Supplemental File 1

Clinical cohort:

From October 2011 to March 2020, we prospectively enrolled a convenience sample of mechanically-ventilated patients with ARF in Medical Intensive Care Units (ICUs) at the University of Pittsburgh Medical Center. We excluded patients unable to provide informed consent or if they were mechanically ventilated for >72 hours prior to enrollment. Informed consent was provided by all participants in accordance with local regulations. The study was approved by the University of Pittsburgh Institutional Review Board (protocol STUDY19050099). Under the same study protocol, from April 2020 to October 2020, we continued enrollment of patients with ARF during the COVID-19 pandemic. During this period, we enrolled both mechanically ventilated patients with COVID-19 ARDS as well as patients with severe COVID-19 pneumonia and ARF managed with high flow nasal cannula oxygen or non-invasive mechanical ventilation in the ICU. We recorded baseline demographics, comorbidities, mechanical ventilation and laboratory variables, and calculated sequential organ failure assessment (SOFA) scores.

Biomarker measurements:

We collected blood samples upon enrollment and measured 10 host-response biomarkers shown to have validated associations with ARDS and/or sepsis with a customized Luminex assay (R&D Systems, Minneapolis) (1). Host-response biomarkers were classified into markers of innate immune response (IL-6, IL-8, IL-10, fractalkine, TNFR-1, suppressor of tumorigenicity-2 [ST-2]), epithelial injury (receptor of advanced glycation end-products [RAGE]), endothelial injury (angiopoietin-2), and response to bacterial infections (procalcitonin and pentraxin-3). We also measured 1-3-beta-D-glucan (BDG), a fungal cell-wall constituent shown to correlate with inflammatory biomarkers, using the commercially available Fungitell® Limulus Amebocyte Lysate

(LAL) assay (Associates of Cape Cod, Inc, East Falmouth, MA, USA) at the manufacturer's facility (2).

Subphenotypic classifications:

In the derivation cohort, we combined baseline data from all six clinical categories of acute respiratory failure (ARF), namely a) ARDS per Berlin criteria (3), b) at-risk for ARDS, based on presence of an identifiable lung injury risk factor upon enrollment but not fulfilling ARDS criteria, c) cardiogenic pulmonary edema from congestive heart failure (CHF), d) acute on chronic respiratory failure (e.g. acute exacerbation of chronic obstructive pulmonary disease [COPD]), e) intubation for airway protection, and f) "multifactorial" category including cases for which the committee could not reach consensus for clinical classification into any of the categories above.

In the combined data set of 498 patients with ARF, we applied latent class analysis (LCA). First, we estimated the optimal number of classes that best fit our patient cohort, as subphenotyping analysis has not yet been performed in this population. LCA has been applied to several recent ARDS cohorts with the goal to identify subgroups of patients defined by a specific group of variables without consideration of clinical outcome. We considered both continuous and categorical clinical and biomarker variables similar to those used in previous LCA-derived models in ARDS trials (Supplemental Table S2). Similar to prior studies we standardized continuous variables to a common z-scale (mean value of 0, standard deviation value of 1) and coded categorical variables as 0 and 1. Data that were highly co-linear (r>0.95) were excluded from the model (e.g. systolic blood pressure was included instead of mean arterial pressure). Prior to performing the final LCA, we examined each continuous and categorical variable for discriminatory value, and selected only variables that were found to be discriminatory for consideration in development in the LCA model. Non-discriminatory variables were removed (defined as not significantly different from 0; $p\geq0.1$). Categorical variables were also compared graphically via Fisher exact tests with non-discriminatory variables being removed. Based off of several prior studies(4, 5), we hypothesized that a two-class model would offer the best fit. Optimal fit was determined using 1) entropy to measure class separation (higher entropy values meaning better class separation), 2) a bootstrapped parametric likelihood ratio test with a level of significance at p<0.05, and 3) low frequency criterion for additional classes. Following selection of discriminatory variables (Table S1), a two class model vs. a single class model had a highly significant parametric likelihood ratio test (log-likelihood difference 1148, p<0.0001) and with entropy of 0.911. Addition of a third class did not improve entropy or the likelihood ratio and included a very small proportion of subjects in the third class (3.4%), considered clinically not useful, and therefore a two class model was considered as optimal fit for our dataset.

The continuous variables were graphically examined by plotting their standardized values to a common z-scale (mean of 0, standard deviation of 1). The continuous variables with higher discriminatory value can be viewed graphically in Supplementary Figure S3 at the extremes of distribution. LCA analyses were performed in MPlus 8.3(6).

We then developed a parsimonious logistic regression model based on a best subsets generalized linear model approach (*bestglm* R package) using Bayesian Information Criteria for selection of the minimal subset of the discriminatory variables that offered optimal predictions (7). We applied subphenotype classifications provided from the parsimonious model in the derivation cohort of patients with ARF to assess model performance, and then to the validation cohort to assess for differences in baseline clinical variables and outcomes between predicted subphenotypes. With an area under the curve (AUC) statistic, we examined for agreement between the predictions from our internal parsimonious model vs. an external predictive model by Famous et al in patients with ARDS that had utilized three biomarker variables (IL-8, bicarbonate, and TNFR-1) that were available in our dataset (8).

Clinical Outcomes:

Patients were followed prospectively for several clinical outcomes. These included 1) shock within the first week of enrollment (defined as need for vasopressors), 2) acute kidney injury (AKI, defined as absolute increase in serum creatinine concentration ≥0.3 mg/dL from baseline or a percentage increase in serum creatinine concentration of more than 50% within a 48 hour period; or oliguria of <0.5 mL/kg per hour for more than six hours), ICU length of stay, ventilatorfree days (VFD) to 28 days(9), time-to-liberation from mechanical ventilation, and 30- and 90-day mortality. For subjects who died prior to day 28, zero VFDs were assigned.

Statistical analyses:

All analyses were performed with R v.3.5.1 except for the LCA analysis which was performed in MPlus 8.3(6, 10). We calculated descriptive statistics for baseline variables. Subphenotype comparisons were made with Wilcoxon test for continuous variables and Fisher's exact test for categorical variables. For the longitudinal outcomes of survival and time-to-liberation from mechanical ventilation, we performed time-to-event analyses with Kaplan-Meier curves and comparisons with a log-rank test. To assess for effects of subphenotype on each of these outcomes, we built Cox-proportional hazard models. For Cox models we tested the proportional hazard assumption. All of these models were adjusted for age and clinical categories of ARF.

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Survival analysis

Subphenotypes - Hyperinflammatory - Hypoinflammatory

- Hyperinflammatory - Hypoinflammatory Subphenotypes

Competing risk likelihood ratio test for difference in time to liberation by subphenotypes: p=0.000031

Subdistribution hazard ratio (95% confidence interval) for time to liberation of hyperinflammatory patients adjusted for the competing risk of death: 0.56 (0.43-0.75), p= 0.000067

Hypo-inflammatory by both parsimonious models

Hypo-inflammatory by 3-variable parsimonious model only

Hyper-inflammatory by 3-variable parsimonious model only

Hyper-inflammatory by both parsimonious models

A.4-variable internal parsimonious model predictions

B.3-variable external parsimonious model predictions

