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# **ORIGINAL ARTICLE**



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# Earliest histopathological changes in COVID-19 pneumonia with comprehensive gene expression analyses: A case series study

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**Summary.** Aims. In COVID-19 pneumonia, early detection and appropriate treatment are essential to prevent severe exacerbation. Therefore, it is important to understand the initiating events of COVID-19 pneumonia. However, at present, the literature about early stage disease has been very limited. Here, we investigated the earliest histopathological changes and gene expression profiles associated with COVID-19 pneumonia.

Methods and Results. We carefully examined 25 autopsied cases with different clinical courses. Dilation of capillaries and edematous thickening of the alveolar septa were found even in areas that macroscopically looked almost normal. Pneumocytes, histocytes/ macrophages, and vascular endothelial cells were immunohistochemically positive for tissue factor, which is an important early responder to tissue injuries. Comprehensive gene expression analyses revealed that those lesions presented differential profiles compared to those of control lungs and were associated with a significant upregulation of the lysosomal pathway.

Conclusions. Alveolar capillary dilation and edematous thickening may be the earliest histopathological change detected in COVID-19 pneumonia. Intensive investigations of such lesions may lead to an understanding of the initiating event of not only COVID-19 pneumonia but also of general diffuse alveolar damage.

**Key words:** COVID-19, Diffuse alveolar damage, Earliest histopathological change

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## Introduction

Coronavirus disease 19 (COVID-19) has rapidly spread worldwide since the end of 2019, causing more than 400-million documented cases and 5.7-million deaths to date (February 2022) (https://ourworldindata. org/coronavirus-data). One crucial feature of COVID-19 is its high mortality rate, which is substantially higher than that of the seasonal influenza (~15% versus ~0.1%) (Okudela et al., 2020). Although the newly developed vaccines supplied worldwide are conquering this pandemic, COVID-19 remains detrimental, causing a large number of deaths every day.

Throughout the COVID-19 pandemic, hundreds of autopsy case reports were published in the English literature (Okudela et al., 2020; Borczuk, 2021; Hooper et al., 2021; Maiese et al., 2021). Accumulating evidence has confirmed that the most critical pathological event is pneumonia, spatially and temporally intermittently inducing alveolar damage (Borczuk, 2021). Different pathological changes can be observed even in a single histological section, such as exudative lesions with hyaline membranes and proliferative lesions with pneumocytes, histocytes/macrophages, and myofibroblastic cell proliferation (Bosmuller et al., 2021; Maiese et al., 2021).

Several recent review articles mentioned temporal histological changes by dividing four main morphological stages: early, exudative, proliferative, and fibrotic. Generally, the exudative stage lasts from 3 to 7 days after the onset, followed by the proliferative and fibrotic stages for several weeks (Thompson et al., 2017; Borczuk, 2021; Bosmuller et al., 2021). However, descriptions of the early stage are very limited and are virtually based on incidental findings from a handful of cases including patients undergoing surgery for lung cancer (Pernazza et al., 2020; Tian et al., 2020; Bosmuller et al., 2021). The reports suggest that focal



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edema, pneumocyte damage and hyperplasia, macrophage desquamation, and endothelialitis/ capillaritis can be observed at this stage (Pernazza et al., 2020; Tian et al., 2020; Bosmuller et al., 2021). Early detection and treatment are necessary to prevent severe exacerbation; thus, it is essential to understand the initiating events.

In this study, we carefully examined a series of COVID-19 autopsy cases, specifically the temporal histopathological changes in alveolar damage, and revealed the earliest histopathological changes.

## Materials and methods

## Autopsy series

A total of 25 COVID-19 autopsy cases from Yokohama Citizens Municipal hospital were carefully examined histologically. Of them, the 5 cases suitable for this study (shorter clinical cause with early COVID-19 pneumonia) were chosen for morphometrical and gene expression analyses. Baseline information, such as age, gender, CT-severity score (Pan et al., 2020), results of PCR test, and essential autopsy results, of all the 25 COVID-19 cases and 5 control causes are summarized in Table 1. The Ethics Committees of Yokohama City University (approving number, A130926004/ B201200074) and Yokohama Citizens' Municipal Hospital (approving number, 20-11-05) approved this study.

## Conventional histopathological examination

Lung tissues were fixed by injecting 10% buffered formaldehyde solution through the bronchus and immersed in the solution for around 10 days. Consequently, tissues were paraffin-embedded and stained with hematoxylin and eosin, Elastica van Gieson, and Alcian blue periodic acid Schiff.

## RT-PCR analysis

RT-PCR on the secretory fluids (nasal swab, saliva, or sputum) for SARS-CoV2 was performed with LightMix (TIB MOLBIOL, Berlin, Germany). Cycle threshold less than 40 was judged as positive. RT-PCR on the autopsied lung tissues was according to the method described elsewhere (Yamaoka et al., 2021). Copy number more than 10 per  $\mu$ g was judged as positive.

## Immunohistochemistry

Tissue sections were incubated with a blocking solution (3% hydrogen peroxide/5% goat serum) to inhibit endogenous peroxidases and non-specific protein binding and were boiled in an antigen retrieval buffer. The sections were then incubated with the primary antibody against CD34 (mouse monoclonal antibody

clone QBEND/10.4.19, Immunotech, Marseille, France), SARS-CoV-2 nucleocapsid (mouse monoclonal antibody clone 001, Sino Biological, Beijing, China), tissue factor (TF) (rabbit polyclonal antibody, Santa Cruz, Santa Cruz, CA), cathepsin B (CSTB) (mouse monoclonal antibody clone CA10, Abcam, Cambridge, MA), followed by incubation with a horseradish peroxidaselabeled anti-mouse immunoglobulin antibody. Immunoreactivity was visualized using diaminobenzidine as a substrate, and the nuclei were lightly counterstained with hematoxylin.

## Morphometry

Glass slides were scanned using a virtual slide system (NanoZoomer slide scanner, Hamamatsu Photonics, Hamamatsu, Japan). Morphometrical analyses were performed using the freely published software NDP.view2 (Hamamatsu Photonics, Hamamatsu, Japan).

## Statistical analysis

The relationships between the diameters of the capillary and alveolar septa and the earliest alveolar damage were analyzed using the Wilcoxon/Kruskal-Wallis test. Statistical analyses were conducted using JMP (version 15.0; SAS Institute Inc., Cary, NC).

## Gene-chip microarray analysis

Total RNA was extracted using an RNeasy® Micro Kit (Qiagen, Venlo, Netherlands) and then subjected to comprehensive mRNA expression analyses with Clariome<sup>TM</sup> D assay (Thermo fisher scientific, Waltham, MA). We here examined 2 COVID-19 autopsied lung tissues and 2 control (autopsied lungs that looked almost normal histologically) for the comprehensive analysis. The Kyoto Encyclopedia of Genes and Genomes (KEGG) pathway analysis was performed using a public software (DAVID, Laboratory of Human Retrovirology and Immunoinformatics, Frederick, MD).

## Results

## Conventional histological examination

A representative case with a 10-day disease history is shown. Grossly, the cut surface of the lung showed a mosaic appearance. Some areas looked slightly graywhiteish, while the others looked almost normal. The macroscopic photograph and corresponding CT slice are shown in Fig. 1. Histologically, the slightly gray-white areas were exudative stage of alveolar damage with hyaline membranes (Fig. 2A (square 1), and 2B), and the areas that looked almost normal also showed faint but interesting histological changes, such as capillary dilation and edematous thickening of alveolar septa occasionally with a small number of assembled

Category, Case	/ Age (year-old)	Gender	Whole duration (from exacerbation) (days)	CT score (at day after onset) (day	RT-PCR Secretory fluid	Cause of death	Main comorbidity	Postmortem (hour)	RT-PCR Autopsy lung	IHC Autopsy lung	His	Jor Jor	tp Sample name
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COV005 COV010 COV011	) 74 ) 77 88	ΣΣĽ	14 (7) 25 (17) 20 (17)	18 ( 7) 23 ( 9) 14 ( 4)	+ + +	DAD / Respiratory failure DAD / Respiratory failure DAD / Respiratory failure	Acute monocytic jeukemia Acute monocytic jeukemia Bronchopneumonia mild Rheumatoid arthritis	 20 25	• + + +	+ • •	* * *	*	E4
	70 70 70 70 70 70 70 70 70 70 70 70 70 7		14 ( 5) 27 (17) 38 (10) 27 (24) 41 (35) 36 (30) 86 (70)	25 (14) AI 14 (11) 14 (18) 18 (4) 20 (7) 13 (7) 17 (8)	• + + + + + + +	DAD / Respiratory failure DAD / Respiratory failure	NIA AMI / Systemic thrombosis AMI / Sepsis AMI / Sepsis Sepsis / Prostatic cancer localized Sepsis / Lung cancer localized Rheunabid arthritis / Gashic cancer localiz Bronchona mid	zed 2.2 2.4 2.4 2.4 1.1 2.4 2.4 2.4 2.4 2.4 2.4 2.4 2.4 2.4 2.4	• + • + + + + •	+ · · · · · ·	* * * * * * *	*	E5
COV015 COV021 COV022 COV022 COV022 COV022 COV022	Mean 80	м м м м м м м м м м м м м м м м м м м	30 (79) 20 (15) 20 (15) 21 ( 9) 40 (36) 6 ( 4) 35 (29)	2 ( 2) 2 ( 2) 13 ( 5) 14 ( 7) 21 ( 5) 13 ( 3) 11 ( 7)		DAD / Respiratory failure DAD / Respiratory failure	Dionciropreumonia mud Cytomegalovirus infection (adrenal glands) Sepsis / Systemic thrombosis Sepsis / Sigmoid colon cancer localized N/A Sepsis / Systemic thrombosis Bronchopneumonia severe Bronchopneumonia mild	8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8	, + + + + , + ,	+ . + .	* * * * * * *	*	ß
Control CTL001 CTL002 CTL003 CTL004 CTL005	75 77 74 74 70 Mean 77	н М. М. 1 0.7				FAR / Circulation failure AM / Circulation failure Parkinsonism / Respiratory failure ALS / Respiratory failure CRC / Cachexia	N/A N/A Emaciation / Bronchopneumonia mild Emaciation / Respiratory muscle atrophy Emaciation / Bronchopneumonia mild	10 22 13 25			* * * * *	* * * * *	C1 C2 C2 C2 C5 C2

Table 1. Essential information of autopsy cases examined in the present study.

mRNA expression analysis; N/A, not applicable; \*, Subjected to the examinations; CT severity score was determined on the first CT image from the disease onset according to the criteria proposed by Pan et al., 2020. The two cases were examined postmortem by autopsy imaging (AI). The three were not determined (N/D) because of lack of full lung image. In SARS-Co-V-2 RT-PCR examination with secretory fluid (nasal swab, saliva, or sputum) samples, cases with cycle threshold less than 40 were judged as positive (+). In SARS-Co-V-2 RT-PCR examination with the autopsied lungs, cases with cycle threshold less than 40 were judged as positive (+). In SARS-Co-V-2 RT-PCR examination with the autopsied lungs, cases with cycle threshold less than 40 were judged as positive (+). In SARS-Co-V-2 RT-PCR examination were signal were judged as positive (+). In RARS-Co-V-2 RT-PCR examination with the autopsied lungs, cases with more than 3 (degenerated) cells showing unequivocally positive signal were judged as positive (+).

## The earliest change in COVID-19 pneumonia



**Fig. 1.** Representative view of a lung surface cut from a case with a 10-day disease history showing a mosaic pattern. Some areas look slightly gray-whiteish (arrows), whereas the others look almost normal **(A)**. Corresponding CT slice from autopsy imaging examination is shown **(B)**. The cervical spine (CS) and trachea (TR) show abnormal anteflexion due to contractile deformation. The dashed square in the panels A and B correspond to each other. Histological appearance in the dashed square is shown in Fig. 2.

Table 2. Result of KEGG pathway analysis on the upregulated genes in the earliest COVID-19 lesions.

Term	Index	Member (Gene Symbol)	FE	P Value
Lysosome	hsa04142	CTSA, ATP6AP1, LAMP1, GLB1, CTSK, GBA, LAPTM5, ARSB, CTSB	7.4	0.00002
Amoebiasis	hsa05146	COL1A1, SERPINB4, LAMA2, COL5A2, PIK3R3, LAMB1, CD14, RAB7A	7.5	0.00008
Glutathione metabolism	hsa00480	GSTM3, G6PD, GPX1, GPX3, ANPEP, GCLM	11.7	0.00013
ECM-receptor interaction	hsa04512	COL1A1, LAMA2, COL5A2, SPP1, TNC, COL6A3, LAMB1	8.0	0.00020
Central carbon metabolism in cancer	hsa05230	G6PD, TIGAR, PKM, PGAM1, PIK3R3	7.8	0.00355
Focal adhesion	hsa04510	COL1A1, LAMA2, COL5A2, SPP1, TNC, PIK3R3, COL6A3, LAMB1	3.9	0.00402
Biosynthesis of amino acids	hsa01230	PKM, PSAT1, PGAM1, TALDO1, BCAT1	6.9	0.00543
PI3K-Akt signaling pathway	hsa04151	COL1A1, LAMA2, COL5A2, DDIT4, SPP1, TNC, PIK3R3, COL6A3, LAMB1	2.6	0.01971
Renin-angiotensin system	hsa04614	CTSA, ANPEP, AGT	13.0	0.02131
Carbon metabolism	hsa01200	G6PD, PKM, PSAT1, PGAM1, TALDO1	4.4	0.02514

FE, Fold Enrichment and P value (Fisher's exact test) were calculated with a public software DAVID.



Fig. 2. Representative histopathological photographs from a case with a 10-day disease history. The scanning view panel **A** shows mosaic pattern, that is, there are different temporal phases of alveolar damage observed in each lobule. The dashed squares 1, 2, and 3 are zoomed-in and shown in panels **B**, **C**, and **D**, respectively. **B** shows the exudative phase, where thickened alveolar septa with hyaline membranes are observed. **C** shows the earlier exudative phase, where thickened alveolar septa with subtle exudate are observed. **D** shows the putative earliest phase, where capillary dilation and edematous thickening alveolar septa are observed. **E** is the control (autopsy lung from a case with unrelated disease), where no pathological change is observed. The insets are zoom-in views from the dashed circles in each panel.



Fig. 3. Immunohistochemical detection of SARS-Co-V2. A representative result from a case with a 10-day disease history is shown. The dashed squares 1, 2, and 3 in the scanning view panel A are zoomed-in and shown in the panels **B**, **C**, and **D**, respectively. SARS-Co-V2-infected cells are occasionally observed in both the overt exudative lesion (**B**, positive; **C**, negative) and putative earliest lesion (**D**, positive; **E** negative). The insets are zoom-in views from the dashed circles in each panel.



Fig. 4. Immunohistochemical visualization of alveolar capillaries stained with an anti-CD34 antibody. A representative result from a case with a 10-day disease history is shown. The dashed squares 1, 2, and 3 in the scanning view panel A are zoomed-in and shown in the panels B, C, and D, respectively. In the overt exudative lesion (B), alveolar capillaries are discontinuously ruptured. In the earlier exudative lesion (C) and putative earliest lesion (D), alveolar capillaries are dilated, compared to the control (E, autopsy lung from a case with unrelated disease). The insets are zoom-in views from the dashed circles in each panel.



Fig. 5. Representative results of morphometrical analyses. Capillary diameters and alveolar thicknesses in the putative earliest lesion (A) and control (B) are measured on CD34-immunostained sections. The insets are closed-up views from the dashed circles in each panel.

neutrophils and monocytes, and slight alveolar hemorrhage (Fig. 2A (square 2, 3), 2C, and 2D). These changes agreed well with the earliest putative tissue response in diffuse alveolar damage/acute respiratory distress syndrome (DAD/ARDS) (Thompson et al., 2017). SARS-CoV-2 were immunohistochemically detected in pneumocytes not only in exudative lesions, but also in these earliest lesions (Fig. 3). Thus, we hypothesized that this could be the earliest histopathological change in COVID-19 pneumonia, likely followed by pneumocyte desquamation and hyaline membrane exudation.

#### Immunohistochemical and morphometrical analyses

To confirm the changes in the alveolar capillaries, we performed immunohistochemistry for a vascular endothelial marker, CD34. To exclude the effect of postmortem congestion, we examined tissue sections from the ventral side of the upper lobe of the lung. The results made the changes clearer, as capillary lumens were found to be dilated (Fig. 4). Morphometric analyses objectively supported the capillary dilation, and also thickening of the alveolar septa (Fig. 5 and Fig. 6).

#### Immunohistochemistry for the early responders

To further support the significance of the earliest changes, we immunohistochemically examined these lesions for expression of pivotal factors involved in diffuse alveolar damage initiation, such as IL-6, TNF- $\alpha$ , IL-1B, and TF (Bokarewa et al., 2002; Thompson et al., 2017; Leisman et al., 2021; Subrahmanian et al., 2021) (data not shown). Among these, TF was mostly associated with these earliest lesions, where pneumocytes, histocytes/macrophages, and vascular endothelial cells were positive (Fig. 7).

## Comprehensive mRNA expression analysis

We also examined these earliest lesions for comprehensive gene expression. Significant changes in expression profiles of these lesions (Fig. 8A) were noted. The KEGG analysis on the upregulated genes whose levels showed 5-fold or more increase in both the two earliest lesions compared to the two controls revealed a remarkable association with the lysosomal pathway (Fig. 8B and Table 2).

Here, we immunohistochemically examined expression of CTSB, one member of the lysosomal pathway, and that confirmed its expression in histocytes/macrophages that were migrating into alveolar interstitium and lumina in these earliest lesions (Fig. 9).

## Discussion

Diffuse alveolar damage occurs through a variety of situations, such as acute exacerbation of chronic diffuse interstitial lung disease, terminal stage of malignancies, and severe infectious disease (sepsis) (Thompson et al., 2017). However, discerning the initiating histopathological event in these situations is challenging because of secondary events from multiple factors in a long clinical course, while in COVID-19 pneumonia, spatially and temporally intermittent alveolar damage occurs within relatively short periods (Borczuk, 2021; Bosmuller et al., 2021). Therefore, we consider COVID-19 pneumonia can be a useful material to investigate the initiating event of alveolar damage.



Fig. 6. Capillary diameters and alveolar thicknesses at 50 to 60 points each in putative earliest lesions from five COVID-19 cases (E1-E5) and in normal controls from five autopsy cases of unrelated disease (C1-C5). The values are shown as dot plots. Both capillary diameters and alveolar thicknesses are significantly larger in the earliest lesion. P values calculated with Wilcoxon/Kruskal-Wallis test are shown.



Fig. 7. Immunohistochemical expression of TF. A representative result from a case with a 10-day disease history is shown. The dashed squares 1, 2, and 3 in the scanning view panel A are zoomed-in and shown in the panels **B**, **C**, and **D**, respectively. In the overt exudative lesion (B), a positive signal is observed in pneumocytes, histocytes/macrophages, endothelial cells, and hyaline membranes. In the earlier exudative lesion (C) and putative earliest lesion (D), a positive signal is observed in pneumocytes, histocytes, histoc

We examined a series of COVID-19 autopsy cases and particularly focused on temporal histopathological changes. Upon investigating the cases, we found that slight capillary dilation and edematous thickening of the alveolar septa already occurred even in areas that looked almost normal macroscopically, where pneumocytes, histiocytes/macrophages, and endothelial cells were immunohistochemically positive for TF. Thus, we concluded that these could be the earliest detectable changes in histological examinations. Actually, previous studies have reported that focal edema, microscopic alveolar hemorrhage, pneumocyte damage and hyperplasia, macrophage desquamation are earlier changes preceding the exudation (Pernazza et al., 2020; Tian et al., 2020; Bosmuller et al., 2021). Our findings well agree with the previous observations. Also, we would like to mention that such earliest change may be detectable by CT examination, since our autopsy imaging demonstrated that the earliest lesion appeared as very light ground glass opacity. That supports previous reports showing that the CT severity scoring system benefits in prognosis (Chung et al., 2020; Pan et al.,



Fig. 8. Comprehensive RNA expression analyses from two earlier lesions (E1 and E2; two different COVID-19 autopsy cases) and two controls (C1 and C2; two different autopsy cases with unrelated disease). A dendrogram is described based on the Ward's hierarchical clustering method (A). E1 and E2 produce distant branches from C1 and C2. The KEGG pathway analysis based on genes whose levels showed 5-fold increase in E1 and E1 compared to C1 and C2 is shown (B). Potentially crucial pathways (horizonal axis) and their significant levels (Fisher's exact test; vertical axis, upper panel) and fold enrichment (vertical axis, lower panel) are presented.



Fig. 9. Immunohistochemical expression of CTSB. A representative result from a case with a 10-day disease history is shown. The dashed squares 1, 2, and 3 in the scanning view panel A are zoomed-in and shown in the panels B, C, and D, respectively. In both the overt (B) and earlier (C) exudative lesions, numerous histocytes/macrophages with strong positive signal are observed mainly in the alveolar lumina. In the putative earliest lesion (D), CTSB-positive histocytes/macrophages are detected mainly in the alveolar interstitium (arrows). In the control (E, autopsy lung from a case with unrelated disease), no positive signal is observed although a few resident alveolar macrophages occasionally show a weak signal. The insets are zoom-in views from the dashed circles in each panel.

2020; Brogna et al., 2021).

Here, we investigated gene expression profiles in these earliest lesions and found remarkable upregulation of pathways related to tissue and cell injury, such as lysosome degradation, and extracellular matrix-receptor interaction (Homolak and Kodvanj, 2020; Bugatti, 2021; Lerum et al., 2021; Sorsa et al., 2021; Syed et al., 2021). The finding confirmed the pathological significance of these lesions. Also, it is of great interest to investigate the potential roles of the differentially expressed molecules, as they are assumed to be initiators for alveolar damage. However, on the other hand, the number of samples examined here may not be enough for statistical analyses to draw firm conclusions. There are critical limitations, such as that the total number of autopsy cases is small due to technical difficulty, and that in most cases RNA quality is insufficient due to postmortem degradation. In our series, only two were possible to be subjected to mRNA expression analysis. Thus, accumulation of more autopsy cases with higher RNA quality and further molecular analysis are needed to clear the potential molecular basis in the initiating event of COVID-19 pneumonia.

In summary, we documented that capillary dilation, edematous thickening of alveolar septa could be the earliest histopathological changes in COVID-19 pneumonia. Hopefully, our findings will provide better understanding of not only COVID-19, but also general diffuse alveolar damage.

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Contribution of each author was as follows: Okudela-K wrote most parts of the manuscript; Okudela-K, Hayashi-H, Iwashita-H, and Hatayama-Y contributed to the pathological diagnoses. Yoshimura-Y, Sasaki-H, and Miyata-N collected the information of the patients and made clinical data base; Okudela-K performed the morphometrical analyses; Okudela-K, Kataoka-T, and Matsumura-M analyzed the expression profiles; Okudela-K, Tachikawa-N, and Ryo-A designed this study and suggested the content of the manuscript; Mitsui-H carried out the immunohistochemical analyses; Yamashiro-T examined CT images and gave severity scores.

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