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Next-generation sequencing for endocrine cancers: Recent advances and challenges

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Abstract

Contemporary molecular biology research tools have enriched numerous areas of biomedical research that address challenging diseases, including endocrine cancers (pituitary, thyroid, parathyroid, adrenal, testicular, ovarian, and neuroendocrine cancers). These tools have placed several intriguing clues before the scientific community. Endocrine cancers pose a major challenge in health care and research despite considerable attempts by researchers to understand their etiology. Microarray analyses have provided gene signatures from many cells, tissues, and organs that can differentiate healthy states from diseased ones, and even show patterns that correlate with stages of a disease. Microarray data can also elucidate the responses of endocrine tumors to therapeutic treatments. The rapid progress in next-generation sequencing methods has overcome many of the initial challenges of these technologies, and their advantages over microarray techniques have enabled them to emerge as valuable aids for clinical research applications (prognosis, identification of drug targets, etc.). A comprehensive review describing the recent advances in next-generation sequencing methods and their application in the evaluation of endocrine and endocrine-related cancers is lacking. The main purpose of this review is to illustrate the concepts that collectively constitute our current view of the possibilities offered by next-generation sequencing technological platforms, challenges to relevant applications, and perspectives on the future of clinical genetic testing of patients with endocrine tumors. We focus on recent discoveries in the use of next-generation sequencing methods for clinical diagnosis of endocrine tumors in patients and conclude with a discussion on persisting challenges and future objectives.

Keywords

Next-generation sequencing, endocrine cancer

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Introduction

Modern challenges in biomedical research demand more data-generating capacity than traditional DNA sequencing technologies such as the Sanger-based methods can offer. Next-generation sequencing (NGS) methods with their extraordinary speed and scalability enable biological researchers to study systems with a definition higher than was ever possible before. The first success in DNA sequencing occurred in the 1970s, and the advent of sequencing using capillary electrophoresis made the technology much more economical.[1–3] In the 2000s, high-throughput sequencing platforms were developed, collectively known as NGS, which led to a significant and rapid expansion of genomic

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