

P0474 Increasing incidence of *Enterococcus faecium* in Copenhagen, Denmark, 2000-2017 and the introduction of a successful clone

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Background: *Enterococcus faecium* is an important nosocomial pathogen. An increase of *E. faecium* bacteraemia has been observed over the past two decades in the Capital Region of Denmark (1.7 million inhabitants). Surveillance data from Europe has also shown an annual increase of approximately 20% for *E. faecium* bacteraemia from 2002-2008. A relative increase in elderly patients, complex medical treatment, co-morbidity and the introduction of a successful clone(s) has been suggested as explanations for the rising trend. The aim of the study was to confirm an increase in the incidence of *E. faecium* bacteraemia. Clinical and demographic characteristics and the genetic epidemiology of *E. faecium* bacteraemia isolates were investigated to understand the increase.

Materials/methods: A population-based cohort study comprising all patients with a first episode of *E. faecium* bacteraemia in the Capital Region of Denmark from 2000-November 2017 was conducted. Clinical and demographic characteristics were collected from a bacteraemia research database (containing data from 2000-2015) and compared for the periods 2000-2008 and 2009-2015. All *E. faecium* isolates sampled in 2005 and 2013 and stored at -80°C were whole genome sequenced on the Illumina MiSeq platform. A core-genome was defined by Roary and a RAxML tree was constructed

Results: During the eighteen-year study, 1879 episodes of *E. faecium* bacteraemia were observed during 29 million person-years of surveillance. The incidence of *E. faecium* bacteraemia showed a rising trend, with an increase from 1.3/100,000 person-years to 10.5/100,000 person-years (Figure 1). No significant differences regarding hospital-acquired bacteraemia (84% vs. 73%), polymicrobial bacteraemia (35% vs. 29%), Charlson co-morbidity index ≥ 3 (47% vs. 52%), the percentage of residents ≥ 60 years (20% vs. 21.6%) and 30-day mortality (43% vs. 41%) were observed between the two periods 2000-2008 and 2009-2015.

The phylogenetic tree of *E. faecium* isolates from 2005 (n=54) and 2013 (n=120) showed high diversity with 16 clonal groups and 28 singletons. However, 64% (n=77) of the isolates from 2013 belonged to one clonal group, ST117.

Conclusions: An increase of *E. faecium* bacteraemia was confirmed. Data supports that the increase was mainly caused by the introduction of a successful ampicillin resistant clone that has spread between hospitalised patients.

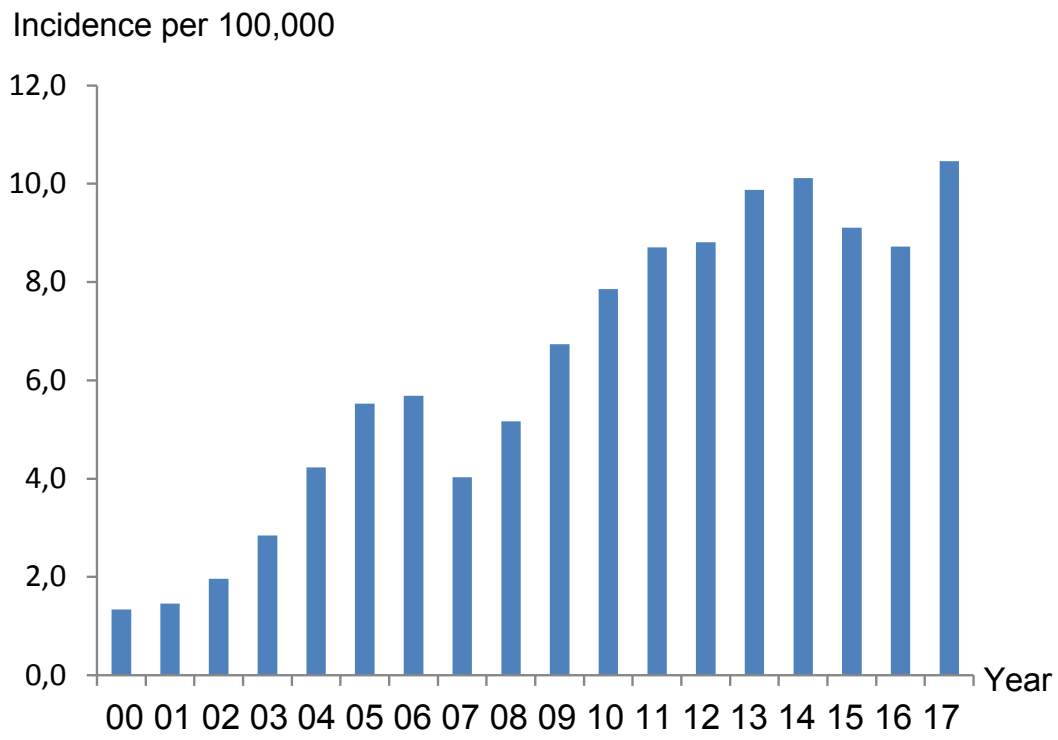


Figure 1: Annual incidence of *E. faecium* bacteraemia