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Plasma-induced nanoparticle aggregation for stratifying COVID-19 patients according to disease severity

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ABSTRACT

Stratifying patients according to disease severity has been a major hurdle during the COVID-19 pandemic. This usually requires evaluating the levels of several biomarkers, which may be cumbersome when rapid decisions are required. In this manuscript we show that a single nanoparticle aggregation test can be used to distinguish patients that require intensive care from those that have already been discharged from the intensive care unit (ICU). It consists of diluting a platelet-free plasma sample and then adding gold nanoparticles. The nanoparticles aggregate to a larger extent when the samples are obtained from a patient in the ICU. This changes the color of the colloidal suspension, which can be evaluated by measuring the pixel intensity of a photograph. Although the exact factor or combination of factors behind the different aggregation behavior is unknown, control experiments demonstrate that the presence of proteins in the samples is crucial for the test to work. Principal component analysis demonstrates that the test result is highly correlated to biomarkers of prognosis and inflammation that are commonly used to evaluate the severity of COVID-19 patients. The results shown here pave the way to develop nanoparticle aggregation assays that classify COVID-19 patients according to disease severity, which could be useful to de-escalate care safely and make a better use of hospital resources.

1. Introduction

Detection systems based on the aggregation of plasmonic nanoparticles have gained popularity due to the marked changes in color they produce, which can be evaluated by eye or with image processing software [1,2]. In these detection systems, the specific detection of a target molecule requires highly controlled assay conditions in order

avoid nanoparticle aggregation in the absence of the analyte. For example, it is well established that citrate-capped nanoparticles tend to aggregate in solutions containing highly concentrated ions or when buffered at low pH values [3]. The presence of biomolecules in these solutions may stabilize or destabilize the colloids depending on their concentration, and may also be modulated by other factors such as the pH or the presence of multivalent ions [4,5]. For instance, proteins may

Abbreviations: Alb, albumin; AST, aspartate aminotransferase; ALT, alanine aminotransferase; C_{1.75}, protein concentration 1.75 × 10⁻⁴ g·dL⁻¹; C_{PImin}, protein concentration at PI_{min}; Creat, creatinine; CRP, C-reactive protein; D-D, D-dimer; Ferr, ferritin; GGT, gamma-glutamyl transferase; Glu, glucose; Hb, hemoglobin; ICU, intensive care unit; INR, international normalized ratio (prothrombin time); LDH, lactate dehydrogenase; LSPR, localized surface plasmon resonance; MCV, mean corpuscular volume; Mono, monocytes; MPV, mean platelet volume; NIR, near-infrared; NLR, neutrophil-to-lymphocyte ratio; NTA, nanoparticle tracking analysis; PDW, platelet distribution width; PI, pixel intensity; PI_{min}, minimum value of pixel intensity; PI_{dil}, pixel intensity at plasma dilution 1:31250; PI_{1.75}, pixel intensity at C_{1.75}; PLR, platelet-to-lymphocyte ratio; RBC, red blood cells; RDW, red cell distribution width; TG, triglycerides; TotProt, total protein concentration; WBC, white blood cells.

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aggregate nanoparticles or protect them from aggregation depending on their concentration and isoelectric point, among other factors [6–8]. These observations have paved the way to develop a new family of sensors that detect changes in the composition of human plasma, which contains proteins and other solutes, using nanoparticle aggregation assays [9,10]. For example, it has been shown that plasma samples from patients with acute COVID-19 have a different composition compared to samples from patients with less severe symptoms [11]. If these differences resulted in a different nanoparticle aggregation behavior, they could be used to identify patients that require critical care. While this approach would not reveal changes in the levels of specific biomarkers, being able to classify patients according to severity with a single measurement could improve their management and make a better use of hospital resources [12].

In this article we show that, in a narrow plasma dilution range, gold nanoparticles aggregate depending on disease severity when exposed to samples obtained from COVID-19 patients (Fig. 1). Specifically, it will be shown that nanoparticles aggregate when the plasma was obtained from patients in the intensive care unit (ICU), but that, in the same conditions, do not aggregate so much when the plasma was obtained from patients that had been discharged from the ICU and were recovering in a hospital ward. Control experiments will demonstrate that plasma proteins are key to trigger the aggregation of the citrate-capped nanoparticles. Our method differs from previous approaches based on probing complex samples with colorimetric arrays of nanoparticles in that we use a single test to query the composition of the sample. Previously, a battery of nanoparticle aggregation conditions such as pH values, ionic strength, and surfactants, among others, were used to create an array of assays [10,13–19]. This yielded a color pattern that was related to the composition of the sample. Instead, we dilute the sample so that the total protein concentration is the same, and then query if nanoparticles aggregate or not with a single test consisting of adding the diluted sample to the nanosensors. While our approach provides no information about the identity of specific proteins in the sample, the test output is a single value, which makes it easier to interpret the results and to correlate them with other clinical variables. It will be shown that the test results have an excellent correlation with prognosis biomarkers that have been shown to be dysregulated in severe COVID-19 patients. The ability to classify hospitalized patients according to disease severity and inflammatory status with a single colorimetric test could be useful to plan hospital resources as well as to guide the de-escalation of patient care, which have been key issues during the management of the COVID-19 pandemic.

2. Material and methods

2.1. Nanoparticle synthesis

Citrate-capped gold nanoparticles with a diameter around 40 nm

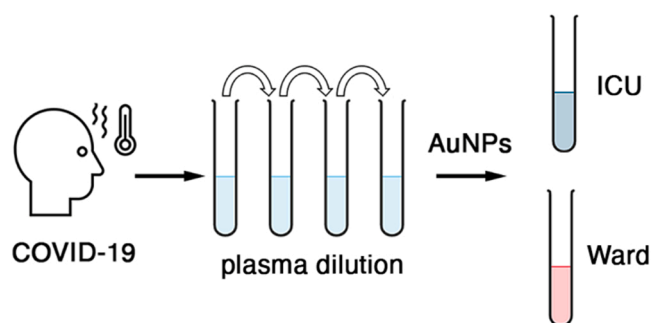


Fig. 1. Schematic representation of COVID-19 severity evaluation with plasma-induced nanoparticle aggregation. Probing a well-defined plasma dilution with gold nanoparticles generates a colorimetric signal associated to disease severity.

were synthesized using the Turkevich method [7]. Briefly, 49 mg gold (III) chloride trihydrate dissolved in 1 mL of Milli-Q water was added to 250 mL boiling Milli-Q water (final gold concentration 0.5 mM) and then sodium citrate was added to a final concentration of 0.75 mM for 15 min while vigorously stirring. The resulting gold nanoparticles were let to cool down at room temperature and then stored at 4 °C until used.

2.2. Sample dilution protocol

Serial dilutions of plasma samples in Milli-Q water were obtained as follows. The first working dilution involved diluting plasma 10^4 times. This was obtained using a 10-fold dilution series starting with 5 μ L of plasma. Samples were then further diluted in the range between 1:250000 and 1:25000.

2.3. Nanoparticle assays

Nanoparticle assays were performed in 96-well plates (Thermo Scientific) previously blocked with 2 % PBS-BSA for 90 min at 37 °C followed by rinsing 5 times with Milli-Q water. Each assay involved mixing 100 μ L of nanoparticles with 100 μ L of diluted plasma. The final nanoparticle concentration was 0.105 nM (Fig. S1). Pictures were taken 20–30 s afterwards using a homemade visible light transilluminator (Figs. S2 and S3). Pictures were taken with a dedicated 5MP Raspberry Pi camera module with Omnivision OV5647 CMOS sensor (model CMT-5MP-RP-OV5647-X010). The camera was controlled with a single board computer (Raspberry Pi Zero WH) and programmed to automatically upload images to a database at the push of a button. Extinction spectra were collected with a PowerWave HT plate reader (Biotek).

2.4. Plasma samples

Blood samples from patients admitted to the ICU were collected in vacuum tubes containing ethylenediaminetetraacetic acid (EDTA) as anticoagulant. Twenty samples were collected from SARS-CoV-2-positive patients admitted to the ICU for less than 10 days, whereas 19 samples originated from patients already discharged from the ICU (ward patients). Gender distribution was similar across ICU and ward cohorts, with 30% and 36.8% females respectively (Fisher's exact test p -value=0.74). Patients' demographic and clinical variables at the time of sampling are provided in Table S1. All samples were collected after informed consent was obtained from the patient or a family member. The study was conducted according to the ethical guidelines of the 1975 Declaration of Helsinki (Ethics and Scientific Committee approval IB 4251/20 PI). Platelet-free plasma samples were obtained by following a double spin cycle. Briefly, whole blood samples were centrifuged at 1500 g for 10 min and then the resulting plasma samples were transferred to new tubes and centrifuged at 2500 g for 15 min. Samples were stored at -80 °C in the Biobank IdISBa and CIBERES Pulmonary Biobank Consortium (integrated in the Spanish National Biobanks Network). In Fig. 5, the total protein concentration was determined in plasma samples diluted 1:2000 using a Bradford assay, whereas albumin levels in samples diluted 1:200,000 were determined with an ELISA test (reference RAB0603 purchased from Sigma-Aldrich).

Experiments with deproteinized plasma samples were addressed after conducting the following deproteinization protocol. Briefly, plasma samples obtained from 3 ICU and 3 ward patients were diluted 1:100 in Milli-Q water (final volume of 500 μ L). These pre-diluted samples were incubated in a bath at 90 °C for 10 min and then centrifuged at 3400 g for 5 min. Next, 400 μ L of the deproteinized supernatants was filtered using Amicon® Ultra-0.5 centrifugal 10 K filters (Millipore) following the manufacturers' instructions.

2.5. Data analysis

The pixel intensity in images was evaluated by quantifying the “a”

channel in the L*a*b color space in the region of interest with Adobe Photoshop. Statistical analysis was performed using GraphPad Prism software. The Mann-Whitney test was used to assess differences between colorimetric signals yielded by plasma samples from ICU and ward patients. A p value < 0.05 was considered statistically significant. Principal component analysis was done to evaluate relationships between patients' clinical variables and colorimetric signals.

3. Results and discussion

The aggregation of gold nanoparticles in a solution that contains proteins depends on the protein concentration, among other factors (Fig. 2A). Therefore, we first endeavored to study the impact of the protein concentration on the aggregation of gold nanoparticles (40 nm diameter). To this end, we serially diluted plasma samples and then

added nanoparticles at the same final concentration. Changes in the state of aggregation of the colloids were observed in the dilution range between 1:2,500,000 and 1:25,000. Fig. 2B shows a representative example of the results obtained from an ICU patient that had an initial total protein concentration value of 8 g·dL⁻¹. In the proposed dilution range, when the concentration of proteins increases from 0 to 1.3×10^{-4} g·dL⁻¹ the color of the colloidal suspension changes from mauve to blue and gray, which indicates that the nanoparticles aggregate (Fig. 2B). In Fig. 2C, extinction spectra taken in this concentration range show that the localized surface plasmon resonance (LSPR) at 530 nm decreases and a new LSPR appears at lower wavelengths, which demonstrates that the nanoparticles are clustering together. This was further supported using nanoparticle tracking analysis (NTA) (supporting Fig. S4). In this concentration range, protein adsorption disturbs the homogenous distribution of negative charges around the colloids and destabilizes them,

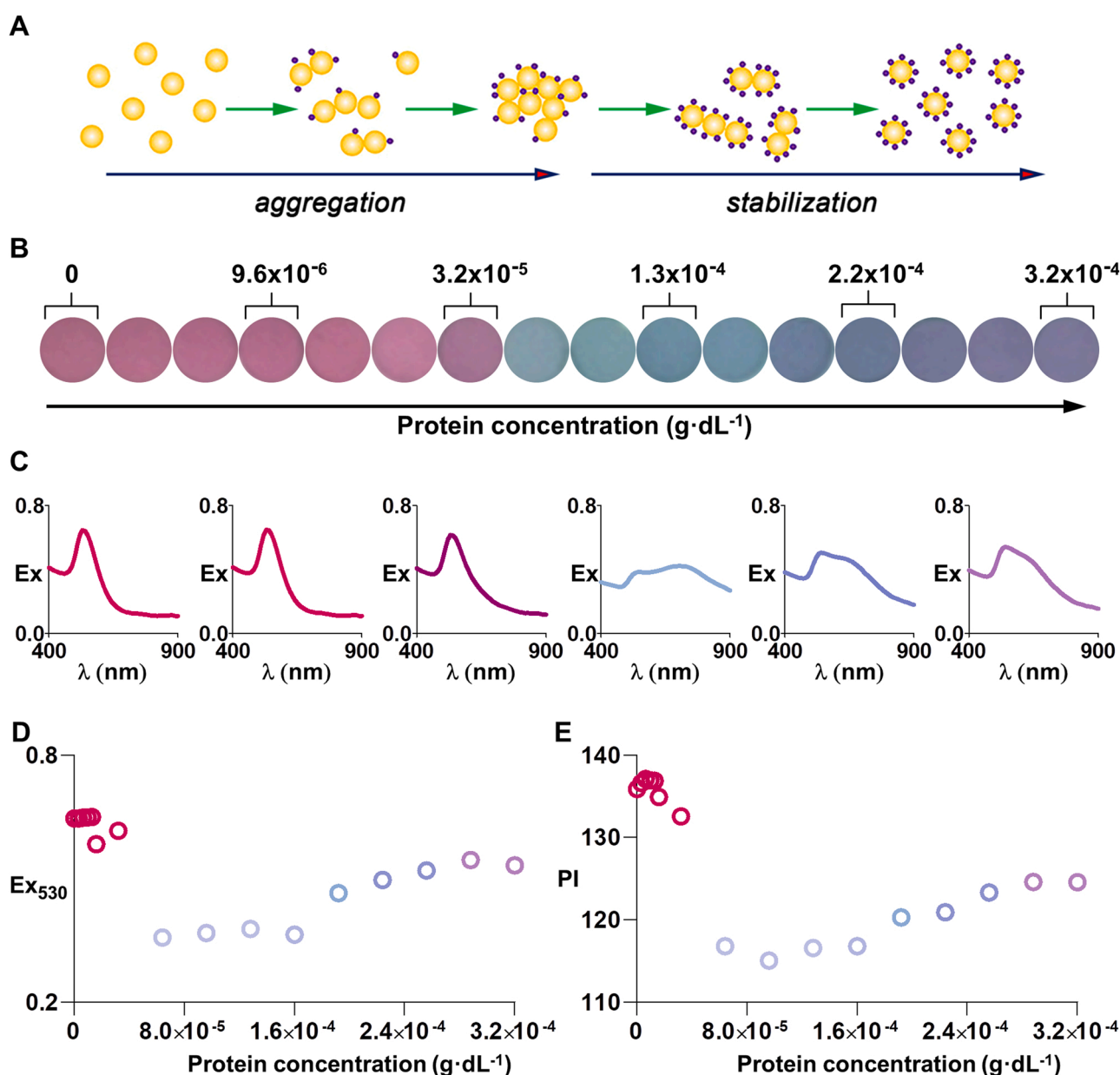


Fig. 2. Representative example of plasma-induced nanoparticle aggregation generated with a sample from a critical patient; A) Schematic representation of the impact of adding proteins (purple dots) at different concentrations to gold nanoparticles (yellow dots); B) Photographs of the colloidal suspensions after adding fifteen decreasing dilutions of a sample from a critical patient with an initial total protein concentration value of 8 g·dL⁻¹ (superscripts indicate the protein concentration in diluted samples prior to nanoparticle addition in g·dL⁻¹) C) Extinction spectra of tests highlighted in panel B; D) Extinction at 530 nm (Ex530); and E) Pixel intensity (PI) as a function of the protein concentration prior to nanoparticle addition in diluted samples.

as schematically shown in Fig. 2A. When the protein concentration increases further the color of the suspension slowly transitions to blue and purple (Fig. 2B). The LSPR at 530 increases and the near-infrared LSPR progressively disappears, which demonstrates that nanoparticles are less aggregated (Fig. 2C). In this concentration range a protein corona is generated that stabilizes the colloids as depicted in Fig. 2A. Figs. 2D and 2E show the evolution of the extinction value at 530 nm, as well as the pixel intensity measured from photographs taken with a raspberry pi camera. Both parameters decrease as the

concentration of protein increases, and then slowly increase after achieving a minimum. These experiments demonstrate that the plasma-induced aggregation of gold nanoparticles depends on the degree of sample dilution, which changes the concentration of proteins and other solutes within it. Changes in nanoparticle aggregation can be monitored by measuring the pixel intensity of a photograph (densitometry), which in the future could be performed with a dedicated instrument or smartphone app [20,21].

After studying the impact of protein concentration on nanoparticle aggregation, we sought to compare the aggregation pattern of nanoparticles after adding diluted plasma samples from patients. Fig. 3 shows the variation of the pixel intensity obtained from 20 ICU patients (red trace), as well as from 19 ward patients that were recovering after staying in the ICU (black trace). The same dilution protocol was applied to all samples. Results were then represented as a function of the actual protein concentration in each plasma sample, which was determined the same day that the sample was collected. In this Figure, the average minimum value of pixel intensity (PI_{\min}) is lower for ICU patients than for ward patients. This means that diluted plasma samples from ICU patients aggregate nanoparticles to a larger extent than plasma samples from ward patients. The average protein concentration at PI_{\min} ($C_{PI_{\min}}$) is higher for ICU patients. This means that more concentrated proteins are required in order to achieve the highest level of aggregation compared to ward patients. Finally, the pixel intensity of ICU samples increases at a slower rate after PI_{\min} compared to samples from ward patients, which means that they stay highly aggregated in a larger range of protein concentrations. Due to this, the pixel intensity at a fixed total concentration value is lower for ICU patients than for ward patients in the range between 1×10^{-4} and 2×10^{-4} g·dL⁻¹. For example, the pixel intensity from ICU patients differs from ward patients in most cases when the protein concentration is near 1.75×10^{-4} g·dL⁻¹ (PI at $C_{1.75}$).

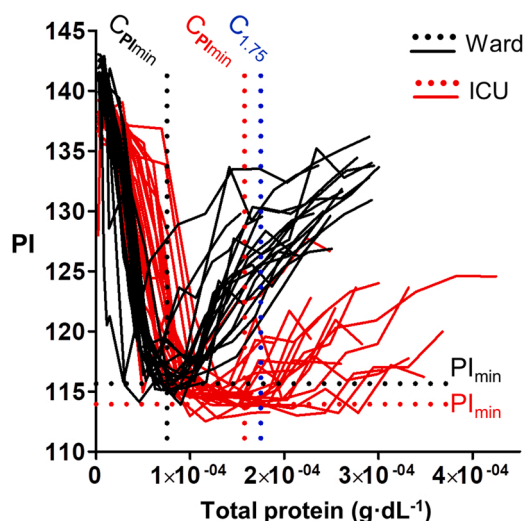


Fig. 3. Pixel intensity as a function of the protein concentration after adding diluted plasma samples from ICU (red) or ward patients (black) to gold nanoparticles. Dotted lines are a guide to eye. PI_{\min} : minimum value of pixel intensity; $C_{PI_{\min}}$: protein concentration at PI_{\min} ; $C_{1.75}$: indicates that the protein concentration is 1.75×10^{-4} g·dL⁻¹.

This.

result indicates that a single aggregation assay at a fixed protein concentration could be enough to identify whether a patient requires critical care or not. This makes our approach different from previous methods based on analyzing the color of nanoparticle suspensions upon exposure to an array of aggregating stimuli [13–19,10].

Fig. 4A–4C show the distribution of PI_{\min} , $C_{PI_{\min}}$, and the PI at $C_{1.75}$ ($PI_{1.75}$) obtained from ICU and ward samples. Statistically relevant differences are observed in all cases. Nevertheless, the parameter that better distinguishes both populations is $PI_{1.75}$ because test results overlap to a lesser extent than when plotting the other parameters. Indeed, only one ICU patient is miscategorized using $PI_{1.75}$, in agreement with our previous observation that a single test at a fixed protein concentration (1.75 g·dL⁻¹) can stratify patients according to severity. However, calculating $PI_{1.75}$ would require measuring the total protein levels first followed by readjusting the dilution protocol in order to test plasma samples at the same final concentration, which would be cumbersome. As an alternative, we investigated if plasma samples could be diluted following the same protocol and then analyze one dilution irrespective of the initial protein concentration. Fig. 4D shows that the PI at dilution 1:31250 (PI_{dil}) also differentiates both sample collections except for the same ICU specimen that overlapped with the ward samples when plotting $PI_{1.75}$. These experiments demonstrate that the color of a single test performed at a fixed dilution can be used to distinguish COVID-19 patients in the ICU from those that do not require intensive care anymore.

Next, we studied the origin of the differences in nanoparticle aggregation behavior observed in Fig. 2. We first checked whether changes in the initial protein concentration or in the concentration of the most abundant protein in plasma (albumin) could be the source of the observed differences. In Fig. 5A and 5B, ICU and ward patients do not have statistically different total protein levels, and there is no correlation between this parameter and PI_{dil} . Similarly, there is no significant difference between the albumin levels of both patient populations, and there is no correlation between the albumin concentration and PI_{dil} (Fig. 5C and 5D). These experiments demonstrate that, although the concentration of protein and albumin may influence the test results, they are not the only factor that determines the color of the test under the proposed conditions. It has been suggested that some drugs (e.g. aminoglycoside antibiotics) can trigger nanoparticle aggregation [22]. Critical patients often show higher lactic acid levels that could lead to small differences in pH [23], which is known to modulate nanoparticle aggregation [7,24]. To demonstrate that proteins, and not other solutes in plasma, are the key to the observed changes in aggregation behavior, we repeated the same experiments with deproteinized plasma samples from 3 ICU and 3 ward patients. Under this condition, no aggregation was observed in the whole range of dilutions proposed, which demonstrates that proteins are essential in order to aggregate nanoparticles in Fig. 3 (Fig. 5E). Moreover, attempts to measure the pH of plasma samples diluted 1:25000 or more were not successful because the dilution factor was so high that the concentration of buffering molecules was negligible, and values fluctuated wildly. Nevertheless, no differences were observed when checking the mean pH after adding nanoparticles to 3 diluted ICU (4.05 ± 0.02) or ward (4.07 ± 0.03) samples. These experiments show that leftover citrate ions from the nanoparticle synthesis rather than intrinsic solutes in the highly diluted samples are responsible for the pH of the mixture. In summary these experiments demonstrate that, although solutes in the plasma may modulate the protein-induced nanoparticle aggregation, the biomolecules are essential to cluster the colloids together and yield the observed color changes.

Fig. 6 shows a principal component analysis (PCA) comparing PI_{dil} and clinical variables that are commonly used to evaluate disease severity and inflammatory status (see also Table S1). Fig. 6A shows two principal components clearly defined by hemostatic and inflammatory biomarkers (clustered in principal component 1, PC1), and albumin levels along with liver function (clustered in principal component 2,

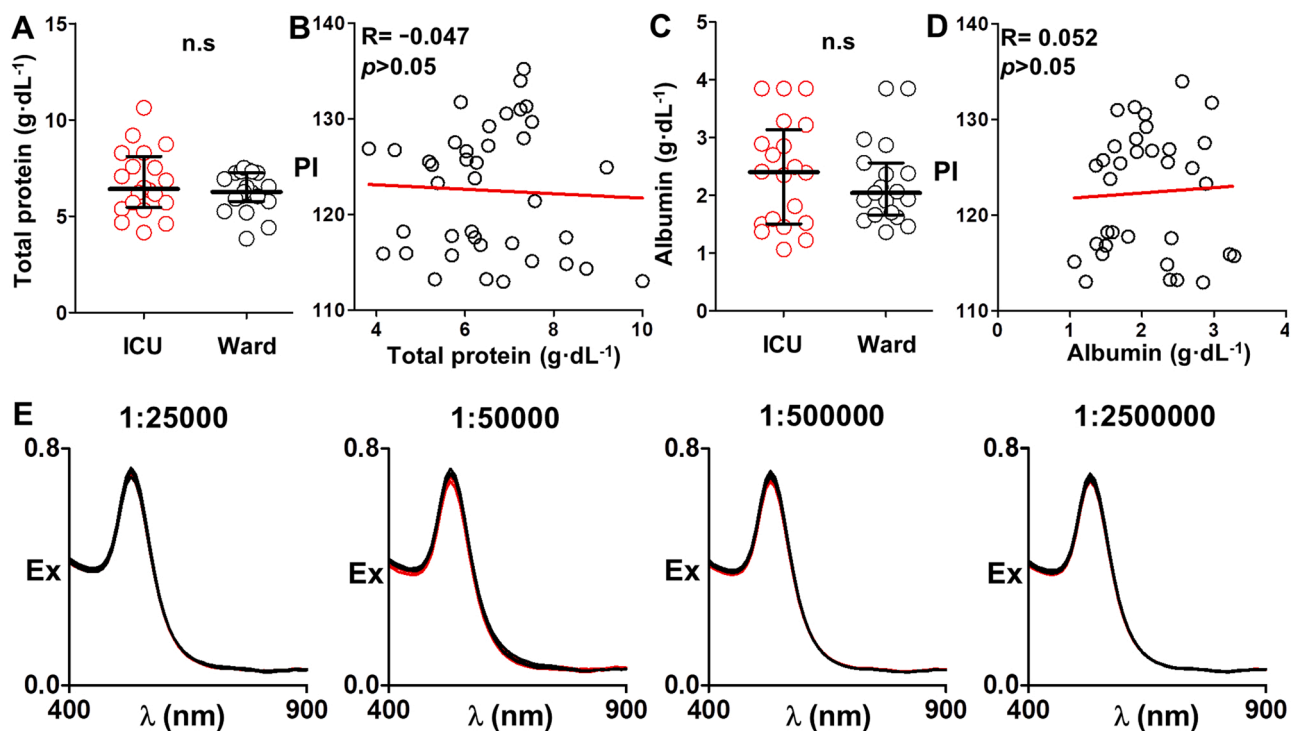


Fig. 5. Potential factors influencing nanoparticle aggregation after adding diluted plasma samples; (A) Distribution of total protein concentration values for ICU and ward patients; (B) Correlation plot comparing the total protein concentration and PI_{dil} ; (C) Distribution of albumin levels for ICU and ward patients; (D) Correlation plot comparing the albumin concentration and PI_{dil} ; (E) Extinction spectra of gold nanoparticles after adding 3 diluted ICU (red) and 3 ward (black) samples covering the whole dilution range shown in Fig. 3. Data in A and C are expressed as median with percentiles 25th and 75th. Mann-Whitney test proved non-significant (n.s.) statistical differences. PI_{dil} : pixel intensity at plasma dilution 1:31250.

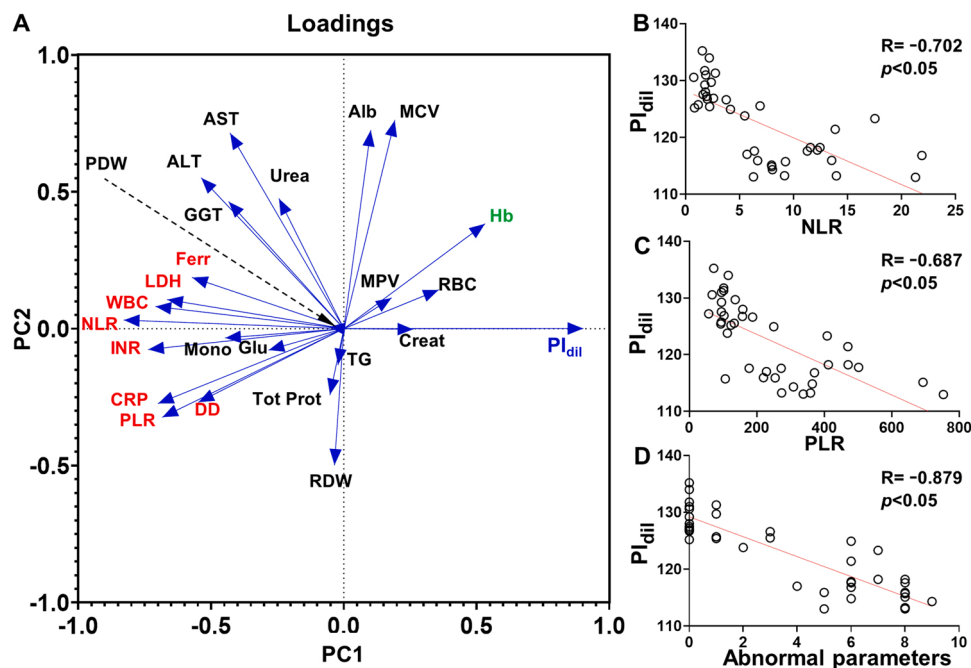


Fig. 6. Correlation studies between PI_{dil} and clinical variables; (A) Principal component analysis; (B-D) Correlation plots comparing PI_{dil} with the neutrophil-to-lymphocyte ratio (NLR, B), the platelet-to-lymphocyte ratio (PLR, C) and the number of biomarkers out of normal range (within selected biomarkers highlighted in red and green in (A), D). PI_{dil} : pixel intensity at plasma dilution 1:31250.

Author Contributions

The manuscript was written through contributions of all authors. / All authors have given approval to the final version of the manuscript.

CRediT authorship contribution statement

Giulia Santopolo: Methodology, Data curation, Validation. **Antonio Clemente:** Conceptualization, Data curation, Formal analysis,

Supervision, Methodology, Writing - review & editing. **Marta Gonzalez-Freire**: Data curation, Resources. **Steven M. Russell**: Methodology, Investigation. **Andreu Vaquer**: Methodology, Investigation. **Enrique Barón**: Methodology, Investigation. **María Aranda**: Investigation, Resources. **Antonia Socias**: Investigation, Resources. **Alberto del Castillo**: Investigation, Resources. **Marcio Borges**: Investigation, Resources. **Roberto de la Rica**: Conceptualization, Funding acquisition; Investigation, Project administration; Resources; Supervision, Writing - original draft; Writing - review & editing.

Declaration of Competing Interest

There are no conflicts of interest.

Data availability

Data will be made available on request.

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Appendix A. Supporting information

Supplementary data associated with this article can be found in the online version at [doi:10.1016/j.snb.2022.132638](https://doi.org/10.1016/j.snb.2022.132638).

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