Editorial

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Does *BRAF* Mutation and Extracellular Signal Regulated Kinase Expression in Patients With Colorectal Cancer Have Any Prognostic Significance?

Moo Jun Baek

Department of Surgery, Soonchunhyang University Cheonan Hospital, Soonchunhyang University College of Medicine, Cheonan, Korea

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Wild-type KRAS acts as a switch during signal transduction; however, somatic mutations that activate regulators and effectors of Ras proteins are common in tumor development and cancer [1-3]. In approximately 35%–42% of early colorectal cancer (CRC) patients, the *KRAS* mutation inhibits KRAS GTPase, resulting in a constitutive KRAS activation and, thus, activating a Ras/Raf signaling pathway. In CRC, 97% of *KRAS* mutations occur in codons 12 and 13 of exon 2, and more than 97% of changes in the protein are attributable to changes in the amino acid sequence by the substitution of seven DNA base pairs [4]. *BRAF* is a human gene that encodes the protein B-Raf, which is considered a proto-oncogene, encoding a serine/threonine protein kinase [5]. B-Raf is a member of the Raf kinase family that regulates the Ras/Raf/MEK/extracellular signal regulated kinase (ERK) pathway and is involved in division, differentiation, and secretion [6]. The most common *BRAF* mutation is a missense mutation (V600E, formally known as V599E), resulting in glutamic acid in place of valine that generates an abnormality in the MEK/ERK signaling pathway in CRC [7].

The mitogen-activated protein kinase (MAPK)/ERK signaling pathway is a highly conserved intercellular signaling system present in multicellular organisms and plays an essential role in cancer progression. MAPK/ERK activation is a common feature of tumors with *KRAS*, *NRAS*, or *BRAF* mutations [8, 9]. A highly activated MAPK/ERK pathway is found in approximately 30% of cancers and over 60% of melanomas, and it is associated with tumor proliferation and migration. BRAF is upstream of the MAPK/ERK pathway, and a single amino acid change, resulting in a valine-to-glutamyl acid substitution at position 600 (V600E), accounts for ~90% of *BRAF* mutations. ERK1/2 are important kinases in the MAPK pathway. Therefore, activation of ERK1/2 could be considered as a target factor related with CRC carcinogenesis through the serrated pathway [8].

The authors of this study investigated the clinicopathologic outcomes of *BRAF* mutation and ERK1/2 expression in patients with CRC and the possibility of their use as prognostic indicators. The authors found that *BRAF* mutation and ERK1/2 expression might be associated with advanced or more aggressive CRC [10].

CONFLICT OF INTEREST

No potential conflict of interest relevant to this article was reported.

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Correspondence to: Moo-Jun Baek, M.D.
Department of Surgery, Soonchunhyang University Cheonan Hospital, Soonchunhyang University College of Medicine, 31 Suncheonhyang 6-gil, Dongnam-gu, Cheonan 330-930, Korea
Tel: +82-41-570-3633, Fax: +82-41-571-0129
E-mail: ssurge@sch.ac.kr

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