

LETTER TO THE EDITOR



Response to commentary by Lu and Wang on “Salivary biomarkers for cancer diagnosis: a meta-analysis”

Dear Editor,

We read with interest the comment by Lu and Wang [1] concerning the potential inclusion of duplicate articles in our meta-analysis [2]. The first article by Xie et al. [2] included 32 supernatant samples from 32 oesophageal cancer and 16 saliva supernatant samples from 16 healthy individuals [3], while the second article by Xie et al. [3] included 46 whole saliva and 46 supernatant samples from 46 oesophageal cancer patients, and 22 whole saliva and 22 supernatant samples from healthy individuals [4]. Although the samples were obtained from the same institution, which implies a certain level of overlap, it should be noted that the sample sizes and characteristics (whole saliva and supernatant in the second study, supernatant only in the first study) are different. Moreover, the designs of the 2 studies are different. While the first study is similar to a pilot study and analyses only the expression of miR-21 by RT-qPCR, the second one comprises two phases: discovery and validation. In the discovery phase a total of 923 mature miRNA sequences integrated into a miRNA microarray design were analysed, and in the validation phase, the expression levels of the six miRNAs were validated by RT-qPCR. Using one study only would have defeated the objective of exhaustivity in our meta-analysis. In addition, due to its small sample size, the exclusion of the first study does not produce a meaningful modification in the pooled measures of our meta-analysis. These are the global results removing Xie et al 2012: DOR: 13.44 (12.29–16.01), sensitivity 0.75 (0.74–0.77), specificity 0.76 (0.75–0.77), NLR 0.31 (0.28–0.34), PLR 3.23 (2.93–3.56) and AUC 0.85 (0.84–0.86).

Sincerely,

References

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