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Poster Session VI

Zoonotic antimicrobial resistance

STAPHYLOCOCCUS AUREUS ISOLATED FROM FARM ANIMALS AND HUMANS IN CLOSE CONTACT, IN GREECE

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Objective: *Staphylococcus aureus* is associated with an increasing number of community and livestock-associated infections. To gain deeper insight into the epidemiology and diversity of *S. aureus* we collected samples from farm animals, their environment and human contacts.

Methods: Isolates were identified as *S. aureus* by conventional tests, followed by MIC determination of oxacillin, vancomycin, linezolid, teicoplanin and daptomycin by the Etest, whereas their antibiotic resistance patterns to antistaphylococcal agents was performed by the disk diffusion method. The genes: *mecA* (encoding PBP2a), *mecC*, *lukS/lukF-PV* (encoding PVL), *tst* (encoding TSST-1) and SCC*mec* types were defined by PCRs with specific primers. Clones were determined by PFGE of chromosomal DNA *Sma*I digests, *spa*-typing and MLST.

Results: A total of 49 *S. aureus* were identified among 220 staphylococci recovered from 100 farm animals, 57 humans and 262 samples from their environment, from January 2011 till December 2012. Ten *S. aureus* were human colonizing isolates, sixteen from animals and twenty-three were recovered from the environment. Thirteen isolates out of 49 (26.5%) were MRSA (5 from farm animals, 2 from humans and 6 from the environment) whereas; three among them were *mecC*-positive (23.1%). The MIC of oxacillin ranged from 0.125 to 24 mg/L, while the MIC<sub>90</sub> of vancomycin, teicoplanin, linezolid and daptomycin were 1.5, 1.5, 1.1 and 0.4 mg/L, respectively. Eighteen *S. aureus* (36.7%) were PVL-positive, while no one carried the *tst* gene. PVL was identified within 7 clones. MRSA belonged to 5 clones according to MLST-SCC*mec* types: ST88-IV (8 isolates), ST109-IV (1), ST149-I (1), ST5-II (1) and ST425-XI (2). Five methicillin-susceptible *S. aureus* (MSSA) were classified to ST398, while the remaining MSSA belonged to ST10 (1 isolate), ST15 (7), ST30 (5), ST80 (12), ST88 (1), ST109 (2), and ST149 (3). Antibiotic resistance patterns were clonal-associated. Common clones were identified among the three different groups. Six different PFGE and seven *spa*-types (predominant: t7558) were identified among MRSA, whereas, in MSSA, 14 PFGE and 15 *spa* types (predominant: t7558, t094) were found.

Conclusion: *S. aureus* has colonized farm animals and their environment, where human-associated clones such as ST80 and ST30 have disseminated. Moreover, ST398 clone of animal origin was found in human close contacts and their environment as well. The transmission of human origin strains in the animal setting and vice versa, creates a group of hosts where resistant isolates can evolve and eventually cause outbreaks.

