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Phylogenetic analysis of Acinetobacter baumannii isolates from raw meat

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BACKGROUND

Acinetobacter baumannii is a significant cause of nosocomial infections and is resistant to a variety of antibiotics. Isolates belonging to three international clones (IC1-3) have spread worldwide and are the main causes of outbreaks. Food is an extra-hospital reservoir of *A. baumannii* of increasing importance. The aims of the study were determining (i) the genomic distance among the genomes of strains found in raw meat and those of isolates from other sources available from NCBI repository and (ii) their antibiotic resistance genes content.

MATERIELS AND METHODS

COLLECTION OF ISOLATES

72 isolates were found in retail raw meat samples in 2 surveillance studies conducted in 2012-2013 and 2018-2019, respectively.

GENOMES SEQUENCING

WGS was carried out on Illumina platforms. Good quality reads were assembled using Shovill v.1.0.4.

BIOINFORMATICS AND PHYLOGENETIC DISTANCE

Sequence types were assigned according to the Institute Pasteur scheme. Phylogenetic distance among genomes was inferred by snp-dist including genomes of *A. baumannii* found in the NCBI that presented the same ST or Single Locus Variant (SLV) of



RESULTS

PHYLOGENETIC DISTANCE Sources Phylogenetic clustering of 295 genomes Figure1: Phylogenetic tree (iTOL v.6) of 72 A. baumannii isolates from raw meat and 223 genomes retrieved from NCBI (November 2022). The ST109 was the most common. Several STS (n=21) were into 4 clades and the repartition of ST/SLV Human Hospital surface common to isolates from raw meat and from humans (n=82, NCBI). The remaining (n=141) were SLV of in each clade. these STs. ST/SLV Strains number Clade Raw meat Environment 4 5 Clade 1 Clade 2 Animal Waste water 56 16 Clade 3 116 16 Unknown Surface Clade 4 36 118 Distribution of sources (n=8) within the Regions clades. Clade 2 Clade 1 Australia Not reported 2% ^{2% 2%} Central America South America 40% 27% South_central Asia Central Europe 64% 60% Eastern Africa South_eastern Asia Clade 3 Clade 4



RESISTANCE GENES

Heatmap of the frequency of selected resistance genes in *A. baumannii* strains from raw meat and NCBI database (n=295). Gene *tet*(39) conferring tetracycline resistance was found in 13 and 48 strains from raw meat and humans, respectively. Two strains of our study carried the *strA* and *strB* genes conferring streptomycin resistance. These genes were present also in 16 genomes from the NCBI database. The numbers in the color-strip gradient represent the positive genomes of a determined STs for the resistance gene.

<u>2 3 4 5 6 7 8 9 10 15 20 25 35 5</u>

ST/SLV	ST1018 ST106 ST108	ST109 ST1133	ST1228 ST1337	ST138 ST1822	ST1890	ST2141 ST7147	ST2143	ST2145 ST7146	ST2147	ST2148 ST2140	ST2150	ST2183 ST240	ST241	51207 ST273	ST331 ST322	ST345	ST348 стало	51349 ST350	ST352 ST352	ST353 стасл	ST356	ST357 ST358	ST361-like	ST362-like ST364	ST367	S1372 ST38	ST388 ctar	5142 ST53	ST624 ST866	ST946	SLV1014 SLV416	SLV659	SLV213	SLV237 SLV1110	SLV1140 SLV1303	SLV1168 SIV164	ыч ти4 SLV1479	SLV584 SIV768	SLV32	SLV 1431 SLV 763		SLV /40 SLV431	SLV203 SLV37	SLV1828 SLV336	
Number of isolates	2 10 10	17 1	1 3	35	1 3	1 1	1 1	1 2	2 1	1	1 1	2 4	191	.3 2	1	2 3	6	2 1	3 1	L 6	1 1	2 2	2 1	1 2	2 1	3 2	7	2 1	4	3 3	2 15	5 1	1 4	1	1 1	162	27	2 2	1 23	1 1	1 1	1 1	11 1	L 1 1	
bla _{OXA-58}																																													
bla _{OXA-23}																																													
bla _{NDM-1}																																													
bla _{CARB-16}																																													
tet(A)																																													



CONCLUSION

The phylogenetic analyses showed that *A. baumannii* isolates from raw meat are heterogenic, clustering in four different clades. Some isolates from raw meat showed large genomic similarity with genomes from isolates causing outbreaks and infections in humans. Isolates from raw meat carried *tet*(39) genes and were carbapenem susceptible. On the contrary, multiple resistance genes have been observed among isolates from humans, including carbapenemase encoding genes and pan-aminoglycosides resistance genes. Our results demonstrate that clones colonizing raw meat samples can circulate among humans and could develop multidrug resistance, nourishing the circulation of this threatening opportunistic pathogen.