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Risk-assessment may improve selection of patients with suspected sepsis for rapid diagnostics

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Background: Selection of high-risk subgroups of patients for rapid diagnostic testing is necessary for cost-effective use. We compared two strategies: selection using clinical sepsis criteria and selection based on risk-assessment by a predictive model.

Material/methods:

Setting and patients: Data were collected retrospectively for patients suspected of infection in the emergency ward, who had blood cultures (BC) drawn either in the emergency or infectious diseases wards at 7 hospitals in Emilia-Romagna, Italy from May 1 to December 31 2016, who also had other laboratory test data available. BCs were excluded if the associated data contained two or fewer infection variables, or if BC results were missing.

Selection for rapid diagnostic testing: Those eligible for a recent trial of the Iridica PCR/ESI-MS platform (Abbott Molecular) conducted by AUSL Romagna were included. In this trial, clinical staff were requested to select “high-risk” patients who fulfilled the Sepsis-3 definitions of sepsis or septic shock at the time of BC prescription.

From the same population SepsisFinder was used to select the same number of BCs with high risk of bacteraemia.

SepsisFinder uses a causal probabilistic network (CPN) to predict bacteraemia based on “infection variables” including C-reactive protein, neutrophil fraction, platelet count and bilirubin. The model is a “lightweight” version of a similar CPN which also included vital parameters (Ward 2016, PhD thesis).

Analysis: Bacteraemia rates were compared for the non-overlapping portions of the high-risk groups. Positivity rates for Iridica were compared for the portions of the clinically selected group that did and did not overlap with the model-based selection.

Results: 1414 BCs for 1322 unique patients were included. Following exclusion, the final dataset consisted of 1264 BCs for 1193 patients. Some bacterial species, primarily *viridans* streptococci and coagulase negative staphylococci, were considered to be contaminants. 408 cases (32.3%) had positive BC. After removal of contaminants, the bacteraemia rate was 26.3% (332/1264). 244 BCs were selected both in the clinical- and model-selected high-risk groups, with 62 common to both. We can define three high-risk groups: “Clinical-only”, “SepsisFinder-only” and “Both” with 182, 182 and 62 patients respectively (Figure). The rate of bacteraemia was significantly higher in “SepsisFinder-only” BCs compared to “Clinical-only” BCs (46.2% vs. 27.5%, p=0.0002). There was no significant difference between the “SepsisFinder-only” and “Both” BCs (46.2% vs. 45.1%, p=0.89). The Iridica positivity rate was 35.2% (86/244) after removal of 9 potential contaminants. The “Both” group had a significantly higher Iridica positivity rate than the “Clinical-only” group (51.6% vs. 30.2%, p=0.002).

Conclusions: The model identified BCs with a higher rate of bacteraemia than clinical selection. Similarly, the model may improve selection for rapid diagnostics: Iridica positivity rates were higher in the “Both” group than in the “Clinical-only” group.

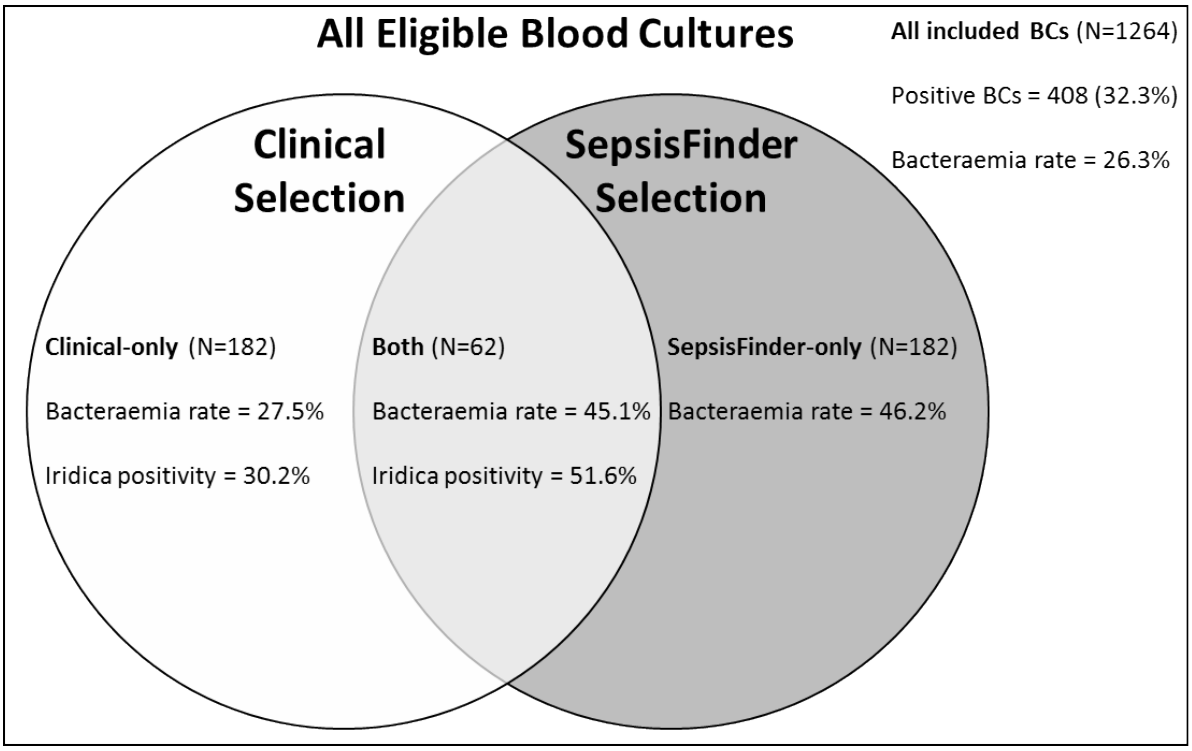

Figure: Patient selection, bacteraemia and Iridica positivity rates