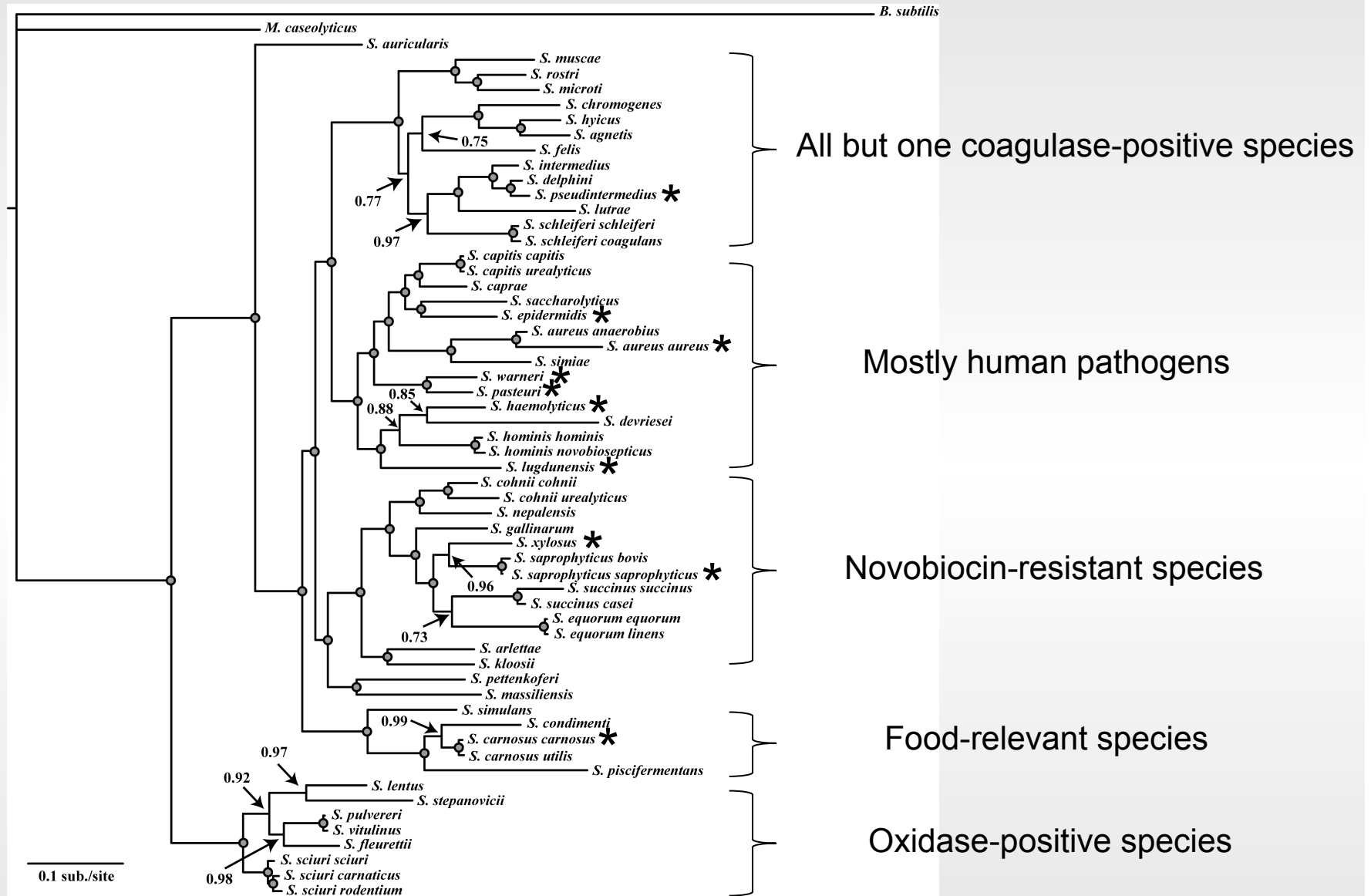
# Staphylococcus: many species (49) / few complete genomes (10)



Bayesian MCMC analysis  
using *rrs*, *dnaJ*, *rpoB*, and *tuf*

from Lamers et al., *BMC Evolutionary Biology*, 2012

# Staphylococcus: many species (49) / few complete genomes (10)

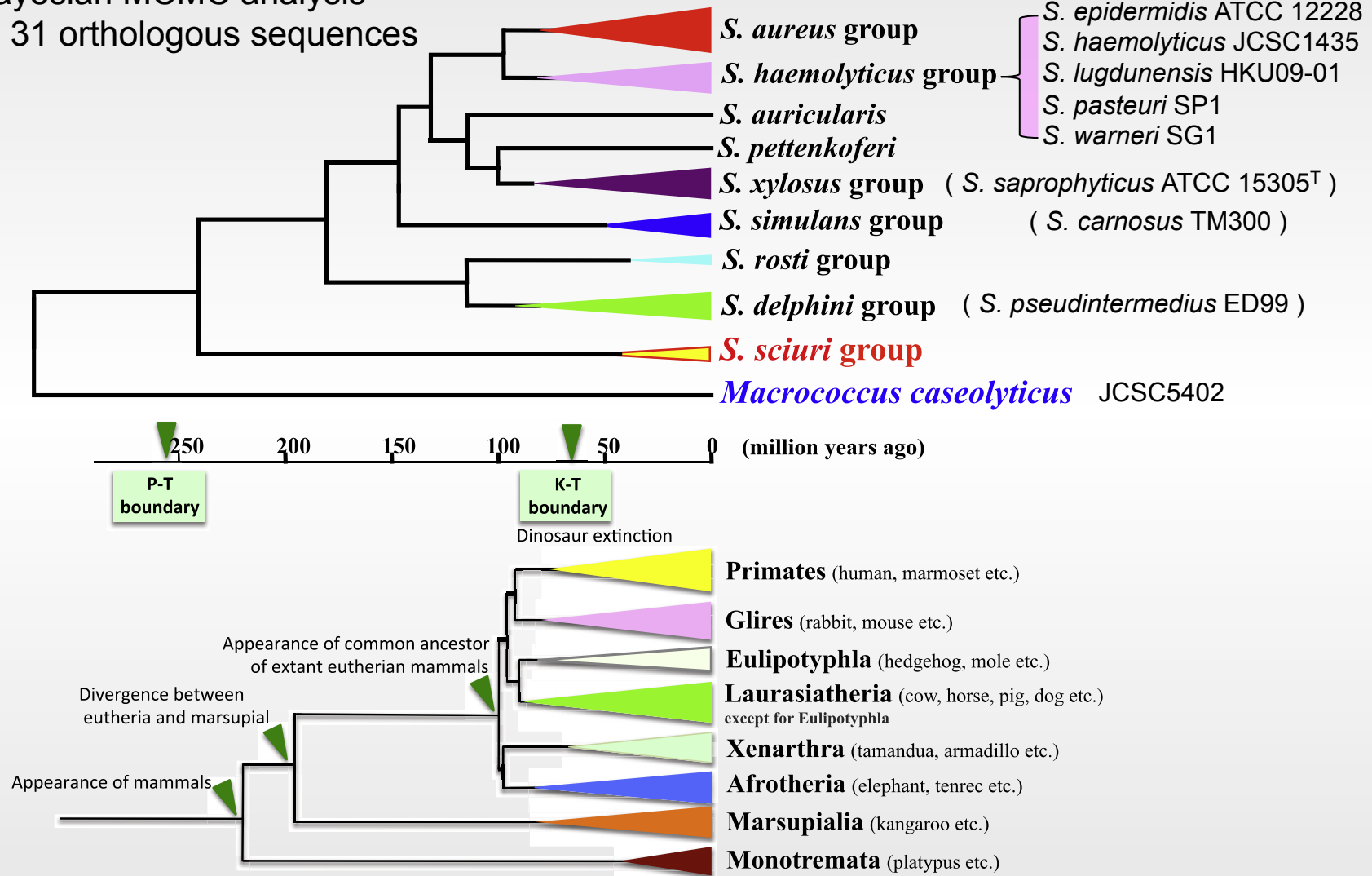


Bayesian MCMC analysis  
using *rrs*, *dnaJ*, *rpoB*, and *tuf*

from Lamers et al., *BMC Evolutionary Biology*, 2012

# Phylogenetic time trees of *Staphylococcaceae* and mammals

Bayesian MCMC analysis  
using 31 orthologous sequences



from Hiramatsu et al., *J. Infect. Chemother.*, 2014

Advanced search

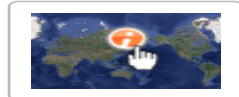
StrainInfo Projects

## Strain Passport

CIP 105824 *Staphylococcus sciuri* subsp. *sciuri*

### overview

species name *Staphylococcus sciuri* subsp. *sciuri* ⬇  
 strain numbers ATCC 29059 , BCRC 15242 , CCRC 15242 , CIP 105824 , DM128



availability map



strain browser



SeqRank

### history

Isolated in 1972 from opossum skin (*Didelphis virginiana*) by Kloos' laboratory

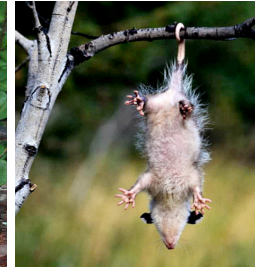
**DM128**

**ATCC 29059**  
Staphylococcus sciuri subsp. sciuri

**CCRC 15242**  
BCRC 15242

**CIP 105824**  
Staphylococcus sciuri subsp. sciuri

Histri for CIP 105824



This Histri was built automatically but not manually verified. As a consequence, the Histri can be incomplete or can contain errors.

### sequences

accession#	description	strainnumber	date	length
KC693025	Staphylococcus sciuri subsp. sciuri strain DM128 ABC superfamily ATP binding cassette transporter (sal(A)) gene, complete cds	CIP 105824	2013/09/01	1626

### publications

2 items found, displaying all items.

Hot C, Berthet N, Chesneau O  
**Characterization of sal(A), a Novel Gene Responsible for Lincosamide and Streptogramin A Resistance in Staphylococcus sciuri**  
 Antimicrob Agents Chemother 58(6), 3335–3341, 2014

Kloos, W E, Schleifer, K H, Smith, R F  
**Characterization of Staphylococcus sciuri sp. nov. and its subspecies**  
 Int J Syst Bacteriol 26, 22–37, 1976

2 items found, displaying all items.

## ARTICLE

Received 30 Nov 2010 | Accepted 11 May 2011 | Published 14 Jun 2011

DOI:10.1038/ncomms1347

# Microorganisms from aphid honeydew attract and enhance the efficacy of natural enemies

Pascal D. Leroy<sup>1</sup>, Ahmed Sabri<sup>2</sup>, Stéphanie Heuskin<sup>3</sup>, Philippe Thonart<sup>2</sup>, Georges Lognay<sup>3</sup>, François J. Verheggen<sup>1</sup>, Frédéric Francis<sup>1</sup>, Yves Brostaux<sup>4</sup>, Gary W. Felton<sup>5</sup> & Eric Haubruge<sup>1</sup>

Aphids are one of the most serious pests of crops worldwide, causing major yield and economic losses. To control aphids, natural enemies could be an option but their efficacy is sometimes limited by their dispersal in natural environment. Here we report the first isolation of a bacterium from the pea aphid *Acyrtosiphon pisum* honeydew, *Staphylococcus sciuri*, which acts as a kairomone enhancing the efficiency of aphid natural enemies. Our findings represent the first case of a host-associated bacterium driving prey location and ovipositional preference for the natural enemy. We show that this bacterium has a key role in tritrophic interactions because it is the direct source of volatiles used to locate prey. Some specific semiochemicals produced by *S. sciuri* were also identified as significant attractants and ovipositional stimulants. The use of this host-associated bacterium could certainly provide a novel approach to control aphids in field and greenhouse systems.

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<sup>2</sup> Walloon Center of Industrial Biology, University of Liege, B40, 4000 Sart-Tilman, Belgium. <sup>3</sup> Department of Analytical Chemistry, University of Liege, Gembloux Agro-Bio Tech, Passage des Déportés 2, 5030 Gembloux, Belgium. <sup>4</sup> Department of Applied Statistics, Computer Science and Mathematics, University of Liege, Gembloux Agro-Bio Tech, Avenue de la Faculté 8, 5030 Gembloux, Belgium. <sup>5</sup> Department of Entomology, Penn State University, University Park, Pennsylvania 16802, USA. Correspondence and requests for materials should be addressed to P.D.L. (email: p.leroy@ulg.ac.be or entomologie.gembloux@ulg.ac.be).

## NATURAL POPULATIONS OF THE GENUS *STAPHYLOCOCCUS*

*Wesley E. Kloos*

Department of Genetics, North Carolina State University, Raleigh,  
North Carolina 27650

We may question the evolutionary course taken by such widespread species as *S. xylosus* and *S. sciuri*, which may be capable of a free-living existence. These species do not require an organic source of nitrogen and have been isolated occasionally from soil and natural waters (44, 45, 103).





## A Highly Pathogenic Strain of *Staphylococcus sciuri* Caused Fatal Exudative Epidermitis in Piglets

Shixi Chen, Yu Wang, Fuyong Chen, Hanchun Yang, Menghou Gan, Shijun J. Zheng\*

Ministry of Agriculture Key Laboratory of Preventive Veterinary Medicine, College of Veterinary Medicine, China Agricultural University, Beijing, China

*Staphylococcus sciuri* are important human pathogens responsible for endocarditis, peritonitis, septic shock, urinary tract infection, pelvic inflammatory disease and wound infections. However, little information is known regarding the pathogenicity of *S. sciuri* to animals. From the pericardial fluid of a diseased piglet with exudative epidermitis (EE), we isolated a strain of *Staphylococcus* in pure culture. Surprisingly, this isolate was a member of *S. sciuri* rather than *S. hyicus* as identified by its biochemical traits and also by analysis of 23S ribosomal DNA using Internal Transcribed Spacer PCR. In addition, inoculation of newborn piglets with  $1 \times 10^{10}$  CFU of the isolate by oral feeding or intra-muscular injection successfully reproduced EE in piglets, which suggested that the oral intake of the pathogen by the animals is one of the major routes of exposure. These unexpected findings prioritized *S. sciuri* as important zoonotic agents, which may have ramifications for human medicine.

Citation: Chen S, Wang Y, Chen F, Yang H, Gan M, et al (2007) A Highly Pathogenic Strain of *Staphylococcus sciuri* Caused Fatal Exudative Epidermitis in Piglets. PLoS ONE 2(1): e147. doi:10.1371/journal.pone.0000147

## *Staphylococcus sciuri* Exfoliative Toxin C (ExhC) is a Necrosis-Inducer for Mammalian Cells

Haihua Li, Yongqiang Wang, Lin Ding, Shijun J. Zheng\*

State Key Laboratory of Agrobiotechnology, Key Laboratory of Animal Epidemiology and Zoonosis, and Ministry of Agriculture, College of Veterinary Medicine, China Agricultural University, Beijing, China

### Abstract

*Staphylococcus sciuri* (*S. sciuri*) is a rare pathogen in humans, but it can cause a wide array of human infections. Recently a *S. sciuri* isolate (HBXX06) was reported to cause fatal exudative epidermitis (EE) in piglets and thus considered as a potential zoonotic agent. To investigate the pathogenicity of this bacterium, we cloned exfoliative toxin C (ExhC), a major toxin of the *S. sciuri* isolate and performed functional analysis of the recombinant ExhC-his (rExhC) protein using *in vitro* cell cultures and newborn mice as models. We found that rExhC could induce necrosis in multiple cell lines and peritoneal macrophages as well as skin lesions in newborn mice, and that the rExhC-induced necrosis in cells or skin lesions in newborn mice could be completely abolished if amino acids 79-128 of rExhC were deleted or blocked with a monoclonal antibody (3E4), indicating aa 79-128 portion as an essential necrosis-inducing domain. This information contributes to further understandings of the mechanisms underlying *S. sciuri* infection.

Citation: Li H, Wang Y, Ding L, Zheng SJ (2011) *Staphylococcus sciuri* Exfoliative Toxin C (ExhC) is a Necrosis-Inducer for Mammalian Cells. PLoS ONE 6(7): e23145. doi:10.1371/journal.pone.0023145

JOURNAL OF CLINICAL MICROBIOLOGY, Mar. 2000, p. 1136–1143  
0095-1137/00/\$04.00+0  
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Vol. 38, No. 3

## Molecular Characterization of *Staphylococcus sciuri* Strains Isolated from Humans

ISABEL COUTO,<sup>1,2,3</sup> ILDA SANTOS SANCHES,<sup>1,3</sup> RAQUEL SÁ-LEÃO,<sup>1</sup> AND HERMÍNIA DE LENCASTRE,<sup>1,2\*</sup>

JOURNAL OF CLINICAL MICROBIOLOGY, June 2005, p. 2782–2785  
0095-1137/05/\$08.00+0 doi:10.1128/JCM.43.6.2782–2785.2005  
Copyright © 2005, American Society for Microbiology. All Rights Reserved.

Vol. 43, No. 6

## Isolation and Molecular Characterization of *Staphylococcus sciuri* in the Hospital Environment

Ivana Dakić,<sup>1</sup> Donald Morrison,<sup>2</sup> Dragana Vuković,<sup>1</sup> Branislava Savić,<sup>1</sup> Adebayo Shittu,<sup>3</sup> Petr Ježek,<sup>4</sup>  
Tomasz Hauschild,<sup>5</sup> and Srdjan Stepanović<sup>1\*</sup>

ANTIMICROBIAL AGENTS AND CHEMOTHERAPY, Dec. 2010, p. 5413–5417  
0066-4804/10/\$12.00 doi:10.1128/AAC.00426-10  
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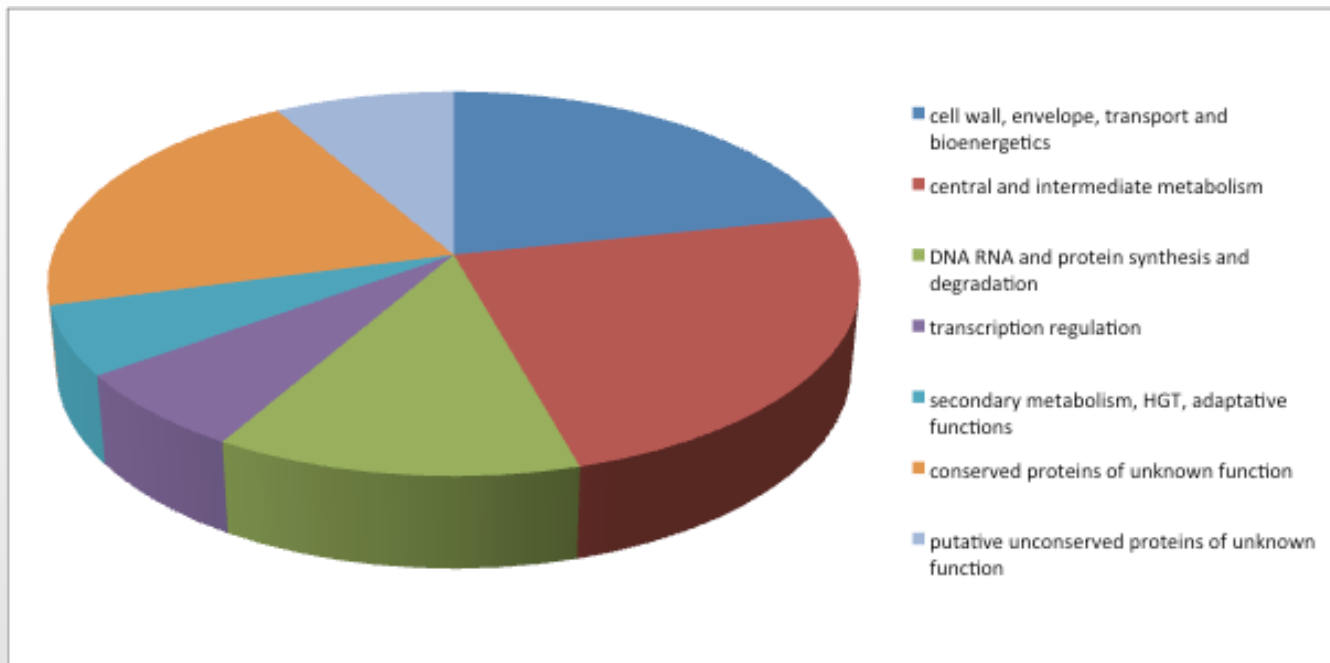
Vol. 54, No. 12

## Nasal Carriage of Methicillin-Resistant and Methicillin-Sensitive Strains of *Staphylococcus sciuri* in the Indonesian Population<sup>∇</sup>

J. A. Severin,<sup>1\*</sup> E. S. Lestari,<sup>2</sup> K. Kuntaman,<sup>3</sup> M. Pastink,<sup>1</sup> S. V. Snijders,<sup>1</sup> N. Lemmens-den Toom,<sup>1</sup>  
D. Horst-Kreft,<sup>1</sup> U. Hadi,<sup>4</sup> D. O. Duerink,<sup>5</sup> W. H. Goessens,<sup>1</sup> A. C. Fluit,<sup>6</sup> W. van Wamel,<sup>1</sup>  
A. van Belkum,<sup>1</sup> and H. A. Verbrugh<sup>1</sup> on behalf of the AMRIN Study Group

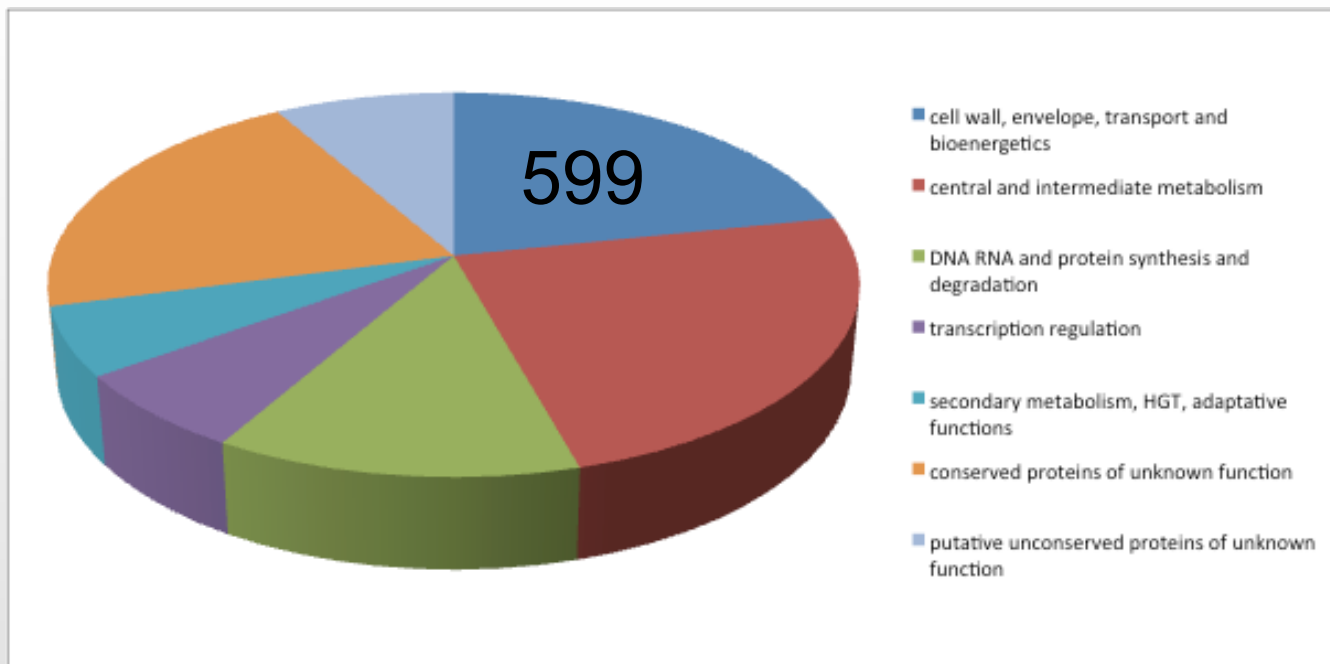
# Characteristics of the CIP 105824 genome project

- Collaboration between INRA, Montpellier University, and Institut Pasteur
- Whole genome shotgun sequencing by 454 method ( $\approx 83,000$  reads)
- More than 20-fold genome coverage (read length  $\approx 700$  bp)
- A total of 166 contigs by *de novo* assembly using Newbler 2.6 software
- Finally  $< 50$  contigs using various means (CLC Workbench / blast / read mapping)
- Automatic annotation of the genes and manual validation using AGMIAL platform



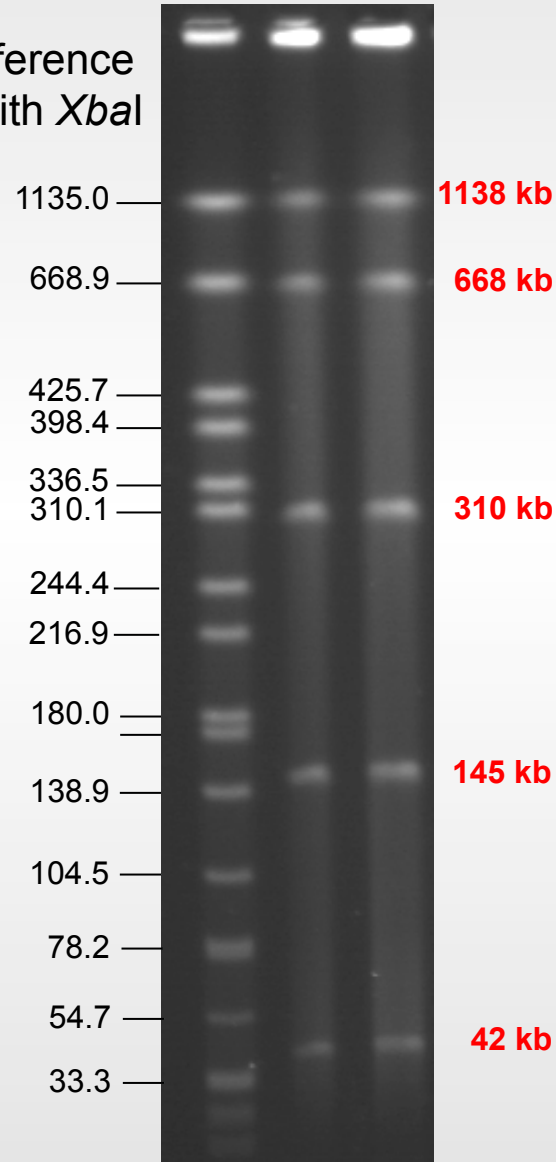
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# Pulsed-field gel electrophoresis of CIP 105824 strain

*Salmonella* reference standard cut with *Xba*I



No plasmid DNA (S1 nuclease)

I-CeuI digest

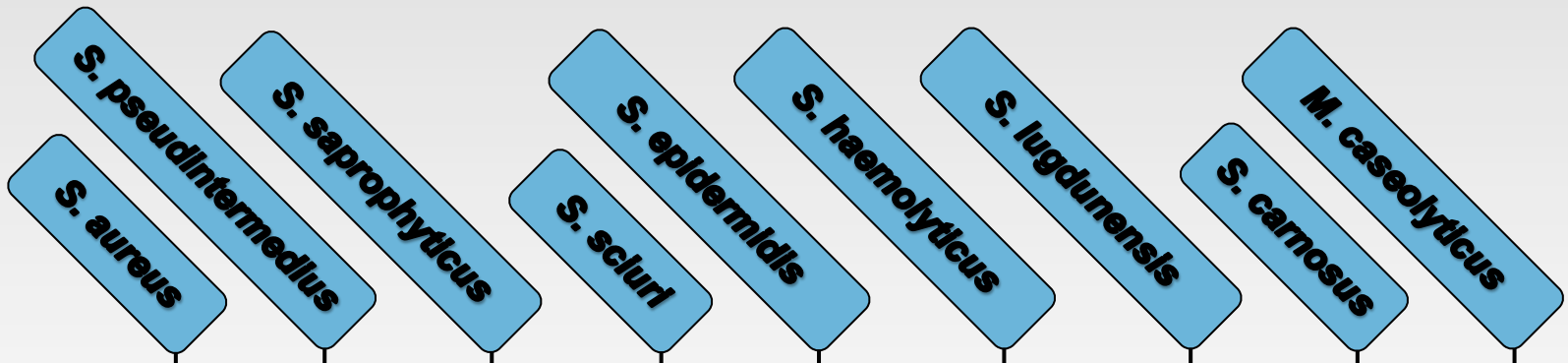


Five copies of rRNA operons



2.3 Mb genome size

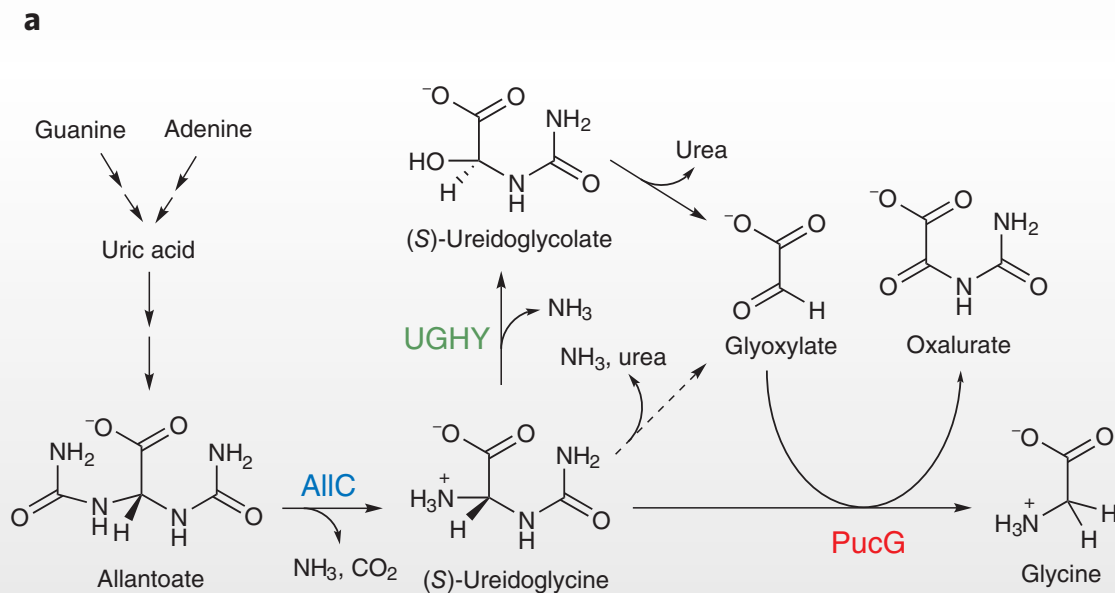
# Some key genomic features of the *Staphylococcaceae* family



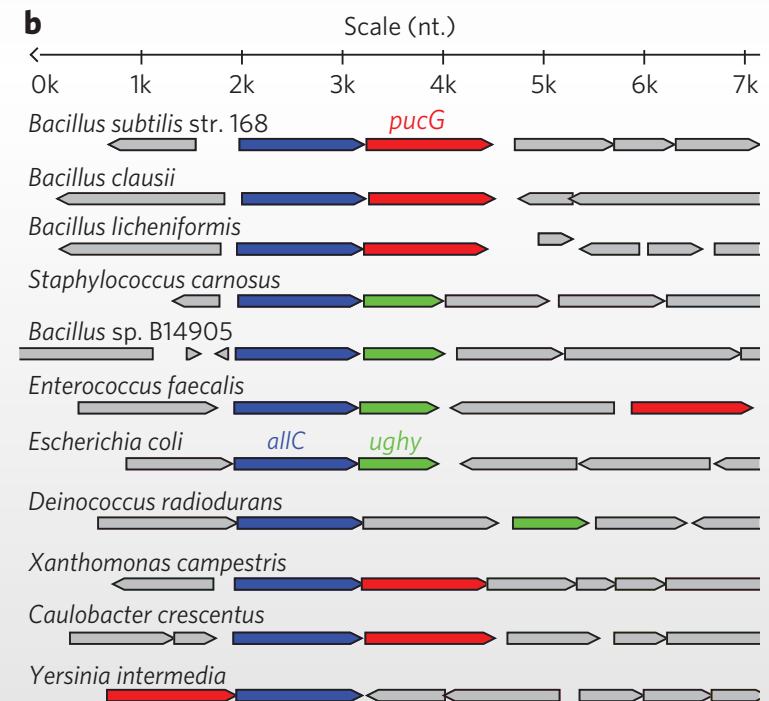
Traits :	Newman	ED99	ATCC 15305	CIP 105824	ATCC 12228	JCSC1435*	HKU09-01	TM300	JCSC5402*
Size (Mb)	2.87	2.57	2.51	≈ 2.3	2.49	2.68	2.65	2.56	2.10
GC%	32.9	37.6	33.2	32.4	32.1	32.8	33.8	34.6	36.9
rRNA operons	5	5	6	5	5	5	6	5	4
Copies of mobile elements									
- Insertion sequences	2 x IS1181	10 (1+7+2)	2 x IS431	0	17 (3+13+1)	60 (6+14+24+16)	5 (4+1)	0	4 (2+1+1)
- Transposons	0	4	0	0	1	2	3 (1+2)	0	0
- Remnant transposases	10	11	9	1	46	22	2	1	2
- Group II introns	0	7 x RT gene	0	0	0	0	0	0	0
- Prophages	4	0	1	2	2	2	1	1	2
- Pathogenicity islands	2	1 very short	0	0	0	0	0	0	0
Sigma factors	4	3	4	5	4	4	4	4	3
Penicillin-binding proteins	4	4	4	5 (PBP2a)	4	5 (PBP4b)	5 (PBP4b)	5 (PBP4b)	4
Pigment biosynthesis	Yes	No	No	Yes	No	No	No	No	No
Major menaquinone	MK-8	MK-7	MK-7	MK-6	MK-7	MK-7	MK-7	MK-7	?
Carboxylate-type siderophores	2	2	1	1 (novel)	1	1	0	1	No
Haem-binding proteins	Yes	No	No	Yes	No	No	Yes	No	No
Phenol-soluble modulins	Yes	No	Yes	Yes	Yes	Yes	Yes	Yes	No
Tagatose-6-P pathway	Yes	Yes	No	Yes	Yes	Yes	Yes	Yes	No
Oxidase ( <i>c</i> -type cytochromes)	-	-	-	+	-	-	-	-	+

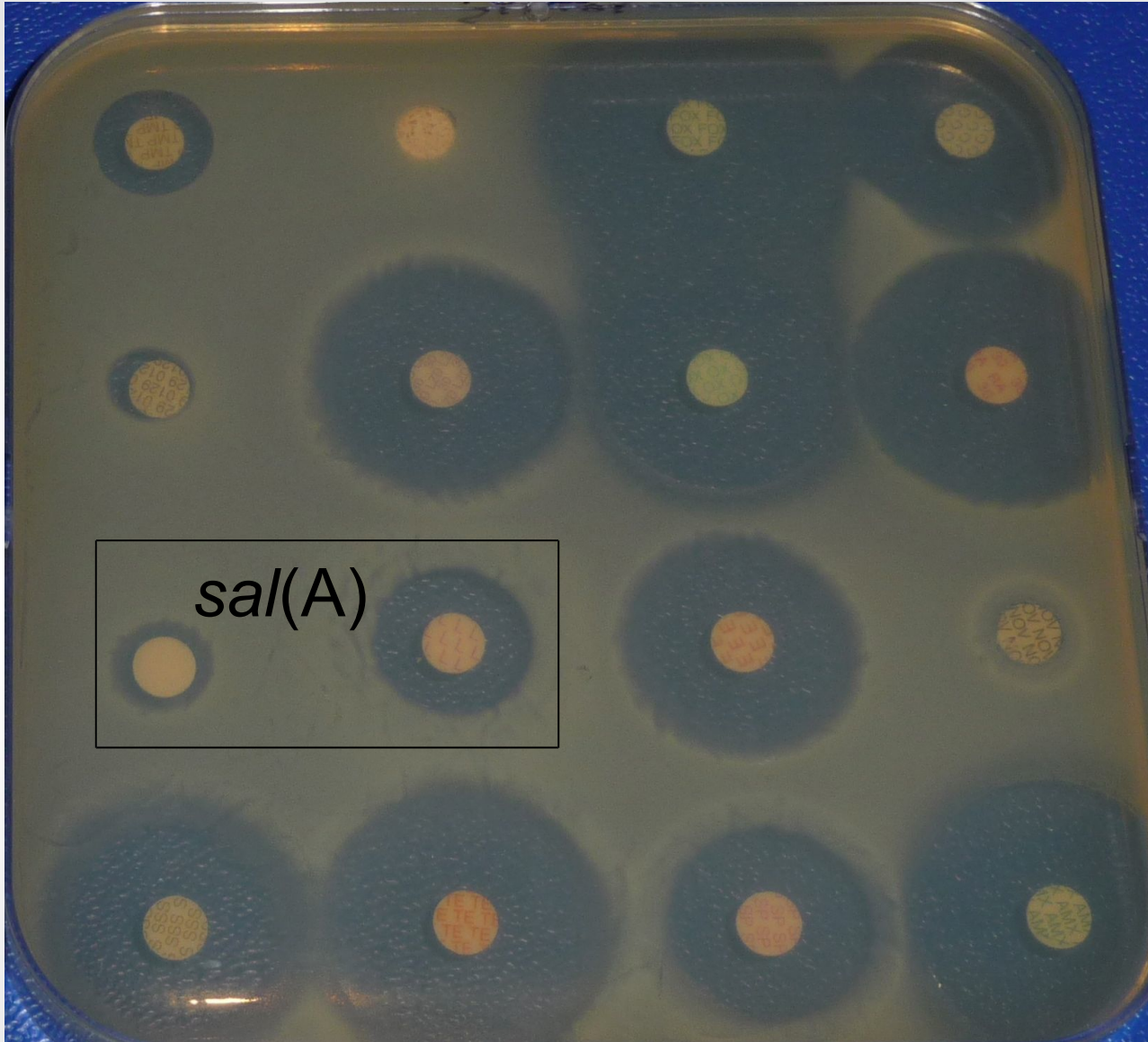
# What makes *S. sciuri* group different from other staphylococci ?

- Oxidase-positive and MK-6 *Staphylococcaceae* organisms
- Growth from  $(\text{NH}_4)_2\text{SO}_4$  (no amino acid auxotrophy)
- A large repertoire of competence genes
- Presence of the MEP pathway for isoprenoid synthesis
- Many more Phospho-Transferase Systems (> 25...)
- A bit more ATP-binding cassette transporters (> 55...)



from Ramazzina et al., *Nat. Chem. Biol.*, 2010

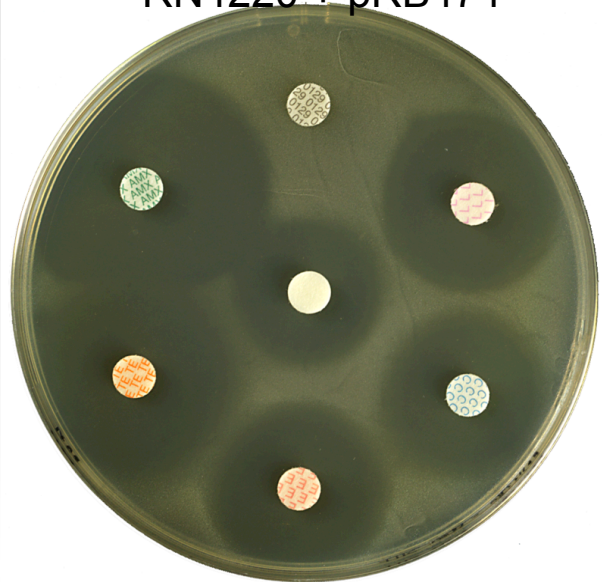




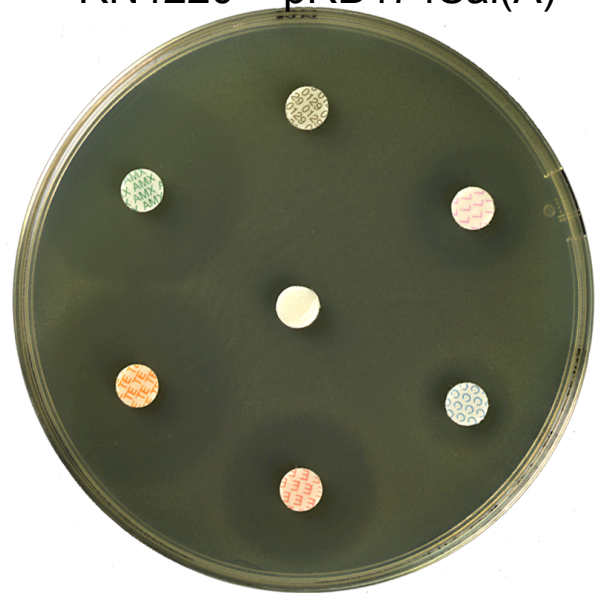


# Sal(A): R to SgA and LIN

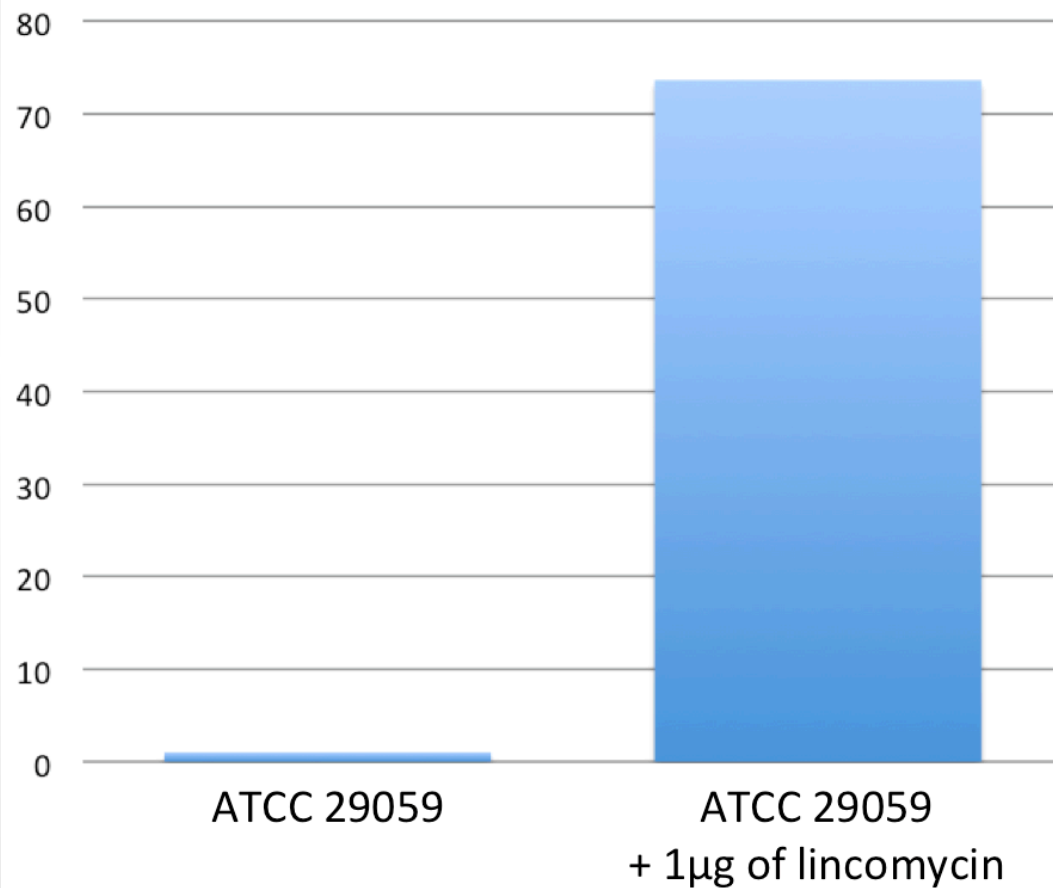
RN4220 + pRB474



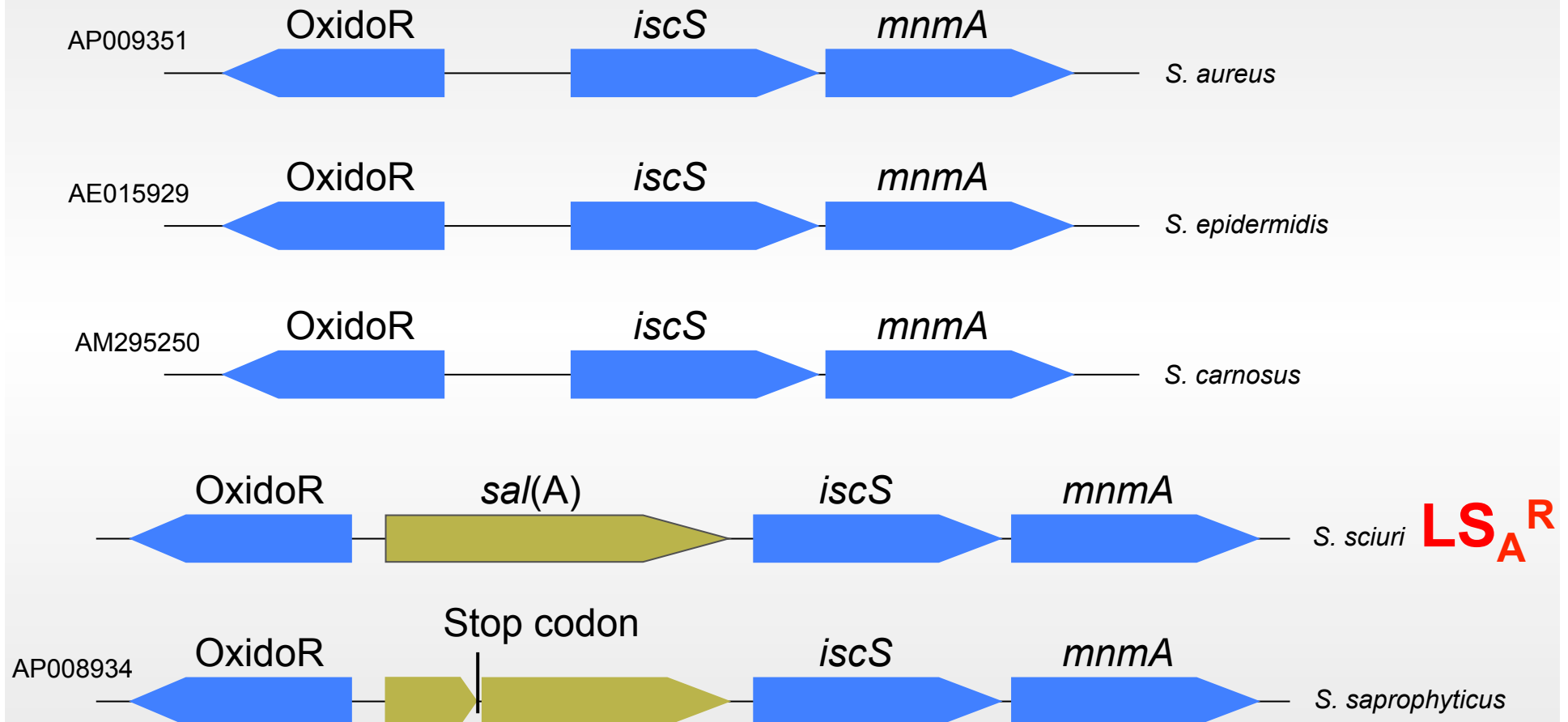
RN4220 + pRB474Sal(A)

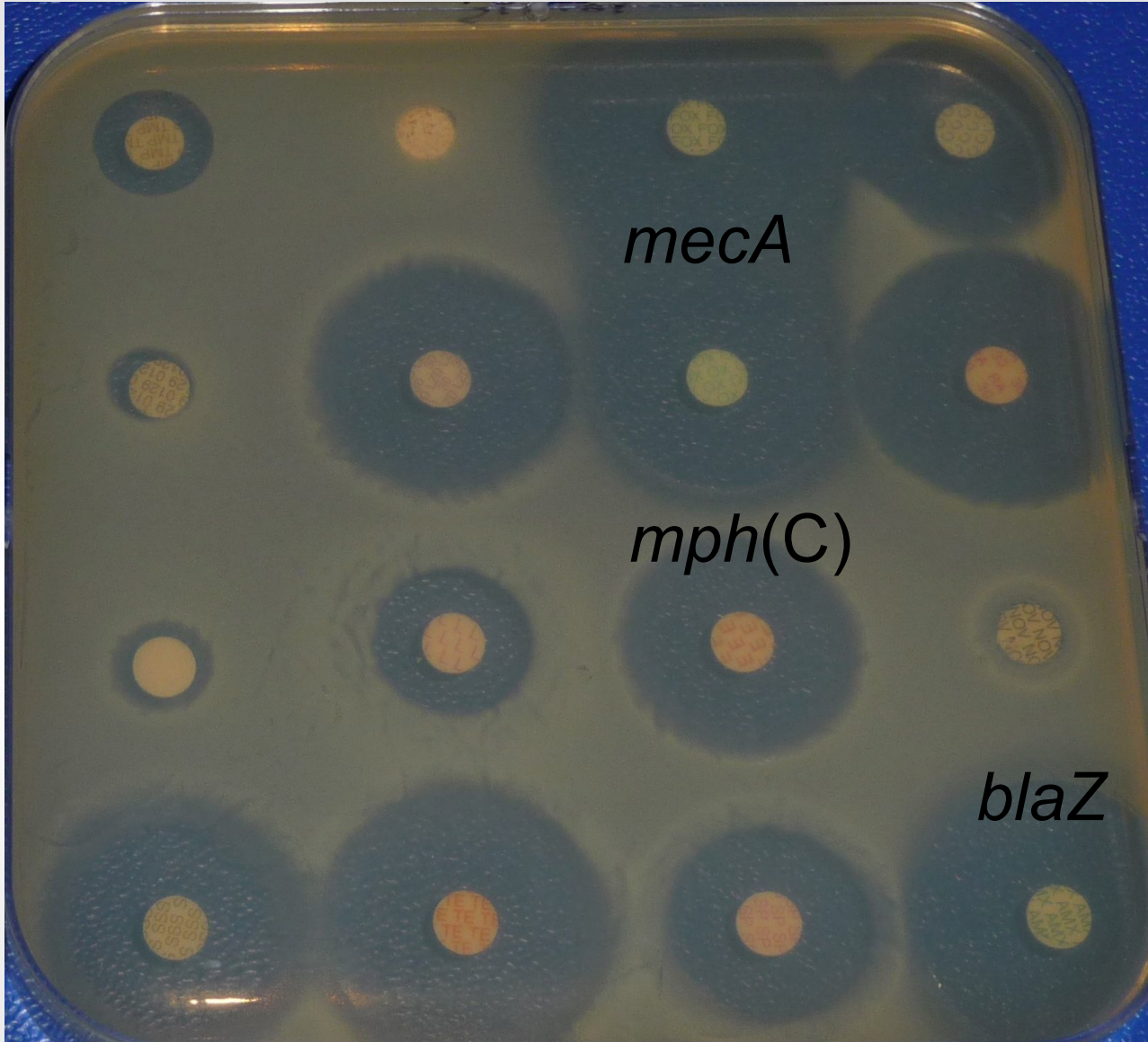


qRT-PCR results



# Saga of *sal(A)* within staphylococci





*mecA*

*mph(C)*

*blaZ*

## Thanks to:

- Tatiana Vallaeys (Montpellier University)
- Valentin Loux and Josef Deutscher (INRA)
- Elie Dassa (Institut Pasteur)

Dedicated to the memory of :

Cécile Wandersman

Head of the Bacterial Membranes Unit  
Microbiology department, Institut Pasteur

