



The frequency of KRAS mutation detection in human colon carcinoma is influenced by the sensitivity of assay methodology: A comparison between direct sequencing and real-time PCR [☆]

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ABSTRACT

Purpose: Kirsten rat sarcoma (KRAS) gene mutations occur early in the progression of colorectal adenoma to carcinoma. The mutation status of the KRAS gene determines the benefits of molecular targeting drugs in patients with advanced colorectal cancer, although many methods are available to detect such mutations. The purpose of this study was to evaluate the influence of assay sensitivity on the detection frequency of mutated genes. **Methods:** Colorectal tumors in 224 colorectal cancer patients were characterized for KRAS mutations using PCR amplification following by direct sequencing as well as a peptide nucleic acid (PNA)-clamp real-time PCR-based assay. **Results:** KRAS mutations were observed in 32.1% (72/224) patients by direct sequencing, and 43.3% (97/224) by PNA-clamp PCR. The chi-square test revealed that the difference in the frequency of KRAS mutations determined by direct sequencing and PNA-clamped PCR (threshold for 1% detection) was statistically significant ($p < 0.015$). **Conclusions:** Our data suggest that assay method sensitivity clearly influences the detection frequency of mutated genes. As more sensitive assays detect more mutated genes in clinical samples, this must be taken into consideration when determining KRAS gene status in clinical practice.

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1. Introduction

Mutations in the Kirsten rat sarcoma (KRAS) oncogene are frequently found in human cancers, particularly those of the pancreas, gall bladder, bile duct, thyroid gland, non-small cell lung cancer, and colorectal cancer [1–4]. The presence of these mutations may determine the prognosis and drug response to new cancer therapies targeting the K-ras protein pathway [5].

Cetuximab and panitumumab, the monoclonal antibodies (mAbs) used to target the epidermal growth factor receptor (EGFR), were recently approved by the US Food and Drug Administration (FDA) and the European Medicines Agency (EMA) for use as single agents or in combination with other chemotherapeutic drugs in the treatment of metastatic colorectal cancer (mCRC). However, the mAbs only benefit a subset of patients that express the wild-type K-ras protein; tumors with mutated K-ras do not respond to this treatment modality [6–9]. A significant improvement

in overall survival and progression-free survival was observed in patients with wild-type K-ras tumors following treatment with cetuximab compared with supportive care alone, but not in those with mutated K-ras tumors [8]. It is therefore important that the KRAS mutation status be determined precisely to maximize the patient's benefit in a clinical setting.

While a variety of methods are available for the detection of KRAS mutations, nested PCR followed by direct sequencing and allele-specific real-time PCR have been widely utilized so far. We hypothesized that differences in the sensitivity of mutation screening methods may influence mutation detection frequency. To test this, we compared the frequency of KRAS mutations detected in clinical colon cancers by two discrete methods. The first involved classical nucleotide sequencing analysis in which PCR amplification is followed by direct sequencing, and the second is a more sensitive method involving the peptide nucleic acid (PNA)-clamp real-time PCR-based assay [10].

2. Materials and methods

2.1. Cell culture

SW480 and HCT116 cell lines were purchased from the American Type Culture Collection (ATCC, Rockville, MD). Cells were

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