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LETTER TO THE EDITOR

Promoter Mutation Analysis of *ALDOA* Gene in Solid Tumors and Acute Leukemias

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To the Editor:

Alteration in the cellular metabolism is one of the cancer hallmarks. *Fructose-1,6-bisphosphate aldolase A* (*ALDOA*) gene encodes an enzyme ALDOA that converts fructose 1,6-bisphosphate into G3P and DHAP, which in glycolysis have proven benefits for cancer cells [1]. High ALDOA expression has been demonstrated in many cancers and is associated with overall survival of the patients, suggesting its functions as a candidate oncogene [2]. However, genetic alterations of *ALDOA* in the coding sequences are reported to be rare. A recent genome-wide sequecning study for promoters in breast cancers discovered somatic promoter mutations in many genes, including *ALDOA* (3.3% of breast cancers) [3]. The *ALDOA* promoter mutation was found at a hotspot (chr16: 30077131). It is well-known that alterations in promoter play a role in the cancer pathogenesis [4], suggesting that *ALDOA* promoter mutation might reside in other cancers as well as in breast cancer.

In this study, human tumor tissues from 1834 patients from diverse organs were analyzed (Table 1). Approval for this study was obtained from the Catholic University of Korea, College of Medicine's institutional review board. Since the *ALDOA* promoter mutation has been found in the hotspot [3], we amplified a region encompassing the hotspot with a primer pair by polymerase chain reaction (PCR) (forward: 5-TCGTAAAG GAAAAAGCTCGGC-3, reverse: 5-GATTCAAG GAGAGAACGCGG-3, size: 174 bps) and subsequently displayed in single-strand conformation polymorphism (SSCP) and DNA sequencing [5].

Overall, we detected *ALDOA* somatic promoter mutations in two cases: one (chr16: 30,077,035 G > A) in a childhood acute lymphoblastic leukemia (ALL) and the other (chr16: 30,077,051 C > T) in a colon carcinoma. Neither of them (Table 1) overlapped with the hotspot [3].

In this study, the prevalence of *ALDOA* somatic promoter mutations (ALL (0.3%) and colon carcinoma (0.3%)) is significantly lower ($P < 0.001$) than that in breast cancers (1.7%) [3]. Also, the mutation sites were different from that in breast cancers [3], indicating that the *ALDOA* mutations might be specific to breast cancer or might be very rare in other tumors, if any. Our results suggest that *ALDOA* promote mutation may not be clinically available for cancer patients due to the low incidence.

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Table 1 Analysis of *ALDOA* promoter mutation in 2018 tumors

Type of tumors	Number of tumors	*ALDOA* promoter		
		Wild type	Mutation	Mutation (%)
Adulthood AML	210	210	0	0
Adulthood ALL	140	140	0	0
Childhood AML	21	21	0	0
Childhood ALL	365	364	1	0.3
Multiple myeloma	75	75	0	0
Myelodysplasia	67	67	0	0
Gastric carcinoma	264	264	0	0
Colon carcinoma	347	346	1	0.3
Prostate carcinoma	239	239	0	0
Hepatocellular carcinomas	37	37	0	0
Squamous cell carcinomas, lung	37	37	0	0
Adenocarcinomas, lung	32	32	0	0
Total	1834	1832	2	0.1

AML, acute myelogenous leukemia; *ALL*, acute lymphoblastic leukemia

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