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***Staphylococcus aureus* Nasal and Intestinal Carriage by Free-Ranging Red Deer: Evidence of Human, Domestic and Wild Animal Lineages**

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STAPHYLOCOCCUS AUREUS

A BRIEF INTRODUCTION

- COMMENSAL BUT ALSO PATHOGEN IN HUMAN AND ANIMAL
- COLONIZATION OF SKIN AND MUCOSA OF HEALTHY POPULATION
- FROM SKIN TO SYSTEMIC INFECTIONS
- EMERGENCE OF STRAINS RESISTANT TO ANTIMICROBIALS
METHICILLIN RESISTANT STRAINS (MRSA)

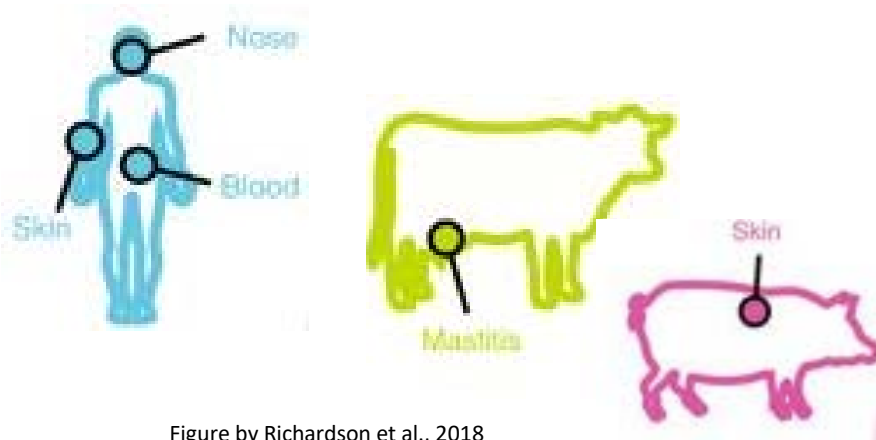
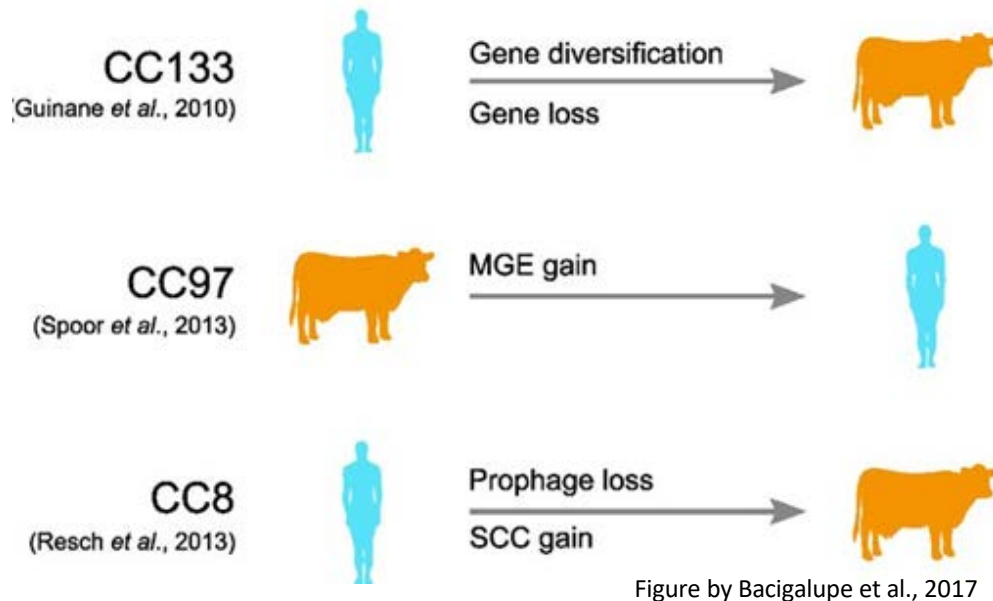


Figure by Richardson et al., 2018

STAPHYLOCOCCUS AUREUS

A MULTI-HOST PATHOGEN

ZOONOTIC EVENTS OF INTERSPECIES TRANSMISSION



- HUMANS AS A MAJOR HUB FOR THE EMERGENCE OF ENDEMIC LIVESTOCK STRAINS
- CATTLE AS THE MAIN ANIMAL RESERVOIR FOR THE EMERGENCE OF HUMAN EPIDEMIC CLONES

(Richardson *et al.*, [Nat Ecol Evol](#), 2018)

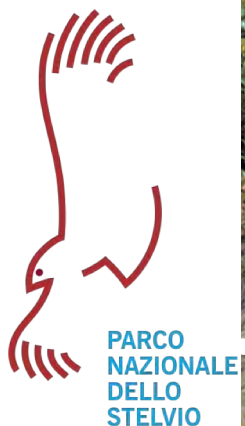
Host-species transitions are associated with horizontal gene transfer and genome diversification for survival in the new host-niche

S. AUREUS IN EUROPEAN WILDLIFE

WILDLIFE ISOLATES SHOWED A HIGH DEGREE OF DIVERSITY IN EUROPE (Monecke et al., PlosOne 2016)

ANTIMICROBIAL RESISTANCE IN WILDLIFE STRAINS IS RATHER LOW (Monecke et al., PlosOne 2016)

SYSTEMATIC STUDIES ARE REQUIRED TO MONITOR
THE TRANSMISSION OF HUMAN- AND LIVESTOCK-ASSOCIATED
S. AUREUS TO WILDLIFE AND *VICE VERSA*



S. AUREUS - WHY FREE RANGING RED DEER?

INCREASE DENSITY AND RANGE DISTRIBUTION IN THE ALPS

- 10.8 red deer /100 ha
- OVERLAPPING WITH HUMAN AND LIVESTOCK
- IMPACT ON BIODIVERSITY
- A CULLING PLAN HAS BEEN AUTHORIZED TO REDUCE RED DEER DENSITY
- CULLED DEER ENTERED THE HUMAN FOOD CHAIN



AIMS and SAMPLING

- Prevalence of *S. aureus* nasal and intestinal carriers in red deer
- *S. aureus* genetic characteristics



75 red deer culled

- 19 <1 year
- 12 1-2 years
- 44 > 2 years

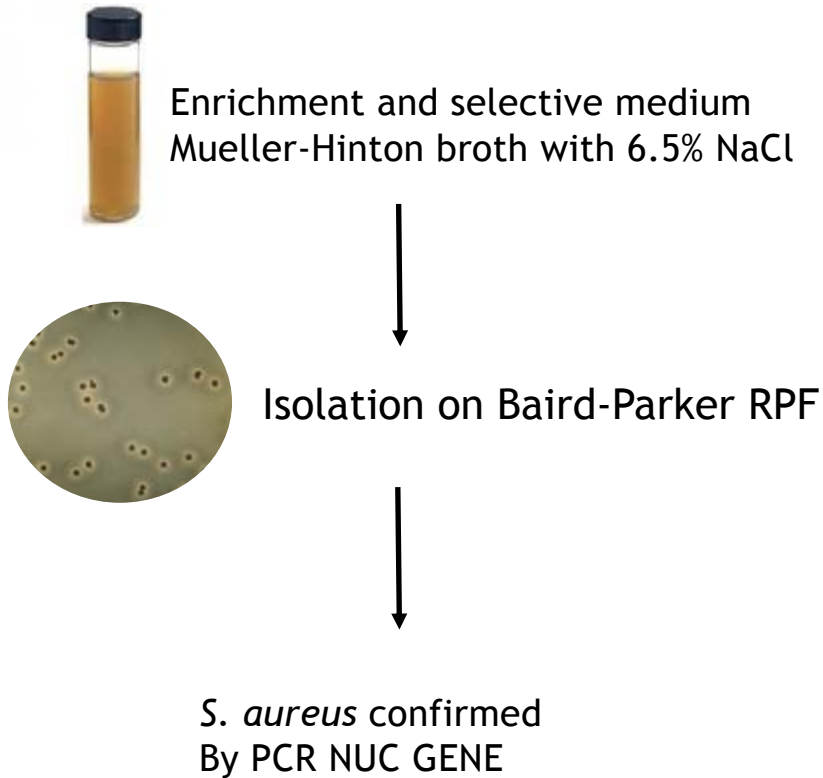
January-February 2017

Nasal swabs

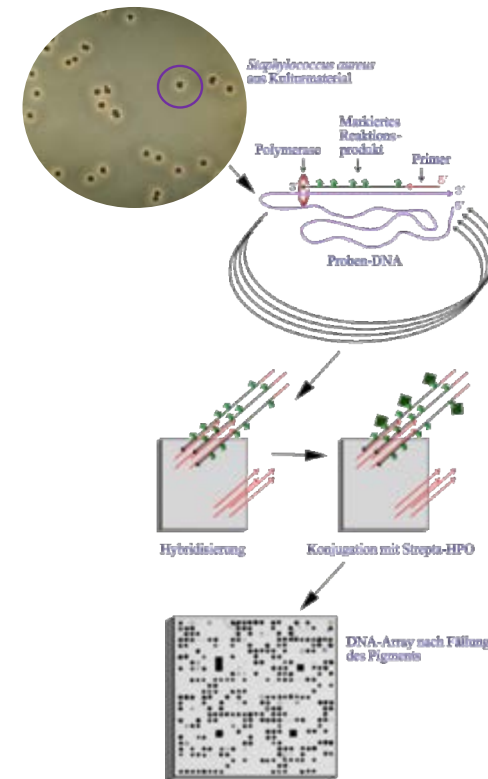
Feces or rectal swabs

BACTERIOLOGICAL ANALYSIS

CHARACTERIZATION OF *S. AUREUS* WITH DNA-ARRAYS



ONE ISOLATE PER COLLECTION SITE
FROM SIMULTANEOUS NASAL AND INTESTINAL CARRIERS



MICROARRAY

- typing genes
- species marker
- MLST
- SCCmec
- all relevant AMR
- virulence genes

S. AUREUS PREVALENCE

NASAL CARRIERS

year	pos/tested	prevalence %	95% CI
2017	68/75	90.67	81.97-95.41
2018	118/134	88.05	81.48-95.52

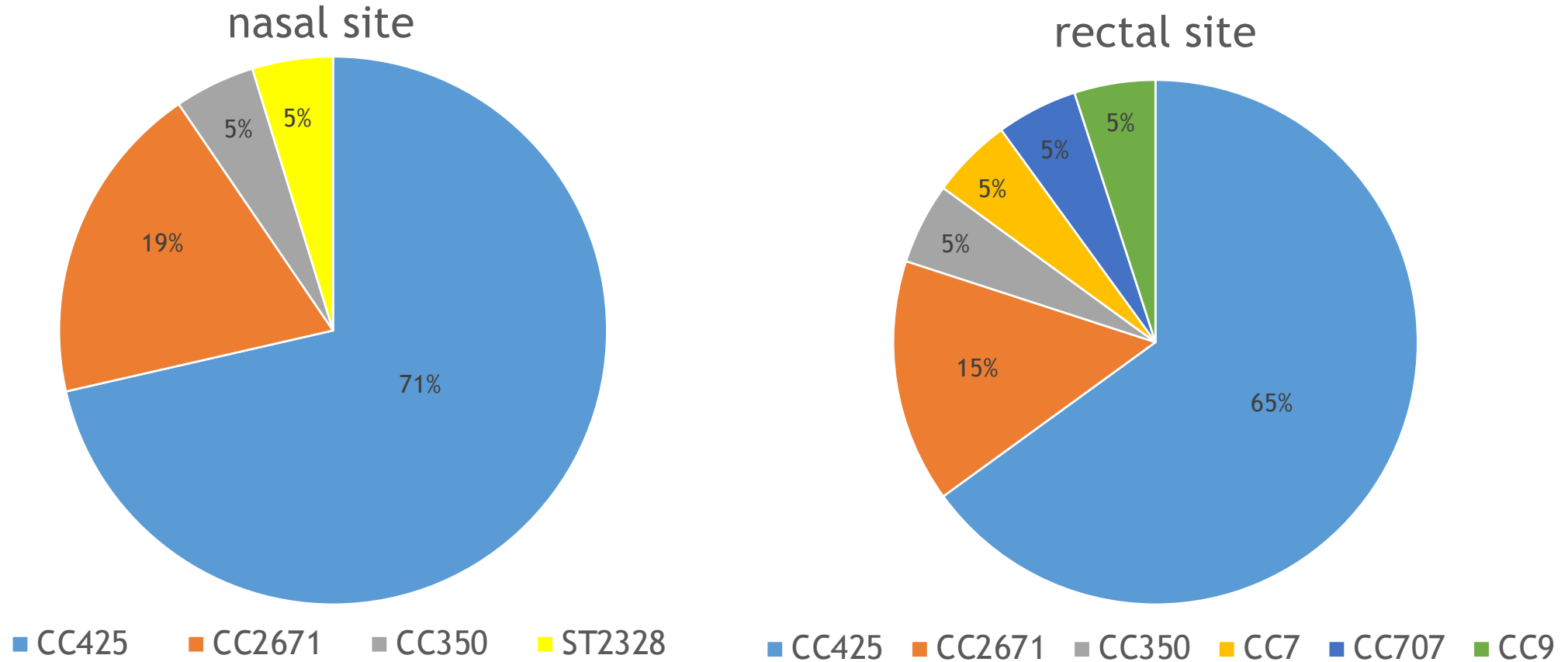
no statistical significant differences within age categories

INTESTINAL CARRIERS

year	pos/tested	prevalence %	95% CI
2017	20/75	26.67	17.98-37.63

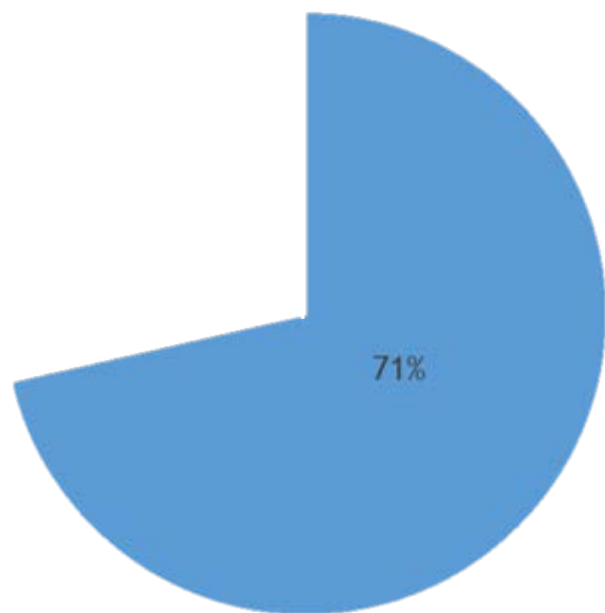
9 positive <1 year age category

***S. AUREUS* TYPING**
simultaneous nasal and intestinal carriers n=20



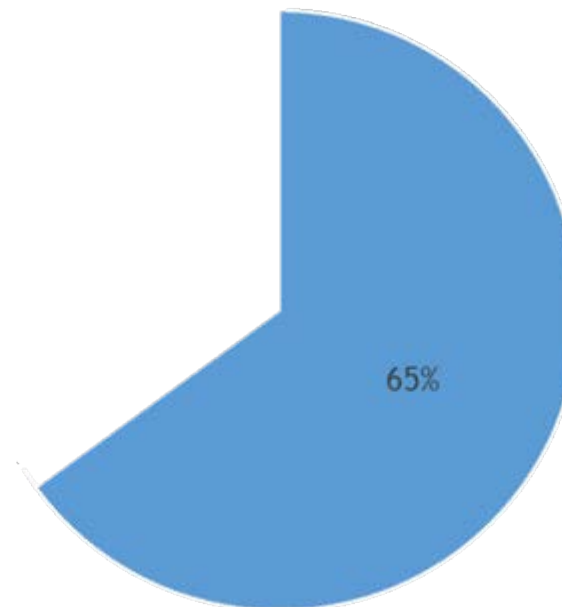
Methicillin susceptible *S. aureus* (MSSA) CC425

nasal site



■ CC425

rectal site



■ CC425

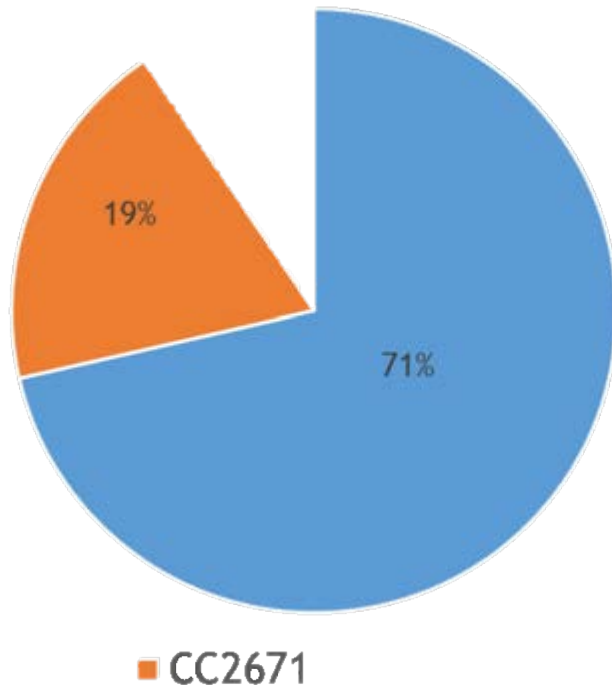
CC425 widespread in ruminants (Monecke et al 2016)

67.86 % of red deer strains carried the leukocidin genes *lukM/lukF-P83*

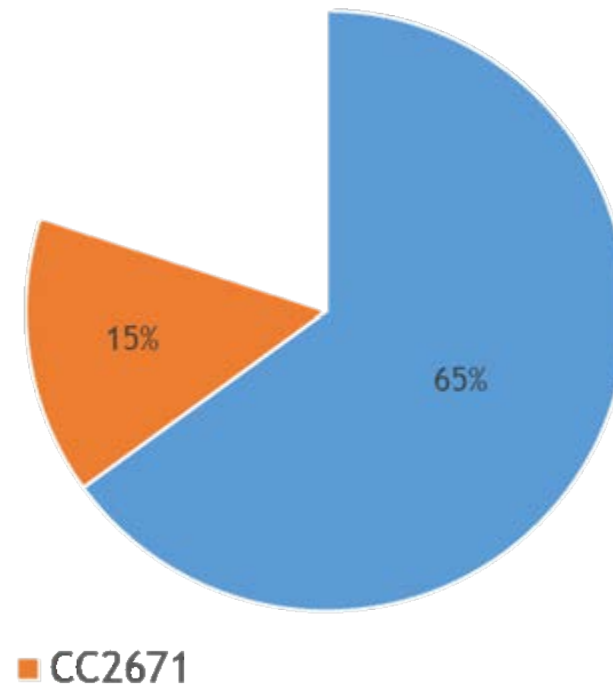
lukM/lukF-P83 are virulence factors harbored by other CC of ruminant origin (Vrieling et al., 2015)

MSSA CC2671

nasal site



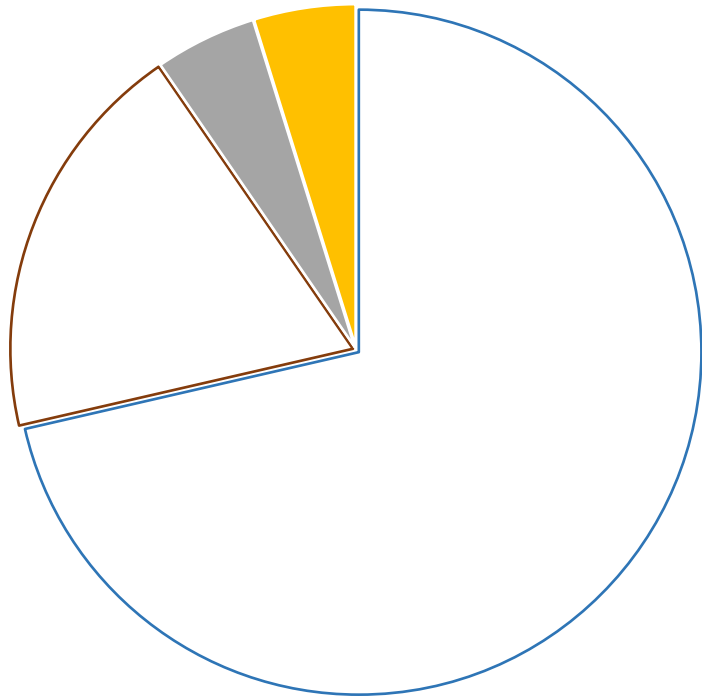
rectal site



Few data available on host range of this CC
Strain detected once in a starved sika deer (Monecke et al 2016)

SPORADIC MSSA CLONAL COMPLEX

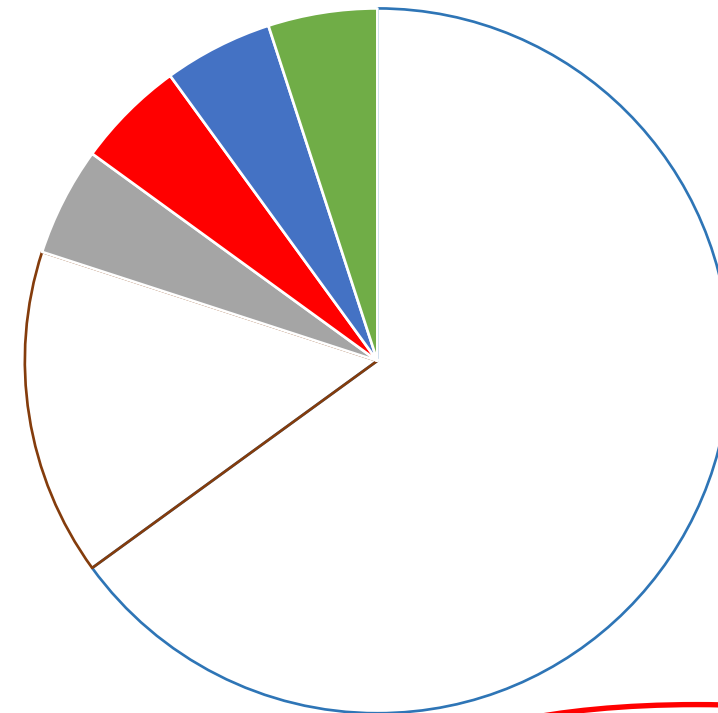
nasal site



■ CC350 ■ ST2328

CC350 rare lineage in human and cattle
CC7, CC707, CC9 human lineages

rectal site



■ CC350 ■ CC7 ■ CC707 ■ CC9

human lineages origin could be caused by habitat anthropization

CONCLUSIONS

- High prevalence of *S. aureus* carriers in red deer free ranging population
- All isolates negative for methicillin resistance genes
- High prevalence of lineages known to occur in domestic and wild ruminants
- Sporadic presence of human lineages
- Microarray convenient tool for rapid typing and selecting strains for whole genome sequencing

Refugia (untreated host population) may dilute the frequency of resistant pathogens in the treated population¹

Free ranging red deer and other wild ungulates as reservoir for native, drug-susceptible pathogens?

¹Park et al., 2015 [Biol Lett.](#)



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A. & D. Scari

