INTRODUCTION

- **Many Neisseria species** are commensal to the human oro-nasopharynx in the same manner as *N. meningitidis*, but with a much reduced association with disease.

- **On rare occasions**, many of these species cause a range of invasive diseases including meningitis, septicemia and endocarditis. Patients may be predisposed to these infections by surgery and immunosuppression but they can occur in seemingly healthy patients. The exact incidence of disease caused by these organisms is unknown, but there are many published case reports.

- **Neisseria species** uptake DNA primarily through type IV pili and undergo frequent horizontal gene transfer (HGT). This includes genes encoding for vaccine antigens and genes encoding antibiotic resistance.

- The **UKHSA Meningococcal Reference Unit** (MRU) received 35 non-meningococcal/gonococcal Neisseria isolates from cases in England between 2010 and 2021.

RESULTS

- Of the 35 isolates characterised (Table 1), *N. subflava* was the most commonly-isolated species (n=11), followed by *N. mucosa* (n=9), *N. polysaccharea* (n=4), *N. oralis* (n=4), *N. cinerea* (n=3), *N. bergeri* (n=2) and *N. elongata* (n=2).

- Almost all (33/35, 94.3%) of isolates were isolated from blood culture, indicating bacteremia/septicemia. The two remaining strains were grown from CSF confirming clinically-suspected meningitis. Four isolates were grown from blood but the clinical notes suggest concurrent meningitis.

- Interestingly, eight cases (23%) were in suspected or confirmed cancer patients; this comprised 100% of *N. polysaccharea* infections and 50% of *N. bergeri* and *N. oralis* cases. The majority of cancer patients (63%) had leukaemia and 36% had lymphoma.

- In 14% of cases, other bacteria or viruses were detected, possibly indicative of coinfection.

- Two cases, an *N. mucosa* infection in a possible cancer patient and an *N. cinerea* and *Parainfluenza* virus coinfection were fatal.

DISCUSSION AND CONCLUSIONS

- **Table 2** shows a subset of isolates that possessed antigens found within licenced MenB vaccines.

- All *N. polysaccharea*, *N. cinerea* and *N. bergeri* isolates harboured fHbp alleles, with a variety of variant 1 (subfamily B) and variant 3 (subfamily A) variants observed. All *N. polysaccharea* and *N. bergeri* isolates possessed NHBA alleles.

METHODS

- *Neisseria* from invasive sites (expected to be sterile in a healthy patient) isolated between 2010 and 2021 were characterized visually, biochemically, and with antimicrobial susceptibility testing.

- DNA was extracted from the isolates, whole-genome sequencing performed and sequences uploaded to the Neisseria BIGSDb database (PubMLST.org) to determine species, antigen profile and genetic similarity.

REFERENCES


