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Single-cell oxygen saturation imaging shows that gas exchange by red blood cells is not impaired in COVID-19 patients

SARS-CoV-2 coronavirus infection is characterised by a marked inflammatory state and viral pneumonitis. A striking clinical feature is severe hypoxaemia, often in the presence of near-normal lung mechanics. Several hypotheses have been put forward to explain these findings,^{1,2} including pulmonary microvascular thrombosis, dysregulated hypoxic pulmonary vasoconstriction and dysfunctional gas transport by red blood cells (RBCs). Derangement in convective O₂ transport is an attractive hypothesis as this would explain why COVID-19 hypoxaemia is often refractory to supplemental oxygen. A controversial *in silico* prediction postulated that the virus attacks haemoglobin (Hb),³ and despite subsequent criticism,⁴ a number of hypotheses have emerged linking Hb with COVID-19, such as the association between thalassaemias or fetal Hb with disease severity.^{5–7} Notwithstanding these opinions, studies in China have confirmed modestly lower Hb levels in severe COVID-19^{8,9} and greater heterogeneity in terms of RBC volume, quantified as RBC Distribution Width-Standard Deviation (RDW-SD).¹⁰

In a recent letter to this Journal, Hb oxygen affinity was shown to be unaltered in a cohort of 14 patients infected with SARS-CoV-2.¹¹ However, steady-state measurements of

affinity cannot predict the kinetics of gas exchange by RBCs, which may become rate-limiting in COVID-19 due to impaired perfusion of the injured lung and inflammation-triggered RBC deformations that expand intracellular diffusion path length. Moreover, measurements on whole blood report an ensemble population average, which cannot resolve the presence of small subpopulations of dysfunctional RBCs, if these emerge in COVID-19. Indeed, given that RDW-SD increases in COVID-19, O₂ handling must be interrogated with cellular resolution.

We recently designed single-cell oxygen saturation imaging to assess O₂ unloading kinetics and O₂ storage capacity on a cell-by-cell basis.¹² We now applied this technique to study blood from COVID-19 patients at the John Radcliffe Hospital, Oxford, UK. Ten SARS-CoV-2-positive patients [9/10 confirmed by polymerase chain reaction (PCR) result, remaining patient diagnosed clinically] were recruited to this study through the Oxford GI Biobank (ethics 16/YH/0247). In half of the patients, blood was sampled within the first two weeks of diagnosis, and for the other half, sampling was in the subsequent fortnight. Three patients were asymptomatic healthcare workers, identified by voluntary PCR testing, and the

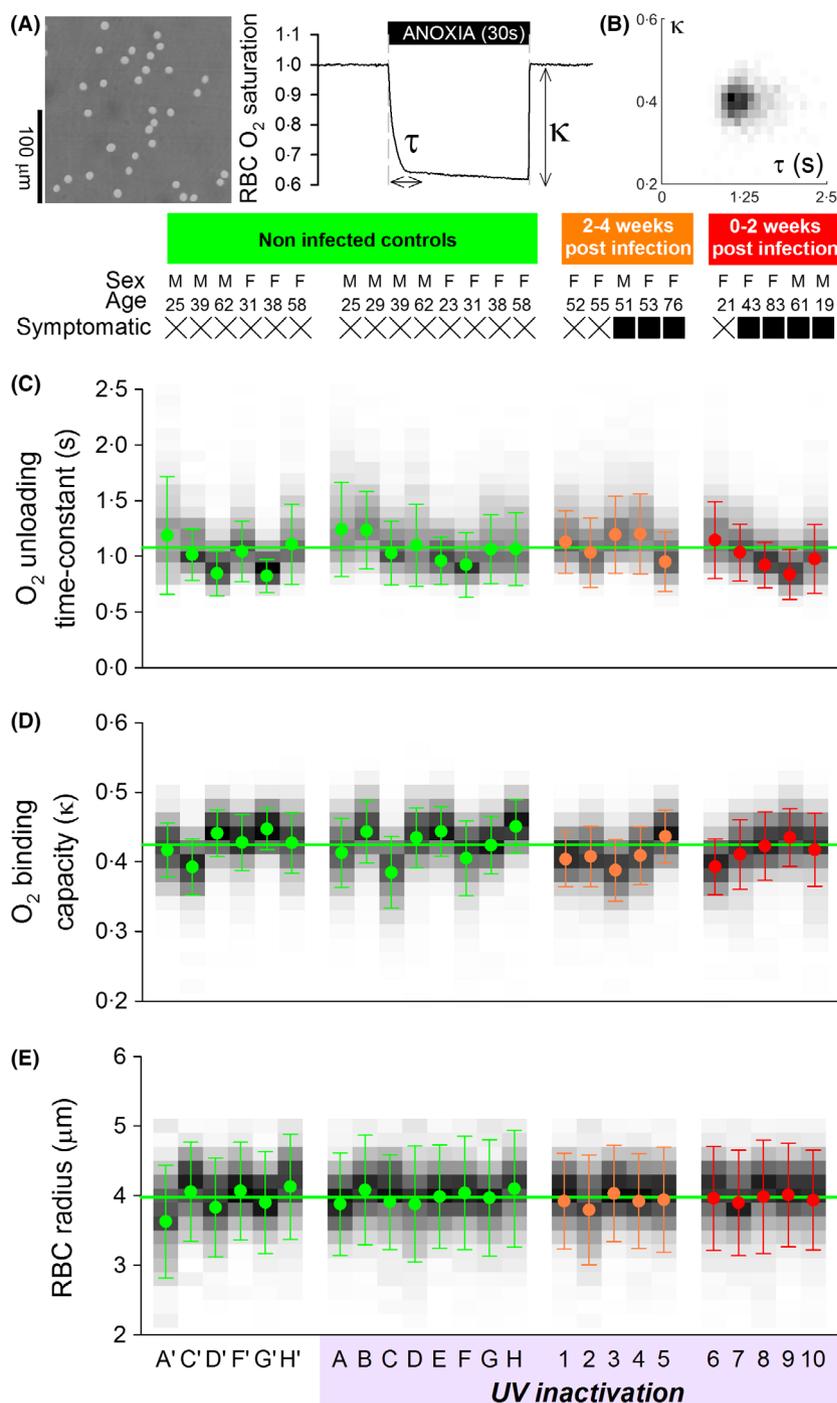


Fig 1. Single-cell characterisation of O₂ handling in red blood cells (RBCs) from patients with SARS-CoV-2 infection. (A) RBCs were loaded with CytoTracker Green and DeepRed to measure O₂ saturation during rapid and transient deoxygenation (N₂-bubbled solution, with 1 mmol/l dithionite). Protocol quantifies O₂ handling in terms of unloading time-constant (τ) and binding capacity (κ) in fresh venous blood sample from COVID-19 patients. (B) Cell-by-cell frequency distribution of τ and κ shows single population. Quantification of (C) τ , (D) κ and (E) radius in non-infected controls (A–H), and patients (1–10) tested positive for SARS-CoV-2 at two time points relative to infection. Viral inactivation by UV light in the presence of 10 mmol/l ascorbate was performed; based on findings from control blood, this treatment had no effect on measured parameters. Greyscale shading illustrates histogram distribution of each parameter. Data presented as mean, and error bars denote width of distribution at half maximal height. >1000 cells per sample.

remaining seven presented with COVID-19 symptoms. None of the patients had a history of RBC disorders or haemoglobinopathy. For reference measurements, healthy

donors were recruited. Venous blood samples were spun down (1200 RCF for 3 min at room temperature) to collect 10 μ l of red cells, which were re-suspended in 4 ml of HEPES-buffered

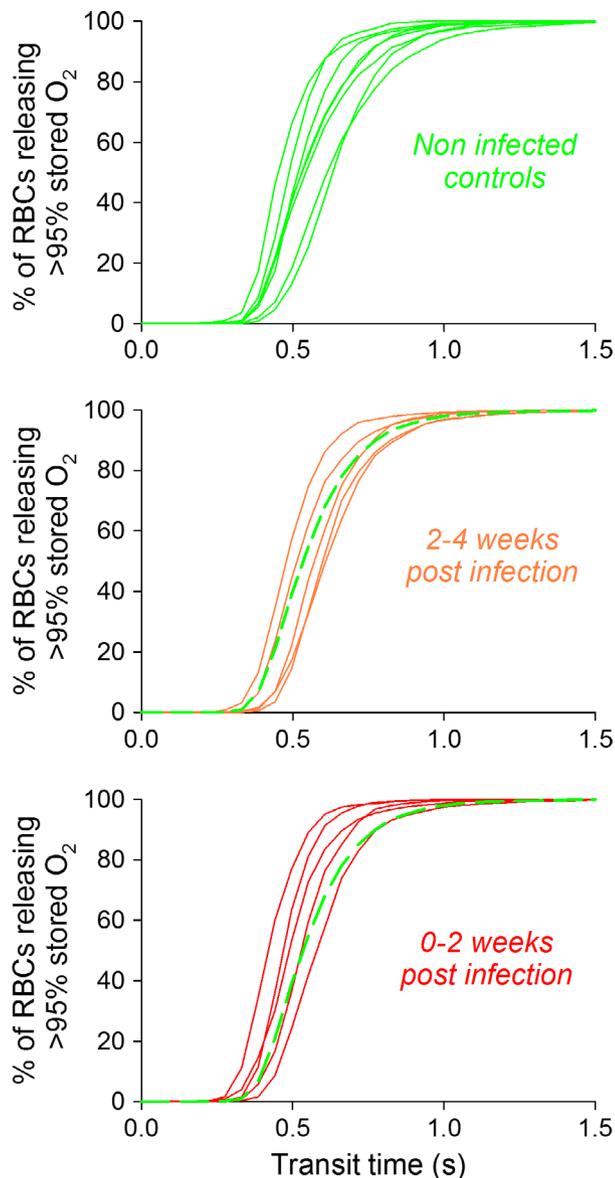


Fig 2. Fraction of red blood cells (RBCs) that deoxygenate by >95% during given transit time. SARS-CoV-2 infection does not affect O_2 release kinetics. Analysis of histogram distributions shown in Fig 1 using equations derived previously in Richardson *et al.*¹²

Tyrode solution containing 10 mmol/l ascorbate and then treated with UV-C light ($4000 \mu\text{W}/\text{cm}^2$ at a distance of 6 cm for 15 min, UVS-18 EL Series UV lamp, Analytik-Jena, Germany) to inactivate the virus. Ascorbate was included to protect Hb from oxidative damage by UV light. After re-suspending in fresh Tyrode solution (containing no ascorbate), cells were loaded with CellTracker DeepRed and Green (ThermoFisher Scientific, Waltham, MA, USA) to produce HbO_2 -sensitive fluorescence on a confocal imaging system.¹² Rapid solution switching between an oxygenated and deoxygenated

microstream triggered O_2 exchange, which was imaged at high temporal resolution for each RBC individually (Fig 1A). Repeating this several times yielded a measure of O_2 unloading kinetics (time constant τ), normalised O_2 binding capacity (κ) and cell radius in the horizontal plane. Data were analysed in terms of their frequency distribution (Fig 1B).

RBC τ , κ and radius were no different in COVID-19 patients, compared to controls (Fig 1C–E). There was also no evidence for a change in the distribution of these functional variables, arguing against the emergence of dysfunctional subpopulations over the course of infection. When expressed in terms of the fraction of cells that release >95% of stored oxygen in a given time (equivalent to capillary transit), there was no effect of SARS-CoV-2 infection on RBC O_2 handling (Fig 2).

Our findings add new evidence that SARS-CoV-2 infection does not lead to dysfunctional convective transport. The cause of hypoxaemia in COVID-19 patients is therefore unlikely to relate to impaired O_2 handling by RBCs, either as a result of direct coronavirus infection or a consequence of the inflammatory state. Our findings argue against a mechanistic link between Hb variants and disease outcomes.

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Author contributions

KCP, NR and PS performed the research. KD, SM and PS designed the research study. NR and PK contributed essential reagents or tools. KCP, KD and PS analysed the data. PS wrote the paper. The authors thank Dr Barbara Kronsteiner and Dr Emily Adland for coordinating blood sample supply.

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