

P2423 Predictors of multidrug-resistant *Pseudomonas aeruginosa* in neutropenic patients with bloodstream infection

Diego Fernando Viasus Perez¹, Pedro Puerta², Celia Cardozo^{*2}, Maria Suárez-Lledó³, Olga Rodríguez Nuñez², Laura Morata², Csaba Feher², Francesc Marco Reverte⁴, Mariana Chumbita², Francesc Fernández³, Gonzalo Gutiérrez³, José Antonio Martínez Martínez², José Mensa², Montserrat Rovira³, Jordi Esteve³, Alex Soriano², Carolina García Vidal²

¹ Health Sciences Division, Universidad del Norte, Colombia, ² Infectious Diseases Department, Hospital Clínic, Barcelona, Spain, ³ Hematology Department, Hospital Clínic, Barcelona, Spain, ⁴ Microbiology Department, Hospital Clínic, Barcelona, Spain

Background: Bloodstream infection (BSI) caused by multidrug-resistant (MDR) *Pseudomonas aeruginosa* (PA) in neutropenic patients is associated to high morbidity and mortality. We aimed to develop a prediction rules to identify MDR-PA BSI to rationalize the use of fast MDR-detection tools in blood cultures and optimize empirical treatments.

Materials/methods: BSI episodes were prospectively collected (2004- 2017). Two multivariate regression models were used to identify independent risk factors for MDR-PA at two different moments: i) once BSI was diagnosed due to positivity of blood cultures; ii) once PA was identified as the etiological pathogen. We constructed easy bedside scores to stratify patients into different risk groups for MDR-PA.

Results: From a total of 1194 consecutive febrile neutropenic patients with BSI, 190 (15.9%) had PA BSI and 70 MDR-PA BSI. Independent factors associated with MDR-PA BSI were stem cell transplant (OR 4.57), shock at onset (OR 10.35), pulmonary source (OR 6.23), prior use of antipseudomonal cephalosporin (OR 91.01) and piperacillin/tazobactam (OR 4.9), and BSI occurring during ceftriaxone treatment (OR 12.42). Figure 1 shows the prediction rule constructed according to the regression coefficients. The rule area under the ROC curve was 0.855 (95% 0.805-0.904), demonstrating a strong ability to predict MDR-PA at BSI diagnosis. Once PA was identified as the BSI causative agent, nosocomial acquisition (OR 7.13), hematological malignancy (OR 3.44), prior use of antipseudomonal cephalosporin (OR 3.82) and quinolones (OR 3.97), corticosteroid use (OR 2.92) and BSI occurring during quinolone (OR 4.88) and beta-lactam (OR 4.51) therapy were independently related with MDR-PA. Figure 1 detailed the constructed prediction rule. The discriminatory power of the clinical prediction rule, was 0.885 (95% 0.835-0.935), demonstrating a robust ability to predict the risk of MDR-PA BSI among patients with PA BSI.

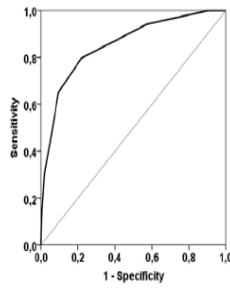
Conclusions: A simple rule allows for the stratification of febrile neutropenic patients according to the risk of MDR-PA BSI. This information is crucial to optimize resources for MDR diagnosis and empirical antibiotic treatments.

Figure 1. Prediction rule and ROC curve for predicting multidrug-resistant *P.aeruginosa* BSI when the diagnosis of bacteremia is performed (left side) and when the etiological identification of *P.aeruginosa* BSI is performed (right side).

Prediction rule

Variable	Points
Hematologic malignancies	1
Nosocomial-acquired BSI	1
Shock at onset of BSI	1
Pulmonary source of infection	1
Prior use of antipseudomonal cephalosporin	3
BSI occurring within carbapenems other than ertapenem treatment	1
BSI occurring within ceftriaxone treatment	2

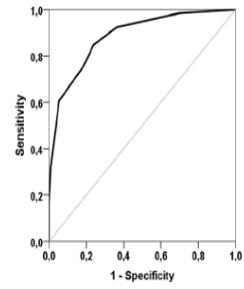
BSI, bloodstream infection



Prediction rule

Variable	Points
Nosocomial acquisition of BSI	3
Hematological malignancy	1
Corticosteroid use	1
Prior use of antipseudomonal cephalosporin	1
Prior use of quinolone	1
BSI occurring within β -lactam other than ertapenem treatment	1
BSI occurring within quinolone treatment	1

BSI, bloodstream infection



29TH ECCMID
13-16 APRIL 2019 AMSTERDAM, NETHERLANDS
POWERED BY M-ANAGE.COM

