The Modern Approach: Group B streptococcus and the importance of microbial whole genome sequencing

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BACKGROUND

Group B streptococcus (GBS, *Streptococcus agalactiae*) is a common cause of early-onset sepsis and meningitis in neonates, therefore intrapartum prophylaxis is widely prescribed. However, there are concerns regarding over-treatment. Antibiotic resistance is increasing in GBS (1) and penicillin resistance has been reported in Japan, spread of resistance is likely to be of significant consequence (2). Modern routine microbiology laboratories are beginning to use Whole Genome Sequencing to improve diagnosis, typing and antimicrobial treatment of bacterial infections as well as for outbreak management (3,4,5).

OBJECTIVE

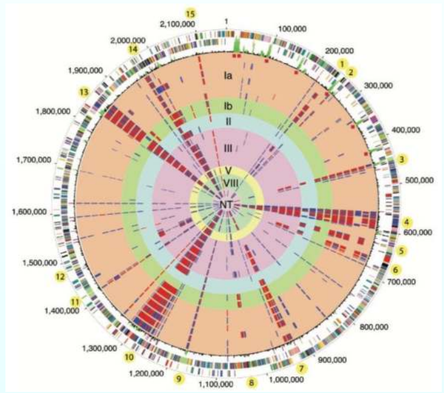
This review seeks to inform clinicians how Whole Genome Sequencing could be used to improve GBS detection and antibiotic choices in the routine management of patients. It also describes the role of WGS in the detection and management outbreaks involving GBS.

METHODS

Literature search

The literature since 2000 was reviewed. In Ovid, Embase, PubMed and Google Scholar, the key words used were “group B streptococcus”, “*Streptococcus agalactiae*”, “molecular”, ”virulence gene”, “antibiotic resistance”, “whole genome sequencing” and “routine microbiology laboratory” and 54 relevant publications were identified. Of these, 12 were cited on this poster and are therefore given below.

LEARNING POINTS / DISCUSSION



Group B streptococcus gene map (6, Copyright (2002) National Academy of Sciences, U.S.A.)

Group B streptococci (6,7)

Serotypes Ia, Ib, II, III, V cause the majority of invasive human GBS disease.

About 50 % of genes are considered as orthologous with *S.pyogenes* and *S.pneumoniae*.

Factors implicated in virulence are genes coding for surface proteins, e.g. *lmb, bca,* and for secreted proteins, e.g. *cylE, cfb*.

Whole Genome Sequencing in the Detection of GBS

- Whole genome sequencing has successfully been used for the identification of GBS directly from clinical samples, but it is not a routine method in the hospital microbiology laboratory (3,4).
- Serotyping with WGS is equivalent to established methods; the *cpsG-K* regions were proposed as the most suitable (8).
- Detection of virulence genes, e.g. for toxins, or their absence might lead to improved understanding of who will benefit from antibiotic prophylaxis (7,9)
- The detection of antibiotic-resistance genes could potentially improve the choice of antibiotics (10, 11).

Outbreak Detection

- WGS can improve outbreak management. Where specific genetic traits are identified, identification of symptomatic cases and improved screening of asymptomatic cases becomes possible. (5)
- GBS colonises different hosts, e.g. humans, dogs, fish, cattle, which could be the source of outbreaks (12).

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CONCLUSIONS

Whole Genome Sequencing has the potential to improve detection and treatment of Group B streptococcus. However, it still has a turn-around time of currently 3-4 days and costs are several times that of bacterial culture. This must improve for it to be used as standard in the modern routine microbiological laboratory.