SmqrR does not equally regulate the expression of Smqrn in all S. maltophilia strains. The intrinsic resistome has been defined as the set of determinants that contribute to the specific phenotype of susceptibility to antibiotics of a given bacterial species. Our results indicate that the contribution to intrinsic resistance (and its regulation) of the elements of bacterial intrinsic resistome (as Smqrn) can be strain-specific. We should therefore be aware that a feature observed in a specific bacterial strain cannot necessarily be extrapolated to the remaining strains of the same species. More studies in other S. maltophilia strains will be required to decipher whether the differential effect observed in these two strains is a general issue or just an exception for one of the analysed isolates.

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Transparency declarations
None to declare.

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Filling the map for antimicrobial resistance in sub-Saharan Africa: ampicillin-resistant Enterococcus from non-clinical sources in Angola

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†Carla Novais and Luisa Peixe equally contributed to the preparation of the study and writing of the manuscript.

Sir,
A recent compilation of antimicrobial resistance (AMR) data from sub-Saharan Africa (sSA) by Leopold et al.1 did not consider the role of non-clinical contexts for the dispersion of AMR. Also, among the microorganisms presented they did not include Enterococcus spp., opportunistic bacteria associated with community and hospital infections worldwide, mainly in individuals with underlying risk factors often identified in sSA (e.g. immuno-compromised).2–6

AMR rates of Enterococcus from diverse sSA environments and hosts were variable among countries, but often included resistance to β-lactams, widely used due to their low cost and ready availability.4–8 Ampicillin resistance (AmpR) is considered a marker of worldwide Enterococcus faecium (Efm) nosocomial epidemic clones [Bayesian Analysis of Population Structure (BAPS) subgroups 2.1a and 3.3a],3 although in sSA the genetic background of AmpR-Efm is barely known in clinical or community settings (http://pubmlst.org/).4

Among the countries pointed out by Leopold et al.1 with very limited AMR data is Angola, an emergent economy with a population of 24 million, recently leaving almost four decades of civil war and still with a precarious health system (http://www.who.int/countryfocus/cooperation_strategy/ccs ago_en.pdf?ua=1). As part of a surveillance project on the occurrence of Gram-positive and Gram-negative bacteria resistant to key antibiotics used to treat human infections, we searched for AmpR-Efm in humans, animals and the environment from Benguela province (June 2013).

Samples (n=62) from different regions of Benguela province, hosts and environments were collected from: (i) healthy humans who did not take antibiotics for 3 months before the sampling (rectal swabs; n=20); (ii) a wild park (free grey monkeys-n=2 and springboks-n=3 fresh faeces; water from animal drinkers and a cistern supplying the drinkers-n=2); (iii) farm production animals

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Table 1. Epidemiological and genetic background of AmpR E. faecium isolated from diverse sources in Angola

<table>
<thead>
<tr>
<th>BAPS</th>
<th>ST</th>
<th>Isolates (n)</th>
<th>Source</th>
<th>Virulence</th>
<th>Ampicillin MIC (PBP5-Sx/Ry)</th>
<th>Resistance to other antibiotics (genes)</th>
</tr>
</thead>
<tbody>
<tr>
<td>2.3a</td>
<td>610</td>
<td>1</td>
<td>CF-A</td>
<td>acm</td>
<td>12 mg/L (S1/R20)</td>
<td>——</td>
</tr>
<tr>
<td>2.1b</td>
<td>245</td>
<td>2</td>
<td>HC-B</td>
<td>acm</td>
<td>64 to &gt;256 mg/L (S2/R19)</td>
<td>TET (tet(M)), ERY (erm(B)), STR, NIT, Q/D</td>
</tr>
<tr>
<td></td>
<td>245d</td>
<td>2</td>
<td>CF-B</td>
<td>acm</td>
<td>48 mg/L</td>
<td>TET (tet(M)), [ERY] (erm(B)), [CIP], STR, NIT, [Q/D]</td>
</tr>
<tr>
<td></td>
<td>650</td>
<td>2</td>
<td>RW-HC</td>
<td>—</td>
<td>&gt;256 mg/L (S1/R20)</td>
<td>TET (tet(M)+tet(L)), ERY (erm(B)), CIP, STR, Q/D</td>
</tr>
<tr>
<td></td>
<td>971</td>
<td>1</td>
<td>P-C</td>
<td>—</td>
<td>12 mg/L (S2/R19)</td>
<td>TET (tet(L)), CIP</td>
</tr>
</tbody>
</table>

CF-A, chicken farm facilities (walls + floor), location A; CF-B, chicken farm facilities (walls + floor), location B; HC-B, healthy chicken pool faeces, location B; RW-HC, residual water from hospital + community; P-C, pig pool faeces, location C; TET, tetracycline; ERY, erythromycin; STR, streptomycin; NIT, nitrofurantoin; Q/D, quinupristin/dalfopristin; CIP, ciprofloxacin; acm, amino-acid residues match the PBP5 ampicillin-susceptible consensus sequence and y indicates that y amino acids match the PBP5 ampicillin-resistant consensus sequence as proposed by Pietta et al.30 (see Table S1).

AmpR E. faecium were isolated from different sources (Table S1). All but one of our AmpR-Efm isolates were MDR. They were resistant to tetracycline [n = 7; tet(M), n = 6 and tet(L), n = 3], high concentrations of streptomycin [n = 6; adaE negative], quinupristin/dalfopristin [n = 5], erythromycin [n = 5; erm(B)], ciprofloxacin (n = 4), and nitrofurantoin (n = 4). Among virulence genes, acm was identified in five isolates of chicken and chicken farm facilities.

In summary, the occurrence of MDR AmpR-Efm outside of an Angolan hospital context suggests ß-lactam selective pressure, supporting the data for other countries and pathogens.1 This is of concern as ß-lactams are critical in the treatment of diverse enterococcal infections in sSA, where antibiotics such as glycopeptides are not readily available. The results of this study (Efm of BAPS groups linked to sSA acute infections and PBPs type previously observed in epidemic clonal lineages), allied to favourable conditions for bacterial transmission and infection (e.g. poor hygiene, high number of immunocompromised persons and non-controlled antibiotic use), suggest that the impact of these strains on sSA public health should be clarified. Besides AMR surveillance in an sSA clinical setting, pointed out by Leopold et al.,1 monitoring non-clinical contexts also seems essential to support empirical therapy in this region.

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Transparency declarations
None to declare.

Supplementary data
Table S1 is available as Supplementary data at JAC Online (http://jac.oxfordjournals.org/).
Rates of faecal colonization by carbapenemase-producing Enterobacteriaceae among patients admitted to ICUs in Spain

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Belen Aracil1 and Jesus Rodriguez-Baño17 on behalf of the Spanish Network for Research in Infectious Diseases (REIPI) and GEIH-GEMARA (SEIMC)

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Sir,

Carbapenemase-producing Enterobacteriaceae (CPE) have rapidly increased in Spain and other countries in recent years, mainly due to the spread of carbapenemase-producing Klebsiella pneumoniae.1,2 However, little information is available about the prevalence of faecal colonization by CPE in ICUs, and most data come from single-institution studies.3,4 Accordingly, we assessed the prevalence of CPE carriers admitted to ICUs in 11 acute-care Spanish hospitals from seven different geographical areas. Rates of faecal carriage of CPE were examined at ICU admission and during ICU stay.

The participating hospitals were located in: Madrid [H.U. La Paz (HUP), H.U. Ramón y Cajal and H.U. Puerta de Hierro (HPUH)]; Barcelona [H.U. de la Santa Creu i Sant Pau, H.U. Vall d’Hebron (HVH) and Corporació Sanitària Parc Taulí]; Seville (H.U. Virgen Macarena); Santander (H.U. Marqués de Valdecilla); Mallorca (H.U. Son Espases); A Coruña (C.H.U. A Coruña (CHUAC)); and Cádiz (H. del SAS de La Línea). In total, 260 intensive care beds were surveyed (range 8–40 per centre): 106 medical, 40 surgical and 114 medical–surgical.

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