Serum Metabolomic Analysis of Pancreatic Cancer—Letter

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In their recent article, Kobayashi and colleagues (1) sought to construct and validate a diagnostic model for pancreatic cancer using gas chromatography-mass spectrometry-based human serum metabolomics approach. The study included a training set (n = 85) and a validation set (n = 106). Using a multiple logistic regression analysis, the authors established a diagnostic model including 4 variables, based on the training set results. The model displayed an area under the curve value of 0.92857 in the training set and 0.76004 in the validation set. The results were interpreted as an evidence that this “metabolomics-based diagnostic model was more sensitive at detecting resectable stage cancer (77.8%) with the lower false-positive rate in chronic pancreatitis (17.4%) than conventional markers,” and that “this novel approach is expected to improve the prognosis of patients with pancreatic cancer by detecting their cancer early, when it is still in a resectable state.”

We are optimistic that the metabolomics approach has the capacity to provide new biomarkers for early detection and diagnosis of pancreatic cancer. However, we are concerned that this study does not provide sufficient proof-of-superiority of this approach over existing diagnostic standards. First, the study had a very small number of resectable cancers (9 in each set). Second, the performance of the model dropped significantly in the validation set. In fact, Fig. 2 in the original article (1) shows an inferior performance to CA19-9, which is likely due to the lack of inclusion of adequate control groups in the training set and the impairment of the diagnostic model in discriminating between cancer and chronic pancreatitis cases.

In the discussion, the authors acknowledge that “the sample size, especially in resectable pancreatic cancer, was not enough to conduct stringent subgroup analyses.” However, this limitation was overlooked in the conclusions when the authors state that their model can detect early-stage pancreatic cancer.

Consequently, the validity of any future study of biomarkers will depend on the thoroughness of study designs that avoid bias and contemplates the specific context of clinical setting and intended biomarker use at the initial discovery phase, to eliminate the cost of validating biomarkers that fail to discriminate between the cancer and its comorbidities (2, 3).

Disclosure of Potential Conflicts of Interest
No potential conflicts of interest were disclosed.

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References
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