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Colonization by multidrug-resistant organisms in long-term care facilities in Italy: a point-prevalence study[☆]

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ABSTRACT

Objectives: To determine prevalence and risk factors for colonization by multidrug-resistant organisms (MDROs) in long-term care facility (LTCF) residents in Italy. Genotypes of MDRO isolates were investigated.

Methods: A point-prevalence study was conducted at 12 LTCFs located in four Italian cities (2 February to 14 March 2015). Rectal swabs, faeces and nasal/auxiliary swabs were cultured for extended-spectrum β -lactamase (ESBL)- and/or carbapenemase-producing *Enterobacteriaceae*, *Clostridium difficile* and methicillin-resistant *Staphylococcus aureus* (MRSA) respectively. Antimicrobial susceptibility testing, detection of ESBL and/or carbapenemase genes and molecular typing of MDROs were performed. Risk factors for colonization were determined by univariate and multivariate analysis.

Results: A total of 489 LTCF residents aged ≥ 65 years were enrolled. The prevalence of colonization by ESBL-producing *Enterobacteriaceae*, MRSA and *C. difficile* was 57.3% (279/487), 17.2% (84/487) and 5.1% (21/409) respectively. Carriage rate of carbapenemase-producing *Enterobacteriaceae* was 1% (5/487). Being bedridden was a common independent risk factor for colonization by all MDROs, although risk factors specific for each MDRO were identified. ESBL-producing *Escherichia coli* carriage was associated with the sequence type (ST) 131-H30 subclone, but other minor STs predominated in individual LTCF or in LTCFs located in the same city, suggesting a role for intrafacility or local transmission. Similarly, MRSA from LTCF residents belonged to the same *spa* types/ST clones (t008/ST8 and t032/ST22) commonly found in Italian acute-care hospitals, but infrequent *spa* types were recovered in individual LTCFs. The prevalent *C. difficile* PCR ribotypes were 356/607 and 018, both common in Italian acute-care hospitals. **Conclusions:** MDRO colonization is common among residents in Italian LTCFs. **M. Giufrè, Clin Microbiol Infect 2017;•:1**

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