Epidemiology of Methicillin Resistant Staphylococcus aureus in nasal cavities of slaughtered small ruminants in a Greek abattoir

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"MRSA is present in

Results

Staphylococcus aureus was detected in 19/30 (63%) of the animals (Table 1)

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Small ruminants constitute a possible risk for the spreading of MRSA into the community. Baseline studies are needed to perform Quantitative Microbial Risk Assessment, determine the MRSA dissemination across the food production chain and evaluate the impact in Public Health

- Methicillin-resistant *Staphylococcus aureus* (MRSA) is a universal threat.
- After being well established in the healthcare setting, emerged also in the community.
- MRSA colonizing or infecting animals and in food of animal origin is of major concern, revealing new reservoirs for MRSA.
- Prevalence studies for MRSA are needed to perform **Microbial Risk assessment.**

- MRSA was detected in 1/30 (3.3%) of the sampled animals
- **Proportion of MRSA was 1/19 (5%) of the** *S. aureus* isolates

Table 1. Prevalence of *S. aureus* and MRSA in studied animals, Greece 2021 (N=30).

	Total samples	S. aureus		MRSA	
	N=30	Ν	%	Ν	%
Farm A	10	10	100	0	0
Farm B	10	8	80	1	10
Farm C	10	1	10	0	0
Total	30	19	63.3	1	3.3

- MRSA isolate was harboring the mecA but, mecC or Panton-Valentine Leucocidin (PVL) genes not detected.
- Enterotoxin producer, seb and sed genes detected
- Weak-biofilm producer
- STSM was conducted during August 2021, funded by **RIBMINS COST** action, to assess the prevalence of MRSA in small ruminants before slaughtering.



Figure 1. Photos of the STSM carried out in Greece August 2021.

- **Resistance** to **penicilli**n, **oxacilli**n, trimethoprim, **tetracycli**ne, and amoxycillin/clavulanic acid
- Assigned to **spa type t13336**
- **PFGE** subtyping did not reveal connection with other pulsotypes origination from food animals, milk, meat, and humans (Fig 2).



Methods

- Nasal swabs collected from 30 goats (3 different farms, 10 animals per farm) at farm level before slaughtering in an abattoir in Thessaloniki, GR.
- 4 presumptive Staphylococcus aureus (S. aureus) colonies were selected from each sample for molecular confirmation, and antimicrobial susceptibility testing versus 19 antimicrobials.
- Genetic characterization (*mecA* and *mecC* genes, virulence-associated genes, Staphylococcus enterotoxin genes, assessment of biofilm-formation ability, Pulsed field gel electrophoresis and spa typing)















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Figure 2. Pulsotypes of the isolated MRSA **t13336** (green arrow) and other MRSA isolates of food and animal origin, Greece August 2021.

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