N. gonorrhoeae (NG) is classified as a superbug because it has developed resistance to all classes of antibiotics used for treatment, including extended spectrum cephalosporins (ESCs) and macrolides such as azithromycin. The later two antibiotics are used in combination therapy to combat antimicrobial resistance (AMR) development. Thus the surveillance of AMR in NG is critical to ensure that appropriate therapies are recommended. The shift from culture-based methods to nucleic acid amplification tests (NAAT) to detect NG infections does not permit AMR detection. Whole genome sequencing methods have been utilized to predict AMR from N. gonorrhoeae cultures and not from NAAT specimens. We evaluated a PCR approach to establish the AMR profiles to 6 antibiotics of 50 Ng positive Aptima remnant NAAT specimens. The AMR strain types were also evaluated.

Background

Methods

Results

1). Viral RNA mini kit showed improved DNA concentration and 260/230 ratio.

2). The utilization of approach 2 was more efficient for amplification of non-amplifiable Aptima urine specimens:

<table>
<thead>
<tr>
<th></th>
<th>% of amplicons obtained</th>
<th>% of Sequences aligned with NGSTAR database</th>
</tr>
</thead>
<tbody>
<tr>
<td>Approach 1</td>
<td>41.7% (146/350)</td>
<td>97% (142/146)</td>
</tr>
<tr>
<td>Approach 2</td>
<td>100% (204/204)</td>
<td>93% (189/204)</td>
</tr>
</tbody>
</table>

3). Emergence of reduced susceptibility to ESCs and Azithromycin resistance in N. gonorrhoeae:

Conclusions

- QIAGEN Viral RNA mini kit improved DNA quality and quantity from NAAT specimens.
- In contrast to the AMR determination from bacterial cultures, this study predicted emerging resistance to cephalosporins and azithromycin in Saskatchewan, with high levels of ciprofloxacin resistance.
- AMR surveillance can be increased by predicting AMR in NAAT specimens.