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RESEARCH ARTICLE

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KRAS, *NRAS*, *BRAF*, and *PIK3CA* mutation rates, clinicopathological association, and their prognostic value in Iranian colorectal cancer patients

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Abstract

Aim: Mutations in *KRAS*, *NRAS*, *BRAF*, and *PIK3CA* genes are critical factors in clinical evaluation of colorectal cancer (CRC) development and progression. In Iran, however, the data regarding genetic profile of CRC patients is limited except for *KRAS* exon2 and *BRAF* V600F mutations. This study aimed to investigate the mutational spectrum and prognostic effects of these genes and explore the relationship between these mutations and clinicopathological features of CRC.

Method: To achieve these objectives, mutations in *KRAS* (exons 2, 3, and 4), *NRAS* (exons 2, 3, and 4), *PIK3CA* (exons 9 and 20), and *BRAF* (exon 15) was determined using PCR and pyrosequencing in a total of 151 patients with colorectal cancer.

Results: *KRAS*, *BRAF*, *NRAS*, and *PIK3CA* mutations were identified in 41%, 5.96%, 3.97%, and 13.24% of the cases, respectively. There were some significant correlations between clinicopathological features and *KRAS*, *PIK3CA*, *BRAF*, and *NRAS* mutations. Mutations in *KRAS* and *PIK3CA* were shown to be independent risk factors for poor survival of the patients at stage I-IV ($p < 0.0001$ and $p = 0.001$, respectively). No significant impact on prognosis was observed in patients with *BRAF* mutations.

Conclusion: Our study revealed the prevalence of CRC biomarkers mutations in Iranian patients and emphasized the role of *KRAS* and *PIK3CA* on shorter overall survival rates in this population.

KEYWORDS
BRAF, colorectal cancer, *KRAS*, *NRAS*, *PIK3CA*

1 | INTRODUCTION

With a prevalence of 10.0%, colorectal cancer (CRC) has been recognized as the third most common cancer worldwide.[1] Like most cancers, colorectal cancer is a multifactorial disease caused by a combination of environmental and genetic factors. The contributing genetic factors include chromosomal abnormalities, epigenetic changes, as well as somatic and germline mutations.