Metagenomic analysis reveals novel links between bacteria, viruses, and cancer

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Video Byte

Abstract

Cancer is a leading cause of mortality worldwide. Some types of cancer are linked to infection by viruses and bacteria, but many such links remain unexplored, indicating that other carcinogenic microbes are likely to exist. A recent study used a large, high-quality collection of 3025 whole-genome sequencing datasets to identify relationships between cancer, bacteria, and viruses. A custom-built pipeline based on the Kraken taxonomic sequence classification system software was used to identify bacterial and viral sequences in the datasets. A total of 3,534,707 read pairs matching 218 bacterial, viral, or phage species-level taxa were detected in tumor and matched healthy tissues. Of these, 27 taxa were identified to be linked to cancer. The findings support known associations between viruses, bacteria, and tumor and patient phenotypes and also reveal entirely new associations. For example, Pseudomonas spp. were found to be associated with bone cancer, while consistent links between microbial taxa and this type of cancer have not been previously described. Although further studies are needed to identify the true connections between these microbes and cancer, this information could be used to prevent certain forms or enhance the treatment of this disease.