have a slightly higher reduction of alcohol consumption over time.

Conclusion Motivational Interviewing proved an acceptable intervention for the nurse practitioner and this cohort of patients. A number of implications for practice were identified including improvements to patient clinical assessment practices and the provision of a MI intervention for alcohol reduction.

P05 - Antimicrobial resistance

P05.01 DRUG TARGET TO INHIBITOR (DT2I) APPROACH OF COMBATING INCREASING DRUG RESISTANCE IN *NEISSERIA GONORRHOEAE*

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Introduction *Neisseria gonorrhoeae* is an etiologic agent of one of the most common sexually transmitted disease in humans. The continuous rise of *N. gonorrhoeae* infection worldwide accompanied by rapid emergence of multidrug-resistant and hypervirulent strains has necessitated the search for novel drug targets and their inhibitors. The present study is undertaken to screen inhibitors against the novel drug targets of N. gonorrhoea.

Methods The putative therapeutic targets in *N. gonorrhoeae* were identified by *in silico* approach which encompassed similarity search between pathogen and host, essentiality study using the database of essential genes and metabolic functional association study using Kyoto Encyclopaedia of Genes and Genomes database. Virtual screening of inhibitors against the major candidate therapeutic targets was further carried out using docking analysis. *In vitro* protein inhibitor binding assays are proposed for the best docked compounds.

Results The study identified various promising drug targets which are non-homologous to human proteins, essential for the pathogen and present in important pathogen-specific pathways. The peptidoglycan biosynthesis pathway is the highest donor to the list of candidate target proteins followed by the two component system. Homology model of one of the identified potential targets from both these pathways, namely, glutamate racemase (product of murI gene) from peptidoglycan biosynthesis pathway and NarL protein from two component system, was constructed. Subsequently, by means of virtual screening approach, potential inhibitors from small molecules databases were predicted against both these targets. Identified inhibitors possesed better docking scores and stronger binding affinity with the target molecules compared to known inhibitors and natural substrate of these proteins. These novel compounds may facilitate the development of new drugs to combat increasing drug resistance associated with *N. gonorrhoeae*.

Conclusion Potential inhibitors predicted against *N. gonorrhoeae* in the present study opens new avenues for the treatment option against multidrug resistant strains.

Disclosure of interest statement There is no conflict of interest.

P05.02 *NEISSERIA GONORRHOEAE* STRAIN TYPES AND ANTIBIOTIC SUSCEPTIBILITY

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Background Molecular surveillance of *Neisseria gonorrhoeae* will help in understanding the transmission patterns of the infection and the acquisition/development of antibiotic resistant strains. We aimed to determine the antimicrobial resistance (AMR) and the genotypes of the *N. gonorrhoeae* isolates.

Methods Of a total of 287 *N. gonorrhoeae* isolates the minimal inhibitory concentration (MIC; mg/L) of penicillin, tetracycline, ciprofloxacin, ceftriaxone, azithromycin, spectinomycin and cefixime was determined employing the gold standard agar dilution method. β-lactamase production was detected using nitrocefin solution. The sequence types (STs) of the isolates was obtained using the NG-Multi Antigen Sequence Typing (NG-MAST) method.

Results All isolates were susceptible to ceftriaxone, spectinomycin, and cefixime. Resistance to ciprofloxacin, tetracycline, penicillin, and azithromycin was 50.9%, 46.3%, 26.5%, and 2.4% respectively. A total of 10.8% of the strains produced β-lactamase. Overall 74 STs were determined. Five STs made up for 50.3% of all the isolates: ST2992 (19.8%); ST1407 (9.7%); ST2400 (7.6%); ST387 (7.3%); ST2212(5.9%). ST387 was isolated in heterosexuals only and ST2400 and ST2992 in mainly men having sex with men. All ST387 were susceptible to all tested antibiotics with 95.2% of the strains having a MIC of 0.001 mg/L for ceftriaxone. All ST2992 were susceptible to ciprofloxacin and all ST1407, ST2212, and ST2400 were resistant. The median MICs for ceftriaxone were 0.03 μg/ml for ST1407, ST2212, and ST2400 and 0.008 μg/ml for ST2292. None of the five STs showed β-lactamase activity.

Conclusions Associations were found between antibiotic susceptibility and sequence type. The most important finding is the absolute susceptibility to the tested antibiotics of ST387, which was identified in heterosexuals only. Our preliminary results are very promising. However, more research is needed to further optimise the NG-MAST method for its use in predicting AMR and in molecular surveillance. Ultimately the method should be applicable directly on biological specimens.

Disclosure of interest Nothing to declare.

P05.03 PERFORMANCE OF TWO ENZYME AND ONE STRIP IMMUNE ASSAY FOR THE DETECTION OF IGM ANTI-*TREPONEMA PALLIDUM* ANTIBODIES

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Background The detection of anti-*Treponema pallidum* (Tp) IgM may be useful in the diagnosis of very early syphilis, re-infection and in the assessment of the newborn. We aimed to evaluate two enzyme and one strip immune assay for the detection of anti-Tp IgM in blood specimens.