**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 asterix 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.