

# Investigation of a Gonorrhoea Outbreak in an Isolated Northern Alberta Community, 2015

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## BACKGROUND

Sexual network analysis describes sexual relationships in a defined group of individuals and helps to understand the spread of sexually transmitted diseases (STI) in populations.

Molecular techniques such as *Neisseria gonorrhoeae* multiantigen sequence typing (NG-MAST) can be used to characterize gonococcal strains to identify clusters of linked individuals and to predict antibiotic resistance. Antibiotic resistance to third generation cephalosporins in gonorrhoea (NG) is an increasing problem in Canada and worldwide.

In 2015, there were 3,400 cases of NG in the province of Alberta, an 80% increase from 2014. In the North-Northwest subzone of Alberta, the NG rate in 2014 was 191/100,000 which was four times higher than the provincial rate (46/100,000).

Nearly 1/3 of cases in the subzone were reported from a small isolated community (population estimate: 2000- 2500 people).

## Objective

To identify transmission networks, risk behaviours and common transmission locations, we used a social network approach with cases, sexual partners, and genetic sequencing of gonococcal specimens.

## METHODS

A descriptive summary of all NG cases reported in 2015 from the community was conducted using routinely collected surveillance and partner data.

During a two week period in the fall of 2015, cases and contacts were contacted to be interviewed to identify local exposure details.

NG MAST was determined and susceptibility to cephalosporins and ciprofloxacin was predicted by RT-PCR using the NAAT specimens.<sup>1,2</sup>

A social network analysis was completed using partner information, transmission locations, and NG MAST.

## RESULTS

In 2015, there were 84 NG cases reported in the community.

- All cases were heterosexual.
- 47.6% (n=40) were female, and 20% (n=8) were pregnant.
- The median age was 24 years (IQR: 20-30).
- 56.0% (n=47) were symptomatic.

Twenty-one clients were interviewed for local exposure details, representing a participation rate of 19.1% for the 110 gonorrhoea cases and contacts.

- 90.5% (n=19) reported limited condom use.
- 66.7% (n=12) met partners through local house parties.
- 61.1% (n=11) reported being under the influence of alcohol or drugs during sexual encounters.

82.1% (n=69) of the cases had specimens that were sequence typed; 6 unique STs were found creating 5 sequence groups (SG).

- 76.8% (n=53) of the cases belonged to SG-7576, 15.9% (n=11) belonged to SG-12621. There were no significant differences in characteristics between these two SG (Table 1).

SNP assay results were available for 19 specimens among the 6 ST; all were predicted to be susceptible to cephalosporins and ciprofloxacin.

There were 5 sexual network components identified, with a total of 79 NG cases and 55 sexual contacts (Figure 1). The largest network component included 94.0% (n=126) of all network members, and was made up of 59.5% (n=75) NG cases. The remaining network components consisted of ≤3 individuals.

Table 1. Characteristics of Gonorrhoea Cases with >2 cases per Sequence Group (2015; N=64)

	SG-7576 (n=53)	SG-12621 (n=11)
Median Age	23 (21-28)	25 (20-41)
Female	24 (45.3)	5 (45.5)
Pregnant	4 (16.7)	1 (20.0)
Symptomatic	31 (73.8)	6 (60.0)
<b>SNP assay Predicted Susceptibility</b>		
Cephalosporins	Susceptible (11/11)	Susceptible (3/3)
Ciprofloxacin	Susceptible (10/10)	Susceptible (1/1)
Susceptibility from cultures at NML	Erythromycin Resistance, Tetracycline Resistance	No cultures available.
NML – National Microbiology Laboratory		

## RESULTS

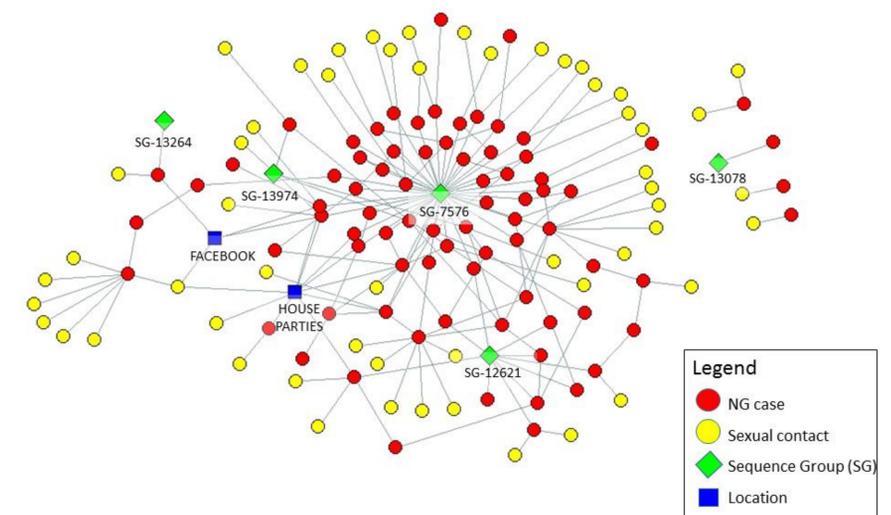


Figure 1. Social and Sexual Networks of NG Cases and Contacts Reported in the Community in 2015, Derived from Contact Tracing, Social Network Interviews, and NG-MAST

## CONCLUSIONS

By combining routine surveillance data, with enhanced exposure details and in depth laboratory data, we were able to ascertain that the outbreak consisted of primarily locally acquired cases and identified key aspects of the outbreak for local intervention.

The identification of key positions in the sexual network allowed local public health staff to engage specific high-risk network members as change agents in the development of interventions that seek to reduce risk behaviour and disrupt large network components.

Predicted antibiotic susceptibility patterns using SNP assay were not suggestive of NG strains resistant to third generation cephalosporins confirming the use of our current first line treatment with cefixime in combination with azithromycin.

## REFERENCES

- Peterson et al. Molecular assay for the detection of ciprofloxacin resistance in *Neisseria gonorrhoeae* from cultures and clinical Nucleic Acid Amplification Test (NAAT) DNA specimens. J Clin Microbiol 2015;53:3606-3608.
- Peterson et al. Molecular assay for the detection of genetic markers associated with decreased susceptibility to cephalosporins in *Neisseria gonorrhoeae*. J Clin Microbiol 2015; 53:2042-2048.