of daptomycin-non-susceptible Enterococcus may occur in the setting of disorders of calcium homeostasis, relatively low doses of daptomycin and end-stage renal disease, which may be associated with limited mutations in the bacterial genome.

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Supplementary data
Figure S1 is available as Supplementary data at JAC Online (http://mc.manuscriptcentral.com/jac).

References

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Spread of NDM-2-producing Acinetobacter baumannii in the Middle East

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Sir,
Resistance of Acinetobacter baumannii isolates to β-lactams and particularly to carbapenems is on the rise. Carbapenem resistance in A. baumannii due to the production of metallo-β-lactamases (MBLs) such as New Delhi MBL (NDM) is increasingly being reported in different parts of the world. To date, two types of NDM (NDM-1 and NDM-2) have been described in A. baumannii1–7 and in other Acinetobacter species.8–11

Five previously described NDM-2-producing A. baumannii isolates recovered from Egypt, Israel and the United Arab Emirates (UAE) were included in the study.2,3,7 The first corresponded to an A. baumannii ML isolate obtained in October 2010 in Germany from a patient who had been hospitalized in Cairo.5 The other four isolates comprised two (AB1 and AB2) clonally related organisms recovered in an Israeli rehabilitation centre in mid-20092 and two recovered 4 months apart in 2009 from the same patient in Al Ain in the UAE.7 All the isolates were confirmed as A. baumannii by matrix-assisted laser desorption ionization time-of-flight mass spectrometry (MALDI-TOF MS) and resistance to carbapenems was confirmed by Etest (AB bioMerieux, Solna, Sweden). Results were interpreted according to CLSI guidelines.12 Although all the isolates had previously been shown to belong to sequence type 103 by multilocus sequence typing according to the Pasteur system (http://www.pasteur.fr/recherche/genopole/PF8/mlst/Abaumannii.html), in this study we performed further epidemiological characterization using PFGE and plasmid profiles13 to confirm they belonged to the same clone.
Analysis of their genomic relationship by PFGE clearly showed the isolates to be clonally related. An identical pattern was observed between the isolates from Egypt and Israel and a similar pattern (a two-band difference) was detected in the two isolates from the UAE (Figure 1a). Likewise, all the isolates showed the same plasmid profile with five plasmid bands (Figure 1b), thereby further confirming that these isolates were clonally related.

The proximity of both the dates of isolation of the organisms reported here and the geographical location of the patients from whom they were obtained strengthens the idea of the dissemination of NDM-2-producing *A. baumannii* in the Middle East. Although the exact location of the original focus of dissemination was not clearly established, the clinical and geographical histories of the patients generate some important clues in this study. The first isolate was recovered in May 2009 from the urine of an Egyptian woman admitted to Tawam Hospital (Al Ain, UAE), who had been repeatedly hospitalized in Cairo and Beirut for cancer treatment in the previous year.7 The second group of isolates was recovered in July 2009 in a systematic surveillance study carried out on patients hospitalized in two wards in the Sourasky Medical Center in Tel-Aviv (Israel). Here, five independent clonally related *A. baumannii* isolates were obtained from elderly women admitted for rehabilitation after orthopaedic surgery.7 However, since the Sourasky Medical Center serves as a referral centre for patients from Gaza (occasionally previously hospitalized in Egypt), as well as for patients from various areas of Israel, spread of the Acinetobacter isolates in the rehabilitation centre is likely. The third case corresponded to an isolate recovered from a patient who had had a traffic accident in Egypt and was transferred to Germany in October 2010;3 since the patient was transferred to the German hospital on this day, the patient must have been colonized by the isolate while she was still in Egypt.

In summary, this is the first known report of the dissemination of the bla<sub>NDM-2</sub>-producing *A. baumannii* clone in three countries of the Middle East with no link to the Indian subcontinent, after the identification of NDM-1-producing *Klebsiella pneumoniae* from the Sultanate of Oman.14 Furthermore, since the isolates were identified over a long period of time, the occurrence of outbreaks has been ruled out, suggesting that the Middle East as well as the Balkan region and the Indian subcontinent may be an important reservoir of NDM-2-producing *Acinetobacter*. Considering the proximity of these territories, international travel to the Middle East region and the transfer of patients between hospitals and reference centres, important surveillance measures are required.

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Co-location of the erm(T) gene and blaROB-1 gene on a small plasmid in Haemophilus parasuis of pig origin

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Sir,

Haemophilus parasuis is the causative agent of Glässer’s disease, characterized by fibrinous polyserositis, polyarthritis and meningitis in pigs, which causes considerable economic losses in the swine industry.1 Macrolide antibiotics inhibit bacterial protein synthesis by binding to the 50S ribosomal subunit. Although macrolides are widely used in the treatment of Gram-positive infections, they are also of clinical relevance in the treatment of infections caused by Gram-negative bacteria such as H. parasuis. The major mechanism of resistance to macrolides is the methylation of the adenine at position A2058 in domain V of the 23S rRNA and the methyltransferases encoded by erm genes generally confer cross-resistance to macrolide, lincosamide and streptogramin B (MLSβ) antibiotics.2,3 In the present study, we report that the erm(T) gene is present in a blaROB-1-positive H. parasuis isolated in China. So far, the erm(T) gene has been described only in lactobacilli, streptococci, enterococci and staphylococci,4–6 all of which are Gram-positive bacteria.

A total of 145 H. parasuis isolates were isolated from pigs suffering from polyserositis, pneumonia or meningitis in China during August 2010 to July 2011. Isolates were confirmed by biochemical tests and 16S diagnostic PCR.1 Due to the unavailability of a CLSI-approved method for H. parasuis, susceptibility tests were conducted using the broth microdilution method according to the CLSI recommendations for Actinobacillus pleuropneumoniae.7 The reference strain A. pleuropneumoniae ATCC 27090 served as a quality control strain. Among the 145 H. parasuis isolates, only strain F539 exhibited high MICs of erythromycin (64 mg/L), lincomycin (64 mg/L), penicillin (32 mg/L), amoxicillin (256 mg/L) and cefaclor (32 mg/L), but showed low MIC values of cefotiofur (<0.064 mg/L) and cefotaxime (<0.064 mg/L). Subsequently, PCR screening for the genes erm(A), erm(B), erm(C), erm(f) and mef(A),2 which have been reported to occur in

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