

July 23-24, 2018 Amsterdam, Netherlands International Conference on

Immuno - Oncology and Cancer Science

Arch Can Res 2018, Volume: 6 DOI: 10.21767/2254-6081-C2-009

TOWARDS VALIDATION OF TARGETED NEXT-GENERATION SEQUENCING ON FFPE COLORECTAL CANCER TISSUES IN EGYPTIAN POPULATION: A PILOT STUDY WITH FEASIBILITY AND CHALLENGES

Neemat M Kassem¹, Sahar Sharaf², Ahmed Abdel Aziz², Mona Mohsen², Hebatallah A Kassem¹, Sara El Khateeb², Nashwa Medhat¹, Basant Nagdy¹, Rabab Ahmed² and Mohammed Abdulla²

¹Kasr Al-Ainy Centre of Clinical Oncology & Nuclear Medicine, Cairo University ²Cairo University

Background: Colorectal cancer (CRC) has been identified as the third most common cancer worldwide. Gene mutation and defective cell regulation are important processes in the development of CRC. Assessment of genetic mutations is an essential element in the modern era of personalized cancer treatment.

Purpose: We performed a pilot study identifying the frequencies of genetic changes in six frequently mutated genes: KRAS, NRAS, BRAF, PIK3CA, PTEN and TP53 in Egyptian CRC patients. The secondary objective was to validate the next-generation sequencing (NGS) technology and to develop a workflow process in the clinical setting.

Methodology: This study investigates the mutations in these 6 genes using targeted NGS. The study included 14 archived Formalin-fixed paraffin-embedded (FFPE) tumor specimens in addition to 11 external quality controls (EQC).

Results: The median age of our CRC patients was 60.5 years, 21.4% of patients were ≤40 years old, females 57.1% and males 42.9% with M/F ratio 0.75:1. The mutation frequencies of KRAS, BRAF, PIK3CA, PTEN and TP53 genes in Egyptian CRC patients were 35.7%, 14.3%, 21.4%, 7.1% and 71.4% respectively, with no mutations detected in NRAS gene which may be due to the limited study population.

Conclusion: Technical validity and clinical efficacy are the two major arguments in the analysis of NGS data. The major benefit of NGS in comparison to more traditional methods is its ability to study multiple genes at once. Implementation of targeted NGS in clinical settings allows for a trustworthy description of the most common mutations, which can direct therapeutic decisions for CRC patients.

Nkkassem@hotmail.com