A Let-7 MicroRNA SNP in the KRAS 3'UTR Is Prognostic in Early-Stage Colorectal Cancer

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Abstract

**Purpose:** Colorectal cancer (CRC) is a common cause of death worldwide. Tumor-node-metastasis-system stage is currently used to guide therapy decisions but lacks precision. Prognostic biomarkers are needed to refine stratification of patients for chemotherapy but validated biomarkers are not yet available. Recently, a SNP in a lethal-7 (let-7) miRNA complementary site (LCS6) in the KRAS 3'untranslated region was suggested to affect survival in metastatic CRC. Effects in early-stage CRC are however unknown. We studied KRAS-LCS6 genotype, hypothesizing that it might identify early-stage cases with a poor prognosis, and could potentially be used in therapy decision-making.

**Experimental Design:** We studied 409 early stage, 182 stage III, and 69 stage IV cases, and 1,886 subcohort members from the Netherlands Cohort Study. KRAS-LCS6 genotype was assessed with TaqMan PCR. Kaplan–Meier analyses or Cox regression were used to assess associations between genotype and CRC risk or cause-specific survival.

**Results:** Early-stage cases with the KRAS-LCS6 variant had a lower CRC risk (incidence-rate ratio 0.68; 95% CI: 0.49–0.94) and a better survival (log-rank \( P = 0.038; \) HR 0.46; 95% CI: 0.18–1.14). In patients with KRAS-mutated CRC carrying the KRAS-LCS6 variant, the better outcome was enhanced as no patients died of CRC (log-rank \( P = 0.017 \)). In advanced patients, no clear association between genotype and CRC risk or survival was observed.

**Conclusions:** Our results indicate that early-stage CRC cases with the KRAS-LCS6 variant have a better outcome. In advanced disease, the better outcome no longer exists. For early-stage patients, KRAS-LCS6 genotype combined with KRAS mutations merits validation as a prognostic biomarker and consideration in therapy decision-making. *Clin Cancer Res;* 17(24); 7723–31. ©2011 AACR.

Introduction

Despite diagnostic and therapeutic innovations, colorectal cancer (CRC) remains the second cause of cancer death in the western world (1). The tumor-node-metastasis-system (TNM) is currently the main tool to provide prognostic information; it is highly predictive for prognosis at the extremes, but less predictive for intermediate stages (2, 3). According to current guidelines, adjuvant chemotherapy is not given to early-stage patients (T1-3-N0-M0 according to the International Union Against Cancer-TNM) as 5-year survival rates in this group are more than 70%. Nevertheless, 20% to 30% of early-stage patients (stage I and II) will die of CRC within 5 years, evoking the question whether these deaths could have been avoided if these patients were identified in advance and therapy was adapted accordingly. Previously, numerous studies have been published claiming a prognostic influence of molecular markers. Results however, are inconsistent and the question which molecular alterations influence prognosis remains unresolved (4).

Over the last years, a new class of gene regulators, micro-RNAs (miRNA), has been identified as important factors in cancer development and progression. Evidence suggests that one miRNA can regulate many mRNAs simultaneously (5) and miRNAs can act as both tumor suppressors and oncogenes (6). One of the first discovered miRNA families is the lethal-7 (let-7) family of miRNAs, and altered expression of these miRNAs has been described in many cancers (7). In lung cancer, let-7 is poorly expressed (8, 9), overexpression of let-7 inhibits cell growth *in vitro* (9) and *in vivo* (10, 11) suggesting that let-7 miRNAs may act as tumor suppressors (6). In colon cancer cells, let-7 expression was significantly decreased in tumor tissue as compared with adjacent
Translational Relevance

We report for the first time that a SNP in a *let-7* (let-7) complementary site (LCS) in the *KRAS* 3′-UTR (*KRAS-LCS6*) might be a prognostic biomarker in early-stage colorectal cancer (CRC). The *KRAS-LCS6* variant is known to cause higher levels of the KRAS oncoprotein and lower levels of the tumor suppressor *let-7* miRNAs. We studied the influence of *KRAS-LCS6* in 409 early-stage (stage I and II), 182 stage III, and 69 stage IV cases from the large, prospective Netherlands Cohort Study (NLCS). Early-stage patients with the *KRAS-LCS6* variant had a better prognosis, especially those that also had KRAS mutations, and this was independent of microsatellite instability or other prognostic factors. In addition, we studied the influence of the *KRAS-LCS6* variant on CRC risk using data from 1,886 subcohort members from the NLCS. The G-allele was associated with a decreased risk on early-stage CRC, but was not associated with advanced stage CRC risk, suggesting that the G-allele is not associated with the likelihood of advanced stage CRC. As our population is the only untreated population studied to date, our results give a first insight into the natural biology of CRC with the *KRAS-LCS6* variant. The *KRAS-LCS6* variant may become a new biomarker in CRC to guide treatment decisions in early-stage patients.

Data collection

Information on tumor localization, stage, differentiation grade, incidence date, and treatment in the 3 months after diagnosis, was available through the NCR. Vital status until May 2005 was retrieved from the Central Bureau of Genealogy and the municipal population registries and could be obtained for all 734 cases. Causes of death were retrieved through linkage with Statistics Netherlands. CRC-related deaths were defined as deaths as a result of a carcinoma in the colon, rectosigmoid, rectum, gastro-intestinal tract (nonspecific) or liver metastases. In the case of gastrointestinal (nonspecific) or liver metastases, we used the information from NCR andPALGA to eliminate the possibility of another primary cancer as cause of death.

DNA isolation and *KRAS-LCS6* SNP determination

A 5-μm section of each tumor tissue block was stained with haematoxylin and eosin and reviewed by a pathologist. Five sections of 20 μm were deparaffinated and DNA was extracted using the Puregene DNA isolation kit (Gentra systems) according to the manufacturer’s instructions. In brief, cell lysis solution and proteinase K (20 mg/mL, Qiagen) were added to the tissue and incubated overnight at 55°C. DNA was extracted for 72 hours at 37°C, protein was removed, and DNA was precipitated using 100% 2-propanol. Finally, DNA was rehydrated in hydration buffer. Isolated DNA was amplified using TaqMan PCR assays designed specifically to identify the T or G allele of the *KRAS-LSC6* SNP (Applied Biosciences). Although we used tumor DNA to assess genotype, it has previously been well documented that the genotype of normal and tumor tissue is the same in *KRAS-LCS6* variant allele carriers (13).

KRAS and Braf mutations were assessed by nested PCR and direct sequencing (KRAS), and restriction fragment

Materials and Methods

Study population

Until 1994, 925 incident CRC cases (ICD-O: 153.0–154.1) were identified within the NLCS which started in 1986 with 120,852 healthy persons between 55 and 69 years. Incident cancer cases were identified by linkage with the Netherlands Cancer Registry (NCR) and PALGA, a nationwide registry of histopathology and cytopathology (21). The NLCS has been described in detail elsewhere (22). A total of 815 patients could be linked to PALGA and paraffin-embedded tumor tissue was collected from 54 pathology registries throughout the Netherlands. We were able to extract sufficient, good quality DNA for 734 (90%) cases (23). At baseline, a subcohort of 5,000 healthy persons was randomly sampled from the entire cohort to estimate person-years at risk of the cohort through biennial follow-up of vital status. For 1,886 persons, DNA from buccal swabs was available for *KRAS-LCS6* genotyping.
length polymorphism (BRAF) as described previously (23, 24). Promoter methylation of RASSF1A, O6-MGMT, CHFR, and CIMP markers as proposed by Weisenberger (25) was assessed by chemical modification of genomic DNA with sodium bisulfite and methylation-specific PCR (MSP; refs. 24, 26, 27). Microsatellite instability (MSI) status was determined using BAT-26, BAT-25, NR-21, NR-22, and NR-24 as described previously (28). All assays were done and analyzed blinded to the main study endpoint, that is, CRC-related death.

Statistical analyses

Cause-specific survival was defined as time from cancer diagnosis until CRC-related death or end of follow-up. Kaplan–Meier curves and log-rank tests were used to estimate the influence of the KRAS variant on cause-specific survival. HR and corresponding 95% CI were assessed by use of Cox proportional hazard models adjusted for potential confounders. Factors were considered possible confounders if they were known prognostic factors for CRC and influenced the crude HR by more than 10%. Confounders that were included were age at diagnosis (continuous), sex, tumor differentiation grade (well, moderate, poor, and undifferentiated), and location (proximal, distal, rectosigmoid, and rectum). The proportional hazard assumption was tested using the Schoenfeld residuals and the log (–log) hazards plots. Survival analyses were restricted to 10 years after diagnosis as CRC-related cause of death was unlikely after that point. Incidence rate ratios (RR) and 95% CI were estimated using Cox proportional hazards models. Standard errors were estimated using the robust Huber–White sandwich estimator to account for additional variance introduced by sampling from the cohort. All analyses were done with the statistical package STATA10.0.

Results

CRC variables and the KRAS-LCS6 variant

Patients in this study were more often male (55.6%), diagnosed with an early-stage tumor (62.0%) or a proximal or distal tumor (65.3%; Table 1). During follow-up, 41.4% of the patients died of CRC. The KRAS-LCS6 variant was detected in 14.0% of early-stage (stage I and II), in 19.2% of stage III and 21.4% of stage IV patients ($P = 0.160; P_{trend} = 0.060$). KRAS-LCS6 variant patients were more often diagnosed with advanced stage disease (47.5% vs. 36.9% in wild-type patients, $P = 0.046$). No other statistically significant differences were found between wild type and variant carriers for sex, age at diagnosis, differentiation grade, tumor location, MSI, or mutations in KRAS (Table 1). BRAF ($P = 0.640$), or RASSF1A promoter CpG island methylation ($P = 0.423$). As expected, patients with stage III or IV disease more often died from CRC ($P < 0.001$) and more often had a poorly differentiated tumor ($P < 0.001$). Advanced stage patients more often had a proximal ($P = 0.036$) or MSS tumor ($P = 0.047$) as compared with early-stage patients.

Stage IV G-allele KRAS-LCS6 carriers were more likely to be female (66.7%; $P = 0.097$), and to present with a proximal tumor (71.4%; $P = 0.004$) as compared with G-allele carriers in other stages (Table 2).

The KRAS-LCS6 variant is associated with better survival in early-stage CRC

No statistically significant difference was observed in Kaplan–Meier analyses for the KRAS-LCS6 variant and cause-specific survival in the total population (log-rank test, $P = 0.864$) (Supplementary Fig. S1).

As survival depends on cancer stage, we conducted analyses stratified for stage. Early-stage G-allele carriers showed a statistically significantly better survival as compared with wild-type cases (log-rank test, $P = 0.038$; Fig. 1A). This difference was not seen for advanced stage cases (Fig. 1B and C; log rank, $P = 0.775$ and 0.875 for stage III and IV cases, respectively).

KRAS/BRAF mutation status enhances the association between the KRAS-LCS6 variant and survival

Figure 2A shows Kaplan–Meier analyses for early-stage (stage I and II) CRC cases with the KRAS-LCS6 variant and KRAS mutations. In our population, none of the 20 G-allele carriers with KRAS mutations died due to CRC. KRAS-LCS6 wild-type patients had a poorer survival, especially if they had KRAS mutations (log-rank test, $P = 0.043$; log-rank test KRAS-LCS6 G-allele carriers with KRAS mutations compared with KRAS-LCS6 G-allele carriers without KRAS mutations $P = 0.017$). This observation was independent of T stage; among 115 KRAS-LCS6 wild-type cases with KRAS mutations, only 5 (4%) were diagnosed as high-risk stage IIb (T4N0M0). Among G-allele carriers, no patients were diagnosed as stage IIb. For advanced stage patients, no survival difference was seen (Fig. 2B and C; log-rank test, $P = 0.535$ for stage III and $P = 0.989$ for stage IV) although results for stage III patients suggest that KRAS-LCS6 wild-type patients with KRAS mutations have the worst prognosis. Subgroup analysis showed that the better outcome for early-stage KRAS-LCS6 variant carriers was mainly caused by stage II cases. Analyses stratified for T stage were not possible due to limited patient numbers (data not shown).

BRAF mutated CRCs carrying the G-allele showed a similar better outcome, although this was not statistically significant (log-rank test, $P = 0.166$) possibly due to small number of patients carrying both events (9 patients). Similarly, G-allele carriers with aberrant RASSF1A promoter hypermethylation, another gene involved in the Ras pathway, had a better prognosis, although only borderline statistically significant, as compared with wild-type carriers without RASSF1A hypermethylation (log-rank test, $P = 0.062$). Analyses combining KRAS, BRAF, and RASSF1A status showed that early-stage G-allele carriers with additional alterations in KRAS, BRAF, or RASSF1A have a better prognosis (log-rank test, $P = 0.026$). In contrast, when adding methylation status of genes not involved in the Ras pathway such as MGMT or CHFR, no survival differences were observed (MGMT: log-rank test, $P = 0.220$; CHFR: log-rank test, $P = 0.118$; data not shown).
<table>
<thead>
<tr>
<th></th>
<th>Overall</th>
<th>KRAS-LCS6 wild-type TT</th>
<th>KRAS-LCS6 variant G-allele (He/Ho)</th>
<th>P</th>
<th>Early-stage (stage I and II) CRC</th>
<th>Stage III</th>
<th>Stage IV</th>
<th>P</th>
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<tr>
<td>Total population, n (%)</td>
<td>734 (100)</td>
<td>567 (83.6)</td>
<td>111 (16.4)</td>
<td>409 (62.0)</td>
<td>182 (27.6)</td>
<td>69 (10.5)</td>
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<td>Sex [male, n (%)]</td>
<td>Male</td>
<td>406 (55.6)</td>
<td>308 (54.3)</td>
<td>66 (59.5)</td>
<td>0.320</td>
<td>219 (53.6)</td>
<td>102 (56.0)</td>
<td>33 (47.8)</td>
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<td>Age at diagnosis (mean, SD)</td>
<td>67.9 (4.3)</td>
<td>67.9 (4.3)</td>
<td>67.9 (4.4)</td>
<td>0.885</td>
<td>68.0 (4.4)</td>
<td>67.5 (4.1)</td>
<td>68.5 (3.8)</td>
<td>0.203</td>
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<td>CRC-related death (yes, n (%))</td>
<td>Yes</td>
<td>302 (41.4)</td>
<td>230 (40.6)</td>
<td>46 (42.2)</td>
<td>0.781</td>
<td>95 (23.3)</td>
<td>107 (8.8)</td>
<td>65 (95.6)</td>
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<td>Cancer stage, n (%)</td>
<td>Early stage (I and II)</td>
<td>409 (62.0)</td>
<td>326 (63.1)</td>
<td>53 (52.5)</td>
<td>0.124</td>
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<td>III</td>
<td>182 (26.7)</td>
<td>137 (66.5)</td>
<td>33 (32.7)</td>
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<td></td>
<td>IV</td>
<td>69 (10.5)</td>
<td>54 (10.4)</td>
<td>15 (14.1)</td>
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<td>Differentiation, n (%)</td>
<td>Well</td>
<td>74 (11.5)</td>
<td>58 (11.8)</td>
<td>9 (8.7)</td>
<td>0.761</td>
<td>46 (12.7)</td>
<td>13 (7.8)</td>
<td>3 (5.0)</td>
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<td></td>
<td>Moderate</td>
<td>457 (71.0)</td>
<td>354 (71.8)</td>
<td>72 (69.9)</td>
<td>0.135</td>
<td>277 (76.5)</td>
<td>109 (65.3)</td>
<td>36 (60.0)</td>
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<tr>
<td></td>
<td>Poor</td>
<td>106 (16.5)</td>
<td>75 (15.2)</td>
<td>21 (20.4)</td>
<td>0.532</td>
<td>37 (10.2)</td>
<td>41 (24.6)</td>
<td>20 (33.3)</td>
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<td></td>
<td>Undifferentiated</td>
<td>7 (1.1)</td>
<td>6 (1.2)</td>
<td>1 (1.0)</td>
<td>0.532</td>
<td>2 (0.6)</td>
<td>4 (2.4)</td>
<td>1 (1.7)</td>
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<tr>
<td>Location, n (%)</td>
<td>Proximal</td>
<td>239 (33.2)</td>
<td>196 (35.4)</td>
<td>34 (31.2)</td>
<td>0.842</td>
<td>128 (31.5)</td>
<td>63 (34.8)</td>
<td>33 (49.3)</td>
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<td>Distal</td>
<td>231 (32.1)</td>
<td>177 (32.0)</td>
<td>37 (33.9)</td>
<td>0.420</td>
<td>125 (30.7)</td>
<td>61 (33.7)</td>
<td>22 (32.8)</td>
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<td></td>
<td>Rectosigmoid</td>
<td>80 (11.1)</td>
<td>59 (10.6)</td>
<td>11 (10.1)</td>
<td>0.382</td>
<td>53 (13.0)</td>
<td>17 (9.4)</td>
<td>5 (7.5)</td>
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<td>Rectum</td>
<td>169 (23.5)</td>
<td>122 (22.0)</td>
<td>27 (24.8)</td>
<td>0.824</td>
<td>101 (24.8)</td>
<td>40 (22.1)</td>
<td>7 (10.5)</td>
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<td>Molecular characteristics, n (%)</td>
<td>MSS</td>
<td>578 (87.3)</td>
<td>463 (87.5)</td>
<td>88 (84.6)</td>
<td>0.149</td>
<td>314 (84.9)</td>
<td>149 (88.7)</td>
<td>63 (95.5)</td>
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<td>MSI</td>
<td>84 (12.7)</td>
<td>66 (12.5)</td>
<td>16 (15.4)</td>
<td>0.420</td>
<td>56 (15.1)</td>
<td>19 (11.3)</td>
<td>3 (4.5)</td>
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<td></td>
<td>CIMP+</td>
<td>167 (27.7)</td>
<td>127 (24.5)</td>
<td>34 (35.4)</td>
<td>0.076</td>
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<td></td>
<td>CIMP−</td>
<td>436 (72.3)</td>
<td>352 (75.5)</td>
<td>62 (64.6)</td>
<td>0.121</td>
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<td>KRAS mutations, n (%)</td>
<td>Wild type</td>
<td>464 (63.2)</td>
<td>362 (63.8)</td>
<td>69 (62.2)</td>
<td>0.736</td>
<td>263 (64.3)</td>
<td>121 (66.5)</td>
<td>39 (56.5)</td>
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<td>KRAS mutated</td>
<td>270 (36.8)</td>
<td>205 (36.2)</td>
<td>42 (37.8)</td>
<td>0.736</td>
<td>146 (35.7)</td>
<td>61 (33.5)</td>
<td>30 (43.5)</td>
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<td>KRAS variant</td>
<td>Wild type</td>
<td>567 (83.6)</td>
<td>326 (86.0)</td>
<td>137 (80.6)</td>
<td>0.336</td>
<td>54 (78.3)</td>
<td></td>
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<tr>
<td></td>
<td>Variant He</td>
<td>107 (15.8)</td>
<td>51 (13.5)</td>
<td>32 (18.8)</td>
<td>0.295</td>
<td>15 (21.7)</td>
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<tr>
<td></td>
<td>Variant Ho</td>
<td>4 (0.6)</td>
<td>2 (0.5)</td>
<td>1 (0.6)</td>
<td>0.295</td>
<td></td>
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</table>
The survival impact of the KRAS-LCS6 variant combined with KRAS mutation status is independent of other prognostic factors

In multivariate analyses, no statistically significant differences in cause-specific survival were found for early-stage (HR 0.46; 95% CI: 0.18–1.14), stage III (HR 0.98; 95% CI: 0.55–1.74) or stage IV cases (HR 0.42; 95% CI: 0.17–1.06) with the G-allele variant as compared with wild types, although early-stage and stage IV G-allele carriers seemed to have a slightly better survival (Table 3). Early-stage G-allele carriers with KRAS mutations seemed to have a good prognosis; none of these patients died due to CRC. In contrast, no statistically significant differences in survival were found between KRAS nonmutated early-stage (HR 0.77; 95% CI: 0.30–1.97), stage III (HR 0.95; 95% CI: 0.44–2.05) or stage IV cases (HR 0.35; 95% CI: 0.11–1.13) with the KRAS-LCS6 variant. However, stage III G-allele carriers with KRAS mutations seemed to have a poor prognosis (HR 1.52; 95% CI: 0.66–3.54) although not statistically significant.

As Dutch guidelines did not advise adjuvant treatment at the time patients were diagnosed with CRC in the NLCS, the proportion of patients that received adjuvant treatment was very low. Within the early-stage cases, only 9% received adjuvant chemotherapy, for the advanced stage patients this was 31% for stage III and 19% for stage IV. Exclusion of treated patients did not alter our conclusions (data not shown) although it even enhanced the difference between early-stage and stage III G-allele carriers with KRAS mutations (early stage: no CRC-related deaths; stage III: HR 2.36 95% CI: 0.99–5.67) implying that stage III G-allele carriers might indeed have a worse natural course of the disease. However, this analysis is based on small patient numbers.

The survival impact of the KRAS-LCS6 variant is independent of MSI

As MSI is currently the only established molecular prognostic marker in CRC, we studied the effect of KRAS-LCS6 genotype stratified for MSI. Exclusion of patients that had an MSI tumor, which is associated with a good prognosis, did not alter our conclusions; both MSI and MSS cases with the KRAS-LCS6 G-variant had a good prognosis. In contrast, patients with the KRAS-LCS6 wild type had a poor prognosis, even if they had an MSI tumor (log-rank test, \( P = 0.036 \)) (Fig. 3). Additional analyses stratified for sex, tumor
The risk of advanced stage CRC is not associated with the KRAS-LCS6 variant

To study the possibility that the KRAS-LCS6 G-allele predisposes for advanced stage CRC, we studied the association between KRAS-LCS6 genotype and CRC risk. The KRAS-LCS6 G-allele was found in 18% of the subcohort members. For CRC, we observed a decreased risk of developing early-stage (stage I or II) CRC when carrying the KRAS-LCS6 G-allele (RR 0.68, 95% CI: 0.49–0.94). The risk of developing advanced stage CRC (stage III or IV) was however not influenced by the KRAS-LCS6 genotype (RR stage III: 1.02, 95% CI: 0.68–1.53; RR stage IV: 1.15, 95% CI: 0.63–2.09).

Discussion

In this study, we tested the hypothesis that a T>G variant in the LCS6 in the 3′UTR region of KRAS affects prognosis in early-stage (stage I and II) CRC. The KRAS-LCS6 G-variant was present in 16.4% of the cases whereas it is only found in 6% of world populations (13), and 12% to 15% in persons from European descent (14). We found an increased frequency of the KRAS-LCS6 G-allele in advanced cases (early-stage 14%, 19.2%, and 21.4% in stage III and IV patients, respectively), which is comparable with previously reported frequencies in stage III (19). The G-allele was found in 18% of the subcohort members. We found a statistically significant association between the KRAS-variant and an increased presentation with advanced colon cancer, perhaps giving some insight into the natural biology of colon cancer in KRAS-LCS6 variant carriers. Furthermore, we found a statistically significant increase in survival for early-stage CRC cases with the KRAS-LCS6 G-variant; among KRAS-mutated patients none of the early-stage patients carrying the G-allele died from CRC. This effect was independent of other prognostic factors such as tumor differentiation or sublocation. As T4 tumors were rare in our group of early-stage cases, a higher frequency of stage IIb cases among KRAS-LCS6 wild types is not the cause of the observed worse outcome. No statistically significant effect was seen in stage III or IV, although results suggested a slightly worse prognosis for stage III cases with the G-variant and KRAS mutations. In addition, we studied the effect of the KRAS-LCS6 G-allele on CRC risk and observed a slightly decreased risk of early-stage CRC, but no effect on the risk of advanced stage CRC, suggesting that the G-allele is not associated with a higher likelihood of advanced stage CRC.

In a number of previous studies, mutations in KRAS have been associated with a poorer prognosis. However, we and others have recently described that results on this topic are inconsistent and the clinical relevance of these findings are unclear (4). Acquired KRAS mutations are however not the same as the KRAS-LCS6 variant, which is congenital and could therefore have a different effect on tumor development, biology, and thus prognosis.

The unexpected finding that the KRAS-LCS6 variant is associated with an increased survival in early-stage CRC is intriguing. Previous research has suggested that cellular senescence can be triggered by overexpression of oncogenic Ras and might contribute to growth cessation in premalignant or benign neoplasms (29). Tumor cell senescence has been reported in human cancers, and premalignant colon adenomas display features of senescence as well (30). Previous studies have often suggested that...
expression had a good prognosis if they had decreased expression of WT1 related genes (31). These results imply that other molecular factors can be involved in the determination of cell fate, and that oncogene-induced senescence can occur after an altered expression of other genetic or epigenetic targets. Hypothetically, this could also play a role in CRC, and the KRAS-LCS6 genotype could either lead to an advanced stage tumor, or an early-stage tumor with a better prognosis based on the other (epi)genetic markers that are affected. However, evidence on this concept is scarce and more research is needed to elucidate whether our findings can be explained by oncogene-induced senescence.

Similar to KRAS mutations, we observed a better outcome for early-stage (stage I and II) cases with the KRAS-LCS6 G-variant and BRAF mutations or RASSF1A hypermethylation, 2 other genes involved in the Ras signaling pathway. BRAF-associated senescence has previously been reported to occur in melanoma (32) but a possible role of RASSF1A in oncogene-induced senescence is currently unknown. As in our population both events are less common, statistical significance was not reached. When combining these (epi)genetic events, the better outcome of patients with the variant G-allele and KRAS, BRAF, or RASSF1A alterations was even more enhanced. Along this line, we hypothesize that Ras overexpression due to the KRAS-LCS6 G-allele, in combination with (epi)genetic alterations in genes from the Ras pathway, could induce senescence in early-stage CRC thereby influencing survival. For advanced cases on the other hand, an increasing number of molecular pathways are affected that all have a role in prognosis. Although intriguing, this is only speculative; more research is needed to determine whether the KRAS-LCS6 G-variant and (epi)genetic alterations in Ras-associated genes can lead to oncogene-induced senescence in early-stage CRC.

Several studies have previously shown a tumor growth suppression effect of the let-7 miRNA (10–12, 33–35), and lower let-7 expression and higher KRAS levels in the presence of the KRAS-LCS6 G-variant (13). Following this, it would be expected that patients with the KRAS-LCS6 variant have a worse prognosis and this has been shown for oral cancer (17). For CRC, there are 2 published reports studying the effect of KRAS-LCS6 genotype (19, 20). One reports a poor survival among a small population of irinotecan-refractory metastatic patients with the KRAS-LCS6 G-variant, and an association with KRAS mutations and the absence of BRAF mutations (19), these findings could not be replicated in our study. The second reports a better response to cetuximab in metastatic CRC and a longer survival in patients with the G-variant without KRAS mutations, but not statistically significant (20). We also observe a slightly better prognosis in stage IV G-allele carriers, although not statistically significant (20). We also observe a slightly better prognosis in stage IV G-allele carriers, although not statistically significant, but our group of stage IV patients is small rendering instable results. Although previous studies used germline tissue to assess the KRAS-LCS6 genotype, we used tumor DNA to assess genotype. However, it has previously been well documented that genotype of

![KRAS-LCS6 Genotype as a Prognostic Marker in Early-Stage CRC](image-url)
Table 3. HRs and 95% CI for cause-specific mortality and clinicopathologic and the KRAS-LCS6 variant in 734 CRC cases from the Netherlands Cohort Study on diet and cancer

<table>
<thead>
<tr>
<th></th>
<th>Early stage (stage I and II) CRC</th>
<th>Stage III CRC</th>
<th>Stage IV CRC</th>
</tr>
</thead>
<tbody>
<tr>
<td>KRAS-LCS6 variant</td>
<td>0.46 (0.18–1.14)</td>
<td>0.98 (0.55–1.74)</td>
<td>0.42 (0.17–1.06)</td>
</tr>
<tr>
<td>KRAS-LCS6 variant without KRAS mutations</td>
<td>0.77 (0.30–1.97)</td>
<td>0.95 (0.44–2.05)</td>
<td>0.35 (0.11–1.13)</td>
</tr>
<tr>
<td>KRAS-LCS6 variant with KRAS mutations</td>
<td>No CRC-related deaths</td>
<td>1.52 (0.66–3.54)</td>
<td>0.60 (0.19–1.91)</td>
</tr>
<tr>
<td>Sex (male)</td>
<td>0.97 (0.60–1.57)</td>
<td>0.92 (0.59–1.45)</td>
<td>0.85 (0.44–1.64)</td>
</tr>
<tr>
<td>Age at diagnosis</td>
<td>0.99 (0.94–1.05)</td>
<td>1.01 (0.96–1.06)</td>
<td>1.02 (0.93–1.10)</td>
</tr>
<tr>
<td>Grade</td>
<td>1 (reference)</td>
<td>1 (reference)</td>
<td>1 (reference)</td>
</tr>
<tr>
<td>Sublocation of the tumor</td>
<td>1 (reference)</td>
<td>1 (reference)</td>
<td>1 (reference)</td>
</tr>
</tbody>
</table>

normal and tumor tissue is the same for the KRAS-LCS6 variant (13).

The conflicting results in early and advanced stage CRC also raise questions on the origin and progression of tumors in different cancer stages, and whether early-stage CRC might develop through a molecular distinct pathway compared with advanced stage. Our results indicate that the KRAS-LCS6 variant is more common among cases with advanced stage disease, however, those patients that are diagnosed early with the KRAS-LCS6 variant seem to have a more advantageous outcome. This might imply a different biology in early-stage as compared with advanced stage cases. In addition, our finding that early-stage KRAS-LCS6 wild-type patients have a poor prognosis, even if they have a MSI tumor, might indicate that these patients are possibly in need of (additional) adjuvant treatment. However, further research including randomized clinical trials, is needed to assess whether these early-stage patients with a poor prognosis would benefit from additional adjuvant treatment. Up until now, MSI has been considered to be a marker for good prognosis (36) however, our data suggest a better outcome for KRAS-LCS6 G-allele carriers independent of MSI status. Even though our study is the largest study on the KRAS-LCS6 genotype in CRC up until now, patient numbers in specific subgroups are still small. Larger, prospective studies and randomized clinical trials are needed to validate the potential role of KRAS-LCS6 genotype as a prognostic biomarker in therapy decision-making.

In conclusion, our assessment of the influence of the KRAS-LCS6 G-variant in early-stage CRC cases showed a better outcome for early-stage G-allele carriers with KRAS mutations. Although the population used in this study is among the largest studies that have been done on the KRAS-LCS6 variant, subgroups were small. However, this population is the only group studied to date that is generally untreated, and for the first time gives insight into the natural biology of CRC with the LCS6 variant. Future studies validating our results are however needed. Nevertheless, our data should be regarded as hypothesis generating providing a first indication that the KRAS-LCS6 genotype is a possible prognostic biomarker for early-stage CRC that can be used to identify CRC patients with a good prognosis.

Disclosure of Potential Conflicts of Interest

I.B. Weidhaas has a consultant and advisory role in MiraDX, her husband is a board member of MiraDX (uncompensated), and she has stock ownership of MiraDX. The other authors disclosed no potential conflicts of interest.

Figure 3. Kaplan–Meier curve for the KRAS-LCS6 variant, MSI status and cause-specific survival in early-stage (stage I and II) CRC.

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