Research team explores 'treasures' from discarded data in cancer research

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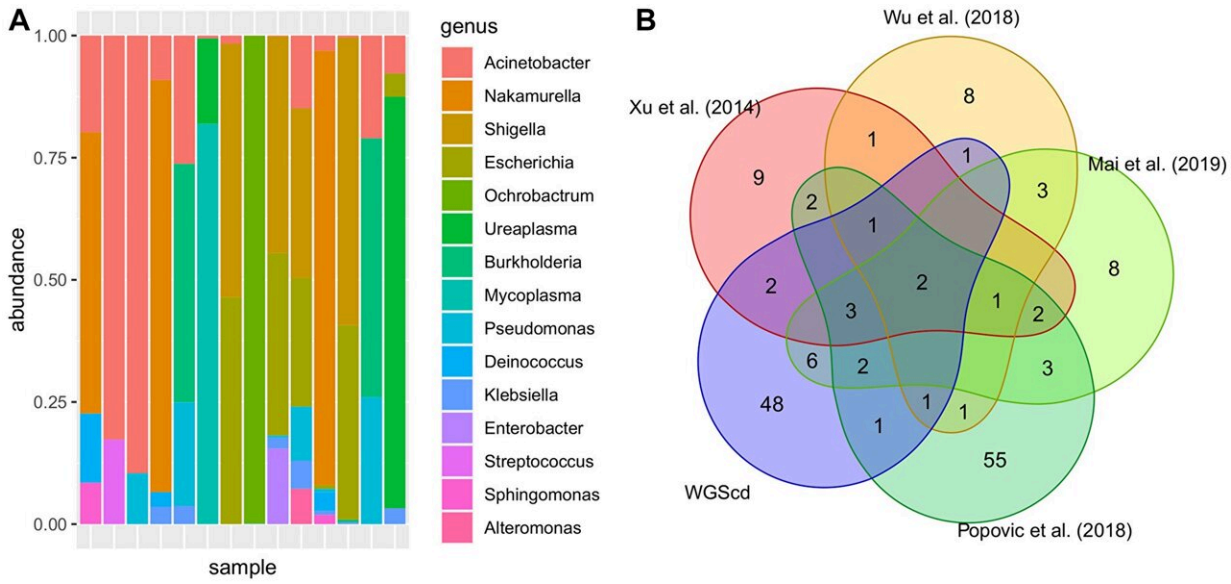

Most abundant bacteria taxa found in bladder analysis. In (A), relative genus abundance among samples. In (B), presence/absence Venn diagram: Bladder cancer tissue metagenomic profile obtained from Whole Genomic Sequencing captured data (WGScd) compared with literature research of urine bladder cancer metagenomic profile obtained from sequencing rRNA 16s amplicon. Taxon data were converted to genus since not all works present results in species resolution. Credit: *Oncotarget* (2022). DOI: 10.18632/oncotarget.28308

Cancer research has significantly improved in recent years, primarily due to next-generation sequencing (NGS) technology. Consequently, an

enormous amount of genomic and transcriptomic data has been generated. In most cases, the data needed for research goals are used, and unwanted reads are discarded. However, these eliminated data contain relevant information. Aiming to test this hypothesis, researchers acquired genomic and transcriptomic data from public datasets.

In a new research perspective published in *Oncotarget*, researchers from Instituto Metrópole Digital at the Universidade Federal do Rio Grande do Norte and Núcleo de Pesquisas em Oncologia and Instituto de Ciências Biológicas at the Universidade Federal do Pará used metagenomic tools to explore genomic cancer data; additional annotations were used to explore differentially expressed ncRNAs from miRNA experiments, and variants in adjacent to tumor samples from RNA-seq experiments were also investigated.

"Here, we demonstrate potential strategies to benefit from nontargeted information resulting from high-throughput cancer investigations," the researchers stated.

In all analyses, new data were obtained: From DNA-seq data, microbiome taxonomies were characterized with a similar performance of dedicated metagenomic research; from miRNA-seq data, additional differentially expressed sncRNAs were found; and in tumor and adjacent to tumor tissue data, somatic variants were found.

These findings indicate that unexplored data from NGS experiments could help elucidate carcinogenesis and discover putative biomarkers with clinical applications. Further investigations should be considered for experimental design, providing opportunities to optimize data, saving time and resources while granting access to multiple genomic perspectives from the same sample and experimental run.

"Altogether, our results strengthen the hypothesis that abundant

additional and potentially useful information can be extracted from NGS. Moreover, the integrated investigation of every available information should provide a broader and more robust interpretation of the molecular scenario from each experiment," the researchers conclude.

More information: Fabiano Cordeiro Moreira et al, Treasures from trash in cancer research, *Oncotarget* (2022). DOI: 10.18632/oncotarget.28308

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