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Gut microbiome modulation by colon surgery

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Colorectal cancer (CRC), the third most widespread malignancy and the second most common cause of cancer-related death worldwide, presents a significant global health burden, particularly in Westernizing countries. CRC is a complex and multifactorial disease with a growing body of evidence suggesting that the gut microbiome plays a crucial role in its development and progression. Surgery remains a cornerstone in the management of CRC, yet its implications extend beyond tumor removal. Recent research has uncovered the interplay between CRC surgery and the gut microbiome; however, only a limited amount of research has been conducted, and the analysis of the virome remains unexplored. In this study, we elucidate changes in the gut microbiome by comparing pre-surgery fecal samples using whole metagenome shotgun sequencing (WMS) with post-surgery fecal samples from 40 patients. Our analysis not only considers the microbiota but also their functional aspects, utilizing HRGM v2, a global and high-quality human gut microbiome catalog comprising only near-complete genomes. Furthermore, we investigate alterations in the gut virome, encompassing changes in viruses themselves, information related to the viruses' host bacteria, lifestyle factors, and their gene contents. To enhance the robustness of our findings, we cross-checked our results with another cohort. In summary, this study significantly advances our understanding of the gut microbial environment after surgery and offers insights into which risk factors may persist or diminish post-surgery from the perspective of the gut microbiome.