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Oral microbiome dynamics during chemotherapy in breast cancer patients

Abstract:

The microbiome of the saliva can be influenced by various factors, including systemic diseases and chemotherapy. Oral dysbiosis manifests as altered bacterial composition and abundance, which often correlates with increased local and systemic inflammation. The aim of the study was to investigate the dysbiosis in the saliva of breast cancer (BC) patients before and during neoadjuvant chemotherapy (NAC).

Saliva samples were collected from 50 breast cancer patients at three timepoints (before, during, and after NAC). Saliva from 10 healthy women was used as control samples. Full-length gene 16S rRNA sequencing and analysis were performed using the Microbiome Analyst platform, R and JADBIO AutomatedML platform to compare the abundances of bacterial taxa.

Alpha and beta diversity measures differed between breast cancer patients and healthy controls. In addition, eight bacterial genera differed significantly between breast cancer patients and controls, including Porphyromonas, Campylobacter, Oribacterium, Veillonella, and Alloprevotella. Longitudinal analysis revealed significant decrease of bacterial diversity in the course of neoadjuvant chemotherapy as well as significant change in the prevalence of a few low-abundant genera. The obtained results confirm BC-related and NAC-related dysbiosis in saliva, which emphasizes the potential of saliva as a diagnostic and prognostic tool in patients with breast cancer.

Keywords: Breast Cancer, Oral microbiome, 16S rRNA sequencing, Neoadjuvant chemotherapy, Nanopore sequencing

Biography: Elżbieta Kaja obtained a PhD in Biological Sciences in 2017 at Adam Mickiewicz University in Poznań. She is also a graduate of Poznań University of Physical Education in the field of Physiotherapy. During her postgraduate studies, she participated in foreign internships, e.g. at the Claude Bernard University in Lyon (France) or Penn State University in the US. In her scientific work, Elżbieta was analyzing microRNA genes in plants and DNA repair pathways in bacteria. In MNM Bioscience Inc. she was involved in the unique project of sequencing 1 200 Polish genomes. Currently, she works at the University of Medical Sciences as a researcher mostly on the oral microbiome