[BIOINFO 2023]

Human reference oral virome

Hanjune Kim[1], Junhyung Cha[1], Insuk Lee[1, *]

[1] *Department of Biotechnology, College of Life science & Biotechnology, Yonsei University*

**Corresponding author: insuklee@yonsei.ac.kr*

The human oral microbiome is one of the most studied metagenomes as well as the human gut microbiome. Dysbiosis of the oral microbiome can contribute to the onset of oral and systemic diseases, including dental caries, periodontitis, oral and other cancers, cardiovascular disease, and diabetes. However, most of the oral microbiome studies has been focused on the bacteriome with least attention on the oral virome. Since been called viral dark matters, oral viral genomes have been reported as direct or indirect modulators of numerous human diseases for decades. Nevertheless, a lack of reference oral viral genome database restricts the human oral virome research, remaining most of the oral viral dark matters unexplored. Here, we established the human reference oral virome database, HROV, which is the most comprehensive, complete, and utilizable human oral viome database. We collected and analyzed 10,172 publicly available oral metagenomes encompassing 21 countries across 5 continents, and created human reference oral virome, HROV, comprising non-redundant high quality oral viral genomes. We also applied viral binning processing for the first time to recover the more complete viral genomes, which has not been viable through conventional contig-based viral genome recovering. Human reference oral virome most comprehensively explains the variations in association to host geography, demography, and multiple associate features including age, diseases, sex, etc. On the whole, human reference oral virome will provide new resources and insights for future metagenomic virome research, enlarging the understanding of the human oral virome.