Chapter 7

Environmental DNA and RNA Metabarcoding:

Advancing Insights in Cancer Research

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ABSTRACT

Environmental DNA (eDNA) and RNA (eRNA) technologies, when integrated with metabarcoding, have emerged as significant instruments in cancer research particularly in exposomics and environmental carcinogenesis. These approaches facilitate the identification and monitoring of genetic material from many environmental sources, yielding insights into the biological and chemical factors that influence cancer risk. Environmental samples can be examined to identify pollutants, microbiota, and other molecular markers that contribute to carcinogenesis through the use of eDNA and eRNA. Metabarcoding enhances this technique by employing high-throughput sequencing to facilitate the comprehensive characterisation of complex ecosystems, the detection of potential carcinogenic exposures, and the elucidation of their interactions with human health. This methodology possesses significant potential for enhancing our comprehension of the environmental factors associated

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with early detection, prevention, and treatments. This chapter explores the concept of the human exposome as evidenced by eDNA and eRNA.

INTRODUCTION

Environmental DNA (eDNA) and RNA (eRNA) metabarcoding have revolutionised molecular ecology by facilitating the identification of genetic material excreted by organisms into their surroundings. These approaches, first designed for ecological study and biodiversity evaluation, are currently being investigated for biological applications, including cancer research. Blood, urine, and saliva contain extracellular nucleic acids, holding potential new gateways in precision medicine, monitoring disease, and cancer diagnosis using non-invasive techniques. Biomarkers for cancer are determined and dynamics of and progression of cancer are revealed using bioinformatics and high-throughput sequencing (Wan et al., 2020; Ogidi et al., 2024a).

Early cancer diagnosis is one of the biggest problems in oncology because conventional methods of diagnosis are not very sensitive and specific. Conventional tumour sample approaches are invasive, costly, and cannot capture all tumour heterogeneity. According to Heitzer et al. (2019), liquid biopsy approaches offer a non-invasive solution to identifying genetic mutations, epigenetic changes, and other molecular alterations in cancer. These techniques measure cell-free DNA (cfDNA) and cell-free RNA (cfRNA) in body fluids. Improved genetic stratification by eDNA and eRNA metabarcoding technologies drives early diagnosis, risk assessment, and patient stratification for therapeutic targeting (Heitzer et al., 2019).

The tumour microenvironment plays an important role in cancer development, such as tumour growth, immune evasion, and metastasis, beyond the early detection phase. Extracellular nucleic acids serve as significant markers of malignant processes derived from cell death of cancer cells, necrosis, and active secretion (Mohan et al., 2022). Metabarcoding analysis of extracellular nucleic acids allows researchers to follow the development of cancer in real-time, the treatment response, and new drug resistance in real-time. It is a useful tool for personalization of therapy in precision oncology, where tumour genomes are dynamically changing. Environmental oncology and cancer epidemiology were established utilizing eDNA metabarcoding and eRNA cancer research. The research has discovered that carcinogens and environmental pollutants can alter the structure and nucleic acid content of extracellular nucleic acids, thereby opening the door to cancer formation (Cheng et al., 2021). Analysis of how environmental determinants affect cancer occurrence and development can be supported by analysis of environmental eDNA and eRNA and hence improve public health interventions and prevention.

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