We report a multidrug-resistant Neisseria gonorrhoeae urogenital and pharyngeal infection with ceftriaxone resistance and intermediate resistance to azithromycin that failed dual therapy with ceftriaxone and doxycycline. This treatment targeted an infection due to Chlamydiae trachomatis; the choice of the clinician was based on recent finding on the efficacy of doxycycline compared to that of azithromycin in urogenital infections [5].

Case description
In November 2017, a heterosexual woman in her early 20s attended a local Hospital in Paris due to a vaginal discharge that had persisted for 3 days. She had only had unprotected sexual relations (oral and intercourse) with one regular French male partner who had urethritis symptoms in the 6 months prior and had received antimicrobial treatment at another clinic. Neither she nor her male partner had travelled abroad or had a known history of sexually transmitted infections. She was treated empirically with ceftriaxone (250 mg intramuscularly) and doxycycline (100 mg orally twice a day, for 7 days). During the same visit, vaginal and pharyngeal swabs were sampled for detection of NG and Chlamydia trachomatis using nucleic acid amplification test (NAAT), RealTime CT/NG assay on the m2000 System, (Abbott Diagnosis, Abbott Molecular Inc., Des Plaines, IL, USA), and NG culture. NAAT and culture detected NG in both vaginal and pharyngeal samples, but all samples were negative for C. trachomatis. HIV, hepatitis B and C viruses, syphilis serological tests were also negative.

At test of cure 4 weeks later, she had no symptoms or signs of gonorrhoea and was not given any additional treatment. However, it was found that only the vaginal swab was negative for NG, as the NAAT and culture taken from the pharyngeal swab remained positive, indicating that only the urogenital infection had been cured. Reinfection was excluded because the patient denied any sexual relations between the first visit and the test of cure. The patient and her male partner were
F90 displayed resistance to ceftriaxone (MIC = 0.5 mg/L), cefixime (MIC = 1 mg/L), tetracycline (MIC = 4 mg/L), ciprofloxacin (MIC = 32 mg/L), and rifampicin (MIC > 32 mg/L). Furthermore, F90 showed intermediate resistance to azithromycin (MIC = 0.5 mg/L), however, it was susceptible to spectinomycin (MIC = 8 mg/L) and had low MIC for ertapenem (MIC = 0.004 mg/L) and gentamicin (MIC = 8 mg/L), for which EUCAST does not state resistance breakpoints.

Molecular investigation
Whole-genome sequencing (WGS) was performed in the Associated laboratory for gonococci of the French National Reference Centre for bacterial STI, Paris, France. DNA extraction was conducted using Wizard Genomic DNA Purification kit (Promega), as previously described [7]. Multiplexed DNA libraries were prepared with the Nextera XT construction protocol (Illumina, San Diego, CA, USA). Paired-end, 1,547,414 150-bp indexed reads with an average depth of 151 were obtained on a MiSeq platform (Illumina). De novo assembly was performed using SPAdes 3.11.1 software [8]. QUAST software [9] revealed that the assembly provided 106 contigs with an average length of 20,394 nucleotides, a N50 of 47,830 nucleotides. The contigs covered 93.7% of the genome of NG reference strain FA1090. The genome annotation was performed using the MicroScope platform (http://www.genoscope.cns.fr//agc/microscope) [10]. The whole nucleotide sequence of the penA gene of F90 is available on GenBank under accession number MH172152.

Using the WGS data, NG antimicrobial resistance determinants were determined in silico with the NG FA1090 genome as reference. Sequence types (ST) were also determined in silico from the WGS data using the NG multi-antigen sequence typing (NG-MAST) online database (http://www.ng-mast.net) [11], the multilocus sequence typing (MLST) from the PubMLST database [12], and the NG Sequence Typing for Antimicrobial Resistance (NG-STAR) [13].

F90 was assigned as MLST1903, NG-MAST ST14395, and NG-STAR233. Regarding ceftriaxone resistance determinants, the isolate harboured a mosaic penA-60.001 allele, sharing a 100% homology with the penAFC428 of the Japanese ceftriaxone-resistant FC428 strain [14]. The penAFC428 gene encodes a mosaic penicillin-binding protein 2 (PBP2) including the amino acid alterations A311V, I312M, V316T, T483S, and G545S associated with resistance to extended-spectrum cephalosporins [15]. Furthermore, F90 contained the adenine deletion in the inverted repeat sequence of the mtrR promoter, resulting in an overexpression of the MtrCDE efflux pump, and G120K and A121D amino acid substitutions in PorB1b, which further increase ESC MICs and contribute to the MDR phenotype of F90. The quinolone resistance determining regions (QRDRs) carried S91F and D95A substitutions in GyrA (subcomponent of DNA gyrase) and a S87R substitution in ParC (subcomponent of Topoisomerase IV), which explained the high-level resistance to ciprofloxacin. No tetM gene was detected but the rpsJ gene contained a mutation conferring the V57M amino acid alteration in the 50S ribosomal protein, which contributes to low-level chromosomally-mediated resistance to tetracycline.

Discussion
In 2010, the first European high-level ceftriaxone-resistant gonococcal isolate was detected in France and characterised in detail [16]. The isolate (F89) harboured a mosaic penA XXXIV allele with an additional A501P alteration in PBP2 and belonged to the internationally spread MDR NG-MAST ST1407 clone [17]. Since 2010, F89 has only been reported in Spain [18] and does not appear to have spread further, which is likely due to a decreased biological fitness of F89 [19]. From 2012 to 2014, the proportion of NG isolates with resistance to cefixime decreased nearly three-fold from 3.3% to 1.2% in France [7].

Here, we report a new MDR NG strain (F90) with ceftriaxone resistance and intermediate resistance to azithromycin that lead to treatment failure of pharyngeal gonorrhoea with ceftriaxone and doxycycline. F90 differs from the French F89 isolate detected in 2010 [16], however, it is similar to a ceftriaxone-resistant clone initially described in Japan in 2016 (FC428 strain; similar antibiogram and an identical mosaic penA-60.001 allele, MLST1903, and NG-STAR233) [14]. The FC428 strain appears to have spread internationally and has been subsequently detected in Australia, Canada and Denmark [20]. In early-2018 the first global strain with ceftriaxone resistance combined with high-level azithromycin resistance was identified in the UK [21], followed by two similar cases in Australia [22].

Unfortunately, the patient presented in this article and her partner are currently lost for further follow-up which is of concern as it creates opportunities for spread of this ceftriaxone-resistant strain.
Conclusion

An MDR gonococcal strain with ceftriaxone resistance and intermediate resistance to azithromycin was found in France in late-2017. The strain might belong to an internationally spread ceftriaxone-resistant clone, which threatens the recommended dual therapy of gonorrhoea and poses a public health threat. Increased awareness of the spread of ceftriaxone-resistant strains, enhanced antimicrobial resistance surveillance, improved implementation of the recommended dual antimicrobial therapy, partner notification and treatment, and TOC are imperative on an international level. Our treatment failure also illustrates the substantial difficulties in treating pharyngeal gonorrhoea and enhanced focus on detection and treatment is, therefore, crucial. Ultimately, novel therapeutic antimicrobials for gonorrhoea are essential.

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Conflict of interest

None declared.

References


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