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SIGNIFICANT CHANGES IN THE EPIDEMIOLOGY OF BLOODSTREAM INFECTIONS (BSI): RESULTS OF A PROSPECTIVE, LONGITUDINAL, REGION-WIDE SURVEY CONDUCTED BETWEEN 2007 AND 2013.

C. Danet[1], H. Gbaguidi-Haore[2], S. Borges Dos Santos[1], N. Girard[3], R. Quentin[1], **N. Van der Mee-Marquet**[1], - BSI Study Group[3]

[1]Microbiology and Hygiene, University Hospital, TOURS, France ; [2]Microbiology and Hygiene, University Hospital, BESANCON, France ; [3]RHC, Réseau des Hygiénistes du Centre, TOURS, France

Objectives

To establish a comprehensive picture of the epidemiology of BSI, a BSI surveillance program in the Centre region of France (2.7 M inhabitants) and a microbiological study of *S. aureus* and ESBL-producing enterobacteriaceae (*ESBLE*) isolates has been under way since 2000. We report the results for the years 2007 to 2013.

Methods

Data are collected for 3 months of each year in a stable cohort of 33 healthcare care institutions (HCIs), comprising 6330 short-stay beds. The survey covered 3,258,015 patient days (PD). The variable studied included patient age and sex, recent history of catheterization (urinary, intravenous) and mechanical ventilation, portal of entry, community- or hospital-acquisition, death within 7 days of BSI diagnosis. The incidence of BSI was determined with respect to the number of PDs. *S. aureus* and ESBLE isolates were collected during the 7 survey periods, tested for antimicrobial susceptibility and genotyped.

Results

During the study period, 6565 BSI cases were recorded (3698 CA- and 2867 HA-BSI) in 3733 males and 2832 females, including 1096 *S. aureus* BSI (268 MRSA, 24 %) and 126 *ESBLE* BSI (including 88 *E. coli*, 27 *K. pneumoniae*).

The incidence of CA-BSI increased significantly (+26% in males and +6% in females), as a result from significant increase in (1) CA-BSI with a digestive portal of entry (+42%), (2) ceftazidime-resistant *E. coli* CA-BSI associated with a digestive portal of entry (none in 2007 and 0.015/1000 PD in 2013) and (3) *MSSA* CA-BSI (+81%).

The incidence of HA-BSI increased significantly (+38%), as a result from significant increase in (1) *E. coli* HA-BSI with a pulmonary portal of entry in males (+102%), (2) *E. coli* HA-BSI with a urinary portal of entry (+16%) and (3) *ESBLE* HA-BSI (none in 2007 and 0.015/1000 PD in 2013). The incidence of MSSA and MRSA HA-BSI was stable.

Genotyping of the *S. aureus* strains revealed highly diverse population of strains and the emergence of strains belonging to clonal complex usually associated with livestock (CC398, CC59, CC97; one BSI in 2007 *vs* 10 % of MSSA BSI in 2013). Among ESBLE, *E. coli* strains showed the highest genetical diversity (only two strains sharing the same PFGE pattern in 2013). By contrast, *K. pneumoniae* showed a low diversity resulting from epidemics.

Conclusion

Our findings showed rapid changes in the epidemiology of BSI, involving the two major pathogens, *E. coli* and *S. aureus*. The major increase of incidence in CA-BSI associated with a digestive portal of entry, the increasing prevalence of ESBL-producing *E. coli* and the emergence of livestock associated *S. aureus* that have been both isolated from food products, alert about the need to study the potential role of food into the changes observed, and consider these changes for the adaptation of infection control strategy.