

**P2685 Molecular analysis of *Staphylococcus aureus* nasal colonisation in nursing home residents**

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**Background:** Nursing homes are known reservoirs of methicillin-resistant *Staphylococcus aureus* (MRSA). The present study investigated the point prevalence and molecular epidemiology of *S. aureus* colonization among nursing home residents.

**Materials/methods:** The study population comprised of 218 residents, living in four nursing homes of the Heraklion, Crete, Greece area, between January 2015 and June 2016. Swabs from the anterior nares of each resident were obtained within a 2-week period. The isolated *S. aureus* strains were identified and screened by standard microbiological and molecular epidemiological methods.

**Results:** *S. aureus* carriage was found in the nares of 62 out of 218 participants (28.4%) with 33 (53.2%) being MRSA. The participants' median age was 82.2 years (range 65-103). Females were more frequently colonized [47 (75.8 %)]. All 33 MRSA isolates were *mecA*-positive carrying SCC*mec* type IV, 30 (91%) the *fnbA*, and 17 (51.5%) the PVL genes, whereas, 30 (91%) were classified to *agr2* group. Thirty-two (97%) belonged to a single pulsotype C, correlated to the ST80 European clone. Among the 33 MRSA isolates, 32 (97%) were clindamycin-resistant, carrying the *ermA* gene. It is worth noting that 85% of the MRSA colonized participants had not been exposed to nosocomial environment during the previous 12 months. Methicillin-susceptible *Staphylococcus aureus* strains showed polyclonality and 76% were PVL-positive.

**Conclusions:** This regional study has shown that nursing homes in the Heralion area are important reservoirs of community-associated MRSA.

