A variant in 3′-untranslated region of KRAS compromises its interaction with hsa-let-7g and contributes to the development of lung cancer in patients with COPD

Hua Hu1
Linlin Zhang1
Geling Teng1
Yanhua Wu1
Ying Chen2

1The Respiratory Department, Shandong Provincial Chest Hospital, Jinan, Shandong, People’s Republic of China
2The Clinical Laboratory of Shandong Provincial Chest Hospital, Jinan, Shandong, People’s Republic of China

Objective: The objective of the present study was to explore the molecular mechanism by which a single nucleotide polymorphism (rs712) interferes with interaction between 3′-untranslated region (3′-UTR) of KRAS and let-7g, and its association with development of lung cancer in the patients with COPD.

Materials and methods: In this study, we confirmed that KRAS is a target of let-7g in lung cancer cells, and that introduction of rs712 minor allele into 3′-UTR significantly compromised the miRNA/mRNA interaction by using a luciferase reporter system. Additionally, a total of 35 lung tissue samples were obtained (TT:17, TG:12, GG:6), and let-7g and KRAS expression levels were determined.

Results: We showed that let-7g level was similar between groups, and the concentration of KRAS in GG genotype group was significantly higher than in TT or GT genotype group. Meanwhile, we found COPD patients with GG genotype had significantly higher risk for lung cancer (odds ratio OR = 6.83, \( P = 0.0081 \)), compared with TT and GT genotypes.

Conclusion: Our study demonstrated that KRAS 3′-UTR rs712 polymorphism interfered with miRNA/mRNA interaction, and showed that the minor allele was associated with an elevated risk for development of lung cancer in COPD.

Keywords: let-7g, chronic obstructive pulmonary disease, lung cancer, KRAS, single nucleotide polymorphism

Introduction
Lung cancer is the cause for more deaths than most other cancers worldwide. Tobacco exposure continues to be a major risk factor for lung cancer and is also closely associated with the pathogenesis of COPD.1 COPD alone also raises the risk of lung cancer independent of tobacco use. As a matter of fact, 50%–80% of patients with lung cancer have COPD.2 In particular, squamous cell carcinoma and adenocarcinoma are the most common histological subtypes among patients with COPD and among long-term smokers.3,4 Therefore, it is believed that lung cancer and COPD may share common etiological factors and similar molecular mechanisms.5

The discovery of microRNAs (miRNAs) in early 1990s revealed an unexpected level of gene expression regulation that proves to be relevant in regulating numerous physiological and pathological conditions, including carcinogenesis, cancer progression, and response to therapy.6 miRNAs are noncoding, evolutionally preserved, small-sized RNA that regulate gene expression through different mechanisms.6 As many as 2,000 human miRNAs have been reported (Sanger miRBase version 18) to be involved in...
the control of important physiological processes and in the
pathogenesis of different diseases.\textsuperscript{6,7} Some miRNAs are
transcribed from polycistronic primary transcripts, either
through independent action or within a coordinated regulatory
network. For lung cancer, miRNA profiling may be useful
in the diagnosis, prediction of recurrence, and assessment
of prognosis in different clinical scenarios.\textsuperscript{8,9} miRNA clusters
have also been recognized as essential components of lung
cancer pathways; for example, the miR-17-92 cluster regulates
growth stimulatory signaling pathways in small-cell lung
cancer.\textsuperscript{10} Better understanding of the molecular networks
regulated by miRNAs may be potentially useful biomarkers
for screening, diagnosis, and/or therapeutic targeting.

There is increasing evidence that single nucleotide poly-
morphisms (SNPs) residing in miRNA binding sites can
differentially express target genes.\textsuperscript{11,12} The impact
of miRNA binding site polymorphisms on cancer risk was
reviewed by Chen et al in 2008.\textsuperscript{13} An SNP in the let-7 comple-
mentary binding site (LCS6) of the KRAS 3′-untranslated
region (3′-UTR) is associated with an elevated risk of non-
small-cell lung cancer,\textsuperscript{14} increased cetuximab responsi-

We hypothesized that KRAS rs712 polymorphism may
increase the susceptibility of lung cancer in the background of
COPD. To test this hypothesis, we examined the relationship
between the rs712 polymorphism and the incidence of lung
cancer in the patients with COPD. In addition, we assessed
the effect of KRAS rs712 polymorphism on the interaction
between the let-7g and KRAS mRNA as well as the expres-
sion pattern of let-7g and KRAS in the lung tissue samples
of each genotype.

Materials and methods
Patients and clinical specimens
A total of 554 patients with diagnosis of COPD, including
132 with lung cancer and 442 without lung cancer, were
enrolled in this study. The included COPD patients were
recruited from Shandong Provincial Chest Hospital. The
disease was staged with the following criteria: classification
of severity of airflow limitation in COPD. Global initiative for
chronic Obstructive Lung Disease (GOLD) 1 (mild): forced
expiratory volume in 1 second (FEV\textsubscript{1}) \( \geq \)80\% predicted;
GOLD 2 (moderate): 50\% \( \leq \) FEV\textsubscript{1} < 80\% predicted; GOLD 3
(severe): 30\% \( \leq \) FEV\textsubscript{1} < 50\% predicted; GOLD 4 (very
severe): FEV\textsubscript{1} < 30\% predicted. To evaluate the effect of
smoking, we evaluated cumulative smoking dose by calculat-
ing pack-years index:

\[
\text{Pack-years} = (\text{Cigarettes per day}/20) \times \text{Years smoked} \quad (1)
\]

Among the recruited participants, resected specimens
were available in 35 patients including 24 COPD patients
who had received surgery for lung tumor resection (at least
2 cm away from tumor tissues), and eleven participants who
had undergone volume reduction surgery. Institutional review
board of Shandong Provincial Chest Hospital approved the
research protocol. Five milliliters of peripheral blood was
donated for genomic DNA extraction after signed written
consent was provided by each participant.

Genotyping
Genomic DNA was extracted from peripheral blood using
the extraction kit (Biotek, Beijing, People’s Republic
of China) as per the manufacturer’s protocol. Chromo-
some segments containing KRAS rs712 polymorphism
were polymerase chain reaction (PCR) amplified using
the primer set: 5′-TAATCTGGGTGTTGATGA-3′ and
5′-GAGTGACCATGACTAATA-3′, and genotyping was
performed using direct sequencing.

Quantification of miRNA and mRNA
expression levels
Real-time qPCR was conducted using Power SYBR
Fast PCR Master Mix and Step-one plus real-time PCR
machine (Applied Biosystems, Foster City, CA, USA).
The human U6 small nuclear RNA was used as an inter-

cal control. The transcription levels of let-7g, KRAS, and
ATK were quantified by the SYBR green-1 Master PCR
Mix with specific real-time PCR primer sets. All reactions
were done in duplicate. Expression levels of miRNA and
mRNA were quantified based on the 2\textsuperscript{-\Delta\Delta C}\textsubscript{T}
relative quantifi-
cation method. The primer sets used for let-7g were:
forward 5′-TGAGGTAGTTTGTACAGTT-3′, reverse
5′-TGACCGGTACGGTTC-3′; KRAS: forward 5′-tgagg
actggtggttt-3′, reverse 5′-tggggtctaatctagga-3′; ATK:
forward 5′-TGGGAAAGTGTACCTGTGAGT-3′, reverse
5′-GGTCGTGGGTCTGGAATGAGT-3′, U6:
forward 5′-CTCGTTCGGAAGCTTACAC-3′, reverse
5′-AAGTTTACTTCTACATTT-3′.

Western blot
Lung tissue samples were homogenized and lysed in radio-
immunoprecipitation assay (RIPA) lysis buffer that contains
protease inhibitor cocktail (Roche, Indianapolis, IN, USA).
The same amount of proteins were resolved on SDS–PAGE and transferred onto nitrocellular membranes. The membranes were blocked with 5% (wt/vol) nonfat milk, washed in Tris-buffered saline Tween 20 solution, and incubated with primary antibody (anti-KRAS antibody, anti-AKT antibody, and anti-p-AKT antibody) at 4°C overnight. After rinsing, the membranes were incubated with horseradish peroxidase-conjugated secondary antibody (Bio-Rad Laboratories Inc., Hercules, CA, USA) at dilutions of 1:10,000 for 1 hour at room temperature, and immunoreactive bands were visualized with Pierce SuperSignal West Pico Chemiluminescent Substrate (Thermo Scientific, Waltham, MA, USA). The relative band intensities were quantified through densitometry using NIH ImageJ software (National Institutes of Health, Bethesda, MD, USA) and normalized with image densities of actin. All antibodies were purchased from Santa Cruz Biotechnology (Santa Cruz, CA, USA).

**Let-7g target validation by UTR luciferase reporter assay**

Two primers were designed to amplify the KRAS 3′-UTR chromosomal segment that contained let-7g binding site and KRAS 3′-UTR rs712 polymorphism (forward: 5′-ATGACTGAAATACAACTTGGTAGGTA-3′; reverse: 5′-ACTAGATAAACACAGATAAGGAT-3′), and the PCR product was inserted into a modified version of pcDNA3.1 with a firefly luciferase inserted. The mutant construct of KRAS 3′-UTR was generated by site-directed mutagenesis.

The luciferase assay with wild-type or mutant KRAS 3′-UTR was performed in two lung cancer cell lines H226 (squamous lung cancer) and H522 (lung adenocarcinoma), respectively. Approximately, 4×10⁴ cells were seeded onto 12-well plates, and after the cells reached 80%–90% confluence, each well was transfected with 300 ng of 3′-UTR reporter vectors, 1,200 ng of let-7g mimics (5′-GAGGUAGUAGUUUGACAGGU-3′), and 40 ng of phRL-TK (Promega, Fitchburg, WI, USA) with 4 μL of Lipofectamine 2000 (Invitrogen, Carlsbad, CA, USA). At 2 days after transfection, the cells were harvested and luciferase activities were determined using the Dual-Luciferase Reporter Assay System (Promega).

**Statistical analysis**

The differences in the characteristics of COPD in patients with or without lung cancer were compared using the chi-square test (for categorical variables) and Student’s t-test (for continuous variables). The risk of the KRAS rs712 polymorphism for lung cancer in COPD was estimated by calculating the odds ratio (OR) and 95% confidence intervals (CI). All statistical analyses were performed using SPSS statistical software package version 21.0 (SPSS, Inc., Chicago, IL, USA). All tests were two-sided and statistical significance was considered if \( P \leq 0.05 \).

**Results**

**Characteristics of the participants**

The demographic and clinicopathological parameters of the participants are described in Table 1. The COPD patients with and without lung cancer were statistically matched regarding age (\( P=0.215 \)), sex (\( P=0.0852 \)), and smoking status (\( P=0.0856 \)) and smoking index (\( P=0.06 \)). However, COPD severity in COPD patients with lung cancer was significantly higher than in those without lung cancer (\( P<0.001 \)). Additionally, all these variables were included in the multivariate logistic regression analysis to evaluate the potential effects of the association between KRAS 3′RAS rs712 polymorphism and the risk of development of lung cancer in COPD patients.

**Association analysis between KRAS 3′-UTR rs712 polymorphism and risk of development of lung cancer in COPD**

Genotype frequency of KRAS 3′-UTR rs712 polymorphism among the COPD patients with or without lung cancers and their associations with lung cancer risk in COPD are presented in Table 2. The frequencies of the TT, TG, and GG genotypes were 65.87%, 31.27%, and 2.86%, respectively, among those COPD patients without lung cancer, and 54.54%, 28.79%, and 16.67%, respectively, among those COPD patients with lung cancer (\( P=0.0282 \)). When we used the TT

**Table 1**

<table>
<thead>
<tr>
<th>Characteristic</th>
<th>COPD (+)</th>
<th>COPD (-)</th>
<th>( P )-value</th>
</tr>
</thead>
<tbody>
<tr>
<td>Sex (M/F)</td>
<td>390/52</td>
<td>108/24</td>
<td>0.0582</td>
</tr>
<tr>
<td>Age (years)</td>
<td>66.7±12.8</td>
<td>65.2±9.6</td>
<td>0.215</td>
</tr>
<tr>
<td>Smoking status</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Smokers</td>
<td>183</td>
<td>68</td>
<td>0.0856</td>
</tr>
<tr>
<td>Ex-smokers</td>
<td>208</td>
<td>54</td>
<td></td>
</tr>
<tr>
<td>Smoking index</td>
<td>32.5±11.2</td>
<td>34.5±8.7</td>
<td>0.060</td>
</tr>
<tr>
<td>COPD severity</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Mild</td>
<td>170</td>
<td>33</td>
<td>&lt;0.001</td>
</tr>
<tr>
<td>Moderate</td>
<td>165</td>
<td>45</td>
<td></td>
</tr>
<tr>
<td>Severe</td>
<td>66</td>
<td>33</td>
<td></td>
</tr>
<tr>
<td>Very severe</td>
<td>21</td>
<td>21</td>
<td></td>
</tr>
<tr>
<td>Lung cancer type</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Squamous</td>
<td>75</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Adenocarcinoma</td>
<td>36</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Large cell</td>
<td>11</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Small cell</td>
<td>10</td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

Note: *Data is mean ± standard deviation.
Table 2 Statistical analysis of the association between the rs712 polymorphism genotype and the presence of lung cancer in COPD patient

<table>
<thead>
<tr>
<th></th>
<th>COPD (+) Lung cancer (-)</th>
<th>COPD (+) Lung cancer (+)</th>
<th>P-value</th>
<th>Adjusted OR (95% CI)</th>
</tr>
</thead>
<tbody>
<tr>
<td>TT</td>
<td>278 (65.87%)</td>
<td>72 (54.54%)</td>
<td>0.0282</td>
<td>1.00</td>
</tr>
<tr>
<td>TG</td>
<td>132 (31.27%)</td>
<td>38 (28.79%)</td>
<td></td>
<td>1.11 (0.71–1.73)</td>
</tr>
<tr>
<td>GG</td>
<td>12 (2.86%)</td>
<td>22 (16.67%)</td>
<td></td>
<td>7.07 (3.34–14.97)</td>
</tr>
<tr>
<td>Combined</td>
<td>410 (97.14%)</td>
<td>110 (83.33%)</td>
<td>0.0081</td>
<td>1.00</td>
</tr>
</tbody>
</table>

**Abbreviations:** OR, odds ratio; CI, confidence interval.

Effect of the KRAS 3′-UTR rs712 polymorphism on KRAS expression in lung cancer cells

It has been previously shown that KRAS is a target of let-7g in human cells. Based on the computational analysis, the KRAS 3′-UTR rs712 polymorphism was found to be located in the flanking sequence close to the predicted “binding site” for hsa-let-7g (Figure 1). To test whether hsa-let-7g targets KRAS 3′ASgets 1 lung cancer cells, we constructed reporter vectors carrying wild-type or mutant KRAS 3′-UTR, as described in Figure 1. Subsequently, we used them for transient transfection with the lung cancer cells together with let-7g mimics or scramble controls. As shown in Figure 2, only the luciferase activity from the cells cotransfected with wild-type KRAS 3′-UTR and let-7g mimics was significantly lower than the control, and activity in all other groups were comparable. The results confirmed that KRAS is a validated target of let-7g in lung cancer cells, that rs712 polymorphism compromised the interaction between let-7g and KRAS 3′-UTR, and that the nucleotide substitution completely abrogates the miRNA/mRNA interaction in lung cancer cells.

Determination of expression patterns of let-7g and KRAS in lung tissues with different genotypes

The lung tissues of three different genotypes (TT, n=17; TG, n=12; GG, n=6) were used to further explore the impacts of the polymorphism on the interaction between let-7g and KRAS 3′-UTR. Using immunohistochemistry analysis, we found that the expression of KRAS was comparable between the TT and TG groups, both of which were substantially lower than GG group (Figure 3). Additionally, to characterize the role and effect of KRAS 3′-UTR rs712 polymorphism on the miRNA/mRNA interaction in lung cancer cells which plays a central role in the development of lung cancer in the patients with COPD, we quantified the expression of let-7g and KRAS by using real-time PCR as well as Western blot. As shown in Figure 4, while the expression levels of let-7g were similarly distributed among each genotype group, the mRNA and protein expression levels of KRAS in GG genotype group were significantly higher than in TT and TG groups. To further confirm the effect of KRAS 3′-UTR rs712 polymorphism on the signaling pathway, we further examined the expression levels of ATK as well as the phosphorylation status of the protein. As shown in Figure 5, even though the mRNA and total protein expression levels of ATK were comparable among each genotype group, the phosphorylated ATK was significantly higher in GG group than in TT or TG group.

Discussion

The occurrence of lung cancer in patients with COPD has been thought to reflect the role of the common etiological agent, cigarettes. High lung cancer incidence rates among nonsmokers in COPD clinics challenge this idea and prompt epidemiological studies to address this question. Little progress has been made toward identifying common mechanistic links for these heterogeneous diseases, as both lung cancer and COPD are characterized by multiple sub-phenotypes. Despite the increased attention, the nature of the link between COPD and lung cancer remains unclear. This is, in a large part, due to the seemingly opposite nature of the two diseases. Emphysema is characterized by the destruction of matrix structures, epithelial cell death, and vanishing blood supply (alveolar capillary dropout). We hypothesized that some molecular defect may be responsible for such changes of opposite direction.
Variant in Kras 3′-UTR increases risk of lung cancer in COPD

WT KRAS 3′-UTR

Luciferase

KRAS 3′-UTR

rs712T

5′-GTGTTTAATTGTACCTACCTAAATTATTAGGTCTTTGCTTTTCTCAGCTAATTCCTTTCTGCTCAATGCAATGCACTGTA

Primary let-7g

3′-ACCGTTCGGTACCGGACATGTCAATAGGCGATCGGCCACGATAGTCTGGAGATTGACATGTGTGACATGTGTGTGAGCGA-5′

MUT KRAS 3′-UTR

Luciferase

KRAS 3′-UTR

rs712G

5′-GTGTTTAATTGTACCTACCTAAATTATTAGGTCTTTGCTTTTCTCAGCTAATTCCTTTCTGCTCAATGCAATGCACTGTA

Figure 1 Schematic sequence comparison of KRAS 3′-UTR and primary let-7g and location of rs712 polymorphism in the 3′-UTR of KRAS.

Abbreviations: MUT, mutant; UTR, untranslated region; WT, wild-type.
miRNAs can act as transacting factors to suppress translation of or induce mRNA degradation of target genes; they are found to regulate gene expression in various cancers. The let-7 miRNA family functions as tumor suppressors in many cancers including GC, and their expressions are downregulated in various other cancers.19–21 Let-7 was reported to target and downregulate RAS by binding to specific sites in the 3′-UTR of the KRAS mRNA and exert its tumor-suppressing function.22,23 Over-expression of let-7g can inhibit the growth of transplanted lung cancer in nude mice model.23 The expression of let-7 is associated with cancer survival in the anti-KRAS monoclonal antibodies. Earlier studies have revealed that let-7f can inhibit tumor invasion and metastasis in human gastric cancer.19

KRAS, also known as V-Ki-ras2 Kirsten rat sarcoma viral oncogene homolog, acts as an intracellular signal transducer. The oncogenic KRAS mutation is an essential part of the development of many human cancers.24–26

Figure 2 Evaluation of rs712 polymorphism on the interaction between let-7g and KRAS 3′-UTR.

Notes: (A) Relative luciferase activity in let-7g over-expressing H226 cells transfected with empty vector, wild-type KRAS 3′-UTR, or mutant KRAS 3′-UTR (***P<0.01, compared with the empty vector; **P<0.01, compared with the empty vector). (B) Relative luciferase activity in let-7g over-expressing H522 cells transfected with empty vector, wild-type KRAS 3′-UTR, or mutant KRAS 3′-UTR (***P<0.01, compared with the empty vector; **P<0.01, compared with the empty vector).

Abbreviations: Luc, luciferase; WT, wild-type; UTR, untranslated region; Mut, mutant.

Figure 3 Determination of expression of KRAS in lungs of each genotype group by using immunohistochemistry.

Notes: Expression of KRAS was comparable between TT (A), TG (B), and GG (C) groups.
Figure 4 Determination of the expression of KRAS in each genotype group.

Notes: (A) Determination of expression of let-7g in lungs in each genotype group (TT, n=17; TG, n=12; GG, n=6) by using real-time PCR. (B) Determination of mRNA expression of KRAS in lungs in each genotype group (TT, n=17; TG, n=12; GG, n=6); (C) Determination of protein expression of KRAS in lungs in each genotype group (TT, n=17; TG, n=12; GG, n=6) by using Western blot. (D) Densitometry analysis of the results of Western blot (**P<0.01, compared with wild type, TT).

Abbreviation: PCR, polymerase chain reaction.

Figure 5 Determination of the expression levels and activities of total AKT and p-AKT in each genotype group.

Notes: (A) Determination of mRNA expression of AKT in lungs in each genotype group (TT, n=17; TG, n=12; GG, n=6). (B) Determination of total protein expression of AKT in lungs in each genotype group (TT, n=17; TG, n=12; GG, n=6) by using Western blot. (C) Determination of phosphorylation level of AKT in lungs in each genotype group (TT, n=17; TG, n=12; GG, n=6) by using Western blot. (D) Densitometry analysis of the results of Western blot described in (B). (E) Densitometry analysis of the results of Western blot described in (C) (**P<0.01, compared with wild type, TT).
reported to be negatively regulated by the let-7 miRNA family.\textsuperscript{22,27} Transfection of human colon cancer cells with let-7g precursor miRNA leads to the inhibition of cell growth and downregulation of KRAS, which suggests that let-7 miRNA may be involved in the growth of colon cancer cells.\textsuperscript{27} In this study, we confirmed that KRAS is a target of let-7g in two lung cancer cell lines. The human KRAS 3′-UTR contains multiple putative let-7 complementary sites (LCS), which enables the let-7 regulation of KRAS activity.\textsuperscript{22} Two polymorphisms have been so far studied in multiple cancer types. Chin et al for the first time reported that the KRAS LCS6 variant allele was significantly associated with an elevated risk of non-small-cell lung cancer among moderate smokers.\textsuperscript{28} The variant allele was reported to confer an elevated risk for triple negative breast cancer\textsuperscript{29} and breast cancer in families with the BRCA1 mutation,\textsuperscript{30} but such finding was not noted for invasive epithelial ovarian cancer.\textsuperscript{31} Another well-studied polymorphism is rs712 polymorphism. Kranenburg reported that the KRAS rs712 polymorphism was associated with an increased risk of CRC and the clinical features of the disease.\textsuperscript{24} AKT is one of the most important downstream effectors along the signaling pathway, and phosphorylation is a necessary step to activate the function of AKT.\textsuperscript{32} In this study, we recruited 554 COPD patients with (n = 132) and without (n = 422) lung cancer, and we did not detect KRAS LCS6 variant in our sample pool; therefore, we focused on rs712 polymorphism. By using luciferase reporter system, we found that introduction of rs712 minor allele into 3′-UTR significantly compromised the miRNA/mRNA interaction. Additionally, to verify such relationship in human samples, we collected 35 human tissue samples genotyped as TT (17), TG (12), GG (6), and let-7g and KRAS expression levels were determined. We showed that let-7g level was similar between groups, and the concentration of KRAS in GG genotype group was significantly higher than in TT or GT genotype group. Meanwhile, we found COPD patients with GG genotype had significantly higher risk for lung cancer (OR = 6.83, P = 0.0081), compared with TT and GT genotypes.

Overall, our study, together with previous reports,\textsuperscript{33} provides the evidence that the rs712 polymorphism compromised the interaction between let-7g and 3′-UTR of KRAS, and was associated with the development of lung cancer in COPD. This polymorphism could be a biomarker to predict the development of lung cancer in COPD and may be of preventive and therapeutic relevance in the clinical practice.

**Disclosure**
The authors report no conflicts of interest in this work.

**References**


