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LETTER TO THE EDITOR

Promoter Mutation Analysis of Long-Non-coding RNA *RMRP* Gene in Solid Tumors

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To the Editor:

A recent study analyzed genome-wide non-coding sequences in breast cancers and found several promoter mutations in coding and non-coding genes [1]. Long noncoding RNAs (lncRNAs) are minimum transcript length of 200 bps and play important roles in many biological processes [2]. Dysregulation of lncRNAs has been found in many cancers and known to be related to cancer pathogenesis [2]. RNA component of mitochondrial RNA (*RMRP*) is an lncRNA that regulates both mitochondrial and ribosomal RNA processing [3]. Alterations of *RMRP* are involved in the development of a genetic disorder cartilage-hair dysplasia [3]. *RMRP* overexpression has been identified in many tumors and considered to have oncogenic functions [4, 5]. Also, somatic *RMRP* mutations in its promoter have been reported in breast cancers [1]. Functionally, *RMRP* expression in cells promotes cell proliferation and invasion, and inhibits cell death [4, 5]. *RMRP* promoter mutations in breast cancers increased *RMRP* expression and its enhanced recruitment of transcriptional activators, suggesting possible gain-of-function (oncogenic) activities [1]. To date, however, presence of *RMRP* promoter mutations in other solid tumors besides breast cancers remains unknown.

In this study, human cancer tissues from 1366 patients from origins were analyzed (Table 1). Approval for this study was obtained from the Catholic University of Korea, College of Medicine's institutional review board. Because *RMRP* promoter mutations in breast cancers have been focused on two regions (chromosome 9: 35658025–63 and 35,658,224) [1], we amplified them with two primer pairs by polymerase chain reaction (PCR) and single-strand conformation polymorphism (SSCP) assay [6].

Overall, we detected *RMRP* somatic promoter mutations in 4 cases: two (Chr9:35,658,037dupA, Chr9: 35,658,174dupT) in gastric carcinomas, one (Chr9:35,658,167G > T) in a colon carcinoma and the other one (Chr9.35,658,015_35,658,031 dupCACGTCCTCAGCTTCAC) in a sarcoma (malignant fibrous histiocytoma). Neither of them (Table 1) overlapped with the mutations previously detected in breast cancers [1]. The mutations consisted of 3 duplication mutations and one point mutation. To confirm the mutation data, we repeated the DNA sequencing twice and found them to be consistent. There were no significant clinicopathologic parameters associated with the mutations including demographic and prognostic data.

Although *RMRP* promoter mutation was found in breast cancers [1], its mutation in solid cancers remained undetermined. We identified *RMRP* promoter mutations in 3 different cancer types, indicating the mutations might be present widely in solid cancers. Despite the presence, low prevalence (0–1.3%) suggests that the promoter mutation is not a generalized driver for cancer pathogenesis. Interestingly, the duplication type mutations in our study were contrast to the *RMRP* promoter mutations previously found in breast cancers (point

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Table 1 Analysis of *RMRP* promoter mutation in common solid cancers

Type of cancers	Number of tumors	*RMRP* promoter mutation site			
		Wild type	Mutation	Location	Mutation (%)
Gastric carcinoma	230	228	2	Chr9:35,658,037dupA, Chr9: 35,658,174dupT	0.9
Colorectal carcinoma	388	387	1	Chr9:35,658,167G > T	0.3
Lung adenocarcinoma	197	197	0		0
Prostate carcinoma	269	269	0		0
Breast carcinoma	95	95	0		0
Hepatocellular carcinoma	46	46	0		0
Esophageal carcinoma	71	71	0		0
Sarcomas	70	69	1 (MFH)	Chr9.35,658,015_35,658,031 dupCACGTCCTCAGCTTCAC	1.4
Total	1366	1362	4		0.3

MFH, malignant fibrous histiocytoma

mutation) [1]. Our results suggest that *RMRP* promoter mutation may be variable depending on the cancer types and not be easy to be used for cancer biomarkers.

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Compliance with Ethical Standards

Conflict of Interest None declared.

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