ASSOCIATION BETWEEN *KRAS* MUTATIONS AND THE ENDOSCOPIC AND HISTOPATHOLOGICAL FEATURES OF COLORECTAL ADENOMATOUS POLYPS

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Colorectal adenomatous polyps are the principal premalignant lesions in colorectal carcinogenesis, and the combined evaluation of endoscopic features, histopathological characteristics, and molecular alterations such as KRAS mutations may help identify lesions with higher-risk features. This analytical cross-sectional study included 123 colorectal adenomatous polyps treated at Can Tho University of Medicine and Pharmacy Hospital from June 2024 to January 2026 to determine the prevalence of KRAS mutations and to assess the associations between KRAS mutation status and endoscopic and histopathological features. KRAS mutations were detected in 38.2% of polyps, predominantly at codon 12 (26.8%), followed by codon 13 (11.4%), no codon 61 mutation was identified. In univariable analyses, KRAS mutation status was associated with a nodular/lobulated surface, JNET type IIB–III classification, polyp size ≥10 mm, tubulovillous adenoma histology, and high-grade dysplasia. In multivariable logistic regression, only polyp size ≥10 mm (OR = 5.71; 95% CI: 2.08–15.67; p < 0.001) and high-grade dysplasia (OR = 6.81; 95% CI: 1.27–36.36; p = 0.025) remained significantly associated with KRAS mutation status. These findings suggest that KRAS mutations may be associated with more advanced features of colorectal adenomatous polyps, particularly larger size and high-grade dysplasia.

Keywords: KRAS mutations, endoscopic features, histopathology, colorectal adenomatous polyps.

I. INTRODUCTION

Colorectal adenomatous polyps are important premalignant lesions in colorectal carcinogenesis. In most cases, colorectal cancer develops through the adenoma-carcinoma sequence, characterized by the stepwise accumulation of genetic and epigenetic alterations, in which conventional adenomas, including tubular adenomas, tubulovillous adenomas, and villous adenomas, serve as the principal precursor lesions.[1] In current practice, magnifying endoscopy combined with narrow-band imaging has improved the stratification of lesion histology with greater accuracy. The Japan NBI Expert Team (JNET) classification, proposed by Japanese endoscopy experts, has demonstrated that surface and microvascular patterns on magnifying narrow-band imaging (NBI) correlate significantly with histopathology and depth of invasion. Notably, because magnifying NBI directly evaluates microvascular and microsurface architecture, these endoscopic

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phenotypes are not merely descriptive findings but may also reflect histologic alterations and neovascular changes accompanying neoplastic progression.[2] This provides a biologically plausible basis for hypothesizing that high-risk endoscopic features may be associated with the underlying molecular alterations of colorectal adenomatous polyps.

Among the molecular alterations identified to date, Kirsten rat sarcoma viral oncogene homolog (KRAS) mutation is a key event in the conventional pathway of colorectal tumorigenesis. *KRAS* encodes a guanosine triphosphatase (GTPase) involved in the epidermal growth factor receptor (EGFR)-rat sarcoma (RAS)-rapidly accelerated fibrosarcoma (RAF)-mitogen-activated protein kinase kinase (MEK)-extracellular signal-regulated kinase (ERK) signaling cascade.[3] When constitutively activated by mutation, *KRAS* promotes cellular proliferation, attenuates apoptosis control, and contributes to adenoma progression toward a more advanced neoplastic phenotype.[4] Several studies have reported that *KRAS* mutations are more frequently detected in adenomas with larger size and with tubulovillous or villous architecture, suggesting a role for this alteration in the morphologic and histopathological progression of adenomatous polyps.[5-6] For example, Yadamsuren et al. reported *KRAS* mutations in 31.0% of non-advanced adenomas, 57.5% of advanced adenomas, and 62.5% of early colorectal cancers; these mutations were predominantly located in codon 12 rather than codon 13 and were associated with villous components and larger lesion size.[7]

Compared with the evidence on histopathological features, the relationship between *KRAS* mutations and the endoscopic characteristics of colorectal adenomatous polyps remains insufficiently elucidated. Although several studies have suggested that *KRAS* may be associated with high-risk features such as larger size, villous histology, and high-grade dysplasia, the available evidence remains inconsistent across study populations and lesion-assessment approaches.[8-10] In Yadamsuren's study, *KRAS* mutation frequency did not differ significantly between low-grade and high-grade dysplasia, indicating that not all markers of histologic progression uniformly reflect *KRAS* mutation status.[7] More notably, a Vietnamese study of colorectal polyps >10 mm found that *KRAS* mutations tended to be more frequent in polyps with villous components and high-grade dysplasia, but no association with endoscopic imaging features was identified.[9] Meanwhile, recent domestic studies have mainly confirmed the diagnostic value of the JNET classification for predicting histopathology or have focused on *KRAS* alterations in colorectal cancer rather than in adenomatous polyps.[11] Therefore, the current knowledge gap lies not only in the limited domestic data, particularly in Can Tho, but also in the scarcity of studies simultaneously evaluating JNET-based endoscopic features, *KRAS* mutation status, and histopathological characteristics in colorectal adenomatous polyps. On that basis, we conducted this study to determine the prevalence of *KRAS* mutations and to assess the associations between *KRAS* mutation status and the endoscopic as well as histopathological features of colorectal adenomatous polyps.

II. MATERIALS AND METHODS

1. Study population

Patients with colorectal polyps confirmed by total colonoscopy and histopathological examination at Can Tho University of Medicine and Pharmacy Hospital from June 2024 to

January 2026.

Inclusion Criteria

Patients who had colorectal polyps ≥5 mm detected on colonoscopy; underwent endoscopic colorectal polypectomy with histopathology confirming an adenomatous polyp; for patients with ≥2 polyps, the lesion with higher histopathological risk (high-grade dysplasia) was selected first, and if the histopathological risk was the same, the lesion with the larger size was selected; and were ≥18 years and agreed to participate in the study.

Exclusion criteria

Patients with polyps ≥5 mm detected on total colonoscopy but with poor bowel preparation, making endoscopic assessment of polyps difficult. Patients with colorectal polyps concomitant with colorectal cancer. Patients with a history of colorectal cancer. Patients with comorbid diseases: colonic Crohn's disease, ulcerative colitis, and ileocecal tuberculosis.

2. Study methods

Study design

Analytical cross-sectional study.

Sample size

Using convenience sampling from June 2024 to January 2026, 123 patients with a total of 123 polyps were recruited and included in the analysis.

Study contents

General characteristics: age, sex, medical history (prior polypectomy; family history of colorectal polyps; family history of colorectal cancer).

KRAS mutation status: *KRAS* point mutations were identified by gene sequencing, including codon 12 variants (G12D, G12V, G12S, G12A, G12C, G12R), codon 13 (G13D), and codon 61 variants (Q61K, Q61L, Q61H, Q61R). A *KRAS* mutation was defined as positivity for any of the 11 variants listed above.[7]

Endoscopic features:

- Polyp location: described according to eight colorectal anatomical sites: cecum, ascending colon, hepatic flexure, transverse colon, splenic flexure, descending colon, sigmoid colon, and rectum.

- Polyp surface appearance: nodular/lobulated and non-nodular/non-lobulated.

- JNET classification: JNET I, JNET IIA, JNET IIB, JNET III.[2]

- Polyp size: defined as the maximum diameter of the colorectal polyp (mm) and categorized into two groups: <10 mm and ≥10 mm.

Histopathological features:

- Adenoma histology: tubular adenoma, villous adenoma, and tubulovillous adenoma.[10]

- Dysplasia grade: low-grade dysplasia and high-grade dysplasia.[10]

Data collection

Participants were directly interviewed and clinically examined by the investigators. Information on endoscopic and histopathological characteristics was recorded in a data collection form based on the patients' medical records. Personal information was coded and kept confidential.

KRAS mutation testing from colorectal adenomatous polyp specimens was performed using Sanger sequencing. Deoxyribonucleic acid (DNA) was extracted from polyp tissue, followed by Polymerase Chain Reaction (PCR) amplification of the target regions in *KRAS* exon 2 and exon 3 to detect mutations at codons 12 and 13 (exon 2) and codon 61 (exon 3). The limit of detection of the assay used in our laboratory for this study was 20% mutant allele frequency. PCR products were bidirectionally sequenced and analyzed by capillary electrophoresis using

the Applied Biosystems 3500 Genetic Analyzer (Thermo Fisher Scientific). Chromatogram data were analyzed using Sequencing Analysis Software, and variant calling was performed using SeqScape Software (Applied Biosystems). For quality control, DNA concentration and purity were assessed after extraction before downstream analysis. Sequence data were reviewed using the software-generated analysis and quality-control outputs and were also manually inspected on electropherograms. Variants were accepted only when the signal quality was adequate and concordant in both forward and reverse reads. Samples with low-quality or ambiguous traces were re-amplified and re-sequenced for confirmation.

Statistical analysis

Statistical analyses were performed using R version 4.5.0. Categorical variables were presented as frequencies and percentages; continuous variables were assessed for distribution using the Shapiro-Wilk test and summarized as mean ± standard deviation when approximately normally distributed. Between-group comparisons (*KRAS* mutation: yes/no) for continuous variables were performed using the independent-samples Student's t test. For categorical variables, comparisons were performed using the Chi-square test or Fisher's exact test as appropriate; for multi-category variables (polyp location and JNET classification), the Fisher-Freeman-Halton exact test was used when Chi-square assumptions were not satisfied. Associations between endoscopic and histopathological features and *KRAS* mutations were evaluated using univariable logistic regression, reporting odds ratio (OR) and 95% confidence interval (95% CI). Variables with $p < 0.20$ in univariable analyses were entered into a multivariable logistic regression model for simultaneous adjustment. When continuous lesion size and categorical size (≥10 mm) were assessed simultaneously, the corresponding variance inflation factor (VIF) values were 1.88 and 1.86, respectively. Although these values did not indicate significant multicollinearity, the two variables represent overlapping information on lesion size; therefore, we did not retain both variables simultaneously in the final multivariable model in order to avoid redundancy and improve interpretability. For clinical applicability, categorical size ≥10 mm was selected for the multivariable model. Multicollinearity among predictors in the final multivariable model was assessed using the VIF, and model fit was evaluated using the Hosmer-Lemeshow test. All tests were two-sided, and $p < 0.05$ was considered statistically significant.

3. Ethics in research

The study was approved by the Biomedical Research Ethics Committee of Can Tho University of Medicine and Pharmacy (No. 25.219.HV/PCT-HĐĐĐ; June 28, 2024). All procedures were conducted in accordance with ethical standards in medical research.

III. RESULTS

From June 2024 to January 2026, a total of 123 patients with colorectal adenomatous polyps who met the eligibility criteria were included in the study. The results are presented as follows:

Table 1. General characteristics and *KRAS* mutation status of the study participants

Characteristics		Frequency (n)	Percentage (%)
Age (mean ± SD), years		59.1 ± 11.8	
Sex	Male	72	58.5
	Female	51	41.5
History of prior polypectomy		28	22.8
Family history of colorectal polyps		11	8.9
Family history of colorectal cancer		16	13.0
KRAS mutation status	Wild-type	76	61.8
	Codon 12 mutation	33	26.8
	Codon 13 mutation	14	11.4
	Codon 61 mutation	0	0.0

The mean age of the study participants was 59.1 ± 11.8 years, and males predominated (58.5%). A history of prior polypectomy was reported in 22.8%. A family history of colorectal polyps was uncommon (8.9%), while a family history of colorectal cancer was 13.0%. *KRAS* mutations were detected mainly in codon 12 (26.8%), followed by codon 13 (11.4%), with no mutations identified in codon 61.

Table 2. Distribution of endoscopic features by *KRAS* mutation status in colorectal adenomatous polyps

Endoscopic feature	*KRAS* mutation		Total	p value
	Yes (n=47)	No (n=76)		
Polyp location, n (%)				
Cecum	1 (2.1)	1 (1.3)	2 (1.6)	0.241[a]
Ascending colon	3 (6.4)	11 (14.5)	14 (11.4)	
Hepatic flexure	4 (8.5)	2 (2.6)	6 (4.9)	
Transverse colon	7 (14.9)	15 (19.7)	22 (17.9)	
Descending colon	5 (10.6)	8 (10.5)	13 (10.6)	
Sigmoid colon	18 (38.3)	33 (43.4)	51 (41.5)	
Rectum	9 (19.1)	6 (7.8)	15 (12.2)	
Polyp surface appearance, n (%)				
Non-nodular/non-lobulated	34 (72.4)	68 (89.5)	102 (82.9)	**<0.001[b]**
Nodular/lobulated	13 (27.6)	8 (10.5)	21 (17.1)	

Endoscopic feature	*KRAS* mutation		Total	p value
	Yes (n=47)	No (n=76)		
JNET classification, n (%)				
JNET I	2 (4.3)	9 (11.8)	11 (8.9)	**<0.001**[a]
JNET IIA	19 (40.4)	58 (76.3)	77 (62.6)	
JNET IIB	23 (48.9)	9 (11.8)	32 (26.0)	
JNET III	3 (6.4)	0 (0.0)	3 (2.4)	
Polyp size category, n (%)				
≥ 10 mm	37 (78.7)	28 (36.8)	65 (52.8)	**<0.001**[b]
< 10 mm	10 (21.3)	48 (63.2)	58 (47.2)	
Polyp size (mean ± SD), mm	13.4 ± 5.0	9.7 ± 4.1	11.0 ± 4.9	**<0.001**[c]

[a]Fisher-Freeman-Halton-Exact test, [b]Chi-square test, [c]Independent-Sample T test

The results showed no statistically significant difference in polyp location between the *KRAS*-mutated and non-mutated groups (p = 0.241), with the sigmoid colon being the most common site in both groups. Polyps with a nodular/lobulated surface were more common in the *KRAS*-mutated group than in the non-mutated group, and the difference was statistically significant (p < 0.001). The JNET classification also differed significantly between the two groups (p < 0.001), with the non-mutated group mainly classified as JNET I and JNET IIA, while the *KRAS*-mutated group tended to be distributed more in JNET IIB and JNET III. Regarding size, the *KRAS*-mutated group had a higher proportion of polyps ≥10 mm, and the mean polyp size in the *KRAS*-mutated group (13.4 ± 5.0 mm) was larger than that in the non-mutated group (9.7 ± 4.1 mm); these differences were statistically significant (p < 0.001).

Table 3. Distribution of histopathological features by *KRAS* mutation status in colorectal adenomatous polyps

Histopathological feature	*KRAS* mutation		Total	p value
	Yes (n=47)	No (n=76)		
Adenoma histology, n (%)				
Tubulovillous adenoma	11 (23.4)	6 (7.9)	17 (13.8)	**0.012**[a]
Tubular adenoma	36 (76.6)	70 (92.1)	106 (86.2)	
Dysplasia grade, n (%)				
Low-grade dysplasia	29 (61.7)	73 (96.1)	102 (82.9)	**<0.001**[b]
High-grade dysplasia	18 (38.3)	3 (3.9)	21 (17.1)	

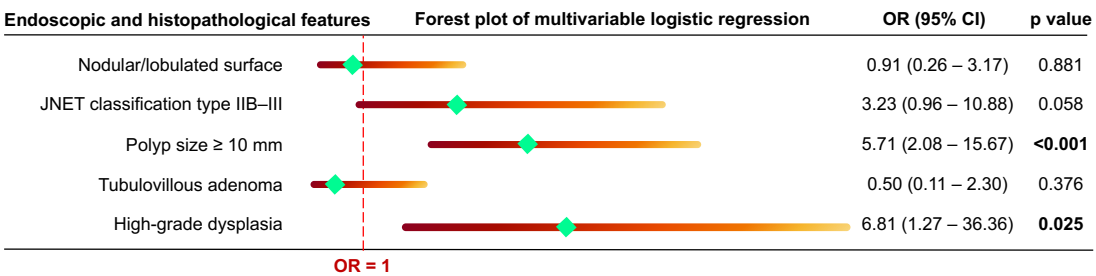
[a]Chi-square test, [b]Fisher's Exact test

Regarding histopathology, tubulovillous adenomas and high-grade dysplasia showed a higher proportion of *KRAS* mutations than tubular adenomas and low-grade dysplasia, with statistically significant differences ($p < 0.012$ and $p < 0.001$).

Table 4. Univariable logistic regression of factors associated with *KRAS* mutations in colorectal adenomatous polyps

Factor	OR	95% CI	p value
Age	0.98	0.95 - 1.02	0.490
Male sex	1.42	0.67 - 3.01	0.350
Nodular/lobulated surface	3.25	1.22 - 8.59	**0.017**
JNET classification type IIB-III	9.21	3.73 - 23.73	**<0.001**
Polyp size ≥ 10 mm	6.34	2.73 - 14.68	**<0.001**
Polyp size (per +1 mm)	1.16	1.06 - 1.27	**<0.001**
Tubulovillous adenoma	3.56	1.21 - 10.42	**0.020**
High-grade dysplasia	15.10	4.13 - 55.18	**<0.001**

In univariable logistic regression analyses, age and sex were not significantly associated with *KRAS* mutations ($p > 0.05$). Morphological features significantly associated with *KRAS* mutations included a nodular/lobulated surface (OR = 3.25; 95% CI: 1.22-8.59; $p = 0.017$), JNET classification type IIB-III (OR = 9.21; 95% CI: 3.73-23.73; $p < 0.001$), polyp size ≥10 mm (OR = 6.34; 95% CI: 2.73-14.68; $p < 0.001$), and each 1-mm increase in size (OR = 1.16; 95% CI: 1.06-1.27; $p < 0.001$). Regarding histopathology, tubulovillous adenoma was significantly associated with *KRAS* mutations (OR = 3.56; 95% CI: 1.21-10.42; $p = 0.020$). Notably, high-grade dysplasia showed the strongest association with *KRAS* mutations (OR = 15.10; 95% CI: 4.13-55.18; $p < 0.001$).



*In the final multivariable model, all predictors had low VIF values (range: 1.45-2.68; highest VIF = 2.68), indicating no significant multicollinearity. The Hosmer-Lemeshow test showed acceptable model fit ($p = 0.205$).

Figure 1. Multivariable logistic regression of factors associated with *KRAS* mutations in colorectal adenomatous polyps

In the multivariable logistic regression model, polyp size ≥10 mm and high-grade dysplasia remained significantly associated with *KRAS* mutation status, with odds ratios of 5.71 (95% CI: 2.08-15.67; p < 0.001) and 6.81 (95% CI: 1.27-36.36; p = 0.025), respectively. In contrast, a nodular/lobulated surface, JNET type IIB-III classification, and tubulovillous adenoma histology were no longer significantly associated after adjustment.

IV. DISCUSSION

In our study of 123 patients with colorectal adenomatous polyps, *KRAS* mutations were detected at a relatively high frequency (38.2%) and were predominantly located in codon 12 (26.8%). Features associated with *KRAS* mutation status included polyp size ≥10 mm, a nodular/lobulated surface, JNET type IIB-III classification, tubulovillous adenoma histology, and particularly high-grade dysplasia. However, after multivariable adjustment, only polyp size ≥10 mm and high-grade dysplasia remained significantly associated with *KRAS* mutation status.

Regarding *KRAS* mutation frequency, our observed rate was higher than the 17.2% reported in 738 adenomatous polyps by Maltzman et al. (2001), higher than the 23.0% observed in the screening-polyp cohort reported by Lorentzen et al. (2016), and higher than the 21.8% reported in the large Chinese population-based study by Yi et al. (2016), but remained lower than the 57.5% reported in advanced adenomas by Yadamsuren et al. (2012).[5-7,12] Domestically, the *KRAS* mutation rate in our study was also higher than the 10.7% reported by Tran Thanh Ha et al. (2022) in colorectal polyps larger than 1 cm, in which all detected mutations were confined to codon 12.[9] These differences likely reflect variations in ethnicity, patient selection, lesion spectrum, and histopathological risk profile across studies. Specifically, Maltzman analyzed sporadic adenomas in a broader population, Lorentzen investigated various types of polyps in the setting of population-based screening, and Yi evaluated the overall spectrum of colorectal premalignant lesions rather than conventional adenomas alone.[5-6,12] In contrast, Yadamsuren stratified non-advanced adenomas, advanced adenomas, and early colorectal cancers separately, making a higher *KRAS* mutation frequency in the higher-risk groups biologically plausible.[7] With regard to the study by Tran Thanh Ha, the difference from our findings may also be partly attributable to differences in mutation-detection methodology, as *KRAS* was assessed at the RNA level rather than the DNA level.[9] Compared with DNA-based analysis, RNA-based testing is additionally influenced by gene-expression levels and RNA integrity, and therefore the reported mutation frequency may not be directly comparable across studies.[13]

Regarding endoscopic features, our univariable analysis showed that *KRAS* mutations were more frequently observed in lesions with a nodular/lobulated surface and were more common in the JNET type IIB-III group. This trend is generally consistent with the study by Metz et al. (2013), in which *KRAS* mutations were more frequently detected in granular-type laterally spreading tumors than in nongranular lesions.[8] This finding may be explained by the fact that the JNET classification and endoscopic surface features primarily reflect the degree of neoplasia and the morphologic progression of the lesion. Specifically, JNET type IIB usually suggests high-grade intramucosal neoplasia or superficially invasive submucosal cancer, whereas JNET type III suggests deeply invasive submucosal cancer.[2] Therefore, endoscopic findings such as JNET type IIB-III or high-risk surface patterns often accompany lesions with

more advanced histopathological features. In our multivariable model, when polyp size, grade of dysplasia, and other factors were adjusted for simultaneously, the effects of a nodular/lobulated surface and JNET type IIB-III were attenuated and were no longer statistically significant. This suggests that these endoscopic features may primarily serve as morphologic markers of more advanced lesions, rather than factors directly linked to *KRAS* mutation status. This interpretation is also in line with the findings of Maltzman et al. (2001), in which *KRAS* was more closely associated with advanced histopathological features such as villous components and high-grade dysplasia.[5] Nevertheless, in our cohort restricted to adenomatous polyps, polyp size ≥10 mm remained associated after adjustment, consistent with the findings of Lorentzen et al. (2016) and Yadamsuren et al. (2012), both of which suggested that *KRAS* mutations are more common in larger or more advanced adenomas.[6-7] In addition, follow-up data from Martínez-Roca et al. (2024) further suggest that *KRAS* may be associated with the risk of developing advanced lesions at subsequent surveillance colonoscopy in patients with high-risk adenomas.[10]

Regarding histopathological features, our findings are also consistent with the overall trend in the literature, in that tubulovillous adenoma histology and, in particular, high-grade dysplasia were associated with *KRAS* mutations in univariable analysis, while high-grade dysplasia remained associated after multivariable adjustment. These results are broadly consistent with those of Maltzman et al. (2001), who reported that *KRAS* mutations were independently associated with tubulovillous/villous histology (OR = 2.3) and high-grade dysplasia (OR = 1.9).[5] Similarly, Yi et al. (2016) showed that villous histology and high-grade dysplasia were independently associated with *KRAS*, with odds ratios of 3.0 and 3.5, respectively.[12] The study by Tran Thanh Ha et al. (2022) also showed a similar trend, with a higher *KRAS* mutation rate in polyps with villous components than in tubular adenomas (33.3% vs 9.2%) and a higher rate in high-grade dysplasia than in low-grade dysplasia (23.1% vs 8.6%).[9] Overall, these data suggest that *KRAS* mutations tend to accompany high-risk histopathological features, particularly villous components and high-grade dysplasia. However, in the context of a cross-sectional design, these associations should be interpreted more cautiously as reflecting the coexistence of *KRAS* mutations with lesions showing more advanced histopathological progression at the time of assessment, rather than as evidence that *KRAS* is an independent causal determinant of disease progression. This interpretation is also consistent with the biological role of *KRAS* in colorectal tumorigenesis. Mechanistically, *KRAS* is a GTPase involved in the EGFR-RAS-RAF-MEK-ERK signaling pathway; when constitutively activated by mutation, *KRAS* can sustain proliferative signaling even in the absence of receptor stimulation and can additionally activate signaling branches involved in cell proliferation, cell survival, and resistance to apoptosis.[14] In the classical model of colorectal carcinogenesis, *KRAS* mutations typically arise after adenomatous polyposis coli (*APC*) alterations and contribute to the progression of lesions from the adenomatous stage toward a more advanced phenotype. Therefore, the tendency for *KRAS* to be associated with histopathological features of more advanced lesions is biologically plausible.[15]

Our study has several limitations that should be considered when interpreting the findings. First, this was a single-center cross-sectional

study using convenience sampling; therefore, the results reflect only observed associations at the time of assessment, do not allow causal inference, and may be subject to selection bias, which limits generalizability to other populations. Second, the sample size was still relatively small for multivariable analysis in a genetic study, so the stability of some estimates may be limited, confidence intervals for some variables were wide, and the possibility of overfitting cannot be completely excluded. Third, in patients with multiple polyps, we selected only one representative lesion for analysis to reduce dependence among observations; however, this approach may have increased the representation of high-risk lesions in the study sample. Finally, *KRAS* mutations in this study were analyzed as a binary variable because the number of cases for each specific variant was limited, precluding a more in-depth analysis of genetic heterogeneity and the biological significance of individual codon-specific mutations. Therefore, the present findings should be regarded as preliminary evidence of an association between *KRAS* mutations and the endoscopic and histopathological features of colorectal adenomatous polyps, rather than evidence supporting a causal role or direct prognostic value of these mutations.

V. CONCLUSION

KRAS mutations were identified in 38.2% of colorectal adenomatous polyps, predominantly at codon 12. In univariable analysis, *KRAS* mutation status was associated with several endoscopic and histopathological characteristics of colorectal adenomatous polyps, including a nodular/lobulated surface, JNET type IIB-III classification, larger polyp size, tubulovillous adenoma histology, and high-grade dysplasia. After adjustment in the multivariable model, only polyp size ≥10 mm and high-grade dysplasia remained significantly associated with *KRAS* mutation status in colorectal adenomatous polyps. However, given the cross-sectional design and relatively small sample size, these associations should be interpreted cautiously, may reflect more advanced lesion status rather than causal or independent determinants of *KRAS* mutation, and require confirmation in larger studies.

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