Infections by *Streptococcus agalactiae* among neonates in Portugal: 2005-2014

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BACKGROUND

Group B streptococci (GBS) is a leading cause of neonatal invasive disease in most countries. We undertook the analysis of 196 GBS isolates recovered from invasive infections in newborns in Portugal, between 2005 and 2014, with the aim of documenting changes in the prevalence of serotypes, antimicrobial resistance patterns and genetic lineages and evaluating their association with either early-onset (EOD) or late-onset disease (LOD).

MATERIALS AND METHODS

All isolates were serotyped and assigned to sequence types (STs) according to the multilocus sequence typing scheme.

Susceptibility to penicillin, erythromycin, clindamycin, vancomycin, chloramphenicol, tetracycline and levofloxacin was tested by disk diffusion according to the CLSI guidelines.

Macrolide and tetracycline resistance genes were determined by PCR. The presence of the surface protein genes *bca*, *alp2*, *alp3*, *alp4*, *eps* and *rib* genes and of the pilus islands 1, 2a and 2b was also tested by PCR.

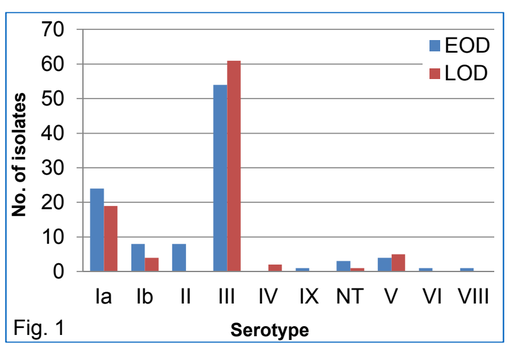

Fig. 1

RESULTS

Serotypes III (n=115) and Ia (n=43) were the most frequent in the population, together accounting for over 80% of the isolates. Serotypes VIII and IX were detected for the first time in Portugal (Fig. 1).

The isolates grouped into 33 STs and 7 clonal complexes (CC). CC17 included 50% of all isolates, highlighting the importance of the hypervirulent lineage represented by serotype III ST17/*rib*/PI-1+PI-2b.

Serotype Ia was found mainly in CC23 (Fig. 2), previously reported as dominant among invasive infections in non-pregnant adults in Portugal (1). Within CC23 we could distinguish two sublineages, ST23/*eps* (n=28) and ST24/*bca* (n=16), the latter at a higher frequency in the GBS population when compared to our previous studies (1,2). While ST23 and its SLVs were associated with EOD, ST24 and its SLVs were dominant among LOD cases (P<0.001), indicating that within the same CC particular sublineages may be better adapted to specific age groups or disease presentations.

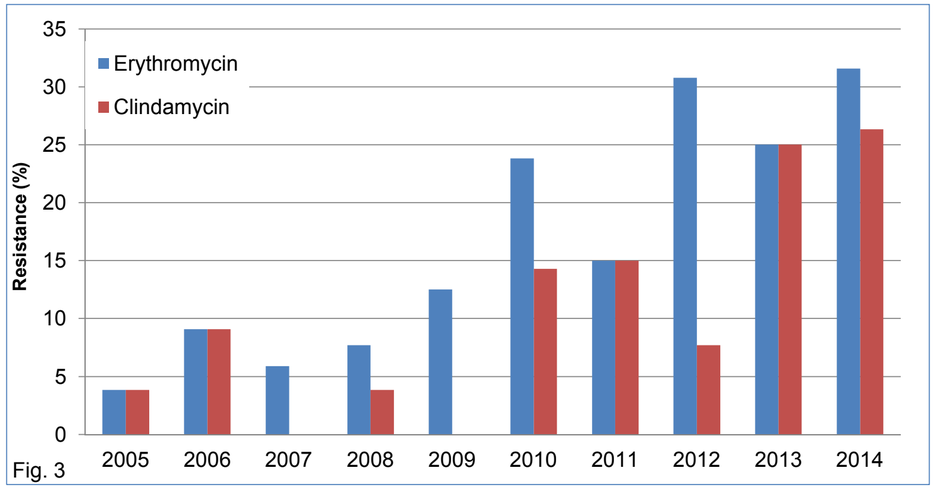

Fig. 3

All isolates were susceptible to levofloxacin, penicillin, and vancomycin. Resistance to chloramphenicol was found in 3 isolates. Most isolates were resistant to tetracycline (n=168; 86%) and carried *tetM* (n=161%). Macrolide resistance increased during the study period (P<0.001), for an overall resistance rate of 15.3% (Fig. 3). Most of the isolates presented the $cMLS_B$ phenotype associated with the *erm*(B) gene. Macrolide resistance was overrepresented among serotype Ib isolates (P=0.004) and particularly associated with CC1 (P<0.001) and CC19 (P=0.003) while most isolates of the hypervirulent CC17 lineage were susceptible (P=0.003).

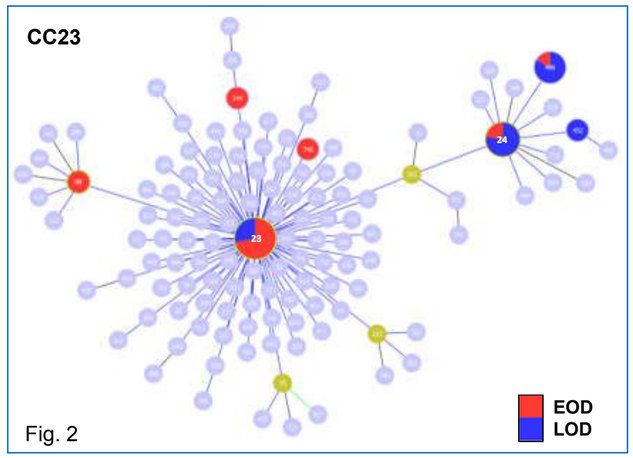

Fig. 2

CONCLUSIONS

The GBS recovered from 10 years of neonatal invasive infections in Portugal were dominated by a small number of genetically distinct lineages that were present over a significant time-span.

The stability and dominance of a few lineages, namely of the hypervirulent serotype III ST17/*rib*, which remains responsible for the majority of infections in spite of continuous antibiotic and immune selective pressures, suggest that these are extremely well adapted to this niche. Still, we have also identified seemingly regionally successful clones, raising the possibility of an ongoing selection and expansion of specific virulent GBS clones.

References

(1) Martins *et al*, 2012. J Clin Microbiol 50(4): 1219-27

(2) Martins *et al*, 2007. J Clin Microbiol 45(10): 3224-9

(3) Martins *et al*, 2011. J Clin Microbiol 49(8): 2911-8.

ACKNOWLEDGMENTS

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