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LETTER

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

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Dear editor

The experimental works performed and recently reported by the group of Zheng et al was read and reviewed thoroughly. The insightful data reported in their study gave the readers novel thoughts and information regarding how to utilize MRI for the texture analysis of papillary thyroid carcinoma accompanied by the prediction of *BRAF* gene mutation which is debatable. Here, a few thoughtful responses are given in order to improve the designs of future studies and communication in sciences.

The mutation in the *BRAF* gene was harbored frequently in various cancer cells including the endocrine malignancy such as thyroid carcinoma.[1,2] Clinical examination such as magnetic resonance imaging (MRI) has been found to be helpful and useful clinically for detecting the structure abnormalities in certain diseases, such as schizophrenia, the chronic brain disorder.[3] In addition, MRI has been developed and utilized for the texture analysis in discrimination of tumors in patients diagnosed with medulloblastoma.[4] In the work reported by Zheng et al, an MRI-based texture feature model was utilized to provide a new approach for noninvasive and preoperative identification of *BRAF* V600E mutation and to find the mutation location in the tissue.[5] This strategy is indeed a needed novel technology in the clinical field used for diagnostic approach as well as the treatment strategy. However, some insightful questions regarding the correlation between MRI-based texture analysis and gene mutation in carcinoma tissue are addressed here for being taken as insightful input for improving the future studies in this particular field.

It was clearly stated and done in the experimental works of Zheng et 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 system (ARMS) real-time polymerase chain reaction (PCR) technology, then confirmed by sequencing was questionable. 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 the *BRAF* gene was clearly not predicted by MRI. Nevertheless, we do agree that the relationship of MRI-structure-based analysis and *BRAF* V600E mutation was likely worth studying even further in order to improve the potential pretreatment medication needed detected by MRI-based prediction in patients with cancer or carcinoma such as PTC.[6,7]

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Author Contributions

NSDP read and reviewed the article of Zheng et al and the cited publications. CSWL and MSM helped in reviewing the cited publications. NSDP, CSWL and MSM discussed the issue written in this letter. Thereafter, NSDP conceived the critical design of the letter. NSDP wrote the whole letter draft. CSWL and MSM read the draft and gave necessary revisions. Lastly, NSDP revised the manuscript accordingly. Novaria Sari Dewi Panjaitan is the main contributor and corresponding author.

Disclosure

There is no conflict of interest regarding the communication.

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