Extra-human epidemiology of Acinetobacter baumannii in Lebanon

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Résumé en anglais	Presence of Acinetobacter baumannii outside hospitals is still a controversial issue. The objective of our study was to explore the extra hospital epidemiology of A. baumannii in Lebanon. From February 2012 to October 2013, a total of 73 water samples, 51 soil samples, 37 raw cow milk samples, 50 cow meat samples, 7 raw cheese samples and 379 animal samples were analysed by cultural methods for the presence of A. baumannii. Species identification was performed by rpoB gene sequencing. Antibiotic susceptibility was investigated and A. baumannii population was studied by two genotyping approaches: Multilocus Sequence Typing (MLST) and blaOXA-51 Sequence-Based Typing (blaOXA-51 SBT). A. baumannii was detected in 6.9% of water samples, 2.7% of milk samples, 8.0% of meat samples, 14.3% of cheese samples and 7.7% of animal samples. All isolates showed a susceptible phenotype against most of the antibiotics tested and lacked carbapenemase encoding genes except one that harboured a blaOXA-143 gene. MLST analysis revealed the presence of 36 sequence types (ST), among them 24 were novel ST(s), reported for the first time in this study. blaOXA-51 SBT showed the presence of 34 variants, among them 21 were novel and all isolated from animal origin. Finally, 30 isolates had new partial rpoB sequences and were considered as putative new Acinetobacter species. In conclusion, animals can be a potential reservoir for A. baumannii and the dissemination of new emerging carbapenemases. The role of novel identified animal clones in community-acquired infections should be investigated.
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Liens
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