Molecular tests for the detection of antimicrobial resistant *Neisseria gonorrhoeae*: when, where, and how to use?

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**Purpose of review**
Molecular methods for the diagnosis of *Neisseria gonorrhoeae* are replacing bacterial culture in many settings. This review focuses on recent progress in the development of molecular tests to detect resistant *N. gonorrhoeae* both to enhance surveillance and to guide decisions about individual patient management.

**Recent findings**
Assays to enhance surveillance have been developed to detect determinants of resistance for all antibiotics used as first-line gonorrhoea treatment, or to detect specific ‘superbug’ strains, but few have been applied in clinical practice. The most advanced strategy relevant to individual case management is to identify ciprofloxacin-sensitive strains so that unnecessary use of ceftriaxone can be avoided. Cross-reactivity with pharyngeal commensal *Neisseria* species reduces specificity and is a challenge for many assays.

**Summary**
Progress with laboratory-based molecular tests to detect gonococcal resistance is being made but substantial challenges remain. No laboratory-based assay has been subjected to a field evaluation and no assay so far can be used as a point-of-care test. Given the threat of antimicrobial resistance, now is the time to exploit the molecular technologies used for diagnosis and to invest in the development of molecular gonococcal resistance tests that can be implemented for public health good.

**Keywords**
antimicrobial resistance, antimicrobial surveillance, *Neisseria gonorrhoeae*, point-of-care tests

**INTRODUCTION**
Antimicrobial resistant *Neisseria gonorrhoeae* is a global public health challenge [1]. New diagnostic strategies and novel antimicrobials are urgently needed to conserve ceftriaxone [2], the last antimicrobial for empirical first-line monotherapy for gonorrhoea in many countries [3,4\textsuperscript{*}]. Gonococcal strains with resistance to extended-spectrum cephalosporins have caused treatment failure with ceftriaxone and/or cefixime in Europe, North America, Asia, and Africa [5–9]. In this evolving situation, dual antimicrobial therapy (ceftriaxone plus azithromycin) has been introduced for first-line treatment in Europe, Australia, and the United States [10].

Detection of antimicrobial resistant gonococci using molecular methods is a necessary innovation [2,6,11,12] because nucleic acid amplification tests (NAAT) are now the most widely used assays for gonorrhoea diagnosis in many countries [11,13,14\textsuperscript{*},15]. The WHO global action plan to mitigate the spread of multidrug-resistant gonococci calls for increased surveillance of antimicrobial resistant *N. gonorrhoeae* globally, strengthened capacity for bacterial culture and research into molecular methods to monitor and detect resistance [1]. We searched the US National Library of Medicine (Ovid Medline) using the medical subject headings 'N. gonorrhoeae' or 'gonorrhoea', ‘drug resistance,
KEY POINTS

- Molecular methods are increasingly used for gonorrhoea diagnosis but, despite the global threat of antimicrobial resistance, commercially available diagnostic assays do not detect gonococcal resistance determinants.

- The requirements of molecular tests to detect gonococcal resistance depend on the purpose of the assay; to enhance surveillance of antimicrobial resistance, or to guide the clinical management of gonorrhoea.

- Molecular detection of resistance determinants in genital and rectal specimens is most accurate; cross-reactivity with nongonococcal Neisseria species particularly in the pharynx reduces assay specificity.

- Detection of ciprofloxacin resistance or susceptibility to spare the use of extended-spectrum cephalosporins is the strategy that has advanced the furthest to date, but is not a long-term solution.

- Now is the time to exploit the molecular technologies used for diagnosis and to invest in the development of molecular gonococcal resistance tests that can be implemented for public health good.

Molecular methods are increasingly used for gonorrhoea diagnosis but, despite the global threat of antimicrobial resistance, commercially available diagnostic assays do not detect gonococcal resistance determinants. The need for molecular detection of antimicrobial resistant Neisseria gonorrhoeae

The molecular technologies have changed patterns of gonorrhoea diagnosis in high-income countries. NAAT are recommended because they have high sensitivity, robust specimen handling conditions, can be automated with high throughput and can be used on noninvasively collected samples like first-void urine and vaginal swabs [39]. The rapid adoption of NAAT has, however, raised two main concerns about the ability to detect, monitor, and manage antimicrobial resistance [1,6,11,14**,15]. First, commercial NAAT specimens provide no viable organism for antimicrobial susceptibility testing. Second, as the number of specimens for culture falls the microbiological skills required for isolation and antimicrobial susceptibility testing are being lost [1]. Countries that have poor healthcare infrastructure and rely on syndromic management of genital urinary symptoms and/or microscopy of Gram-stained smears have a particularly urgent need for better diagnostics and knowledge of gonococcal antimicrobial resistance patterns [40].

Molecular technology is redefining expectations about the detection of antimicrobial resistant gonorrhoea. The paradigm for sexually transmitted infection treatment reflects the clinical priority to treat symptomatic patients on presentation [3]. In the absence of results of antimicrobial susceptibility testing, the first-line treatment regimen should cure at least 95% of infections [3]. Bacterial culture and antimicrobial susceptibility testing underpin the success of this strategy and have many advantages [11,14**]. First, culture on selective media directly provides the biological material for assessing a strain’s susceptibility to multiple antimicrobials simultaneously [3]. Second, breakpoints for the MIC that determines resistance correspond with clinical treatment failure for many antimicrobials. Third, organised surveillance programmes can monitor changes in the resistance prevalence for many antimicrobials [41–43]. Fourth, clinicians can use the antimicrobial susceptibility profile to alter therapy, or choose an antimicrobial for an untreated patient. The use of NAAT’s alone precludes monitoring of antimicrobial resistance, but has also highlighted the limitations of culture. First, considerable technical skills and time are required to culture the fastidious N. gonorrhoeae and test for antimicrobial resistance. Second, culture has poor sensitivity for extragenital sites such as the pharynx [3], where horizontal transfer of resistance determinants from commensal Neisseria species is thought to be the origin of resistance to extended-spectrum cephalosporins [4*,6].

Requirements of molecular tests to detect antimicrobial resistant N. gonorrhoeae

Ideally, molecular resistance testing should reflect the exact MICs of different antimicrobials.
Resistance to many antimicrobials in *N. gonorrhoeae*, however, is affected by multiple genes. Different mutations and an accumulation of these mutations result in the high MIC of the specific antimicrobial agent(s). This characteristic makes it exceedingly difficult to use molecular assays to predict exact MICs of the antimicrobials, but by targeting the main resistance determinants the resistance/susceptibility phenotypes might be predicted. The principal genes associated with gonococcal antimicrobial resistance are shown in Table 1.

### Table 1. Main genes associated with antimicrobial resistance in *Neisseria gonorrhoeae*

<table>
<thead>
<tr>
<th>Antimicrobial</th>
<th>Principal gene(s) and position*</th>
<th>Other genes with verified impact on resistance in clinical strains*×†</th>
</tr>
</thead>
<tbody>
<tr>
<td>Ciprofloxacin</td>
<td>gyrA S91 (D95)</td>
<td>parC</td>
</tr>
<tr>
<td>Ceftriaxone</td>
<td>penA mosaic allele [A501-altered penA alleles]</td>
<td>mtrR, porB</td>
</tr>
<tr>
<td>Azithromycin</td>
<td>23S rRNA gene: C2611 (lower level of resistance) and A2059 (high-level resistance)b</td>
<td>mtrR, mefA, erm genes</td>
</tr>
<tr>
<td>Spectinomycin</td>
<td>16S rRNA gene: C1192</td>
<td>rpsE</td>
</tr>
<tr>
<td>Tetracycline</td>
<td>tetM-carrying plasmid (high-level resistance) and rpsJ V57 (lower level of resistance)</td>
<td>mtrR, porB</td>
</tr>
<tr>
<td>Penicillin</td>
<td>β-lactamase plasmid (blaTEM gene; high-level resistance) and penA (D345 insertion or mosaic allele; lower level of resistance)</td>
<td>mtrR, porB, ponA</td>
</tr>
</tbody>
</table>

*With the exception of the tetM-carrying plasmid and the β-lactamase plasmid, listed genes, and positions are involved in chromosomally-mediated resistance. Wild type positions are listed, which can have many different mutations resulting in resistance.

*There are four alleles of the 23S rRNA gene in each gonococcal strain. *Escherichia coli* numbering used.

†There are additional efflux pumps, for example, MacAB and NorM, in *N. gonorrhoeae* that affect the minimum inhibitory concentrations of several antimicrobials.

Some assays have been used in real-life settings. A real-time polymerase chain reaction (PCR) assay was developed to detect penicillinase producing gonococci [30] in remote regions of Australia where resistance to penicillin remains below 5%. The molecular assay had 100% sensitivity and 98.7% specificity compared with phenotypic tests. When applied subsequently to *N. gonorrhoeae* positive NAAT specimens from Western Australia, the assay detected penicillinase producing gonococci in 15/915 (1.6%) of specimens from remote areas and 34/303 (11.2%) of specimens from more heavily populated areas [44]. As a result, the treatment regimen of amoxicillin, probenecid, and azithromycin was continued in remote areas and, in populous areas, changed from ceftriaxone alone to ceftriaxone plus azithromycin [44]. This assay has been further optimised to include additional β-lactamase plasmid targets [19]. Molecular tests for surveillance can also be used to monitor specific strains. For example, real-time PCR assays have been developed to screen clinical specimens for extensively drug resistant gonococcal strains (‘superbugs’) that were first detected in Japan (H041) [29] and subsequently in Europe (F89) [24].

An antibiogram gives information about susceptibility to multiple antimicrobials. Most molecular assays detect resistance determinants and relate to a single antibiotic (penicillin [19,30,44]).
ciprofloxacin [18,31,32]; azithromycin [21,45]; extended-spectrum cephalosporins [17]; or a single strain [24,29]. Molecular assays aiming to detect resistance to several antimicrobials have been run in series [26] or as multiplex reactions [27,36], but their analytical sensitivity was too low to be used in clinical specimens [36] or, if assessed on clinical specimens, was not validated against a culture-based MIC reference standard [26,27].

Laboratory-based molecular tests to guide individual patient management

Laboratory-based molecular assays could have advantages if they produce faster results and have greater sensitivity than bacterial culture, particularly when used on extragenital specimens for NAAT testing. Laboratory-based assays will usually not help, however, in the management of patients who present with symptoms or who need same-day treatment for other reasons.

The strategy that has advanced furthest aims to spare overuse of ceftriaxone plus azithromycin (the only remaining first-line empirical treatment in many countries) by targeting ciprofloxacin to patients with ciprofloxacin-sensitive gonococcal strains before treatment is initiated. Several laboratory-based molecular assays for use in clinical specimens detect one or more chromosomal mutations in gonococci that are associated with ciprofloxacin resistance [18,26,27,31,32]. Siedner and colleagues [31] designed a real-time PCR assay to detect resistance using a single target mutation in urine specimens. The prototype assay amplified the target sequence in only 85% of all urine NAAT specimens tested [31]. Further optimisation of this assay has improved sensitivity in cultured isolates, which should be validated in clinical specimens [37]. The suboptimal diagnostic test accuracy of real-time PCR assays to detect ciprofloxacin resistance in clinical specimens presents ongoing challenges. In a study that tested 24 NAAT specimens, real-time PCR assays correctly identified only 4/6 ciprofloxacin-resistant specimens with S91 mutations and 16/18 ciprofloxacin-sensitive specimens [18]. Three of four specimens that failed were from the pharynx or rectum. Cross-reactivity occurred with N. meningitidis, N. lactamica, N. subflava, and N. polysaccharea. In another study, real-time PCR failed in 10% (28/290) of clinical specimens, particularly those from nongenital sites [38].

An alternative strategy is to identify wild type gyrA sequences that predict ciprofloxacin susceptibility rather than resistance [32]. To exclude cross-reactivity, a N. gonorrhoeae specific target (dcmH) was also detected in this molecular assay. When used in male urine NAAT specimens in South Africa, the assay correctly identified 15/15 ciprofloxacin-sensitive and 18/18 strains with intermediate susceptibility or resistance [32].

Point-of-care molecular tests to guide individual patient management

Point-of-care tests have a rapid turnaround time that guides clinical decisions and allows results and treatment to be given to the patient at the same visit [47]. None of the molecular assays developed so far to detect antimicrobial resistance in N. gonorrhoeae is a "transformative point-of-care diagnostic test that will conserve antibiotics for future generations..."
Neisseria/C223 allele in one species with similar porB mosaic gene encoding isolates or in alleles with A501 mutations are the main species and in 33% (7/21) N. gonorrhoeae porB alleles. Low and Unemo (mtrR allele sequences in cultured pseudogene), mosaic targets with commensal alleles and mutations in additional resistance determinants of decreased susceptibility and resistance to extended-spectrum cephalosporins [4*,6,8]. Furthermore, cross-reactivity in the penA, mtrR, porB, and ponA targets with commensal Neisseria isolates or in clinical specimens was identified. All three clinical cross-reactive specimens were from the pharynx [17*].

Molecular detection of azithromycin resistance
Azithromycin alone is not a first-line treatment for gonorrhoea, but detecting resistance is important because of its use in dual treatment regimens. Two mutations in the 23S ribosomal RNA genes (A2059G and C2611T) are associated with azithromycin resistance with MICs depending on how many of the four alleles are mutated [45,54]. Two real-time PCR assays could characterise the 23S rRNA 2059 and 2611 positions as wild type or mutated in 87% (266/306) of genital and rectal specimens. However, cross-reactivity was observed with both assays testing commensal Neisseria species and in 33% (7/21) of pharyngeal samples [21*]. Furthermore, among 64 samples with MIC results, 3% (2/64) with raised MICs (1 μg/ml), which indicates resistance, were identified as 23S rRNA wild type.

Challenges for molecular detection of antimicrobial resistant N. gonorrhoeae
The number of assays and techniques used to detect genetic determinants of antimicrobial resistant N. gonorrhoeae is increasing and some assays are beginning to be adopted for surveillance [14**]. Progress in molecular assays to guide clinical management, however, is lagging. In addition to the challenges to developing usable and commercially viable point-of-care tests [47], there are many remaining roadblocks for the development of diagnostic tools to contain antimicrobial resistance in general [40] and for gonorrhoea in particular. First, molecular tests can only detect known targets and new mutations and resistance mechanisms will remain the most urgent threat. The development of molecular assays to detect any resistance to extended-spectrum cephalosporins in clinical specimens is inherently challenging because multiple mechanisms are involved and are still evolving [4*]. Mosaic alleles of the penA gene encoding penicillin-binding protein 2 (PBP2) and nonmosaic penA alleles with A501 mutations are the main determinants of decreased susceptibility and resistance to extended-spectrum cephalosporins [4*]. The gonococcal ‘superbug’ F89 strain is a good example of how resistance to extended-spectrum cephalosporins evolves. This strain contains a penA mosaic allele (type XXXIV), which is common worldwide [4*,5–7], with an additional A501P alteration, resulting in high-level ceftriaxone resistance [9]. Molecular test specificity is a major challenge, particularly for pharyngeal specimens that frequently harbour nongonococcal Neisseria species with similar penA sequences. Several assays have examined the presence of mosaic penA allele sequences in cultured isolates [25,50,53]. One real-time PCR assay that detects N. gonorrhoeae (porA pseudogene), mosaic penA alleles and mutations in additional resistance-determining loci (mtrR, porB, and ponA) was tested on 24 gonococcal-negative NAAT specimens and 34 gonococcal-positive NAAT specimens [17*]. The assay detected a mosaic penA allele in one specimen with the highest ceftriaxone MIC (0.25 μg/ml), but lacked specificity in the prediction of decreased susceptibility to extended-spectrum cephalosporins (in clinical specimens and culture isolates). This suboptimal specificity will be exceedingly difficult to overcome because this assay and other similar assays detect many different mosaic penA alleles which result in highly divergent MICs of the extended-spectrum cephalosporins [4*,6,8]. Furthermore, cross-reactivity in the penA, mtrR, porB, and ponA targets with commensal Neisseria isolates or in clinical specimens was identified. All three clinical cross-reactive specimens were from the pharynx [17*].
Sexually transmitted diseases

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Conflicts of interest
N.L. and M.U. are co-investigators in the RaDAR-Go project which aims to develop a point-of-care test to detect antimicrobial resistance in N. gonorrhoeae.

REFERENCES AND RECOMMENDED READING
Papers of particular interest, published within the annual period of review, have been highlighted as:

© of special interest
★ of outstanding interest


The comprehensive review describes N. gonorrhoeae resistance mechanisms and determinants. The extensive literature review can be used as a source for potential targets for molecular resistance tests.


The review explains in detail how molecular tests can be used to enhance surveillance for antimicrobial resistant gonorrhoea.


The study describes the most recent assay for the detection of gonococcal resistance to extended-spectrum cephalosporins in clinical specimens. Assay sensitivity was sufficient to detect a raised ceftriaxone MIC but lacked specificity.

CONCLUSION
Progress with the development of molecular tests to detect gonococcal resistance is significantly more advanced for enhancing surveillance than for guiding clinical decision making but substantial challenges remain. Gonococcal culture and antimicrobial susceptibility testing remain essential tools for surveillance and as a reference standard for assay validation. The prioritisation of molecular resistance determinants for inclusion in assays needs to consider both short and longer term antimicrobial resistance threats. In addition, cross-reactivity with nongonococcal Neisseria species, particularly in the pharynx, is a challenge for all assays and suggests that assay development should focus first on genital and rectal clinical specimens. Now is the time to exploit the molecular technologies used for diagnostics and to invest in the development of molecular gonococcal resistance tests that can be implemented for public health good.

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None.

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Detection of antimicrobial resistant Neisseria gonorrhoeae Low and Unemo


This study describes a multiplex assay applied to clinical specimens, but lacks validation against a culture reference standard.


The study is the first to show how an assay to detect antimicrobial resistance in N. gonorrhoeae was used in surveillance to change treatment guidelines.


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