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Abstract (oral session)

A binational cohort study of colonisation with ESBL-producing Proteus mirabilis in patients admitted to rehabilitation centres

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Objectives: Our aims were 1) to analyze the risk factors for colonization with extended-spectrum beta - lactamase-producing Proteus mirabilis (ESBLPM) and 2) to characterize the molecular features of these strains. Methods: The study was conducted in 2 rehabilitation centers; in Tel-Aviv, Israel (TA), and Rome, Italy (RM), from October 2008 to April 2011. Carriage of ESBLPM was surveyed by rectal swabs. ESBLs, confirmed by DDST, were identified by PCR and sequencing. Typing was carried out by PFGE. Clinical and demographic data were collected retrospectively from patients' charts. Patients admitted to the same institutions without ESBLPM carriage (TA-50, RM-100) were controls. Results: The study group included 73 and 31 patients from RM and TA, respectively. The mean age was 62 years, ranging from 18 to 99 years. Most patients (91%) were admitted from acute-care hospitals following either acute neurologic disorder or musculoskeletal injury. Compared with the control group, ESBLPM carriers were more likely to have a history of long-term care facility stay in the last 6 months (11/104 vs. 8/150, $p<0.01$), have an invasive device in the preceding month (80/104 vs. 94/150, $p<0.05$), be admitted with active infection (16/104 vs. 6/150, $p<0.01$), and receive antimicrobial treatment in the preceding month (52/104 vs. 56/150, $p<0.05$). In multivariate analysis, active infection on admission remained the single significant risk factor (OR=4.03, C.I. 95% 1.47-11.1, p=0.007). No patient died during the hospitalization. ESBLPM carriers were less likely to be discharged home (61/104 vs. 140/150, $p<0.01$). In RM, most ESBLPM produced TEM-92 (n=66, 90%); other ESBLs were TEM-72 (n=3), TEM-177 (n=3) and CTX-M-15 (n=1). In TA, CTX-M-2 was the most common ESBL (n=29, 93%); others were CTX-M-39 and CTX-M-94 (n=1 each). The clonal structure in RM consisted of 5 major clones, grouping 48 isolates (65%), and 17 minor clones. In TA, there were 3 major clones, comprising 25 isolates (80%), and 5 minor clones. No similarities in PFGE patterns between the institutions were observed. Conclusions: Active infection upon admission was the main risk factor for ESBLPM colonization. The ESBLPM populations were clonally diverse, suggesting that the dissemination of the blaTEM-92 and blaCTX-M-2 genes in RM and TA, respectively, was probably due to transfer of mobile genetic elements.