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RESPONSE TO LETTER

Thoughtful Response on "MRI-Based Texture Analysis for Preoperative Prediction of BRAF V600E Mutation in Papillary Thyroid Carcinoma" [Response to Letter]

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Dear editor

We are pleased to receive a letter from readers regarding our publication entitled "MRI-Based Texture Analysis for Preoperative Prediction of BRAF V600E Mutation in Papillary Thyroid Carcinoma". (ID: 405040).

The responses to the readers' comments are as following:

1) Comment: It was clearly stated and done in the experimental works of Zheng T el al. that the BRAF gene mutation was confirmed by sequencing which was performed before MRI-based texture analysis. The inclusion criteria of the samples used in this study regarding the detection of BRAF V600E mutation detected by AB Diagnostic kit, which is based on the amplification-resisted mutation Information Classification: General system (ARMS) real-time polymerase chain reaction (PCR) technology, then confirmed by sequencing was questionable.

Response: I apologize for the misunderstanding caused by the unclear presentation. Our institution sent specimens out to companies for testing until October 2021, using the Sanger sequencing method. After that, the amplification-resisted mutation system (ARMS) real-time polymerase chain reaction (PCR) technology has been used. Fifty-nine of our 80 patients were Sanger sequencing method and 21 were tested with ARMS real-time PCR technology.

2) Comment: In this study, the samples used were originally grouped based on their characteristics, BRAF V600E mutant (72.5%) and wild-type (27.5%). The question addressed here is regarding the conclusion taken in the study. It was mentioned that MRI-based texture analysis could be a potential method for predicting BRAF V600E mutation in PTC preoperatively in the conclusion section. However, based on the data, the mutation in BRAF gene was clearly not predicted by MRI.

Response: Thank you for your comments. We used the results of genetic testing as a criterion to explore MRI-based texture with statistically significant differences between the mutant and wild groups and build the prediction model. The area under the ROC curves (AUCs) for the T2WI model, CE-T1WI model, and combined model were 0.83 (95% CI: 0.75–0.91), 0.83 (95% CI: 0.73–0.90), and 0.88 (95% CI: 0.81–0.94), respectively. The ICCs of the features we used for modeling were all greater than 0.75 with good agreement. So we think MRI-based texture analysis could be a potential method for predicting BRAF V600E mutation in PTC.

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Disclosure

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