ABSTRACT

Objective: The predictive and prognostic role of KRAS mutations in cervical cancer remains inconclusive. The aim of this study was to explore the clinicopathological and prognostic relevance of KRAS mutations in invasive cervical cancers (ICC).

Methods: Reverse transcription polymerase chain reaction (PCR) and Sanger sequencing were employed to detect KRAS mutations in 876 ICC patients. Quantitative real-time PCR was used to detect human papillomavirus (HPV) 16 and HPV 18.

Results: Non-synonymous mutations of KRAS were identified in 30 (3.4%) patients. These mutations were more common in non-squamous cell carcinoma than in squamous cell carcinoma (SCC) (8.2% vs. 2.2%, respectively, p<0.001) and were associated with HPV 18 infection (p=0.003). The prevalence of mutations was highest (18.2%) in the uncommon histological subtypes followed by adenocarcinoma (AC, 7.3%) and adenosquamous carcinoma (ASC, 5.8%). During the median follow-up of 55 months, compared to patients with wild-type KRAS, a greater percentage of patients with mutant KRAS relapsed (20.0% vs. 42.9%, respectively, p=0.007). The 3-year relapse-free survival was poorer in patients with mutant KRAS than in patients without KRAS mutations (57.1% vs. 81.9%, respectively, p=0.001). Furthermore, the multivariate analysis showed that the presence of a KRAS mutation was an independent predictor for disease recurrence (hazard ratio [HR]=2.064; 95% confidence interval [CI]=1.125–3.787; p=0.019).

Conclusion: KRAS mutations were predominant in non-SCCs of the cervix and were associated with HPV 18 infection. A combination of KRAS mutation detection and HPV genotyping would be useful in identifying patients with poor prognosis for further interventions.

Keywords: KRAS; Uterine Cervical Neoplasms; Papillomaviridae; Prognosis

INTRODUCTION

In China, cervical cancer is the eighth leading cause of cancer-related death among women and is responsible for more than 20,000 deaths annually [1]. Despite improvements in cervical cancer screenings and treatments over the past 50 years, the incidence and mortality rates of cervical cancer in China have increased annually since 2000 [2]. Treatment of advanced or
Funding
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Conflict of Interest
No potential conflict of interest relevant to this article was reported.

Author Contributions

To date, RAS proteins have not yielded any successful targeted therapies and have been viewed as “undruggable” for many years. Some drugs have been designed to block pathways downstream of RAS, such as RAF, MAPK-MEK, and ERK; however, their efficacy has been generally disappointing [13-15]. Nevertheless, the patient’s KRAS mutation status has been confirmed to be a criterion for implementing treatment with anti-epidermal growth factor receptor (EGFR) antibodies [16], as this treatment modality is more successful in patients with RAS wild-type metastatic CRC than in patients with mutant RAS. The combination of a MEK inhibitor and a fibroblast growth factor receptor 1 (FGFR1) inhibitor leads to tumor cell death in KRAS-mutant lung cancer cells but not in corresponding KRAS wild-type cells [17]. Thus, detecting KRAS mutations has been shown to be useful in selecting patients who could benefit from some of the available targeted treatments.

KRAS mutation has been identified as the second common oncogenic mutation following PIK3CA in our previous comprehensive analysis of 16 targetable oncogenic mutations in 285 cervical cancers [18]. In this study, a larger cohort of patients with cervical cancer (876 patients) were enrolled to explore its association with clinicopathological characteristics and prognosis over a longer follow-up period as well as to determine the relevance of human papillomavirus (HPV) infection in the incidence of KRAS mutations.

MATERIALS AND METHODS

1. Patient data
This study was approved by the Ethics Committee at the Fudan University Shanghai Cancer Center (FUSCC 050432-4-4121B) and was conducted in accordance with the approved guidelines. Patients with cervical cancer were enrolled between January 1, 2010 and December 30, 2012 if they satisfied the following conditions: pathologically determined primary cervical carcinomas, stages IB1–IIA2 disease according to the 2009 International Federation of Gynecology and Obstetrics (FIGO) staging system, and no prior neoadjuvant chemotherapy or radiation. Cervical tumor specimens were collected during either radical hysterectomy or trachelectomy procedures and stored at −80°C in RNAlater solution (Ambion; Thermo Fisher Scientific, Waltham, MA, USA). After the specimens were assessed...
by 2 independent pathologists (Xuxia Shen and Wentao Yang), those with either insufficient
tumor material for a comprehensive mutational analysis or fewer than 50% malignant cells
within the entire tissue sample were excluded. In total, 876 patients were eligible for this
study. Among these, 553 patients received adjuvant therapy after surgery according to the
guidelines, including 64 patients who received pelvic radiotherapy alone, 68 patients who
received chemotherapy alone and 421 patients who received concurrent chemoradiation
with or without subsequent systemic chemotherapy. The specific clinicopathological
characteristics, including age, menopausal status, histological type, tumor size, depth
of myometrial invasion, lymphovascular space involvement (LVSI), regional lymph node
metastasis, parametrical involvement, and distant metastasis, were recorded. The patients
were followed up for disease recurrence and survival duration either in the clinic or by
telephone. All patients provided written informed consent for the analysis of their tumor
specimens and the collection of clinical information.

2. Detection of **KRAS** mutations
Genomic DNA and total RNA were extracted from the tumor tissues using a DNA/RNA
isolation kit (Tiangen Biotech, Beijing, China) according to the manufacturer's instructions.
cDNA was obtained by reverse transcribing 2 μg of total RNA using an M-MLV Reverse
Transcriptase kit (Invitrogen, Waltham, MA, USA) and was used for mutational analysis
and HPV detection. Mutational analyses were conducted according to our previous protocol
[18]. **KRAS** (exons 1–4) was amplified using KOD-Plus-Neo DNA polymerase (Toyobo, Tokyo,
Japan) with the following primers: **KRAS**-F: CCATTTCGGACTGGGAGCGA, and **KRAS**-R:
GGCATCATCAACACCCA GAT. The polymerase chain reaction (PCR) products were directly
sequenced using the Sanger sequencing technique, and all mutations were confirmed by an
additional independent PCR experiment.

3. Quantitative real-time PCR assay for the detection of HPV
A TaqMan quantitative real-time PCR assay was used to detect HPV 16 and HPV 18
[19] using the following primers: HPV 16 (F: 5'GAACCGAAACCCTTAGTATAA
3', R: 5'ATGTATAGTTGTTGGCAGCTGTG3') and HPV 18 (F:
5'GGACCGAAAAACGGTTATATAAA 3', R: 5'CAGTGAAGTGTCCAGTCTGGT 3'). The
probes for HPV 16 and HPV 18 were CATTTATGCACCAAAGAGAATCGCAAATGTTC
and ATGTGAGAAACACACCACACACACACACTATGGCGCG, respectively. The PCR reaction (10
μL) comprised 5 μL of Premix Ex Taq™; 1 μL of Primer Mix (10 μM); 1 μL of Probe Mix (40
nM for HPV 16, 200 nM for HPV 18); 1 μL of sample cDNA and 2 μL of dH2O. The PCR was
performed on an ABI 7500 instrument (Applied Biosystems, Foster City, CA, USA) as follows:
denaturation step at 95°C for 30 seconds and 40 cycles of 5 seconds at 95°C, 10 seconds at
55°C, and 20 seconds at 72°C.

4. Statistical analysis
All statistical analyses were performed using IBM SPSS statistics software, version 19 (IBM
Corporation, New York, NY, USA). Either the χ² test or Fisher’s exact test was used to analyze
the association between **KRAS** mutations and the patients’ clinicopathological characteristics.
Relapse-free survival (RFS) was defined as the period from the completion of surgery to the
date of documented evidence of disease recurrence. The end of the observation period was
March 31, 2016, and patients without disease recurrence were censored at their last follow-
up visit. Survival curves were calculated using the Kaplan-Meier method, and differences
between the groups were tested using the log-rank test. The Cox proportional hazards model
was used for multivariate survival analysis. Statistical significance was set at p<0.050.
RESULTS

1. Characterization of KRAS mutation in cervical cancers

Among 876 patients, 30 non-synonymous mutations of KRAS were identified (3.4%), the majority (86.7%, 26/30) of which were found on exon 2. Ten percent (3/30) of the mutations were located on exon 3, and only one (3.3%) mutation existed on exon 4. The detailed mutation and clinicopathological information were provided in Supplementary Table 2.

Fig. 1 demonstrated the distribution of the mutation sites in KRAS-mutant carcinomas. The G12 residue on KRAS was the most frequently mutated (17/30, 56.7%) followed by G13 (4/30, 13.3%). KRAS G12 mutations are predominant in non-squamous cell carcinomas (SCCs) (73.3%), and the rates of KRAS G12 & G13 mutations in SCC were 40% and 20%, respectively. A mutation of residue Q61 was only found in one patient in this cohort despite its status as a common mutation of KRAS in other human cancers [6]. In addition, 3 novel KRAS mutations (G15C, S39Y, and F156Y), which have not been previously described in cervical cancer according to the Catalogue of Somatic Mutations in Cancer (COSMIC) database (http://cancer.sanger.ac.uk/cancergenome/projects/cosmic; Jun 8, 2017), were identified in our patient cohort.

2. Clinicopathological association of KRAS mutations

Table 1 summarizes the association between KRAS mutations and the patients’ clinicopathological characteristics. KRAS mutations were more common in non-SCC than in SCC (8.2% vs. 2.2%, p<0.001). The highest prevalence of mutations (18.2%) occurred in uncommon histological subtypes (neuroendocrine carcinoma, clear cell carcinoma, carcinosarcoma, and poorly differentiated carcinoma) followed by adenocarcinoma (AC; 7.3%), adenosquamous carcinoma (ASC; 5.8%), and SCC (2.2%) (p<0.001, Table 1).

Either HPV 16 or HPV 18 was detected in 631 patients (71.9%), with 487 (55.6%) patients positive for HPV 16, 136 (15.5%) patients positive for HPV 18, and 8 (0.9%) patients positive for both. HPV 18 positive patients were more likely to harbor a KRAS mutation than either HPV 16 positive or negative patients (8.1% vs. 2.1% vs. 3.7%, respectively, p=0.003, Table 1). KRAS mutations were not found to correlate with other clinicopathological characteristics such as lymph node metastasis, larger tumor size, deep myometrial invasion and the presence of LVSI.

Fig. 1. Identification of KRAS mutation hotspots in cervical cancers. (A) KRAS mutations identified in 30 cervical cancers. (B) KRAS mutations identified in 15 non-SCCs. (C) KRAS mutations identified in 15 SCCs.

SCC, squamous cell carcinoma.
3. The association between KRAS mutation and treatment outcome

A total of 767 (87.6%) patients were included in the survival analysis with a median follow-up duration of 55 months (range: 1-75 months). Disease recurrence was documented in 160 patients (20.9%) during the follow-up intervals, with 12 (42.9%) of 28 patients with mutant KRAS experiencing recurrence during follow-up; this rate was significantly higher than rate of patients with wild-type KRAS (20.0%, 148/739, p=0.007; Fisher’s exact test). Detailed recurrence information was available for 759 patients. Distant metastasis outside of the pelvis was documented in 113 (14.9%) patients, and pelvic recurrence was documented in 39 patients (5.1%). In patients with a KRAS mutation, distant metastasis and pelvic recurrence within the surgical or radiation area were documented in 29.6% and 11.1% of the patients, respectively; these rates were significantly higher than those in patients with wild-type KRAS (14.3% and 4.9%, respectively, p=0.023). Furthermore, a significant relation was found between KRAS mutation and distant metastasis (p=0.016), but not for local recurrence (p=0.101) (Supplementary Table 1).

Table 1. Association between KRAS mutations and clinicopathological parameters

<table>
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AC, adenocarcinoma; ASC, adenosquamous carcinoma; FIGO, International Federation of Gynecology and Obstetrics; HPV, human papillomavirus; LVSI, lymphovascular space involvement; SCC, squamous cell carcinoma.

*Eight Cases positive for both HPV 16 & 18 were excluded in χ² test. All the 8 cases were negative for mutations. †Others include neuroendocrine carcinoma (16), clear cell carcinoma (2), carcinosarcoma (2), and poorly differentiated carcinoma. ‡Fisher’s exact test was used.
KRAS mutations were confirmed to be associated with patient survival in both univariate and multivariate analyses. The 3-year RFS of patients with mutant KRAS was significantly poorer than that of patients with wild-type KRAS (57.1% vs. 81.9%, respectively, p=0.001) (Fig. 2A). The multivariate analyses revealed that KRAS mutations were an independent predictor for worse RFS (hazard ratio [HR]=2.064; 95% confidence interval [CI]=1.125–3.787; p=0.019) (Table 2).

Furthermore, survival analysis was performed in patients with SCC or non-SCC. Among the 166 patients with non-SCC, the 3-year RFS was significantly poorer in patients with a KRAS mutation than in those with wild-type KRAS (46.7% vs. 75.5%, p=0.013) (Fig. 2B); however, this finding was not replicated in patients with SCC (Supplementary Fig. 1).

Among patients positive for HPV 18, those with a KRAS mutation had a shorter survival than patients with wild-type KRAS (3-year RFS: 40.0% vs. 85.2%, respectively, p=0.001). However, an association between KRAS mutations and RFS was not observed in patients positive for HPV 16 (p=0.478) (Fig. 2C).

In addition, the 3-year RFS was compared among 4 patients with KRAS G13 mutations and 17 patients with KRAS G12 mutations. A worse survival trend was revealed in patients harboring KRAS mutations in cervical cancers.
G13 mutations than in patients with KRAS G12 mutations (25.0% vs. 70.6%); however, due to the limited number of cases (21 cases), this difference was not statistically significant (p=0.153) (Supplementary Fig. 2).

DISCUSSION

The features of KRAS mutations in lung and colon cancer have become increasingly clear, whereas the clinicopathological and prognostic characteristics of KRAS mutations in cervical cancer remain inconclusive. There are some uncertainties regarding the predictive and prognostic role of KRAS mutations in previous studies due to their relatively small sample sizes. In this study, with a large cohort of 876 patients with cervical cancer, KRAS mutations were found to be more associated with non-SCC and a positive HPV 18 infection status. In these specific subtypes of cervical cancer, patients with a KRAS mutation have a worse prognosis.

The development of a KRAS mutation is a rare event in SCCs of the cervix. According to the COSMIC database (http://cancer.sanger.ac.uk/cancergenome/projects/cosmic; Jun 8, 2017), the prevalence of KRAS mutations in SCC is approximately 2%, which was confirmed in our patient cohort (2.2%). In comparison, KRAS mutations were predominant in non-squamous cell cervical carcinomas, including AC, ASC, and other uncommon subtypes. Spaans et al. [20] demonstrated that KRAS mutations occurred more frequently in AC than in SCC (24% vs. 3%, p < 0.001), and Wright et al. [21] indicated that KRAS mutations were detected only in AC but not in SCC (17.5% vs. 0%, p = 0.010). In our cohort of patients with AC, the KRAS mutation rate was 7.3% (8/110), which is similar to the results observed by Ojesina et al. [22] using whole exome sequencing of 24 patients with AC (2/24, 8%). Regarding neuroendocrine carcinomas, Frumovitz et al. [23] reported that the prevalence of KRAS mutations was 14% (6/44), which is lower than observed in this study (4/16, 25%). Due to its small sample size, both studies may have some bias. Thus, the reported prevalence of KRAS mutations in non-SCC is highly variable.

In the present study, KRAS mutations were detected in 3.4% (30/876) of Chinese patients with cervical carcinoma, which was relatively low compared with data from other studies. According to the COSMIC database, the frequency of KRAS mutations in cervical cancer is 5.83% (http://cancer.sanger.ac.uk/cancergenome/projects/cosmic; Jun 8, 2017). As the data above indicated, the distribution of the different histological subtypes accounts for the variance of the mutation rate among the studies [21]. In addition, the disease stage might
also contribute to the low frequency of KRAS mutations in our cohort of cervical cancer patients. Wegman et al. [24] reported that KRAS mutations were more commonly found in patients with advanced stage disease (FIGO stages III–IV) than in those with early stage disease (FIGO stages I–II) (35.3% vs. 5.6%, respectively, p<0.001); however, all our patients were diagnosed with FIGO stages IB–IIA disease.

In accordance with the result of most studies, we confirmed that the 3-year RFS in patients with KRAS mutations was significantly lower than that in patients without KRAS mutations in our large patient cohort [18,21,24]. Wegman et al. [24] found that among patients treated with definitive chemoradiation, those harboring mutant KRAS had significantly worse recurrence-free survival than those with wild-type KRAS (p=0.030). Our cohort of patients underwent surgery-based multimodal treatment, and disease recurrence outside of the pelvis was the primary recurrence pattern. Wegman et al. [24] reported that there was a significant association between KRAS mutation and distant metastases but not local recurrence, which is consistent with our previous findings. In clinic, the finding of the association between KRAS mutation and worse 3-year RFS suggests that detection of KRAS mutation could be used as a prognostic marker. Close follow-up is needed in those patients with KRAS mutation for early detection of recurrence. In addition to conventional adjuvant therapy, such as concurrent chemoradiation and systemic chemotherapy, further management might be considered in patients with KRAS mutation to prevent from recurrence. Novel therapy is needed to be identified including KRAS-targeted therapy.

An association between KRAS mutations and HPV infection has not been confirmed in the literature, as Wright et al. [21] did not observe an association between HPV infection and KRAS mutations in a cohort of 80 patients with cervical cancer. In our study, we demonstrated that KRAS mutations were associated with HPV 18 infection but not HPV 16 infection. Moreover, KRAS mutations were a predictor of poor disease-free survival (DFS) only in patients with HPV 18 infection. This result is consistent with the finding that an association between KRAS mutations and disease recurrence was only observed in patients with non-SCC but not with SCC. Epidemiological studies have confirmed that HPV 18 infection accounts for majority of cervical ACs. In this study, we found that HPV 18 infection was predominantly present in ACs (19.9%), ASCs (23.5%), and uncommon histological subtypes (8.1%) at significantly higher rates than HPV 16 infection (6.0%, 2.5%, and 0.4%, respectively, p<0.001). Compared to SCC, these specific histologic subtypes present poorer survival. Thus, a combination of KRAS mutation detection and HPV genotyping might be useful in identifying patient with poor prognosis for further interventions.

According to the literature, KRAS mutations at residues G12 and G13 have different risks of tumor progression in lung cancer and CRC [7-9,25,26]. The mechanism of different KRAS mutations on tumor progression has not been completely elucidated. It has been revealed that different amino acid changes result in the involvement of different signaling pathways [27-29]. In this study, patients with mutant KRAS at codon 13 are more likely to have a shorter DFS than patients with mutant KRAS at codon 12, although this difference was not statistically significant. More cases are required to confirm these results. Functional studies of those KRAS mutations warrant further studies, especially for the newly identified mutants in cervical cancer.

There are some limitations in our study. First, eligible patients did not include those with advanced cervical cancer, and the frequency, clinicopathological features and prognostic relevance of KRAS mutations were obtained from patients with relatively early stage disease.
which could lead to an incomplete analysis of KRAS mutations in cervical cancer. Second, the presence of concurrent mutations may also influence the clinical phenotype and prognostic outcomes. Our other study discovered a subset of cervical cancer patients with concurrent ERBB2, PIK3CA, and/or KRAS mutations (sent to publication). A study of a large patient cohort based on whole-genome sequencing is required to fully analyze oncogenic mutations in cervical cancer. Third, the detection of HPV was just limited in HPV 16 and HPV 18. Finally, because a small group of people died of cervical cancer, overall survival was not analyzed in our study.

In summary, KRAS mutations were predominant in non-SCC of the cervix and are associated with HPV 18 infection. These mutations were an independent predictor for disease recurrence in patients with cervical cancer who received surgery-based multimodal treatment. Further intervention might be necessary in patients with KRAS mutations because of their increased risk for recurrence and distant metastasis. A combination of KRAS mutation detection and HPV genotyping would be useful in identifying patients with poor prognosis for further interventions.

ACKNOWLEDGMENTS

The authors thank Wentao Yang for the contribution in histopathological diagnosis.

SUPPLEMENTARY MATERIALS

Supplementary Table 1
The association between KRAS mutation and disease recurrence

Click here to view

Supplementary Table 2
Detailed mutation and clinicopathological information

Click here to view

Supplementary Fig. 1
Kaplan-Meier curves of RFS for 601 patients with SCCs.

Click here to view

Supplementary Fig. 2
Kaplan-Meier curves of RFS for patients with KRAS G12 and G13 mutations.

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REFERENCES


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https://ejgo.org

https://doi.org/10.3802/jgo.2018.29.e4
KRAS mutations in cervical cancers


