



Serum heart-type fatty acid-binding protein as a predictor for the development of sepsis-associated acute kidney injury: methodological issues

Masoumeh Abbasi & Mehdi Naderi

To cite this article: Masoumeh Abbasi & Mehdi Naderi (2019): Serum heart-type fatty acid-binding protein as a predictor for the development of sepsis-associated acute kidney injury: methodological issues, Expert Review of Molecular Diagnostics, DOI: [10.1080/14737159.2020.1689819](https://doi.org/10.1080/14737159.2020.1689819)

To link to this article: <https://doi.org/10.1080/14737159.2020.1689819>



Accepted author version posted online: 04 Nov 2019.
Published online: 05 Nov 2019.



Submit your article to this journal [↗](#)



Article views: 3



View related articles [↗](#)




View Crossmark data [↗](#)

LETTER TO THE EDITOR



Serum heart-type fatty acid-binding protein as a predictor for the development of sepsis-associated acute kidney injury: methodological issues

Masoumeh Abbasi^a and Mehdi Naderi ^b

^aDepartment of Health Information Technology, School of Paramedical, Kermanshah University of Medical Sciences, Kermanshah, I.R. Iran; ^bClinical Research Development Centre, Taleghani and Imam Ali Hospital, Kermanshah University of Medical Sciences, Kermanshah, I.R. Iran

ARTICLE HISTORY Received 30 July 2019; Accepted 4 November 2019

KEYWORDS Acute kidney injury; sepsis; heart-type fatty acid-binding protein; prediction; methodological issue

Dear Editor,

We read with great interest the study of Jiang et al. entitled 'Serum heart-type fatty acid-binding protein as a predictor for the development of sepsis-associated acute kidney injury'. The aim of the authors was to determine the predictive capacity of heart-type fatty acid-binding protein (HFABP) for sepsis-associated acute kidney injury (SAKI) [1]. For this purpose, 442 patients with sepsis included in the study. Patients were divided into the no-AKI group (n = 317) and AKI group (n = 125). Logistic regression analysis was used to analyze the correlation between HFABP and SAKI. Predictive performance of the HFABP to SAKI evaluated by c-index, net reclassification improvement index (NRI) and integrated discrimination improvement index (IDI). The results showed HFABP concentration is an independent risk factor for SAKI (OR: 11.398; 95% CI: 6.218–20.891, P < 0.001). The AUC for prediction model with HFABP significantly improved (0.867 vs 0.755, P < 0.001), NRI 25.03% (95% CI 9.72–38.51%) and IDI 14.33 (95% CI 11.04–17.62) [1].

To develop a prediction model, we need two different data sets or at least one data set divided into two data (groups of patients with both failure and success) to predict an outcome. Generally, if the prediction model is not validated, the main outcome of research has spurious results. Different approaches apply for validation of a prediction model such as the split file, bootstrapping, or other well-known validation methods [2–4]. In the limitation of the study mentioned that data from single-center and data set was small. Bootstrapping is particularly recommended when the data set is small with many candidate predictors and when predictor selection techniques have been used regardless of the modeling technique. Also, since all of the data is applied to model development and model evaluation, generally bootstrapping resampling methods are recommended [5]. Another point is that interactions between important variables should be evaluated, especially when there are qualitative interactions, the final results will be significantly affected [5]. C-index, NRI and IDI are indexes to measures of discrimination. We cannot say that these indexes determine alone the predictive ability of the HFABP to SAKI. There are various measures such as calibration,

discrimination, reclassification and overall measures of performance to evaluate the model performance [6].

The authors concluded that the Serum HFABP is correlated with SAKI development and could become a potential predictive biomarker [1]. Briefly, in prediction studies, the main purpose is to provide a model, index, or score applicable to an individual (patient). Finally, associations, even those that are statistically significant, do not guarantee prediction [2–6].

In this letter, we discussed methodological issues in the study. Any prediction study should consider the above points.

Funding

This paper was not funded.

Declaration of interest

The authors have no relevant affiliations or financial involvement with any organization or entity with a financial interest in or financial conflict with the subject matter or materials discussed in the manuscript. This includes employment, consultancies, honoraria, stock ownership or options, expert testimony, grants or patents received or pending, or royalties.

ORCID

Mehdi Naderi  <http://orcid.org/0000-0002-5608-6582>

References

1. Jiang D, Shen M, Yuan X, et al. Serum heart-type fatty acidbinding protein as a predictor for the development of sepsis-associated acute kidney injury. *Expert Rev Mol Diagn.* 2019;19(8):757–765.
2. Abbasi M, Naderi M. What does need to know about developing clinical prediction models? *J Geriatr Oncol.* 2019;10(2):369.
3. Grobbee DE, Hoes AW. *Clinical epidemiology: principles, methods, and applications for clinical research.* London: Jones & BartlettPublishers; 2009.
4. Szklo M, Nieto FJ. *Epidemiology beyond the basics.* 3rd ed. Manhattan, New York: Jones and Bartlett Publisher; 2014.
5. Altman DG, Royston P. What do we mean by validating a prognostic model? *Stat Med.* 2000;19(4):453–473.
6. Moons KGM, de Groot JAH, Bouwmeester W, et al. Critical appraisal and data extraction for systematic reviews of prediction modelling studies: the CHARMS checklist. *PLoS Med.* 2014;11(10):e1001744.