

**P2635 Characterisation of *Mycobacterium chimaera* isolates from cardiologic patients with post-surgical infections and from heater-cooler units in France**

Emmanuel Lecorche<sup>1,2,3</sup>, Daniau Côme<sup>4</sup>, Sylvain Kumanski<sup>2</sup>, Faïza Mougari<sup>1,2,3</sup>, Hanaa Benmansour<sup>1,2</sup>, Thomas Kohl<sup>5</sup>, Stefan Niemann<sup>5</sup>, Sandra Fournier<sup>6</sup>, Anne Berger-Carbonne<sup>4</sup>, Emmanuelle Cambau<sup>\*1,2,3</sup>

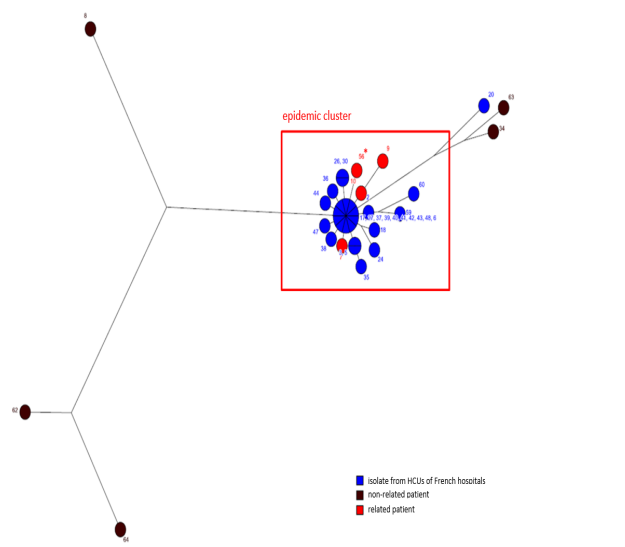
<sup>1</sup> Hospital Lariboisière Ap-Hp, Paris, France, <sup>2</sup> National Reference Center for Mycobacteria and Antimycobacterial Resistance, Paris, France, <sup>3</sup> INSERM IAME UMR1137, Paris, France, <sup>4</sup> Public Health France, Saint-Maurice, France, <sup>5</sup> Leibniz-Center for Medicine and Biosciences, Research Center Borstel, Borstel, Germany, <sup>6</sup> Assistance Publique des Hopitaux de Paris APHP, Paris, France

**Background:** Since the Rapid Risk Assessment alert issued by the European Centre for Disease Prevention and Control in 2016, over 100 cases of invasive cardiovascular infections and disseminated disease with *Mycobacterium chimaera* have been notified worldwide. The outbreak was shown to be related to the contamination of heater-cooler units (HCUs), especially those provided by one manufacturer. The aim of our study was to characterize the *M. chimaera* strains isolated in France in comparison to the epidemic strain.

**Materials/methods:** A retrospective analysis was conducted in cardio-thoracic surgery wards and HCU water tanks were screened for mycobacteria. We obtained 40 *M. chimaera* isolates: 3 isolates from the 2 cardiac surgery-related patients detected in France, 33 from HCUs of French hospitals, 4 from unrelated patients and one from environmental source. Isolates were analysed by next-generation whole-genome sequencing (WGS) using Illumina technologies, and compared with 4 published *M. chimaera* genomes.

**Results:** 27 isolates (3 from patients and 24 HCUs) belonged to the epidemic cluster, cf. Figure 1, with 2 to 10 SNPs difference. The remaining isolates distributed in two groups: 3 with a genome showing 20-40 SNPs difference, and 10 with > 100 SNPs.

Figure 1: Maximum parsimony phylogeny showing the relationship between a subset of *Mycobacterium chimaera* isolates; epidemic patients are represented by red circles (isolate 56 marked by an asterisk is the epidemic strain Zurich1), French isolates from HCUs are represented by blue circles and non-related isolates are represented by grey circles.



**Conclusions:** WGS comparison of *M. chimaera* isolated in France from the two patients with post-surgery disseminated infection and HCUs used in cardiac-surgery wards showed that all isolates are clonal with the *M. chimaera* epidemic cluster found on the HCUs production site.

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