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Codon 91 Gyrase A Testing Is Necessary and Sufficient to Predict Ciprofloxacin Susceptibility in *Neisseria gonorrhoeae*

To the Editor—We read with great interest the article by Grad et al [1]. We agree with their conclusion that gyrase A (*gyr*A) genotype testing of *Neisseria gonorrhoeae* is a valuable means of resistance testing; however, we believe that *gyr*A testing, specifically of codon 91, is both necessary and sufficient for predicting susceptibility to ciprofloxacin. There have been 11 studies (N=4777 specimens) comparing real-time polymerase chain reaction (RT-PCR) genotype results with conventional antimicrobial susceptibility testing methods, all of which have demonstrated high sensitivity and specificity (93.8%–100% and 93.2%–100%, respectively). Positive and negative predictive values were similarly impressive (94.4%–100% and 87.5%–100%, respectively). Furthermore, 4 studies found that mutation at codon 91 of the *gyr*A gene as determined by RT-PCR was 100% specific for *N. gonorrhoeae* compared with other *Neisseria* species [2–5].

Other mutations have been shown to contribute to ciprofloxacin resistance, but previous studies have shown that other mutations in general occur in conjunction with a mutation in the *gyr*A gene [6, 7]. In addition, it is estimated that approximately 80% of *N. gonorrhoeae* infections in the United States are susceptible to ciprofloxacin [8]. Those 2 facts support the implementation of *gyr*A genotype testing to promote the use of targeted ciprofloxacin therapy. That may in turn reduce overuse of ceftriaxone. A recent article showed that treatment may be a major driver of ceftriaxone resistance in *Neisseria gonorrhoeae* [9], which has been called one of the top 3 urgent threats to public health by the Centers for Disease Control and Prevention [10].

We developed a rapid codon 91 *gyr*A genotypic assay using RT-PCR techniques [6], and we verified the assay in accordance with Clinical Laboratory Improvement Amendments [2]. UCLA Health introduced that assay into routine clinical practice for all *N. gonorrhoeae*–positive specimens in November 2015. Further studies are underway to characterize the impact of that implementation.

Notes

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Both authors have submitted the ICMJE Form for Disclosure of Potential Conflicts of Interest. Conflicts that the editors consider relevant to the content of the manuscript have been disclosed.

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Reply to Allan-Blitz and Klausner

To the Editor—We thank Allan-Blitz and Klausner [1] for the citations to their group's work in this area and to the efforts underway to test diagnostics for quinolone resistance in *Neisseria gonorrhoeae*. Although our study investigated the genetic basis of resistance and assessed the positive and negative predictive values of specific mutations for resistance in the set of samples we analyzed [2], we take no position on the suitability of particular diagnostics. We note, however, that the US Food and Drug Administration has published guidance for antimicrobial susceptibility test systems [3]. The lower end of the range in negative predictive value cited by Allan-Blitz and Klausner (87.5%) is considerably lower than the 99% we observed,