

Letter

Using surface molecule expression on lymphocytes to classify septic shock patients

Jorge Monserrat¹, Raul de Pablo², Alfredo Prieto¹, Eduardo Reyes¹ and Melchor Álvarez-Mon^{1,3}

¹Laboratory of Immune System Diseases and Oncology, National Biotechnology Center—Department of Medicine (CNB-CSIC) Associated Unit, University of Alcalá, Carretera Madrid-Barcelona, Km 33,600, Alcalá de Henares, 28871 Madrid, Spain

²Intensive Care Unit, Hospital Universitario Príncipe de Asturias, Alcalá de Henares, 28871 Madrid, Spain

³Immune System Diseases and Oncology Service, Hospital Universitario Príncipe de Asturias, Alcalá de Henares, 28871 Madrid, Spain

Corresponding author: Melchor Alvarez-Mon, jorge.monserrat@uah.es

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See related commentary by McDunn and Hotchkiss, <http://ccforum.com/content/13/2/127>, and related research by Monserrat *et al.*, <http://ccforum.com/content/13/1/R26>

In agreement with McDunn and Hotchkiss [1], we hypothesized that the simultaneous analysis of different immune system cell subsets would improve the prediction of outcome in septic shock patients. Abnormal redistribution of T-lymphocyte, NK-lymphocyte and B-lymphocyte subsets has been found to be involved in the pathogenesis of other diseases, but the evidence reported in critical illness is less compelling [2]. In addition to the results described in our previous paper, and following a cytomic analysis [3], we have also studied the predicting value for outcome of combining different T-cell, B-cell and NK-cell markers in the 52 septic shock patients reported in our article [4].

Receiver operating characteristic curves were built for each phenotypic variable. The sensitivity and specificity of each variable to predict the real outcome was thus obtained [5]. The variables with higher sensitivity values were selected and combined to create multiple variable combinations or masks. The mask with the highest sensitivity and specificity was selected to predict the outcome of these patients.

According to this methodology we have found a set of five immunophenotypic variables (CD3⁺CD8⁺CD28⁺, CD3⁺CD8⁺CD45RA⁺CD45RO⁻, CD19⁺CD80⁺, CD56⁺CD69⁺, CD3⁺CD11A^{br}CD11B⁺) and their cutoff values (163, 114, 67, 114, 250 lymphocytes/ μ l, respectively) that are able to improve the prediction for outcome in septic shock patients to a sensitivity of 94% and a specificity of 100%. We therefore conclude that the immunophenotypic study of peripheral blood mononuclear cells is useful to predict the outcome of septic shock patients.

Competing interests

The authors declare that they have no competing interests.

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