Colonization as a reservoir for *Streptococcus agalactiae* infections – lessons from non-pregnant adults

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BACKGROUND

Streptococcus agalactiae (group B streptococci, GBS) is a colonizing agent of the genitourinary and gastrointestinal tracts. It is also recognized as a leading cause of bacterial sepsis and meningitis in neonates and is increasingly associated with invasive infections in adults.

The aim of this study was to evaluate GBS colonization among community dwelling non-pregnant adults and to characterize their genetic diversity. Comparison of adult colonization isolates with those causing invasive disease could help identify lineages with propensity to colonize different anatomical sites or with an enhanced invasive disease potential.

MATERIALS AND METHODS

We evaluated GBS gastrointestinal, genitourinary and oral colonization among 336 non-pregnant adults in the community. We characterized the isolates by serotyping, multilocus sequence typing, surface protein gene and pili profiling, and antimicrobial susceptibility and compared with contemporary invasive isolates.

RESULTS

The colonization rate (32%) among non-pregnant adults was similar to that of pregnant women. Colonization increased with age (Fig. 1), potentially explaining the higher incidence of disease with older age and was more frequent among the diabetic.

Participants who were colonized at multiple sites (73%) were frequently carrying the same strain (93%), consistent with the existence of a single reservoir of colonization and transfer of GBS between sites within the same individual.

The most frequent lineages found were serotype Ib/CC1 (23%), serotype V/CC1 (17%), serotype Ia/CC23 (11%), serotype III/ST17 (11%), and serotype Ib/CC11 (10%). Comparison with contemporary isolates causing invasive infections in Portugal (Fig. 2) revealed that GBS colonization and disease appear to be restricted to a limited number of lineages represented equally in carriage and infection.

Fig. 1. GBS colonization rate by gender and age group.

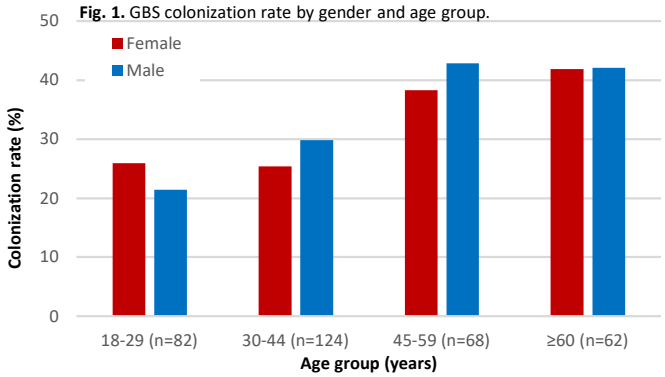
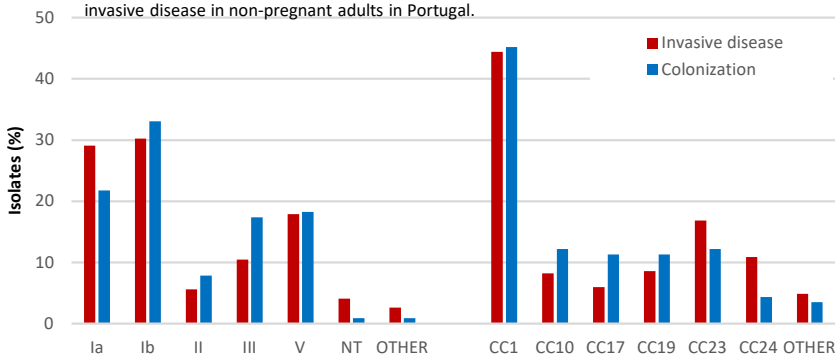


Fig. 2. Comparison of serotype and clonal complex distribution of GBS colonizing and causing invasive disease in non-pregnant adults in Portugal.



All isolates were susceptible to penicillin, vancomycin, chloramphenicol, and gentamicin. Tetracycline resistance was found in 89.6% of the isolates (n=103), mostly associated with the tet(M) gene. The overall rates of erythromycin and clindamycin resistance were 41.7% (n=48) and 40.9% (n=47), respectively. Erythromycin resistance was overrepresented within CC1 ($p<0.001$) and serotype Ib ($p<0.001$), with all serotype Ib/CC1 isolates presenting the cMLSB phenotype and carrying the erm(B) gene. Three isolates (2.6%) presented high-level resistance to streptomycin, of which two belong to the serotype III/CC17/PI-2b subset of the hypervirulent lineage, being simultaneously resistant to macrolides, lincosamides and tetracycline, a sublineage previously reported among neonatal and adult invasive disease cases in Portugal.

CONCLUSIONS

Our study shows a similar distribution of serotypes and genetic lineages in contemporary colonizing and invasive disease isolates in a geographically restricted adult population.
Asymptomatic colonization of non-pregnant adults is significant and could act as a reservoir for invasive disease but, in contrast to infant disease, in which there is a documented enhanced invasiveness of the serotype III/ST17 lineage, we found no GBS lineages with an increased potential for causing invasive disease in adults.