cough (OR = 17.29, 95% CI: 1.09–274.92, P =0.043) were significantly associated with adrenal insufficiency with fever.

Table. Risk factors for adrenal insufficiency with fever using a multivariable logistic regression model

Table. Risk factors for adrenal insufficiency with fever using a multivariable logistic regression model

		Univariate analysis		Multivariate analysis	
	No.	OR (95% CI)	*P*-value	OR (95% CI)	*P*-value
Age >70					
No	38	1.00	-	-	-
Yes	68	1.25 (0.53-2.97)	0.606	-	-
Female sex					
No	42	1.00	-	1.00	-
Yes	64	0.37 (0.16-0.86)	0.020	0.32 (0.12-0.86)	0.024
Charlson's comorbidity index >2					
No	76	1.00	-	-	-
Yes	30	1.33 (0.55-3.25)	0.525	-	-
History of infectious diseases within 1 month					
No	84	1.00	-	-	-
Yes	22	2.08 (0.79-5.46)	0.135	-	-
History of surgical procedure within 6 months					
No	85	1.00	-	1.00	-
Yes	21	2.97 (1.11-7.91)	0.030	4.35 (1.23-15.39)	0.023
General weakness					
No	28	1.00	-	1.00	-
Yes	78	5.50 (1.53-19.78)	0.009	7.21 (1.71-30.37)	0.007
Headache					
No	97	1.00	-	1.00	-
Yes	9	2.93 (0.73-11.71)	0.128	4.11 (0.79-21.27)	0.092
Myalgia					
No	86	1.00	-	-	-
Yes	20	2.58 (0.96-6.99)	0.062	-	-
Cough					
No	100	1.00	-	1.00	-
Yes	6	0.08 (0.00-0.73)	0.025	17.29 (1.09-274.92)	0.043

Abbreviations: OR, odd ratio; CI, confidence interval

Conclusion. Approximately 30% of adrenal insufficiency presented fever. In patients with adrenal insufficiency and male sex, history of surgical procedure within 6 months, general weakness, and cough may be associated with presenting fever.

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1215. Evaluation of the Carba-R NxG Assay in a Global Challenge Set of Pseudomonas aeruginosa

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Session: P-55. New Approaches to Diagnostics

Background. Carbapenem-resistant *P. aeruginosa* (CRPA) is a growing clinical challenge. Carbapenemase production is particularly problematic due to high transmissibility and limited treatment options. Carbapenemase prevalence and diversity are largely driven by geography and thus testing spectrum will dictate utility in certain regions. The purpose of this study was to evaluate the performance of the research-use-only Xpert® Carba-R NxG (Carba-R NxG) and commercially available Xpert® Carba-R (Carba-R) in a global collection of *P. aeruginosa*.

Methods. The challenge set included 123 clinical *P. aeruginosa* isolates from 11 countries. Isolates were previously categorized via PCR or whole-genome sequencing. Carbapenemase classes tested include: VIM, IMP, NDM, SPM, KPC, and GES. Non-carbapenemase (non-CP) harboring isolates were also tested (negative control). Isolates were tested using the Carba-R NxG and the Carba-R per manufacturer instructions. Carba-R NxG testing was completed by Cepheid (Sunnyvale, CA) blinded to genotype. Test performances were tabulated for each assay by carbapenemase class.

Results. Both assays gave negative results for all non-CP isolates and positive results for all VIM, NDM, and KPC isolates. An improvement in IMP detection among isolates was observed (Carba-R NxG 100% vs. Carba-R 58% detection). All SPM and GES isolates, targets not present in the current Carba-R, were positive by Carba-R NxG. Two isolates harbored both VIM and GES, while a third isolate contained VIM and NDM. The Carba-R NxG identified both targets in all 3 isolates while the Carba-R was negative for both GES-containing isolates. **Table 1** provides the test performance of both assays. Overall, the Carba-R NxG successfully categorized 100% of isolates tested compared with 68% for its predecessor.

Table 1. Test performance of Carba-R NxG and Commercially Available Carba-R by Carbapenemase Class.

		Carba-R NxG [a]		Commercially Available Carba-R[b]	
Target	**Number of Isolates**	**Sensitivity**	**Specificity**	**Sensitivity**	**Specificity**
VIM	31	100% (89-100)	100% (95-100)	100% (89-100)	100% (95-100)
IMP	26	100% (87-100)	100% (96-100)	58% (37-77)	100% (96-100)
NDM	13	100% (75-100)	100% (97-100)	100% (75-100)	100% (97-100)
SPM	14	100% (77-100)	100% (97-100)	--[c]	--[c]
KPC	8	100% (63-100)	100% (97-100)	100% (63-100)	100% (97-100)
GES	14	100% (77-100)	100% (97-100)	--[c]	--[c]
Non-CP	20	--[c]	--[c]	--[c]	--[c]

[a] Carba-R NxG detects VIM, IMP, NDM, SPM, KPC, GES, OXA-48, and NMC/IMI
[b] Carba-R detects VIM, IMP, NDM, KPC, and OXA-48
[c] Not Determined

Conclusion. As the prevalence and diversity of carbapenemase-producing CRPA continues to expand, the Carba-R offers a rapid and sensitive assay to identify clinically relevant carbapenemase genotypes to inform infection prevention and therapeutic interventions. The Carba-R NxG will expand the current targets including SPM, GES, NMC/IMI, and IMP-subtypes, outside the previous testing spectrum, increasing the global utility of the test.

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1216. Benchmarking Published Gene Signatures for Robust Infection Classification

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Session: P-55. New Approaches to Diagnostics

Background. Host gene expression has emerged as a promising diagnostic strategy to discriminate bacterial and viral infection. Multiple gene signatures of varying size and complexity have been developed in various clinical populations. However, there has been no systematic comparison of these signatures. It is also unclear how these signatures apply to different clinical populations. This meta-analysis examined 19 published signatures, validated in 49 publicly available datasets for a total of 4750 patients. The objectives were to understand how the signatures compared to each other with respect to composition and performance, and to evaluate their performance in different patient subgroups.

Methods. Signatures were characterized with respect to size, platform, and discovery population. For each of the 19 signatures, we ran leave-one-out cross-validation to generate AUCs for bacterial classification and viral classification. We then applied dataset-specific thresholds to generate accuracies, pooling patients across datasets.

Results. Signature performance varied significantly with a median AUC across all validation datasets ranging from 0.55 to 0.94 for bacterial classification and 0.79 to 0.96 for viral classification. Signature size varied (1- 341 genes) with smaller signatures generally performing more poorly for both bacterial classification ($P < .001$) and for viral classification ($P = 0.02$). Viral infection was easier to diagnose than bacterial infection (85% vs. 80% overall accuracy, respectively; $P < .001$). Host gene expression classifiers performed more poorly in children < 12-years compared to those older than 12-years for both bacterial infection (77% vs. 83%, respectively; $P < .001$) and for viral infection (82% vs. 89%, respectively; $P < .001$). We did not observe differences based on illness severity as defined by ICU care for either bacterial or viral infections.

Conclusion. We observed significant differences among gene expression signatures for bacterial/viral discrimination, though these were not due to variations in the discovery methods or populations. Signature size directly correlated with test performance, which was generally better for the diagnosis of viral infection and in populations >12-years.

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