|  |
| --- |
| **The tuberculosis lung virome of 18th Century mummified lung tissue.** |
| *Talya Conradie1,2, Jose Caparros-Martin1, Abhinav Sharma3, Anthony Kicic1,4,5,6,* *Siobhon Egan2,7, Sulev Koks2,8,9, Stephen M. Stick1,4,5 and Patricia Agudelo-Romero1,10,11* |
| *1Wal-yan Respiratory Research Centre, Telethon Kids Institute, WA, Australia**2Medical, Molecular and Forensic Sciences, Murdoch University, WA, Australia**3Division of Molecular Biology and Human Genetics, Faculty of Medicine and Health Sciences, Stellenbosch University, Cape Town.**4Department of Respiratory and Sleep Medicine, Perth Children’s Hospital for Children, WA, Australia.**5Centre for Cell Therapy and Regenerative Medicine, School of Medicine and Pharmacology, WA, Australia.**6School of Population Health, Curtin University, WA, Bentley, Australia**7Centre for Computational and Systems Medicine, Health Futures Institute, Murdoch University**8Perron Institute for Neurological and Translational Science, Perth, 8 Verdun Street, Nedlands, WA, 6009, Australia**9Centre for Molecular Medicine and Innovative Therapeutics, Murdoch University, Perth, WA, Australia**10Australian Research Council Centre of Excellence in Plant Energy Biology, School of Molecular Sciences, The University of Western Australia, Perth, WA, Australia**11European Virus Bioinformatics Center, Jena, TH, Germany.* |
| **Keywords:** Virome, tuberculosis, viral genomics**Introduction/Aim:**  To gain an insight into the ancient lung virome possibly associated to Tuberculosis (TB), we reanalysed metagenomics data from lung tissue samples of mummified remains found in a crypt in Hungary (DOI:10.1038/ncomms7717). These 18th Century crypts contained remains from individuals who died from TB and underwent shotgun metagenomic sequencing to identify TB strains. Therefore, this study aimed to assess the virome associated with TB by characterising and taxonomically classifying the viral contigs (vContigs) associated with the TB-infected mummified remains.**Methods:**  Two lung virome studies utilising shotgun metagenomics on mummified lung tissue were collated from the public database Sequence Read Archive (SRA) public database. The bioproject data was then run through the EVEREST pipeline (https://agudeloromero.github.io/EVEREST/). Additionally phylogenetic analyses were performed on both viral contigs to confirm their taxonomic classification.**Results:**  vContig-Cressdnaviridae and vContig-Caudovirales captured 87 vContigs, of which two were scored with medium and high-quality genomes and were found to belong to the orders Cressdnaviridae and Caudovirales. The length of the vContigs were 7180 base pairs (bp) and 98030 bp, respectively. Genomic annotation showed GC contents of 58.23% and 67.55% for vContig-Cressdnaviridae and vContig-Caudovirales, respectively. Gene coding densities of 87.16% (12 CDS, 25% known function) and 95.77% (162 CDS, 20.37% known function), including genes related to host takeover and tail proteins.**Conclusion:**  Two complete vContigs were identified from publicly available mummified lung tissue metagenomic samples through the EVEREST pipeline. This has given a historic insight into the lung virome from Eastern Europe related to TB, and the lineage of historic bacteriophages.**Grant Support:** Pawsey Supercomputing Research Centre, and Australian Government Research Training Program Scholarship. |