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## Phylogenetic and resistome analysis of epidemic multidrug-resistant *Acinetobacter baumannii* clone

Agnese Lupo, Benoit Valot, Antoine Drapeau, Estelle Saras, Bour Maxime, Marisa Haenni, Plésiat Patrick, Jean-Yves Madec, Anais Potron

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A. Lupo,<sup>1</sup> B. Valot,<sup>2</sup> A. Drapeau,<sup>1</sup> E. Saras,<sup>1</sup> M. Bour,<sup>3</sup> M. Haenni,<sup>1</sup> P. Plésiat,<sup>3</sup> J-Y. Madec,<sup>1</sup> A. Potron<sup>3</sup>

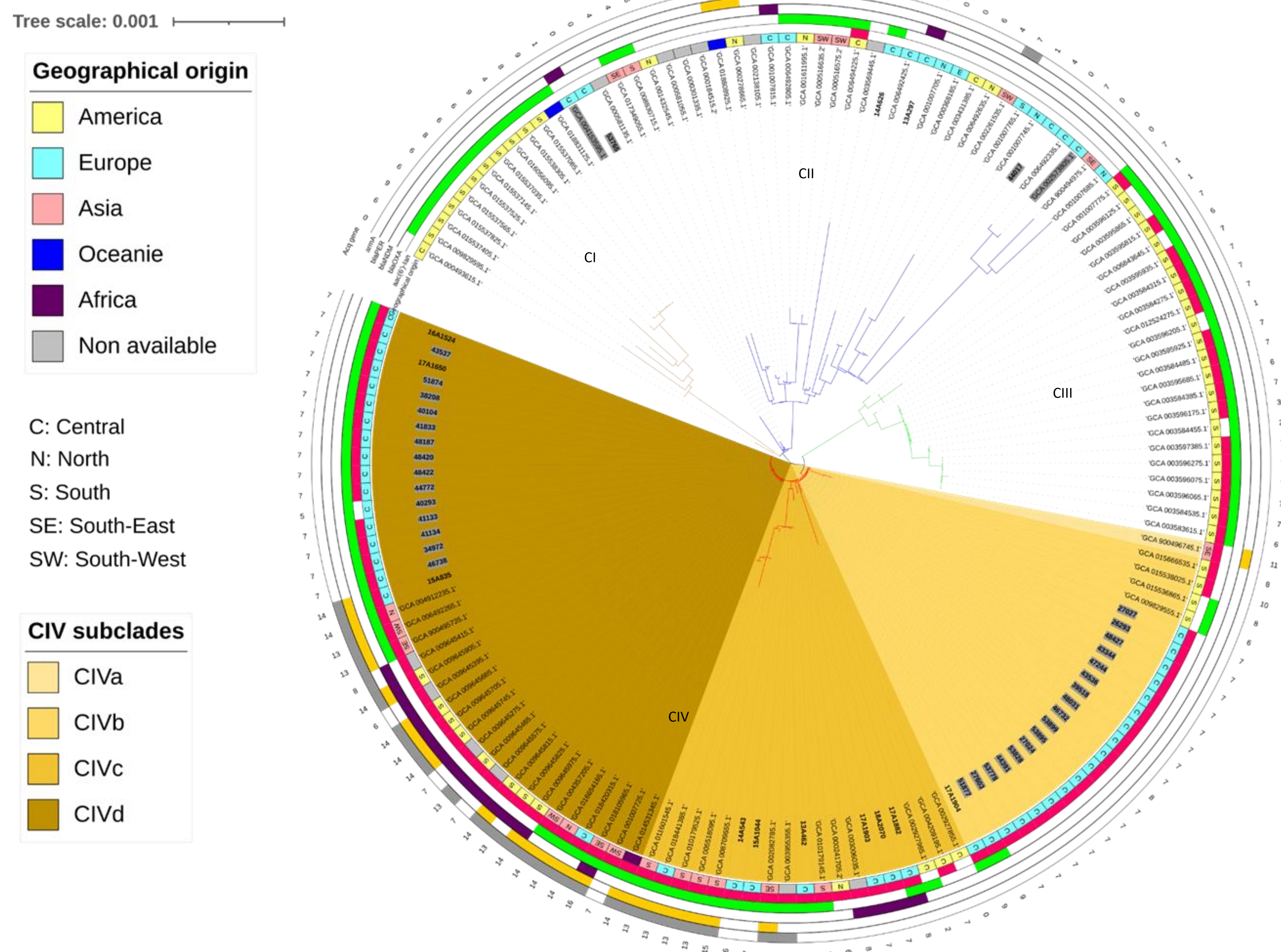
<sup>1</sup>:Université Lyon 1 - ANSES-Lyon, Unité Antibiorésistance et Virulence Bactériennes; <sup>2</sup>:CNRS-Université de Bourgogne/Franche-Comté, UMR 6249Chrono-Environnement; <sup>3</sup>:CNRS de la Résistance aux Antibiotiques, Centre Hospitalier Universitaire de Besançon.

Contact: [agnese.lupo@anses.fr](mailto:agnese.lupo@anses.fr)

**Background:** ST25 *Acinetobacter baumannii* includes multidrug-resistant isolates responsible for severe infections, which are propagating globally.

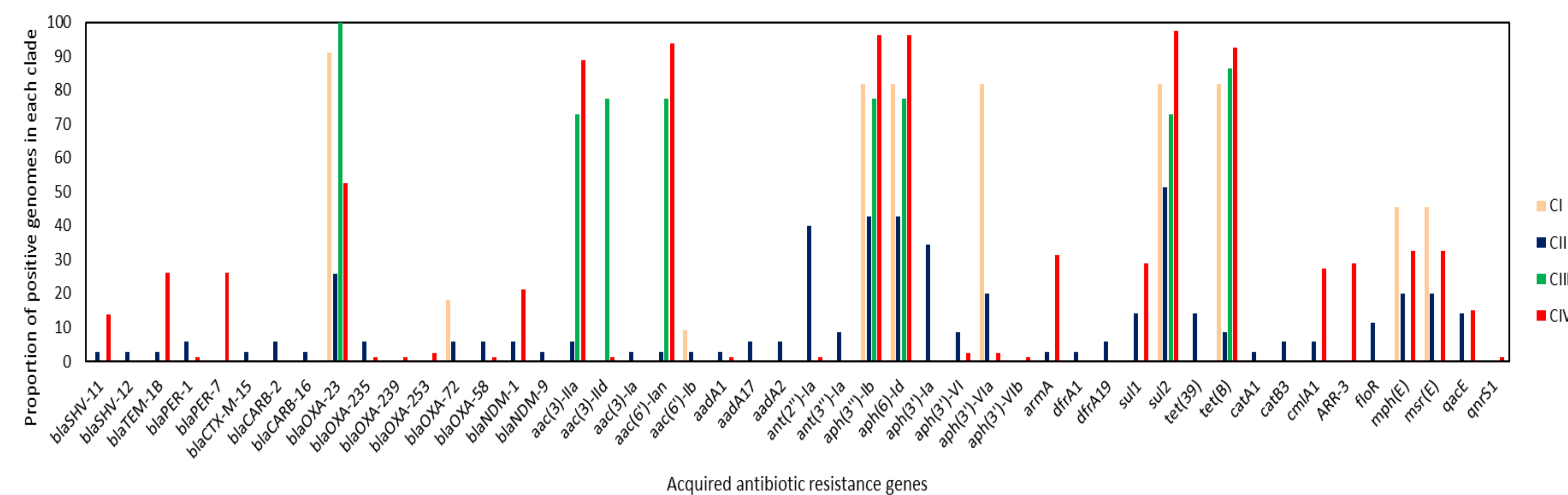
**Objectives:** To analyze genomic relationships and resistome of ST25 *A. baumannii* French isolates from humans (n=11) and animals (n=34), together with all ST25 genomes (n=103) publically available from the NCBI database.

## Phylogenetic analysis of ST25 *Acinetobacter baumannii* clone



**Figure1.** Representation of the bayesian phylogenetic analysis of 148 ST25 *A. baumannii* genomes (MrBayes; iTOLv6) generating four clades: Cl, light orange; CII, blue; CIII, light green; CIV, red. In bold: isolates sequenced for this study (Illumina); gray shadowing: genome of an isolate from animal.

## Resistome of ST25 *Acinetobacter baumannii* genomes



**Figure 2.** Fifty-two acquired genes conferring antibiotic resistance were found (ResFinder v4.1). The *bla*<sub>OXA-23</sub> gene was the most common carbapenemase encoding gene and was mainly located on an AbaR4 element. Clade CIII-IV included most of multidrug-resistant isolates.

## Conclusion

The ST25 *A. baumannii* clone is globally expanded but presents genomic divergence among isolates. Clades I and III concerned mainly South America. Genomes of clades II and IV had more diverse geographical origin. The highest number of acquired resistance genes occurred in genomes of clade CIV. Furthermore, ST25 multidrug-resistant isolates are able to colonize humans and animals overcoming host-related barrier, warranting surveillance of this clone to limit its further spread and preserving global health.