Uncontrolled innate and impaired adaptive immune responses are prognostic features of COVID-19 ARDS

Online supplement

Content

Methods

Non-COVID-19 ARDS patients

All patients with moderate/severe pneumonia-related ARDS were included consecutively with the following inclusion criteria: tracheal intubation and mechanical ventilation since less than 48 hours; pulmonary infection diagnosed less than 7 days before ICU admission ; bilateral pulmonary infiltrates on chest x-ray; a PaO₂/FiO₂ ratio \leq 200 mm Hg with a positive endexpiratory pressure (PEEP) \geq 5 cm H₂O. Non-inclusion criteria were as follows: age <18 years; pregnancy; chronic respiratory failure requiring long-term oxygen therapy; Child-Pugh C liver cirrhosis; lung fibrosis; immunosuppression (*i.e.*, HIV infection, active hematological malignancy or solid cancer receiving chemotherapy, corticosteroids therapy for more than 0.5 mg/kg/day since more than 4 weeks, organ transplant patients), SAPS II (Simplified Acute Physiology II score) >90, irreversible neurological disorders, patients with withholding/withdrawing of life-sustaining therapies and profound hypoxemia (PaO₂/FiO₂ <75 mm Hg). Seventy patients with non-COVID-19 ARDS were included during the study period, 36 of whom underwent at least two blood samples drawn at days 1-2 and days 4-6 time points, as depicted in the flow chart (Figure E1).

Study design and patients

ARDS patients received mechanical ventilation using a standardized protective ventilation strategy (1). Other treatments, including neuromuscular blocking agents, nitric oxide inhalation, prone positioning and venovenous extra-corporeal membrane oxygenation were administered depending on the severity of ARDS and according to National guidelines (2). The prevention of ventilator-associated pneumonia followed a multifaceted program (3). Sedation and mechanical ventilation weaning followed standardized protocols.

Data collection

Demographics, clinical and laboratory variables were recorded upon ICU admission, at samples collection time points and during ICU stay. Other recorded variables included the use of adjuvant therapies for ARDS, the need for hemodialysis or vasopressors, corticosteroids administration, and the number of organ failure-free days at day 28. The primary clinical endpoint of the study was day-28 mortality.

Flow cytometry analyses

Blood samples were collected within 48 hours of ICU admission (Days 1-2 sample) and 4 days thereafter (Days 4-6 sample) in EDTA tubes, shipped at room temperature and analyzed within 2 h. Immuno-staining was performed as follows: 100 μL of whole blood was incubated for 10 min at RT in the dark with the different combinations of the following conjugated-monoclonal antibodies: anti-CD4-PE (clone 13B8.2), anti-CD3-AA750 (clone UCHT1), anti-CD8-AA700 (B9.11), anti-CD38-PC5.5 (LS198-4-3) or isotype control, anti-CD279 (PD-1)-PC7 (clone PD1) or isotype control, anti-HLA-DR-PB (Immu-357) or isotype control, anti-CD14-ECD (RMO52) and CD45-Krome Orange (clone J33) (all reagents were from Beckman Coulter). Red-blood-cells were then lysed using VersaLyse Solution (Beckman Coulter) according to the manufacturer's instructions. Washed samples were immediately acquired on a 10-multicolor Navios flow cytometer (Beckman Coulter) and analyzed with the Kaluza 2.1 software (Beckman Coulter).

Independent T and B cell counts were performed using standardized procedures. For non COVID-19 patients, absolute cell counts were performed using FC500 cytometer (Beckman Coulter) and a routine bead‐based single platform technology according to the manufacturer instructions (All reagents and materials were from Beckman Coulter). For COVID-19 patients, T and B cell counts were performed using a fully automated AQUIOS cytometer. Of note, the two lymphocytes counts methods have an excellent correlation and agreement.

Monocytes, and lymphocytes were first gated on a side scatter-area (SSC-A) versus CD45 (the leukocyte common antigen) flow cytometry dot plots. Monocytes were defined as Side Scatter (SS) intermediate, CD45+ and CD14+ cells (Figure E2). Expression of HLA-DR was then analyzed (Figure E2, upper panel). T CD8+ lymphocytes were identified as CD45+ CD3+ CD8+ cells within the CD45+ SS low lymphocyte gate. Expression of HLA-DR, CD38 and PD-1 was then analyzed on T CD8+ lymphocytes (Figure E2, lower panel).

Measurements of serum cytokine concentrations

Blood samples collected at days 1-2, days 4-6 and days 8-12 for patients who still had ARDS criteria were immediately centrifuged for storage at – 80°C. Cytokines were measured at distance in serum inactivated for 20 minutes at 56°C using Luminex® multiplex bead-based technology (R&D Systems, Minneapolis, MN. USA) and a Bio-Plex 200® instrument (BioRad, Hercules, CA. USA), according to the manufacturers' protocols on serum diluted to 1/2. Laboratory technician who performed the assays was blinded to all clinical data. The following cytokines/chemokines were evaluated CCL2/MCP-1, CCL4/MIP-1β, CCL19/MIP-3β, CD40L, CXCL10/IP-10, FGF-basic, G-CSF, GRZ-B, IFN-β, IL-1α, IL-1ra, IL-3, IL-5, IL-7, IL-10, IL-13, IL-17A, PD-L1, TNF-α, VEGF, CCL3/MIP-1α, CCL11/Eotaxin, CCL20/MIP-3α, CX3CL1/Fractalkine, EGF, Flt-3L, GM-CSF, IFN-α, IFN-γ, IL-1β, IL-2, IL-4, IL-6, IL-

8/CXCL8, IL-12p70, IL-15, IL-33, TGF-α, TRAIL, CCL5/RANTES, IL-17E/IL-25. All samples, including those obtained from both COVID-19 and non-COVID-19 patients, were inactivated during 20 minutes at 56°C, as previously described (4). We analyzed cytokines/chemokines which displayed more than 80% of concentration values above the lower limit of quantification (n=19). For each of these analytes, extrapolated concentration values calculated by Bioplex Manager 6.1 sofware were taken into account and undetectable values were imputed to the lowest extrapolated concentration value.

Statistical analyses

Descriptive results are presented as means (\pm standard deviation [SD]) or medians ($1st$ -3rd) quartiles) for continuous variables, and as numbers with percentages for categorical variables. Log-transformation was applied to non-normally distributed variables, as assessed by graphical methods and the Shapiro-Wilk test. Boxplots were plotted to illustrate differences in cytokines levels according to time and COVID-19 status.

Bivariate correlation analyses between cytokines and COVID-19 status were conducted by computing Spearman and biserial correlation coefficients for continuous-continuous and binary-continuous variables correlations, respectively. A correlation network plot was built from those results to graphically illustrate relationships.

Unadjusted between-groups comparisons between conditions (COVID-19 *versus* non-COVID-19) and outcome (alive *versus* dead at ICU day-28) were performed using Mann-Whitney tests for continuous variables, and Chi² or Fisher's exact tests for categorical variables, as appropriate. Within-groups comparisons between baseline and subsequent assessments were conducted using paired Wilcoxon signed ranks test. Association between cytokines, other covariates and final outcome were further assessed after systematically adjusting for age and SOFA score, using logistic regression (categorical variables) and linear regression modeling (continuous variables) to compute adjusted odds ratios (95% confidence interval) and adjusted means (±standard error), respectively.

Longitudinal analyses were finally performed to assess the temporal evolution of cytokines levels over a 12-day period using mixed effects linear regression models to account for the correlation between repeated data over time. Models included a COVID-19 status variable, a time variable and an interaction term COVID-19*time to test for differences in average cytokines levels between COVID-19 and non-COVID-19 patients, significant positive or negative trends over time (slopes), and differentiated trends over time between COVID-19 and ARDS patients.

Two-tailed p-values < 0.05 were considered statistically significant, applying Benjamini-Hochberg correction for test multiplicity in correlation analyses. Analyses were performed using Stata V16.0 statistical software (StataCorp, College Station, TX, USA), R 3.6.3 (R Foundation for Statistical Computing, Vienna, Austria; *corrplot* and *qgraph* packages) and GraphPad Prism v8.0 (GraphPad Software, San Diego, CA, USA).

References

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- 4. Darnell MER, Taylor DR. Evaluation of inactivation methods for severe acute respiratory syndrome coronavirus in noncellular blood products. *Transfusion* 2006;46:1770–1777.

Results

Table E1**. Results from longitudinal analysis by mixed effects linear regression model assessing the association between COVID-19 status, time elapsed since hospital admission and serum cytokines concentrations**

Results are p-values from mixed effects linear regression model, testing for a differences in average cytokines levels between COVID-19+ and ARDS patients, b significant positive or negative trends over time (slopes), and c differentiated trends over time between COVID-19 and ARDS patients.

Table E2**. Results from longitudinal analysis by mixed effects linear regression model assessing the association between COVID-19 status, time elapsed since first symptoms of disease onset (COVID-19 or non-COVID-19) and serum cytokines concentrations.**

Results are p-values from mixed effects linear regression model, testing for a differences in average cytokines levels between COVID-19+ and ARDS patients, b significant positive or negative trends over time (slopes), and c differentiated trends over time between COVID-19 and ARDS patients.

Table E3. Serum cytokines concentrations according to the microbiological etiology of acute respiratory distress syndrome (non-COVID-19 viral or bacterial/non-documented (ND) or COVID-19.

Results are presented as median (1st-3rd quartiles); **bolded** results are statistically significant at the p<0.05 level; ^a Missing data, n=5; ^b Missing data, n=3; ^c pvalues come from the Kruskal-Wallis test; ^b Post-hoc comparisons were performed when the global p-value was <0.05 and corrected for multiple testing using *the Bonferroni correction.*

Table E4**. Clinical and biological variables associated with day-28 mortality in COVID-19 patients and non-COVID-19 patients**

Results are presented as median (1st-3rd quartiles); bolded results are statistically significant at the p<0.05 level; a P-values comes from the Mann-Whitney

test; b Missing data, n=3 for COVID-19 patients and n=5 for non-COVID-19 patients; c obtained from naso-pharyngeal swabs

Results are presented as median (1st-3rd quartiles) or means±standard deviation (SD) or ±standard error (SE). as appropriate;

bolded results are statistically significant at the p<0.05 level; ^aResults from linear regression modeling (continuous variables) or

logistic regression modeling adjusting for age and SOFA score; ^bobtained from naso-pharyngeal swabs

Figure E1**.**

Flow chart of patients with non-COVID-19 acute respiratory distress syndrome (ARDS) included between January 2014 and December 2018. CRD: chronic respiratory disease; LTO: long-term oxygenotherapy; OTI: oro-tracheal intubation; WH/WD of LST: withholding/withdrawal of lifesustaining therapies.

Figure E2**.**

Flow cytometry gating strategies. Monocytes, and lymphocytes were first gated on a side scatter-area (SSC-A) versus CD45 (the leukocyte common antigen) flow cytometry dot plots. Monocytes were defined as Side Scatter (SS) intermediate, CD45+ and CD14+ cells (Figure E2). Expression of HLA-DR was then analyzed (upper panel). T CD8+ lymphocytes were identified as CD45+ CD3+ CD8+ cells within the CD45+ SS low lymphocyte gate. Expression of HLA-DR, CD38 and PD-1 was then analyzed on T CD8+ lymphocytes (lower panel).

Figure E3**.**

Flow cytometry analysis of lymphocytes subsets and monocytes in COVID-19 (sky blue) and non-COVID-19 patients with viral (red) or bacterial/non-documented (ND) acute respiratory distress syndrome at days 1-2 of intensive care unit admission. A) Blood T CD4+ lymphocytes counts; There was no significant effect of ARDS group by the Kruskal-Wallis test (p=0.454); B) Blood T CD8+ lymphocytes counts; There was a significant effect of ARDS group by the Kruskal-Wallis test (p=0.021) but no significant between group differences on *post-hoc* comparisons; C) Blood B (CD19+) lymphocytes counts; There was a significant effect of ARDS group by the Kruskal-Wallis test (p=0.007) and a significant between group (viral *vs* COVID-19) difference on *post-hoc* comparisons (p-value comes from the Dunn's test); D) Percentage of T CD8+ CD38+ HLA-DR+ lymphocytes; There was no significant effect of ARDS group by the Kruskal-Wallis test (p=0.850); E) Percentage of T CD8+ PD1+ lymphocytes; There was a significant effect of ARDS group by the Kruskal-Wallis test (p=0.004) and a significant between group (viral *vs* COVID-19) difference on *post-hoc* comparisons (p-value comes from the Dunn's test); F) Percentage of HLA-DR+ monocytes; There was a significant effect of ARDS group by the Kruskal-Wallis test (p<0.0001) and a significant between group (viral *vs* bacterial/ND and bacterial/ND vs COVID-19) difference on *post-hoc* comparisons (p-value comes from the Dunn's test); Horizontal lines indicate the median value and the $1st$ and $3rd$ tertiles.

Figure E4**.**

Evolution of serum concentrations of cytokines over time in patients with COVID-19 (thick red lines) and non-COVID-19 (thick blue lines) acute respiratory distress syndrome. The y-axis represents serum concentrations expressed in (log) ng/mL. Individual trajectories of COVID-19 (thin red lines) and non-COVID-19 (thin blue lines) patients are represented in the background; The x-axis represents the time elapsed since symptoms onset.

Figure E5**.**

Correlation matrix of serum cytokines concentrations, age and SOFA score in patients with COVID-19 (n=38) and non-COVID-19 (n=36) ARDS. A) Spearman and biserial correlation coefficients are provided for continuous-continuous and binary-continuous variables correlations, respectively, with positive (blue) and negative (red) correlation coefficients indicating statistical significance at the p<0.05 level after Benjamini-Hochberg correction for test multiplicity; B) Spearman and biserial correlation coefficients are provided for continuous-continuous and binary-continuous variables correlations, respectively, with p-values indicated as follows: * p<0.05, ** p<0.01, *** p<0.001, **** p<0.0001.

COVID-19 $GN-CSF$ CX3CL1 **CCL19 CCL20** CCL4 VEGF CCL₂ CCL5 SOFA CCL₃ L1ra 15 \overline{L} 10 $\frac{1}{2}$ Fit₃ Age $\frac{8}{1}$ ڡ \overline{u} 1 EGF -0.32 -0.35 0.29 0.25 0.69 -0.4 0.64 **SOFA** 0.49 0.36 0.36 0.28 0.28 0.51 0.28 0.3 0.8 CCL₂₀ -0.31 0.41 0.37 0.33 0.62 0.66 0.53 0.54 0.72 0.67 0.36 0.27 0.25 **IL15** 0.34 0.25 0.35 0.35 0.46 0.67 0.26 0.36 0.29 0.63 0.6 0.37 0.6 IL6 0.37 0.34 0.39 0.41 0.4 0.48 0.62 0.46 CX3CL1 0.39 0.45 0.28 0.31 0.24 0.43 0.43 0.43 $0.5\,$ 0.25 0.4 FIt₃ 0.25 0.53 0.53 0.32 0.56 0.36 0.26 IL1ra 0.45 0.45 0.44 0.37 0.43 0.42 0.39 0.28 0.62 0.2 CCL19 0.32 0.45 0.42 0.33 0.47 0.43 0.42 CCL₄ 0.34 0.42 0.38 0.36 $0.32 \begin{array}{|l} 0.61 \end{array}$ 0 **VEGF** 0.32 0.3 0.29 $0.48 \quad 0.32$ CCL₂ 0.48 0.47 0.52 0.5 0.38 0.37 -0.2 IL₈ 0.53 0.34 GM-CSF 0.29 0.35 -0.4 **IL10** 0.35 $IP10$ 0.29 0.35 -0.6 CCL₃ 0.39 Age -0.8 IL7 0.42 CCL₅ 0.33

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