

No total, existiam 11 doentes com trissomia 8 isolada, um valor ligeiramente inferior ao descrito na literatura.

CONCLUSÃO

A ocorrência de trissomia 8 em diferentes tipos de leucemias está descrita na literatura, e a sua importância está também para além do estabelecimento dos grupos de risco, no facto de cerca de 25% dos doentes com síndrome mielodisplásico com trissomia 8 estarem em risco de desenvolver leucemia. Para este estudo as percentagens dos doentes com trissomia 8 são ligeiramente inferiores às descritas na literatura. Provavelmente utilizando as técnicas de FISH, uma técnica mais sensível, poderemos obter valores mais próximos dos descritos.

CL3 – Worldwide prevalence and distribution of acquired AmpC- β -lactamases in Enterobacteriaceae lacking inducible AmpC

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INTRODUCTION

Acquired AmpC beta-lactamases (qAmpC) which confer resistance to cephamycins and reduced susceptibility to extended-spectrum cephalosporins and β -lactamase inhibitors have increasingly been recognized as an emerging problem worldwide. qAmpCs enzymes are grouped according to the DNA sequence similarity with natural chromosomal AmpCs of some *Enterobacteriaceae* species, namely *C. freundii* (CMY-2-like, LAT-1, CFE-1), *Enterobacter* spp. (ACT-1-like, MIR-1-like), *M. morgannii* (DHA-1-like) and *H. alvei* (ACC-1-like), and with *Aeromonas* spp. (CMY-1-like, FOX-1-like, MOX-1-like). Isolates harbouring qAmpCs are usually multir-resistant, and inappropriate empirical therapy is associated with high mortality ratios in invasive infections.

OBJECTIVES

Estimate the worldwide prevalence and distribution of qAmpC types.

METHODS

We conducted a literature review on pertinent articles published between 2000 and 2011 on qAmpC detection and prevalence in *Enterobacteriaceae* lacking inducible AmpC [*E. coli* (EC), *K. pneumoniae* (KP), *K. oxytoca* (KO), *P. mirabilis* (PM) and *Salmonella* spp. (SM)] isolated from human infections. Estimated relative frequencies were calculated for qAmpC types detected in each country with relevant articles.

RESULTS

A total of 26 relevant studies from 21 countries on qAmpC epidemiology were retrieved, comprising 216648 isolates (182573 EC, 18858 KP, 8117 SM, 2340 PM, and 2278 KO). qAmpCs were detected in all but one study from Brazil, being the worldwide overall prevalence 0.55% (1194/216648, or 5.5 qAmpC producers per 1000 isolates). Countries with higher prevalence were China (4%), South Korea (3.5%), Portugal (3%) and Poland (3%), and the lowest were observed in Brazil (0%), Japan (0.08%), Switzerland (0.16%) and Belgium (0.16%). The overall species specific prevalence was 4.1%, 3.5%, 1.4%, 0.5% and 0.2% in SM, PM, KP, KO, and EC respectively. China presented the higher prevalence for KP (7%) and KO (3%), Thailand for EC (2%), while for PM and SM it was Poland (20.5%) and Mexico (7.7%), respectively. Globally, the main qAmpC variants detected were CMY-2 (53.1%), DHA-1 (30.6%) and CMY-2-like (11.7%). CMY-2 was predominantly present in EC, PM and SM isolates while DHA-1 was detected mostly among KP and KO. In countries like South Korea, China, and Portugal DHA-1 is the dominant variant, while in North America, Norway, Denmark, Thailand, Japan, Algeria and Spain is CMY-2.

CONCLUSION

Although qAmpC prevalence is globally low, the results suggest that it is rising. This study also demonstrates that CMY-2 is the most prevalent qAmpC followed by DHA-1. Future studies are needed in order to monitor the spread of this emerging resistance mechanism.