last accessed). This isolate (submitted in 2010) originated from Poland and is described as methicillin susceptible. Multilocus sequence typing showed that the isolate belonged to the novel sequence type ST2497, a single-locus variant of ST1943 with one nucleotide difference in the glpF gene.

The isolate described in this study represents the first detection of an mecC-containing MRSA from an animal host in Norway. The mecC gene has been detected recently in a total of eight MRSA isolates from humans in Norway7 (and K. W. Larssen, unpublished data). All eight mecC MRSA, isolated during 2006–12, belonged to CC130. The genotype of the feline isolate represents a new mecC-positive genotype identified in our country; however, isolates within this clonal lineage with mecC have been described from other countries.1,4

The detection of mecC in an MRSA from a clinical sample from a cat submitted to our diagnostic bacteriological service unit demonstrates the importance of taking mecC into consideration in diagnostic units that examine samples from companion animals. Our finding extends our knowledge of MRSA carrying mecC from animals and demonstrates that detection of mecC is not only a rare event when screening historical isolate collections.

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None to declare.

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HIV-1 integrase variability and relationship with drug resistance in antiretroviral-naive and -experienced patients with different HIV-1 subtypes

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Keywords: human, viruses, sequences, nucleotides
Sir,

The prevalence of natural polymorphisms and mutations associated with integrase (INI) inhibitor (INI) resistance in the HIV-1 IN has already been analysed. The aim of the study was to characterize the HIV-1 IN variability in antiretroviral (ARV)-naive and -experienced patients, never treated with INIs, in a panel of different HIV-1 subtypes, and the relationship with drug resistance. This multicentre study included 590 HIV-1-infected individuals never treated with INIs (308 drug-naive and 282 ARV-experienced patients) who were enrolled in seven clinical centres in France and one centre in Switzerland. Nucleotide and amino acid sequences were compared with the HxB2 HIV-1 clade B consensus sequence (GenBank accession number K03465.1) using the BioEdit software program. The sequences of the samples have been submitted to GenBank and assigned accession numbers JX425421 to JX425885 and JX451875 to JX451963. Thirty-seven of the 590 sequences are not available in the NCBI database because we have only the JX451875 to JX451963. Thirty-seven of the 590 sequences are not available in the NCBI database because we have only the JX451875 to JX451963.

We have identified and assigned accession numbers JX425421 to JX425885 and JX451875 to JX451963 to the HIV-1 IN sequences of the samples. No difference in reverse transcriptase and IN sequences was observed between ARV-naive and -experienced patients. The primary mutations detected in patients failing on raltegravir-containing regimens (Y143R/C, Q148H/K/R and N155H) or on elvitegravir-containing regimens (T66L, E92Q, E138K, S147G, Q148H/K/R and N155H) was detected. The E157Q mutation was observed among 2.9% (n = 17) of patient samples, including four of subtype B, one of subtype H, seven of subtype CRF02_AG, one of subtype A, two of subtype D, one of subtype CRF11_cpx and one of subtype G, without a significant difference in polymorphism between ARV-naive and -experienced patients. The primary mutations detected in patients failing on raltegravir-containing regimens (V151I, S153Y, T66K/L74M, E92Q/N155H, E138A/K/Q148H/K/R, G140C/S/Q148H/K/R and Q148R/N155H) were completely absent.

In our study, dolutegravir resistance-associated mutations, in particular R263K, were not found to be polymorphic. Only the mutations L101I and T124A, which were previously shown to be selected in vitro in the presence of dolutegravir, either alone or in combination, were common in both naive and experienced patients. However, these mutations have shown little impact on virological response to dolutegravir. Recently, the HIV-1 CRF01_AE IN coding region of the pol gene was evaluated for the prevalence of natural polymorphisms in 87 ARV-naive individuals from Cambodia, Thailand and Vietnam. Amino acid substitutions occurred in 60% of the subjects and none of these substitutions have been reported to be associated with resistance to INIs. Many polymorphisms in non-B viruses are considered to be secondary resistance mutations since they emerge in B subtype viruses after drug exposure. Nevertheless, the selection of resistance mutations could be influenced by the naturally occurring variations between the different non-B subtypes.

In conclusion, all patients in our study lacked previously described major resistance mutations to raltegravir, elvitegravir and dolutegravir. However, we found evidence of important variations regarding the IN polymorphisms according to the different HIV-1 subtypes. Further studies of INI-treated patients will be needed to fully elucidate the role of polymorphic IN mutations in the context of HIV-1 variability.

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Figure 1. Distribution of variants among group M HIV-1 IN sequences. Amino acid polymorphism in HIV-1 IN from 308 plasma samples from drug-naive patients and 282 samples from experienced patients are reported. The consensus subtype B sequence is shown in bold at the top of each 30 amino acid section. Numbers given as superscripts below each position are the numbers of isolates with that specific polymorphism. Grey boxes signify positions associated with in vivo resistance defined according to the algorithms from the ANRS (update October 2012, v.22, http://www.hivfrenchresistance.org/2012/Algo-sep-2012.pdf). Highly conserved motifs, the HHCC motif (coordinates zinc binding), the DDE motif, catalytic core domains I–VI and the Q sequence, are indicated by boxes.
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Transparency declarations
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Pharmacokinetic interaction of maraviroc with tacrolimus in a patient coinfected with HIV and hepatitis B virus following hepatic transplant due to hepatocellular carcinoma

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Keywords: HIV antiviral pharmacology, hepatic transplantation, immunosuppression, HBV

Sir,
Limited data are available regarding interactions between tacrolimus and commonly used highly active antiretroviral therapies, such as first-line nucleoside reverse transcriptase inhibitors, non-nucleoside reverse transcriptase inhibitors (NNRTIs) and some protease inhibitors (PIs). When first-line combinations are contraindicated and newer antiretroviral agents are required, there are even less data on the interactions between newer agents such as maraviroc (a CCR5 inhibitor) with immunosuppressants such as tacrolimus (a calcineurin inhibitor). There are some animal model data of the beneficial effects on cardiac allograft survival when using maraviroc alongside immunosuppressants, with the potential that CCR5 inhibition could improve long-term outcomes after transplantation. In our patient undergoing hepatic transplant, with limited antiretroviral therapy options such as tacrolimus (a calcineurin inhibitor). There are some animal model data of the beneficial effects on cardiac allograft survival when using maraviroc alongside immunosuppressants, with the potential that CCR5 inhibition could improve long-term outcomes after transplantation. In our patient undergoing hepatic transplant, there was no indication of the benefit of using maraviroc at the time of transplantation. However, we set out to observe concentrations of the immunosuppressant tacrolimus and the necessity to be started on a newer agent, we set out to observe concentrations of the immunosuppressant tacrolimus and the necessity to be started on a newer agent, we set out to observe concentrations of the immunosuppressant tacrolimus and the necessity to be started on a newer agent.

We describe a 49-year-old man from Sierra Leone, recently diagnosed with fully sensitive HIV clade C and chronic hepatitis B virus (HBV). After routine blood tests revealed abnormal liver