Professor Ulrich Mahlknecht

Editor-in Chief

Clinical Epigenetics

Nov 11st, 2013

Dear Professor Mahlknecht,

Enclosed please find out our recent research paper entitled “Diagnostic Role of APC Promoter Methylation in Non-Small Cell Lung Cancer (NSCLC): An Integrate-Analysis of Published Articles and Microarray Data”. APC has been considered one of most important biomarker for early diagnosis of cancer while there was still not yet any quantitative assessment for the sensitivity and specificity in NSCLC. In this report, we made a comprehensively assessment on the diagnosis ability of APC promoter hypermethylation in NSLCL with a combination of Meta-analysis and independent Microarray dataset from TCGA project. Three credible heterogeneity sources to the association between APC methylation and NSCLC were identified, including primer set, proportion of adenocarcinoma in NSCLC samples. The present study shows that the methylation status of APC would be an excellent diagnosis biomarker in remote non-invasive media. In addition, APC methylation test has better diagnosis ability in adenocarcinoma than that in squamous cell carcinoma. The study made a professional analysis for methylation diagnostic ability with summary receiver operating characteristic curve (SROC) and independently validation with methylation microarray data, which we believe, will become to a novel methodology and template for the future methylation meta-analysis.

I would greatly appreciate could you consider its suitability for publication in Clinical Epigenetics

All authors have agreed the current version of the paper submitted here and myself as its corresponding author. The manuscript has not been and is not submitted to elsewhere for considering publication.

Thank you very much for your consideration and help with handling the paper for us.

Sincerely,

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The survival time of Non-small cell lung cancer could be significantly increased if NSCLC could be diagnosis in the early stage. DNA methylation has been considered one of most promising biomarkers for early detection for NSCLC. Integration analysis to inter-platform genome-wide DNA methylation datastes with appreciated data normalization and batch effect elimination could provide optimal biomarker combination in a large sample population to obtain maximum diagnosis efficiency. With this approach, we identified a 5 gene signature including *AGTR1*, *GALR1*, *SLC5A8*, *ZMYND10* and *NTSR1*, which could provide highly diagnosis sensitivity and specificity. It demonstrates that computational biomarker selection combined with independent sample validation would be a promising strategy for diagnosis biomarker identification.