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# ***Staphylococcus aureus* and methicilin-resistant *Staphylococcus aureus* (MRSA) in Greek dairy farms: A “one health” perspective**



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# 1. Background

- *Staphylococcus aureus* (*S. aureus*) → the third most common food-borne pathogen that causes food poisoning worldwide.
- Methicillin-Resistant *S. aureus* (MRSA) represents a serious public-health concern
- Transmission may occur by
  - direct contact with infected animals (personnel in farms and food handlers)
  - handling and consumption of food of animal origin- contaminated with MRSA
- Greek dairy farms work in a mixed model –animals, in the same farm, are used for milk and meat production
- Personnel in these farms work both for meat and milk production

**We investigated the prevalence and genetic characteristics of *S. aureus* and MRSA in animals and farm personnel of dairy farms in Northern Greece.**

## 2. Materials/Methods

- A total of 571 samples (nasal swabs) from 64 dairy farms
  - Farmers: N=109
  - Dairy cows: N=124
  - Sheep: N=215
  - Goats: N=123
- *S. aureus* detection according to ISO 6888-1 (ISO 1999)
- Epirus, East Macedonia/Thrace and Central Macedonia



- Susceptibility towards 14 antimicrobials
- Interpretation using EUCAST criteria
- All phenotypically confirmed MRSA strains:
  - presence of *mecA*, *mecC* genes
  - presence of Pandon-Valentine Leucocidin (*PVL*) genes
  - presence of the *sea*, *seb*, *sec*, *sed* and *see* genes that encode for the “classic” staphylococcal enterotoxins
  - characterized by *spa* typing
  - characterized by PFGE typing

## 3. Results

- Overall 320/571 (56%) samples were *S. aureus* positive
- 19/571 of the samples were MRSA positive
  - 10/109 (1%) of the employees were MRSA carriers\*
  - 9/462 (0,2%) of the animals were MRSA carriers\*

**\*based on their phenotypic resistance to oxacillin**

## 3. Results

- Antimicrobial Susceptibility testing
  - Penicillin 98%,
  - Amoxicillin/clavulanic acid acid 87%
  - Tetracycline 37%
- 16/19 MRSA isolates carried the *mecA* gene, while the *mecC* and PVL genes were not detected.
- 95% of MRSA isolates carried one or more enterotoxin-coding genes, with *sec* being most prevalent.

# 3. Results

- 10 different *spa* types : t012, t034, t127, t192, t253, t1773, t3536, t4038, t13336.
- t127 being the most prevalent 5/19.
- One novel *spa* type was identified.
- One MRSA strain was un-typeable via *spa* typing.
- *Spa* type t034 (CC398) was isolated for the first time from livestock (goat) in Greece.
- PFGE did not identify common PFGE types among isolates of animal and personnel origin.

## 4. Conclusions

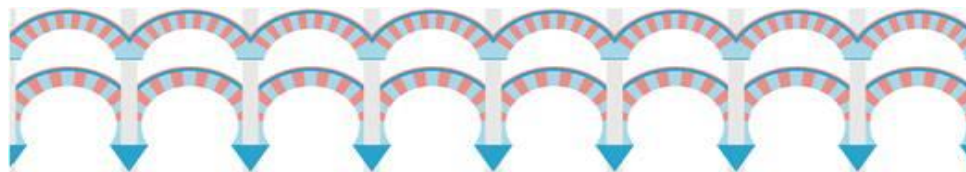
- Animal farms may contribute to the dissemination of MRSA strains (even enterotoxinogenic ones) in the community
- Personnel could potentially spread MRSA strains to the animals and to the food chain
- The fact that MRSA isolates originated from both human and animal sources, indicates the importance of the One Health approach in the prevention of the spread of *MRSA* through the food chain.



# Thank you!



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