Background. Colorectal cancer (CRC) is one of the most common types of cancer, affecting 3 - 5% of the global population. K-ras proto-oncogene and TP53 tumour suppressor gene mutations are among the most common genetic alterations detected in advanced colorectal tumours.

Objective. To investigate the role of K-ras codon 12 and TP53 exons 5 - 9 mutations in late-stage CRC patients.

Methods. Blood samples were collected from 249 CRC patients, of whom 147 presented with advanced carcinoma. K-ras codon 12 mutations were analysed using polymerase chain reaction-restriction fragment length polymorphism, while direct sequencing was used in screening for TP53 exons 5 - 9 mutations.

Results. No significant changes were observed in TP53 exons 5 - 9, except for two cases in which nucleotide replacements were observed in the non-coding regions in intron 4 (c.376-19C>T) and intron 9 (c.993+12T>C). Heterozygous mutations in K-ras codon 12 were observed in 79 individuals suffering from advanced CRC (53.7%). Colon and rectal tumours were equally distributed among the heterozygotes, but colon tumours were mostly present in wild-type homozygotes (84.6%). There was also a predominance of Caucasians among heterozygotes and a predominance of Asians among the wild-type homozygotes.

Conclusion. Analysis of peripheral blood samples of CRC patients suffering from advanced carcinoma has prognostic value only for K-ras codon 12 mutations, and not for TP53 mutations.

Colorectal cancer (CRC) is one of the most common cancers, affecting 3 - 5% of the population, with an incidence peak in the age range 50 - 70 years. CRC is the third leading cause of cancer death in both men and women worldwide, and continues to be one of the most common fatal types of cancer. Worldwide, approximately 1.5 million individuals are diagnosed with CRC and 500 000 die from the disease annually. Among Eurasian countries, Kazakhstan has the seventh-highest incidence of CRC. CRC develops slowly over several years and progresses through cytologically distinct benign and malignant stages of growth, ranging from single-crypt lesions through adenoma to malignant carcinoma with the potential for invasion and metastasis. The majority of CRC cases are sporadic, with 20 - 30% being familial.

The classic model of colorectal tumourigenesis includes several genetic changes that are required for cancer initiation and progression. The earliest genetic trigger is the inactivation of the APC pathway. Mutations in other tumour suppressor genes (APC, SMAD2, SMAD4, DCC, TP53) and oncogenes (K-ras) and several other genes/pathways accompany the transition of the tumour towards malignancy and metastasis. In addition to the gene mutations, deregulated expression of oncogenes and/or tumour suppressor genes can also be mediated via epigenetic modifications such as DNA methylation and histone acetylation. Rapidly developing insights into the molecular genetics of CRC have led to the identification of predictive and prognostic biomarkers for CRC.
The TP53 gene product is a nuclear phosphoprotein that is expressed at low levels in normal tissues and plays a key role in the control of cell cycle progression, genome stability and apoptosis. TP53 is one of the most frequently mutated genes in human cancers. Somatic mutations of TP53 are associated with more advanced stages of the disease, with loss of TP53 gene heterozygosity being a marker for the conversion of adenoma to carcinoma. In CRC tumours, more than 50% of mutations occur in the TP53 gene. The most common mutations are single-base substitutions that alter protein function. However, in contrast to the activating K-ras gene mutations, which are concentrated in only a few positions, mutations in the TP53 gene are scattered over a large region of the gene. Most TP53 gene mutations in CRC tumours occur in exons 5 - 9, which contain four highly conserved domains that are important in the clinical outcome of CRC and have been associated with increased malignant potential. 

Several studies have reported combined mutations in K-Ras and TP53 genes in CRC tumours, but the clinical usefulness of K-Ras and/or TP53 gene mutations is still somewhat controversial. The data on K-ras and TP53 aberrations and their relationship to patient survival and prognosis are insufficient to recommend the use of such mutations as prognostic indicators. It is therefore clear that prospective studies to assess the prognostic utility of these genetic abnormalities are required. Although most reports indicate that altered K-Ras and TP53 genes in tumour tissues present at advanced stages, it would be interesting to assess the status of these genes in peripheral blood samples of CRC patients, because the gene heterozygosity can have a predictive value for determining prognosis.

The Kazakhstan National Screening Program for malignant neoplasms of the colon and rectum, initiated in 2011, showed that most cases were diagnosed at a very late stage when treatment is expensive and ineffective. The prediction of malignant potential and resistance to EGFR or 5FU chemotherapy at earlier stages of CRC development before surgery may improve patient survival.

### Methods

#### Sampling

Blood samples were collected from 249 CRC patients at Almaty Oncology Centre, Almaty, Kazakhstan. Informed consent and detailed demographic information were obtained. Histological testing showed that 147 of these patients (59.0%) had presented with advanced CRC, and they were chosen as subjects for this study. The study protocol was approved by the Ethics Committee of the Asfendiyarov Kazakh National Medical University.

#### DNA isolation

Genomic DNA was isolated from peripheral blood leukocytes of the 147 patients with advanced CRC (stages III and IV) using the standard phenol-chloroform method with modifications in the composition of the lysis buffer (0.2M sodium acetate and 1% sodium dodecyl sulphate, pH 8.0) and precipitated in ice-cold ethanol. The quantity and quality of the DNA samples were evaluated spectrophotometrically using an Eppendorf BioPhotometer (Eppendorf, Germany), and they were stored at −20°C until required.

#### Detection of K-ras mutations in codon 12

All known nucleotide mutations in codon 12 were screened by polymerase chain reaction-restriction fragment length polymorphism (PCR-RFLP). One hundred nanograms of total DNA was amplified in a 20 μL reaction mixture containing 10 pM of each specific primer (sense-5’-AICTGAATATAACCTTGAGTTGACCTGACC-3’, anti-sense-5’-TCAGAATAGGTCTCAGGACC-3’), 10 mM of each deoxynucleotide triphosphate (dNTP), 1 mM MgCl2, 0.5 KCl, 0.1% gelatin and 1 U Taq-polymerase (Sigma-Aldrich, USA). Denaturation was performed at 95°C for 5 minutes, followed by 40 cycles at 95°C for 30 seconds, at 54°C for 40 seconds and at 72°C for 1 minute, with a final elongation step at 72°C for 7 minutes. Five microlitres of each PCR product (157 bp) was digested with 1 U MvaI (BstN1, ThermoScientific, USA) at 60°C for 3 hours. Digestion products were analysed on 1.4% agarose gels. The normal K-ras allele is indicated by the presence of a 114-bp fragment as opposed to the 143-bp fragment in the mutant K-ras allele. Heterozygotes display both the 143- and 114-bp fragments.

#### Sequencing of exons 5 - 9 of the TP53 gene

Direct sequencing was used to screen for mutations in exons 5 - 9 of TP53. The PCR was performed in a final volume of 20 μL containing 50 ng template DNA, 1 × PCR buffer, 0.2 mM of each dNTP, 1.5 mM MgCl2, 0.4 μM of each primer (Table 1) and 0.5 U of FastStart Taq DNA polymerase using the Veriti Dx 96-well Thermal Cycler (Applied Biosystems, USA). PCR products were visualised by electrophoresis on 1.5% agarose gels.

PCR products were purified using Nucleofast 96-well PCR plates (Macherey-Nagel, Germany). Sequencing reactions were performed using BigDye Terminator v3.1 Cycle sequencing kit (Applied Biosystems, USA). The negative strand of the gene was sequenced.

### Objective

Because the K-ras codon 12 and TP53 mutations are the most promising biomarkers of CRC tumour progression, the objective of this study was to assess K-Ras and TP53 gene status in blood samples of patients with advanced colorectal carcinoma.

### Table 1. The PCR amplification primers and parameters used for direct sequencing of TP53 exons 5 - 9

<table>
<thead>
<tr>
<th>Amplified regions of TP53 gene</th>
<th>Primer pairs (5 ′ → 3 ′)</th>
<th>PCR conditions</th>
<th>Length of PCR products</th>
</tr>
</thead>
<tbody>
<tr>
<td>Exons 5 - 6</td>
<td>f-TGTTCACTTGTCCTGACTr-TTAAACCCCTGGTCCACAGAGA</td>
<td>1 cycle of 2 min at 94°C, 20 cycles (94°C for 30 s, 63°C for 45 s with –5°C per cycle, 72°C for 1 min), followed by 30 cycles (94°C for 30 s, 60°C for 45 s, 72°C for 1 min), and a final cycle of 10 min at 72°C</td>
<td>467 bp</td>
</tr>
<tr>
<td>Exon 7</td>
<td>f-CTTGCACAGGTTCCTCCCAAr-AGGGTGACAGGCGAACGA</td>
<td>1 cycle of 2 min at 94°C, 20 cycles (94°C for 30 s, 63°C for 45 s with –5°C per cycle, 72°C for 1 min), followed by 30 cycles (94°C for 30 s, 60°C for 45 s, 72°C for 1 min), and a final cycle of 10 min at 72°C</td>
<td>237 bp</td>
</tr>
<tr>
<td>Exons 8 - 9</td>
<td>f-TGGGGATAGATGGGACCTr-AGTGTAGACTGGAAAACCTT</td>
<td>1 cycle of 2 min at 94°C, 20 cycles (94°C for 30 s, 63°C for 45 s with –5°C per cycle, 72°C for 1 min), followed by 30 cycles (94°C for 30 s, 60°C for 45 s, 72°C for 1 min), and a final cycle of 10 min at 72°C</td>
<td>445 bp</td>
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</table>
using specific primers and the BigDye Terminator v3.1 sequencing kit (Applied Biosystems) and an ABI 3730xl Genetic Analyser (Applied Biosystems). The cycle sequencing reactions contained 50 - 100 nmol of purified PCR product, 2 μl of BigDye Terminator, 1 μl of Sequencing Buffer and 3.2 pmol of primer in a total volume of 20 μl. Cycle sequencing was performed using 55 cycles at 96°C for 5 minutes, 60°C for 5 minutes and 96°C for 5 minutes. After cycle sequencing, sodium dodecyl sulphate was added and the samples were purified on Sephadex columns using a Tecan EVO150 robotic workstation (Agilent Technologies, USA). The purified sequencing products were dried, suspended in Hi-Di (Life Technologies, USA) and denatured at 95°C for 2 minutes before sequencing electrophoresis. Electrophoresis was performed on an ABI 3730xl using a 50 cm capillary array and POP7 (Applied Biosystems).

DNA sequencing data were analysed using ChromasPro version 1.7.4 software, confirmed by reverse sequencing and compared with the Leiden Open Variation and Universal Mutation databases to search for mutations.

Statistical analysis
Student’s t-test was used to compare the distribution of variables between groups, with a p-value of <0.05 considered significant.

Results
Characteristics of the study population
Adenocarcinoma was the predominant tumour type among the 249 CRC patients first diagnosed with CRC in the period 2012 - 2014, and 55.8% of the tumours were well or moderately differentiated. Table 2 summarises the data on tumour localisation and stage, showing that rectal tumours predominated at 47.7% of all sites.

For the analysis of K-ras codon 12 mutations and TP53 exons 5 - 9 mutations as potential markers of cancer progression, the advanced carcinoma cases were chosen after histological verification. A total of 147 patients (59.0%) had advanced CRC (stages III and IV by TNM criteria). In this cohort there were 73 women (49.7%) and 74 men (50.3%), and the ethnic distribution was as follows: Kazakhs n=39 (26.5%), Russians n=86 (58.5%), other Asians (Turks, Uzbeks, Tatars, Uighurs, Koreans, Dungans) n=17 (11.6%), and other Caucasians (Armenians, Ukrainians, Belarusians, Germans) n=5 (3.4%). There were 50 cases of rectal cancer (34.0%) and 97 of colon cancer (66.0%), with 126 cases of stage III cancer (85.7%) and 21 of stage IV cancer (14.3%). Among patients suffering from advanced CRC there were 5 smokers (3.4%), 14 ex-smokers (9.5%), and 128 non-smokers (87.1%).

K-ras mutations in codon 12 in patients with advanced CRC
The 147 selected CRC patients with advanced carcinoma were screened for K-ras codon 12 mutations (Gly12Asp (GGT→GAT), Gly12Ala (GGT→GCT), Gly12Val (GGT→GTT), Gly12Ser (GGT→AGT), Gly12Arg (GGT→CGT), Gly12Cys (GGT→TGT)).

The genotyping data for the K-ras codon 12 mutations (Fig. 1) revealed 79 heterozygous individuals (53.7%), while 68 (46.3%) of the patients were homozygous wild type. Some differences were observed in the stage of cancer progression between individuals who were mutant heterozygous and normal homozygous for K-ras codon 12 (Table 3). The percentage of patients who had progressed to stage IV was higher among the mutant allele carriers than...
amplification using the primers defined in Table 1, and the PCR products were subjected to direct sequencing, as shown in Fig. 2. However, three cases of nucleotide replacements were noticed in intron 9 (c.993+12T>C) (Fig. 2, A), and another two cases in intron 4 (c.376-19C>T, Fig. 2, B), all in the heterozygous state. Table 4 summarises the DNA sequencing data in individuals with TP53 mutations. Two different types of mutations were detected in five patients from among the 147 patients with advanced carcinoma.

**Discussion**

It is well known that mutations in the tumour suppressor gene TP53 and K-ras oncogene are not responsible for initiation of the development of CRC, but are critical for tumour progression and metastasis.

The most common TP53 gene mutations are single-base substitutions that alter protein function. While loss-of-function mutations are generally inherited or early events, some of the oncogenic mutations that confer gain-of-function properties are late-stage events, mostly exon 5 - 9 mutations, that play an important role in the clinical outcome of CRC.

Our study on peripheral blood samples of 147 patients with advanced CRC did not show any significant changes in TP53 exon 5 - 9 mutations, except for two novel heterozygous nucleotide replacements in the non-coding regions of the gene. One change in intron 4 (c.376-19C>T) was observed in two patients, and another nucleotide substitution was detected in intron 9 (c.993+12T>C) in three patients. No information on the significance of these mutations detected in CRC patients from Kazakhstan is available in the literature. It should also be noted that the TP53 mutations were examined in the peripheral blood DNA of the patients and not in the tumours; these are therefore inherited mutations. However, it cannot be ruled out that additional genetic events may occur along the way. Although intronic mutations do not alter the amino acid sequence of a gene product, they can influence the regulation of gene activity by altering the binding of regulatory proteins or miRNA, leading, for example, to aberrant splicing (IARC TP53 Database).

The most common K-ras codon 12 mutations result in the substitution of glycine for valine, thus changing the spatial conformation of the RAS, leading to a constitutively activated form where the RAS signalling cascade to other participants occurs regardless of EGFR status. This explains why the predictive value of K-ras mutations in determining whether or not patients will respond to anti-EGFR therapy is of much interest..

Screening of all known K-ras codon 12 mutations (Gly12Asp, Gly12Ala, Gly12Val, Gly12Ser, Gly12Arg, Gly12Cys) in the blood DNA of 147 CRC patients with advanced CRC showed heterozygous mutations in more than 50% of the patients (79/147). Our data are in agreement with the published data showing K-ras codon 12 mutation frequencies ranging from 30% to 60% in tissue samples from rectal and colon tumours.

We could not find any significant differences regarding gender, age or smoking habit between patients carrying the K-ras codon 12 mutation and the wild-type homozygotes. The percentage of patients with stage IV cancer carrying the mutant allele was higher than among the normal homozygotes (32.9% v. 14.7%), but this was not statistically significant. Tumours of the rectum and colon were equally distributed among heterozygous patients; however, the prevalence of colon tumours (84.6%) in normal homozygous patients was statistically significant. The relationship between K-ras mutations and the clinical/morphological parameters of CRC has been extensively investigated.

There is some evidence that K-ras codon 12 mutations are significantly
associated with poor survival at all stages of cancer progression. Estimated event-free survival correlates with poor tumour differentiation status, pericolic fat invasion and metastasis.\textsuperscript{10, 11} CRCs with \textit{K-ras} mutations are associated with distinctive morphological features. \textit{K-ras} codon 12 mutations are more frequently observed in carcinomas of the proximal-distal axis of the colorectum, mucinous differentiation, and contiguous polyps. Our findings are in agreement with these findings.

Some ethnic differences were observed in the Kazakhstan patients: there was a higher prevalence of mutant allele carriers among the Caucasians (Russians and others) and a higher prevalence of normal homozygotes among the Asians (Kazakhs and others). It is well established that ethnic differences and lifestyle have a strong influence on the frequency of \textit{K-ras} mutations.\textsuperscript{13} \textit{K-ras} codon 12 mutation is a good biomarker in stage IV CRC, predicting lack of benefit from the anti-EGFR targeted antibodies cetuximab (Erbitux) and panitumab (Vectibix).\textsuperscript{14, 15} It is possible that the findings on \textit{K-ras} codon 12 carriers in our population will help in the choice of adjuvant therapy.

Several studies have detected compound mutations in the \textit{K-ras} and \textit{TP53} genes in CRC.\textsuperscript{11, 16} A Tunisian CRC study reported the detection of a \textit{K-ras} somatic mutation in 31.5% of patients, with 81.2% having a single mutation at codon 12 and 23% having a single mutation at codon 13; 43.75% of the patients harboured combined \textit{K-ras} and \textit{TP53} mutations, with 71.42% of them showing \textit{TP53} over-expression.\textsuperscript{17} In our study two of the five patients (a woman born in 1967, rectal carcinoma, stage III T3NxMo, and a man born in 1937, rectal carcinoma, stage IV T4NxM1) with \textit{TP53} intron mutations were also heterozygous for the \textit{K-ras} codon 12 mutation. In both cases the mutation was in intron 9 of \textit{TP53} (c.993+12T>C). Because the percentage of \textit{TP53} mutations among advanced CRC patients from Kazakhstan is very low (3.4%) and nothing is known about the pathological significance of these intronic mutations, there is no evidence for an association with poor prognosis. However, our observation of the prevalence of inherited \textit{K-ras} codon 12 mutation carriers in advanced CRC patients (53.7%), together with the literature data, supports the idea that these mutations may be a predictive marker of cancer progression and anti-EGFR therapy.

**Conclusion**

The study demonstrates that the analysis of peripheral blood samples of patients suffering from advanced CRC may have prognostic value only for \textit{K-ras} codon 12 mutations, and not for \textit{TP53} mutations.

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**References**