

The Author Response

***EML4-ALK* Fusion Gene in Korean Non-Small Cell Lung Cancer**

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I would like to thank the interest and comments on our paper entitled “*EML4-ALK* fusion gene in Korean non-small cell lung cancer” (1). In this study, we examined *EML4-ALK* fusion variants in Korean non-small cell lung cancers (NSCLCs) via reverse-transcriptase-polymerase chain reaction (RT-PCR) using primers designed to detect *EML4-ALK* fusion variants (variants 1, 2, 3a, 3b, 4, 5a, 5b, 6, and 7) that have been previously identified (2, 3). Our study demonstrated the spectrum and frequency of *EML4-ALK* fusion variants in Korean NSCLCs, which were different from those in other ethnic populations.

I agree with the comment that the RT-PCR technology for identification of *ALK* fusion variants has several limitations. As pointed out in this comment, there are multiple *EML4-ALK* fusion variants and non-*EML4* fusion partners, such as *KIF5B*, and *KLC1* (2-5); therefore, any PCR-based strategy must incorporate validated primer pairs for all known *ALK* fusions. Another limitation is that given that most specimens from lung cancer patients are stored as formalin-fixed paraffin embedded tissue, the RNA may have been substantially degraded relative to non-fixed, fresh-frozen tissue. In addition, it has been reported that PCR-based detection of *EML4-ALK* can yield positive results in the absence of detectable *ALK*-rearrangement in both tumor and non-tumor tissues, suggesting a propensity for false positive results (6). The aim of our study was to examine the profile of known *EML4-ALK* fusion variants in Korean NSCLCs and was not to detect the presence of *ALK* fusion to other gene partners. The limitations of the RT-PCR analysis, such as the necessity of available high-quality RNA and the propensity of false positive results, were briefly discussed in the paper. I agree with the suggestion that long-distance-PCR or long distance inverse-PCR could be used to identify all *EML4-ALK* fusion variants as well as other *ALK* rearrangements having known or even unknown fusion partner genes (7, 8).

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