93% of the isolates (n=297) had MICs of <0.03 mg/l which were classified as susceptible (CroS). All CroRed isolates were analysed for mutations in penA (FPB2), mtrR (MtrR), porB (PorB) and ponA (FPB1). 123 (42%) CroS isolates were randomly selected as coselected strains. No ceftriaxone and spectinomycin resistant strains were found, but the proportions of isolates with a high level of resistance to penicillin, tetracycline, ciprofloxacin and spectinomycin were determined by the agar dilution method, according to CLSI and WHO protocols.

**Results**
In total, nine mutation patterns were observed in penA. Patterns I (31.7%), IX (29.2%) and XXII (26%) were most common in the 123 CroS isolates; while patterns IX (60.8%, p<0.05) and XXII (21.5%, p>0.05) were predominant in the 23 CroRed isolates. The mosaic penA pattern X was observed in only one isolate (Cro MIC=0.06 mg/l). Seven mutation patterns were noted in mtrR. Among the CroS isolates, 35.8% had a single mutation (G45D or A39T) in the DNA binding domain (DBD) and 17.8% of the isolates carried an A' nucleotide deletion (A-) in the mtr promoter coupled with a G45D mutation. Among the CroRed isolates, 65.2% carried G45D or A39T single mutations, significantly higher than that of CroS isolates (p<0.05). The mutation of A-/H105Y was observed in 21.7% of CroRed isolates as compared to 4% of CroS isolates (p<0.05). Five mutation patterns at residues G120 and A121 of PorB were observed in the CroRed isolates including double (47.8% vs 15% CroS isolates, p<0.05) or single (21.7% vs 26% CroS isolates, p<0.05) mutations. L421P in FPB1 was detected in 87% CroRed and 15% CroS isolates, respectively (p<0.05).

**Conclusions**
Mosaic penA pattern X was only observed in one CroRed isolate. The mutations associated with CroRed phenotypes include pattern IX of FPB2, mutations in DBD and a double mutation of A-/H105Y in mtrR, double mutations in PorB (positions G120 and A121) and L421P of FPB1.

**EMERGENCE OF AN AFRICAN ANTIMICROBIAL RESISTANCE GENOTYPE IN NEISSERIA GONORRHOEAE STRAINS ISOLATED IN GUANGZHOU, CHINA, 2001—2009**

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**Background**
The continuing spread of drug-resistant gonococci has posed a challenge for successful treatment worldwide. Recently third-generation cephalosporins-resistant strains are isolated in Japan. Guangdong Province in South China has one of the highest gonococcal resistance rates in China and a large number of international migrants. We investigated the invitro antimicrobial susceptibility and genotypes of Neisseria gonorrhoeae strains isolated in Guangzhou, the capital city, from 2001 to 2009.

**Methods**
MICs to penicillin, ceftriaxone, tetracycline, ciprofloxacin, and spectinomycin were determined by the agar dilution method, according to CLSI and WHO protocols. The resistant plasmids were determined for penicillinase-producing Neisseria gonorrhoeae (PPNG) and high-level tetracycline resistant Neisseria gonorrhoeae (TRNG) by PCR and the isolates were genotyped.

**Results**
Of 1132 consecutive gonococci isolated from 2001 to 2009, no ceftriaxone and spectinomycin resistant strains were found, but the prevalence of strains less susceptible to ceftriaxone rose from 18.2% to 38.5%. The MIC90 for ceftriaxone showed intermediate sensitivity (0.06–0.125 μg/ml) and spectinomycin near the resistant level (16–52 μg/ml). The resistance to penicillin, tetracycline and ciprofloxacin increased from 8.1%, 84.5% and 72.5% in 2001 to 90.1%, 91.4% and 98.7% in 2009, respectively. A total of 313 (27.7%) PPNG and 486 (42.9%) TRNG strains were detected. 206 (18.2%) strains were both PPNG and TRNG. PPNG from 21.5% to 29.5% and TRNG rapidly increased from 27.2% to 56.3%. Genotyping TEM-1 gene showed 267 (99.6%) PPNGs in 2001–2008 carried the Asian-type β-lactamase plasmids and one African-type in 2008. Genotyping of tetM gene showed that all 486 TRNGs were Dutch variants.

**Conclusion**
Gonorrhoea resistance continues to be a major public health problem in Guangzhou. The emergence of an African gonorrhoea resistance variant may be related to the large African diaspora in Guangzhou, migration of Chinese to Africa, or other migration patterns. More research is needed to determine what practices, and behaviours contribute to escalating resistance patterns.
Methods In 2010, all N. gonorrhoeae strains isolated in clinical laboratories throughout the province were submitted to the Laboratoire de santé publique du Québec where their susceptibility profile to azithromycin, cefixime, ceftriaxone, ciprofloxacin and spectinomycin was determined by the agar dilution method.

Results A total of 831 strains isolated from 607 males and 224 females were tested. The strains were recovered from (data available for 819 strains) the following specimens—urethra, 452; cervix, 191; anus, 100; throat, 90; eye, 4; and synovial fluid, 2. All strains were susceptible to cefixime, ceftriaxone and spectinomycin, 270 (32.5%) were resistant to ciprofloxacin and 11 (1.3%) were resistant to azithromycin (MIC ≥ 2 mg/l). The azithromycin resistant isolates were retrieved from 11 males aged 16–55 years (mean, 30) from the Montreal area (urethra, 8; throat, 3). The azithromycin MIC distribution was as follows—4 mg/l (n = 1), 8 mg/l (n = 6), 16 mg/l (n = 4). No highly resistant organism (MIC > 128 mg/l) was identified. Among the azithromycin resistant isolates, one was resistant to ciprofloxacin but all were susceptible to cefixime, ceftriaxone and spectinomycin. In 2010, 68 (8.2%) isolates exhibited decreased susceptibility to cefixime (MIC = 0.125 mg/l [n = 62] and 0.25 mg/l [n = 6]). Of these 68 isolates, all were susceptible to azithromycin and ceftriaxone but all were resistant to ciprofloxacin. Only one isolate showed decreased susceptibility to ceftriaxone (MIC = 0.125 mg/l)—this isolate also showed decreased susceptibility to cefixime.

Conclusions As observed elsewhere, N. gonorrhoeae strains are showing a worrisome drift in susceptibility to cefixime, a first line treatment for gonococcal infections associated with resistance to ciprofloxacin. Furthermore, resistance to azithromycin, a second line treatment option, is emerging. Sustained collaborative laboratory surveillance programs are mandatory for the design of public health interventions to prevent and control gonococcal infections.

Background and molecular epidemiological characteristics of Neisseria gonorrhoeae circulating in 2009 and 2010 in Belarus

Methods N. gonorrhoeae isolates cultured in 2009 (n = 80) and 2010 (n = 78) in the two different cities Minsk (n = 45) and Mogilev (n = 113) were examined using Etest for nine antimicrobials and nitrocefin solution for β-lactamase production. Where available, breakpoints for susceptibility and resistance according to the European Committee on Antimicrobial Susceptibility Testing (EUCAST; http://www.eucast.org) were used. Moreover, screening for penA mosaic alleles, full-length porB gene sequencing, and N. gonorrhoeae multiantigen sequence typing (NG-MAST) were performed.

Results The levels of resistance in 2009–2010 to antimicrobials evidently used in the gonorrhoea treatment in Belarus were—ceftaxone 0%, spectinomycin 0%, azithromycin 14.4%, tetracycline 30.9%, ciprofloxacin 54.6%, and erythromycin 59.2% (only tested in 2009). The levels of resistance to other antimicrobials of international interest but not used in Belarus were—cefixime 0%, gentamicin 1.3%, and penicillin G 9.9% (only tested in 2009). Extraordinarily, no β-lactamase producing isolates were detected. The circulating N. gonorrhoeae population identified was very heterogeneous and contained many divergent NG-MAST STs, of which more than half have not been previously described worldwide.

Conclusions Due to the high levels of resistance to all antimicrobials previously recommended as first-line treatment, only ceftriaxone and spectinomycin can be recommended for empirical gonorrhoea treatment in Belarus. Continuous and quality assured gonococcal AMR surveillance in Eastern Europe is crucial, in Belarus this surveillance is now initiated using WHO protocols.