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Red Blood Cell Susceptibility to Pneumolysin: Correlation with Membrane Biochemical and Physical Properties

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Running title: *Red Blood Cell Properties and Susceptibility to Pneumolysin*

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ABSTRACT

This study investigated the effect of the biochemical and biophysical properties of the plasma membrane as well as membrane morphology on the susceptibility of human red blood cells to the cholesterol-dependent cytolysin pneumolysin, a key virulence factor of *Streptococcus pneumoniae*, using single cell studies. We show a correlation between the physical properties of the membrane (bending rigidity, surface and dipole electrostatic potentials) and the susceptibility of red blood cells to pneumolysin-induced haemolysis. We demonstrate that biochemical modifications of the membrane induced by oxidative stress, lipid scrambling and artificial cell aging modulate the cell response to the toxin. We provide evidence that the diversity of response to pneumolysin in diabetic red blood cells correlates with levels of glycated haemoglobin (Hba1c) and that the mechanical properties of the red blood cell plasma membrane are altered in diabetes. Finally, we show that diabetic red blood cells are more resistant to pneumolysin and the related toxin perfringolysin O relative to healthy red blood cells. Taken together, these studies indicate that the diversity of cell response to pneumolysin within a population of human red blood cells is influenced by the biophysical and biochemical status of the plasma membrane and the chemical and/or oxidative stress prehistory of the cell.

The interaction of toxins with their target cells is generally characterised by a dose-response curve that is sigmoidal in shape (1). This shape is taken to reflect the differing susceptibilities of individual cells within the population. The fact that red blood cells (RBCs), with their less developed glycocalyx compared to other cell types (2), exhibit such a response is evidence that the initial interaction between the toxin and the plasma membrane is subject to, and probably the main determinant of, such variability. Therefore, it is important to understand the biochemical and biophysical factors affecting toxin-membrane interactions and the resulting variability of susceptibility within the same cell population.

Individual RBCs within a population differ significantly (3) with respect to their shape, volume and surface area. Some of these changes are related to cell age, due to the variety of

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mechanical and chemical stresses that a RBC undergoes in its life span of approximately 120 days (4,5), and others can be associated with diseases, such as diabetes and with acute conditions, such as sepsis, amongst many others (6) and thus, are likely to be present in the membranes of many other cell types.

Previous work on bulk cell preparations revealed that in addition to its normal discocytic shape, the RBC at rest can assume a variety of other distinct shapes, such as echinocytes and acanthocytes, characterised by exterior projections, and stomatocytes with cup-shaped invaginations (7). Many of these unusual shapes appear in normal blood at a frequency of about 1 %. However, during blood bank storage and in many inflammatory, degenerative and microvascular disorders the frequency of RBCs with altered morphology increases (8-12). For example, an increase of 13% in echinocytes was observed in patients suffering from chronic hepatitis (13) and in neuroacanthocytosis syndromes, a group of rare neurodegenerative diseases that mainly affect children and young adults, acanthocytes appear with a frequency of 12% to 45% (14).

High heterogeneity in the size of circulating erythrocytes can also have a dramatic impact on the health and function of the entire cell population (4,5,15). Recent studies indicate that the RBC distribution width (RDW), a measure of the size variation of circulating erythrocytes with a normal reference range of 11–15% (16), is a strong predictor of cardiovascular and thrombotic disorders (15,17), with a positive correlation between increased RDW and peripheral artery diseases (18).

Aging RBCs are characterised by a decrease in size, usually explained in terms of a decrease in cell area due to loss of lipids (19), and by surface modifications that include external exposure of membrane phosphatidylserine (PS) and decreased levels of sialic acid (20,21). Exposure of PS on the outer leaflet of the membrane marks the cell for recognition and phagocytosis by macrophages.

A number of studies have shown that aging of RBCs influences their sensitivity to bacterial toxins. For example, human RBCs during blood bank storage become more susceptible to sublytic concentrations of phospholipase C from either *Bacillus cereus* or *Clostridium perfringens* (12,22). Age-development changes in susceptibility of RBCs to the pore-forming toxin (PFT) perfringolysin O (PFO) from *C. perfringens*, a member of the cholesterol-dependent cytolysin (CDC) family of PFTs, have been demonstrated in mice, with RBCs of old mice being more susceptible to the toxin than those of young mice (23). Old RBC populations and peroxyl-oxidized RBCs also showed more susceptibility to hemolysis by the PFT stycholysin II from the sea anemone *Stichodactyla helianthus* compared to young cell populations (21). In contrast, old RBCs from rabbits are less susceptible to *Staphylococcus aureus* α-toxin relative to young RBCs (24-26). This is due to degradation of the membrane protein Band 3 in older RBCs (27), a binding site for staphylococcal α-toxin. The chemistry of lipid rafts (e.g. cholesterol content) is also known to change with age and such changes could alter the susceptibility of the host cell to toxin action (28).

Like PFO, pneumolysin (PLY) is also a member of the CDC family of PFTs (29). PLY is a key virulence factor of the bacterial pathogen *Streptococcus pneumoniae* (30,31) and plays a role in a range of human diseases, such as pneumonia, sepsis and meningitis (32). Disease is especially common in children, the elderly and in immunocompromised and diabetic individuals (30).

PLY is released from the bacterium as an inactive, water-soluble monomer (53 kDa). Monomeric PLY is an elongated molecule organised into four domains (33,34). Three short hydrophobic loops and the highly conserved tryptophan-rich loop at the base of domain 4 anchor the toxin to the membrane (35,36), with a highly conserved threonine-leucine pair in loop 1 critical for cholesterol binding (37), the receptor for most CDCs (38,39). Two putative carbohydrate-binding sites have also been identified in PLY: one near the conserved tryptophan-rich loop in domain 4 and the other at the domain 3-domain 4 interface (33,40).

Pore-formation by PLY is a multistep process. Upon binding to the membrane, PLY monomers interact with each other and form an oligomeric pre-pore complex on the membrane surface that contain 30-50 monomers (41,42). Pre-pore to pore transition is associated with

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significant conformational changes in the complex and consequent membrane insertion of the oligomer that leads to the formation of large pores of 32-43 nm in diameter and ultimately, to cell lysis (43-45).

A wide range of host cells are susceptible to the action of PLY, and although erythrocytes are not the primary target for the toxin *in vivo*, they are the cell type most commonly used to measure activity towards host cells (46).

To date, the relationship between the plasma membrane properties and the variability in cell response to toxin within a population has largely been unexplored. Therefore, the aim of this study was to investigate the effect of the biochemical (oxidative stress, lipid scrambling and artificial cell aging) and biophysical properties (bending rigidity, surface and dipole electrostatic potentials) of the plasma membrane and the effect of membrane morphology on the susceptibility of RBCs to PLY (47), using single cell studies. Finally, we sought to establish whether the response to PLY in populations of RBCs derived from diabetic subjects correlates with levels of glycated haemoglobin (Hba1c), which is elevated in people with diabetes and is likely to alter membrane physical characteristics via glucose induced biochemical modifications.

EXPERIMENTAL PROCEDURES

Materials–Chemicals were purchased from Sigma-Aldrich, UK unless otherwise stated. Recombinant wild-type pneumolysin with N-terminal 6x His tag (PLY), recombinant wild-type pneumolysin with N-terminal 6x His and eGFP tags (eGFP-PLY) and perfringolysin O (PFO) were generated, expressed and purified as described in (48-50); eGFP-PLY is monomeric in solution as judged by size exclusion chromatography and analytical ultracentrifugation experiments and has a specific activity similar to unlabelled PLY at equivalent molarity (data not shown). Recombinant plasmid pET-33b(+) containing the non-lytic and aggregation negative variant of eGFP-PLY, termed eGFP-Δ6PLY^{L363A}, was generated as described in (49).

Expression and purification of eGFP-Δ6PLY^{L363A}–For expression of eGFP-Δ6PLY^{L363A}, recombinant plasmid was transferred into *E. coli* Rosetta 2 (DE3) cells (Merck, Darmstadt, Germany) and expression of eGFP-Δ6PLY^{L363A} was induced using the autoinduction system as described in (51).

Time course of hemolysis induced by PLY within a population of human RBCs–Fresh whole blood from healthy (n = 17) and diabetic individuals (n = 36) was collected by venepuncture from the University of Exeter Medical School, NIHR Exeter Clinical Research Facility, Diabetes and Vascular Medicine Centre, Exeter, UK into neutral tubes and 1 mL whole blood was immediately transferred into 20 mL DPBS buffer with pH 7.0-7.2 (Invitrogen) supplemented with 1 mg/mL bovine serum albumin (BSA) (DPBS/BSA). RBCs were washed three times in DPBS/BSA, resuspended in DPBS/BSA at a concentration of 3 x 10^7 cells/mL and cells (90 µL) were incubated with PLY at a final concentration of 118 ng/mL (2.2 nM) for 30 minutes at room temperature, similar to the dose (1 nM) frequently used in the literature under comparable experimental conditions (40,52). The time course of hemolysis was monitored by phase contrast microscopy (Zeiss Axiophot upright microscope equipped with a Plan Neofluar 20x / 0.5 Air objective). Images were captured every 2 minutes for 30 minutes using a Spot Pursuit™ 1.4 MP Monochrome CCD camera (Visitron Systems). The number of lysed cells was counted and the percentage of lysed cells was calculated for each time point.

Analysis of binding of recombinant eGFP-PLY and eGFP-Δ6PLY^{L363A} to human RBCs by microscopy–To investigate whether the variation of cell response to PLY within a population of RBCs correlates to the amount of toxin bound to the membrane, RBCs (Innovative Research) were diluted to 6 x 10^7 cells/mL in DPBS/BSA and cells (90 µL) were incubated with eGFP-PLY at a final concentration of 0.67 µg/mL to allow optimal detection of eGFP fluorescence by microscopy.

To investigate whether increased sensitivity of stomatocytes to PLY correlates to the amount of toxin bound to the membrane, fresh blood was collected from healthy volunteers using a pin-prick lancet and immediately suspended in DPBS/BSA (approximately 3 x 10^7 cells/mL). Cells (90 µL) were incubated with eGFP-Δ6PLY^{L363A} at a final concentration of 1.12 µg/mL.

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Cells were imaged at room temperature using an Olympus IX81 microscope (Olympus Optical, Hamburg, Germany) equipped with a PlanApo 100x / 1.40 oil objective and eGFP filter sets equipped with a 470/40 ET Bandpass, Beamsplitter T 495 LPXR and a 525/50 ET Bandpass filter (Chroma Technology Corp. Olching, Germany).

Each image had its background intensity subtracted and the GFP intensities of cells were measured 2 minutes after exposure to toxin using ImageJ software (53).

Simulated oxidative stress and aging–Fresh whole blood from healthy individuals was collected by venepuncture from the University of Exeter Medical School, NIHR Exeter Clinical Research Facility, Diabetes and Vascular Medicine Centre, Exeter, UK into neutral tubes and 1 mL whole blood was immediately transferred into DPBS/BSA. Cells were washed three times with DPBS/BSA and resuspended in DPBS/BSA to 3 x 10^7 cells/mL.

To simulate oxidative stress we used two different oxidants, the water-soluble hydrogen peroxide (H_2O_2) and the membrane-soluble cumene hydroperoxide (cumOOH). Solutions were prepared in DPBS/BSA immediately before each experiment to minimise peroxide degradation. To disperse cumOOH at the necessary concentration into DPBS/BSA, the mixture was vigorously vortexed for a few minutes.

We used two different approaches to simulate cell aging. The first one relies on cell treatment with the steroid hormone dehydroepiandrosterone (DHEA). In DHEA treated cells, inhibition of glucose-6-phosphate dehydrogenase (G6PD) activity results in decreased levels of NADPH, an essential cofactor that helps maintain glutathione (GSH) in its reduced, antioxidant form (54). Thus, decreased levels of GSH weaken the cell's antioxidant defence system. The second approach used calcium ionophore A23187. It has been demonstrated that treatment of RBCs with calcium ionophore A23187 causes internalisation of Ca^{2+} leading to fast phosphatidylserine (PS) translocation from the inner monolayer to the outer monolayer of the plasma membrane, as well as cell shrinkage and membrane blebbing, which are typical signs of apoptosis (55-58).

Human RBCs from healthy individuals were diluted to 3 x 10^7 cells/mL in DPBS/BSA and cells (1 mL) were incubated with H_2O_2 (100 μM), cumOOH (100 μM), DHEA (35 μM), calcium ionophore A23187 (20 μM, in the presence of 0.9 mM calcium chloride) or DPBS/BSA (as control) for 2 hours at 37 °C. The solvent concentration in DHEA and calcium ionophore A23187-treated samples was kept below 1% (v/v). After incubation, cells were washed three times in DPBS/BSA and resuspended in 1 mL DPBS/BSA. Cells (90 μL) were exposed to PLY at a final concentration of 118 ng/mL or perfringolysin O at a final concentration of 72 ng/mL and the time course of hemolysis was monitored by phase contrast microscopy (Zeiss Axiophot upright microscope equipped with a Plan Neofluar 20x / 0.5 Air objective). Images were captured every 2 minutes for 30 minutes using a Spot Pursuit™ 1.4 MP Monochrome CCD camera (Visitron Systems). The number of lysed cells was counted and the percentage of lysed cells was calculated for each time point.

Flow cytometry analysis of calcium ionophore A23187-treated RBCs exposed to eGFP-Δ6PLY^{L363A}–Human RBCs from healthy individuals were diluted to 5 x 10^6 cells/mL and cells (1 mL) were incubated with calcium ionophore A23187 (20 μM, in the presence of 0.9 mM calcium chloride) or ethanol aqueous solution (as control) for 1 hour at 37 °C; the solvent (ethanol) concentration in both samples was 0.1 % (v/v). After incubation, cells were washed three times in DPBS/BSA and resuspended in annexin V binding buffer (10 mM HEPES, 140 mM sodium chloride and 2.5 mM calcium chloride, pH 7.4, BD Biosciences) at a concentration of 1 x 10^6 cells/mL. Cells (100 μL) were labelled with 5 μL annexin V Alexa Fluor® 594 Conjugate (Molecular Probes) for 15 minutes at room temperature followed by incubation with eGFP-Δ6PLY^{L363A} at a final concentration of 1.67 μg/mL for 2 minutes at room temperature. After the incubation period, 400 μL of ice-cold annexin V binding buffer was added to each sample and cells were analyzed by flow cytometry using 488 nm and 633 nm excitation on a BD FACSARIA II Cytometer with 530/30 and 660/20 bandpass filters. The number of events noted for each sample was 10,000.

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Ratiometric measurement of the membrane dipole potential–In separate experiments, the membrane dipole potential was measured before exposing RBCs (100 µL at 3 x 10^7 cells/mL in DPBS/BSA) to PLY (5.9 ng/mL) in a µ–Slide $I^{0.4}$ Luer poly-L-lysine imaging chamber (Ibidi). The membrane dipole potential was measured using ratiometric fluorescence imaging of Di-8-ANEPPS labelled RBC membranes. 5 µL of 1 mg/mL Di-8-ANEPPS in ethanol was added to 1 mL RBC suspension and cells were incubated at 37 °C for 1 hour. Subsequently, cells were washed three times in DPBS/BSA to remove excess dye and resuspended in 1 mL DPBS/BSA. Ratiometric measurement of the membrane dipole potential was performed on an Olympus IX50 inverted microscope using a 63x oil immersion objective. Excitation light with a selectable wavelength was provided by a Till Photonics Polychrome V monochromator and the images were recorded using a high-sensitivity CCD camera (AVT Stingray F-145B) attached to the microscope in conjunction with a 650/50 nm emission filter (Thorlabs). Two consecutive images using excitation at 420 nm and 520 nm (each with an exposure time of 500 ms, with 5 ms between them) were recorded. Each image (n = 24) had its background intensity subtracted before the 420 nm excitation image was divided by the 520 nm excitation image to produce a matrix of the ratiometric intensity, $R = I_{420}/I_{520}$ using ImageJ software (53). The value of the membrane dipole potential ψ_d (in mV), averaged over the whole cell, can be found from the following calibration dependence (59): $\psi_d = \frac{R+0.3}{0.0043}$

Measurement of the membrane surface potential–Similarly to the membrane dipole potential, the membrane surface electrostatic potential of RBCs (100 µL at 3 x 10^7 cells/mL in DPBS/BSA) was evaluated before exposing the cells to PLY (5.9 ng/mL) in a µ–Slide $I^{0.4}$ Luer Poly-L-Lysine imaging chamber (Ibidi). The membrane surface potential was measured using fluorescence intensity measurements of fluorescein-phosphatidylethanolamine (FPE; Molecular Probes) incorporated in the RBC membrane. The quantum yield of this probe is sensitive to the charge density of its immediate environment. Therefore, changes in the membrane surface electrostatic potential are manifested by changes in the fluorescence intensity recorded (60,61). A decrease in the net negative charge of the surface results in deprotonation of fluorescein and a consequent increase in its fluorescence intensity.

Human RBCs were labelled with FPE following a protocol adapted from (62). In brief, 12.5 µg FPE dissolved in 2.5 µL ethanol was added to 3 x 10^7 RBCs in 1 mL DPBS/BSA and cells were incubated at 37 °C for 1 hour. Subsequently, cells were washed three times in DPBS/BSA to remove excess dye and resuspended in 1 mL DPBS/BSA. Fluorescence intensity measurements of FPE-labelled cells (n = 108) were performed using an Olympus IX81 microscope (Olympus Optical, Hamburg, Germany) equipped with a UPlanFL N 40x / 1.3 oil objective and eGFP filter sets equipped with a 470/40 ET Bandpass, Beamsplitter T 495 LPXR and a 525/50 ET Bandpass filter (Chroma Technology Corp. Olching, Germany).

Measurement of the membrane bending elasticity using thermal fluctuation spectroscopy–Human RBCs were also interrogated for their mechanical properties, in particular membrane bending elasticity, using thermal fluctuation spectroscopy as described in more detail earlier (63,64). In brief, individual RBCs (n = 9) were recorded using phase contrast microscopy (Leica DMLFS upright microscope equipped with 63× PL Fluotar objective). Video sequences (about 1000 frames) of fluctuating RBCs were recorded at an exposure time of 10 ms using a QImaging QIClick CCD camera attached to the microscope and interfaced with a computer, and each frame was analysed by a sub-pixel precision algorithm to obtain a series of 2D equatorial contours. Each contour was decomposed into a Fourier series used subsequently to calculate the thermal fluctuation spectrum of the entire contour sequence as described in (63,64). The bending elastic modulus of the membrane was obtained by fitting a flat-membrane model to the experimentally obtained thermal fluctuation spectrum (a full discussion of the bases of this methodology can be found in (64)). For these experiments, 5 µL samples of fresh blood was collected from a healthy volunteer using a pin-prick lancet and immediately suspended in 1 mL DPBS/BSA. A small volume (approximately 20 µL) of this suspension was

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introduced in an imaging chamber that consisted of a microscope slide and a glass coverslip spaced apart by two strips of Parafilm® (Pechiney Plastic Packaging, USA) along the long edges of the slide, bonded together by heating briefly on a hot plate. Within a few minutes the cells settle down onto the bottom of the chamber (due to their slightly higher density than that of the surrounding buffer), which allowed their fluctuations to be recorded before introducing the toxin solution (DPBS/BSA containing PLY at a final concentration of 59 ng/mL) by placing excess solution on one side of the chamber and pulling it through with filter paper introduced to the opposite side.

Monitoring the changes in the radius of RBCs exposed to PLY over time–Changes in the radius of the equatorial contour of RBCs are an indicator for the onset of lysis. Therefore, we measured the radius of individual cells before and after introducing the toxin solution into the imaging chamber using the same methodology as for the thermal fluctuation analysis (in fact, radius evaluation is a part of the Fourier representation of the contour). In all experiments, cell membrane radii were initially recorded while in DPBS/BSA after the cells have stabilised on the bottom of the chamber. The buffer was then exchanged with buffer containing PLY (59 ng/mL) and RBCs were recorded at regular time intervals (typically every 2 minutes for a period of up to 30 minutes).

Measurement of Hba1c levels in RBCs from diabetic individuals–Levels of glycated haemoglobin (HbA1c) were determined with the Gold standard Ion-Exchange method using the Tosoh G8 HPLC Analyzer, (Tosoh Bioscience, South San Francisco, CA).

Measurement of the modulus of shear elasticity–To measure the RBC shear elastic modulus, we employed the micropipette aspiration method. In brief, a micropipette is brought in close proximity to a cell, which is then partially aspirated into the pipette by applying small suction pressure. Subsequent incremental increases in the suction pressure leads to a stepwise aspiration of the cell membrane into the pipette, which allows the establishment of the relationship between the applied suction pressure, ΔP, and the projected length of the membrane inside the pipette, L. The shear elastic modulus, μ, can then be evaluated from such dependences according to the following equation (65,66):

$$\Delta P R_{\mathrm{p}} = \mu \left[K_1 \left(\frac{L}{R_p} \right) - K_2 \right] \qquad (1)$$

where R_{p} is the pipette radius, and K_1 = 2.45 and K_2 = 0.603 are numerical constants. Equation 1 is valid for $1 \leq L/R_{\mathrm{p}} \leq 4$.

Micropipettes were drawn from glass capillaries of 0.86 mm internal diameter (Harvard Instruments GC 150-11) using a microelectrode puller (Micro Instruments Ltd, Oxford). The end of the pipette was then manually forged with a heated filament until a smooth aperture was produced with typical diameters of 1 – 2 μm. The pipette was filled with buffer and attached to a pressure-generating apparatus capable of controlling the suction pressure via careful adjustments of the height of a buffer reservoir. The micropipette was then mounted on a hydraulically-driven micromanipulator (Narishige Co. Ltd) and its tip was introduced into the chamber containing the cell suspension. Images were acquired using a Leica DMLFS upright microscope (40× long working distance objective), a video camera (JVC KY-F55B) and acquisition software (AcQuis Bio 3.01).

The University of Exeter Medical School, NIHR Exeter Clinical Research Facility, Diabetes and Vascular Medicine Centre provided blood samples from individuals with diabetes (n = 12) and healthy (n = 14) subjects, stored at 4 °C in 9.5 mL heparinised tubes and used within 48 hours. The individuals with diabetes were males over the age of 45 with no known diabetic complications and neither on insulin nor on metformin therapy. Control samples were obtained from age-matched healthy subjects.

Statistical analyses–The software GraphPad Prism 6 (GraphPad Software, La Jolla, USA) was used to perform statistical analysis. In all analyses, P values of < 0.05 were considered significant. All data represent the means and standard deviations of three independent experiments performed in triplicate, unless stated otherwise.

RESULTS

Variation of response to pneumolysin within a population of human RBCs–In the initial experiments, we sought to establish the behaviour of human RBC populations in response to PLY.

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Fresh RBCs from healthy individuals (n = 17) were incubated with purified recombinant PLY (118 ng/mL) and the time course of haemolysis induced by the toxin on individual cells within each population was monitored by phase contrast microscopy. Figure 1A shows representative phase contrast images of a population of RBCs exposed to PLY at time points 0, 15 and 30 minutes. In phase contrast, lysed cells appear as dark circles while live cells appear with a distinctive halo around their edges. Figure 1B shows the average (± SEM) haemolysis time profiles of 17 different donations treated with PLY. As evident from these results, the interaction between RBCs and PLY is characterised by a sigmoidal curve, which suggests a considerable degree of variability in the RBC response. At the toxin concentration used, a lag phase of approximately 3 minutes (on average) was followed by lysis where most cells lysed by 30 minutes. Experiments carried out in the absence of PLY did not show any noticeable changes in the number of live cells on the time scale of the assay (data not shown).

In order to characterise the variability of RBC response to PLY within the same population, we compared the lysis behaviour of RBCs exposed to PLY for each of the 17 individual samples. Figure 1C shows three representative individual haemolysis time profiles from different healthy individuals. It can be seen that, although all samples exhibit the characteristic S-shaped curve, there are considerable quantitative variations between the individual populations. Figure 1D shows a dot plot of the percentage of live RBCs from 17 healthy individuals 30 minutes after exposure to PLY, where on average 6.6 % ± 1.7 % (SEM) of RBCs remain resistant to PLY-induced lysis, despite all cells having been subjected to the same concentration of toxin.

Another important observation illustrated in Figure 1C is the considerable degree of variability of RBC response to PLY within the same population, in which the time scale for cell lysis could differ by many minutes, despite the fact that all cells were derived from the same individual. To further investigate the variation of response to PLY within a population of RBCs, we monitored the changes in the radius of RBCs exposed to PLY over time. This revealed two distinct stages of interaction (Figure 2). In the first stage (lasting different periods for different cells) the radius remains relatively constant. This is followed by a rapid drop in the radius in the second stage of interaction that corresponds to cell lysis. Figure 2 shows typical time courses of the radius change for two RBCs from the same sample exposed to PLY, where the onset of cell lysis, marked by arrows, differs between the two cells by some 21 minutes. These results prompted us to further investigate the factors that influence the diversity of response to PLY within a population of cells. The experiments that follow were designed to address this question.

The variation of response to PLY within a population of human RBCs correlates with the amount of toxin bound to the membrane–To investigate if there is a correlation between the RBC response to PLY and the amount of toxin bound to the membrane, we incubated RBCs with recombinant GFP-tagged PLY (eGFP-PLY). Figure 3A shows representative DIC and GFP fluorescence images obtained after exposure of RBCs to eGFP-PLY (0.67 µg/mL). The GFP fluorescence intensity of cells (n = 38) was measured 2 minutes after exposure to toxin. Most cells exposed to the toxin lysed within 2 minutes of exposure, indicated by the appearance of faint circles in the DIC image. However, some cells showed prolonged resistance to the toxin and in the DIC image appeared with a halo around their edges. Statistical analysis using Student t test revealed that cells with prolonged resistance to the toxin showed significantly lower GFP fluorescence intensity values compared to cells that lysed within 2 minutes of exposure to toxin, indicating that variation of cell response to PLY within a population of RBCs correlates with the amount of toxin bound to the membrane (Figure 3B). The punctate pattern of fluorescence on the RBC membrane probably corresponds to high molecular weight aggregates of the GFP-labelled toxin in the form of close-packed pores that have also been observed for the small β-PFTs, lysenin and epsilon toxin (67-69). The pores can also be observed by analytical ultracentrifugation of membranes solubilised from toxin treated cells or by electron microscopy (data not shown).

Effect of cell morphology on susceptibility of RBCs to PLY–To investigate the effect of cell morphology on the susceptibility of RBCs to PLY, RBCs from 17 healthy individuals were incubated with PLY, as described above, and lysis was

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monitored by phase contrast microscopy. The shape of RBCs in each population was assessed using ImageJ and the percentage of lysed discocytes and stomatocytes 15 minutes after exposure to PLY was determined (Figure 4A). Statistical analysis using Mann–Whitney *t* test revealed that stomatocytes are more susceptible to PLY relative to discocytes, indicated by increased percentage of lysed cells 15 minutes after exposure to toxin (Figure 4A).

To investigate if the increased sensitivity of stomatocytes relative to discocytes correlates with increased levels of toxin bound to the membrane, we incubated live RBCs with eGFP-Δ6PLY^{L363A}, a non-lytic variant of recombinant eGFP-PLY with preserved binding activity (49). As shown in Figure 4B, stomatocytes showed significantly higher GFP fluorescence intensity values compared to discocytes.

In a separate group of experiments, we performed DIC and fluorescence imaging of echinocytic RBCs (formed spontaneously in the blood sample) incubated with eGFP-Δ6PLY^{L363A} (1.67 μg/mL) for 2 minutes. As can be seen from Figure 4C, we observed clusters of eGFP-Δ6PLY^{L363A} bound preferentially to the spikes of the echinocytes, where the curvature of the membrane is high.

Simulated oxidative stress, artificial aging and membrane lipid scrambling of RBCs leads to changes in susceptibility to PLY–To determine whether the variation of cell response to PLY might be due to differences in the biochemical status of the RBC membrane, we selectively modified the membrane using four different treatments. Oxidative stress was simulated by exposing RBCs to either hydrogen peroxide (H_2O_2, 100 μM) or cumene hydroperoxide (cumOOH, 100 μM). These two oxidants were used to selectively target different cell constituents. Hydrogen peroxide is water-soluble and upon addition to the cell suspension it permeates the plasma membrane relatively quickly and partitions in the cytoplasm, thus targeting mainly haemoglobin (64,70). In contrast, cumOOH is membrane-soluble and partitions predominantly into the lipid bilayer due to its hydrophobicity, where it is able to cause oxidative damage to lipids as well as to membrane-bound proteins and to the membrane skeleton (64,70). To simulate aspects of the aging process in RBC, we exposed cells to the steroid DHEA (35 μM), as described in the Experimental Procedures section. In a separate series of experiments, membrane lipid scrambling was induced using calcium ionophore A23187 (20 μM) in the presence of calcium chloride (0.9 mM).

Figure 5 is a representative summary of the obtained results, along with a control of untreated cells. The typical sigmoidal response is observed again. However, there are considerable quantitative differences between the different treatment protocols. Treatment with H_2O_2 had no effect on the sensitivity of RBCs to PLY (the haemolysis profile in this case was similar to the control sample), while cumOOH-induced oxidative stress resulted in increased resistance to PLY relative to control cells, indicated by the low percentage of lysed cells over the time course of the experiment (30 minutes). A similar effect was observed in cells treated with calcium ionophore A23187. In contrast, artificially aged cells treated with DHEA exhibited higher susceptibility to PLY relative to control cells, indicated by the increased percentage of lysed cells over the time course of the experiment.

Increased resistance of calcium ionophore A23187-treated RBCs to PLY corresponds to reduced toxin binding–The drastic changes in membrane lipid composition and loss of asymmetry between the two leaflets of the RBC membrane induced by the calcium ionophore A23187 treatment required further investigation to assess the binding affinity of PLY to scrambled membranes. First, we labelled calcium ionophore A23187-treated and control RBCs with AlexaFluor® 594-annexin V. Since annexin V binds to phosphatidylserine (PS), the expectation was that only cells in which PS is transferred to the outer membrane leaflet will become labelled with annexin V (for healthy RBCs PS is exclusively located in the inner membrane leaflet). These preparations were then incubated with either eGFP-Δ6PLY^{L363A} or buffer only and toxin binding was analysed by flow cytometry.

The first group of experiments was carried out on annexin V-labelled cells treated with calcium ionophore A23187 or ethanol aqueous solution (as control) before exposure to toxin. Flow cytometry analysis of dot plots that reflect cell shape revealed that calcium ionophore

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A23187-treated cells had altered cell morphology relative to control cells, with reduced forward scatter (FSC), indicating reduced size, and a narrow range of side scatter (SSC), indicating echinocytic morphology (71) (Figure 6A). Further microscopy analysis revealed projections of the cell membrane in calcium ionophore A23187-treated cells, leading to echinocytes (Figure 6B).

Fluorescence analysis of calcium ionophore A23187-treated cells revealed that 36.2 % of cells were labelled with Alexa Fluor® 594-annexin V (Figure 7B, bottom right panel), indicating transfer of PS to the outer membrane leaflet, while control cells showed only background red fluorescence of 0.09 % (Figure 7A, bottom right panel), indicating that PS is located exclusively in the inner membrane leaflet.

The second group of experiments was carried out on annexin V-labelled control and A23187-treated RBCs after exposure to eGFP-Δ6PLY^{L363A}. Flow cytometry analysis of annexin V-labelled control cells exposed to eGFP-Δ6PLY^{L363A} showed green fluorescence in 99.5 % of cells (Figure 7C, top left panel), indicating eGFP-Δ6PLY^{L363A} binding to most cells. Annexin V-labelled calcium inonophore A23187-treated cells exposed to eGFP-Δ6PLY^{L363A} showed green fluorescence in 59.1% of cells (Figure 7D, top left panel) and double fluorescence of green and red in 39.2 % of cells (Figure 7D, top right panel), indicating eGFP-Δ6PLY^{L363A} binding to RBCs with both externalised and non-externalised PS. However, double fluorescence plots of red and green fluorescence show that the green fluorescence intensity in annexin V-labelled calcium ionophore A23187-treated cells exposed to toxin is reduced in comparison to annexin V-labelled control cells exposed to toxin (top left panels of Figure 7D and C, respectively). This tendency is especially visible for calcium ionophore A23187-treated cells with externalised PS (Figure 7D, top right panel). These results indicate that increased resistance of A23187-treated cells to PLY is most probably due to reduced toxin binding to membranes with scrambled lipids.

Differences in the membrane physical properties of individual cells within a population of human RBCs are correlated with their susceptibility to PLY–The physical properties of the lipid bilayer membrane, such as membrane elasticity and its electrostatic status, are likely determinants of the susceptibility of cells to toxin, as they have been shown to contribute to, as well as control, the interactions between the plasma membrane and various proteins (72-74). This motivated us to investigate whether differences in the membrane physical properties of individual cells within a population of RBCs are correlated with their susceptibility to PLY. We measured the membrane bending elastic modulus (a primary measure of the mechanical compliance of the lipid bilayer (75)), the membrane electrostatic dipole potential (76,77) and the membrane electrostatic surface potential (60,61) for a number of individual cells within a population of RBCs before toxin exposure. The buffer surrounding the cells was then exchanged with buffer containing toxin and the time to lysis, i.e. the period of time the cell survived intact and without haemolysis after the addition of toxin, was monitored for each cell by microscopy.

Figure 8A shows the dependence of the membrane bending elastic modulus (in units of k_BT, where k_B is the Boltzmann constant and T is the absolute temperature) on the time to lysis for nine individual cells. There is a clear correlation between these two parameters, where cells that are more rigid with respect to bending show reduced time to lysis, indicating increased susceptibility to the toxin's lytic activity.

In separate experiments, using ratiometric fluorescence microscopy measurements on Di-8-ANEPPS-labelled RBCs, we found a similar correlation between the membrane dipole potential and the time to lysis, as illustrated in Figure 8B. Higher dipole potentials appear to be correlated with reduced time to PLY-induced lysis.

Finally, we measured the membrane-associated fluorescence intensity of FPE-labelled RBCs before toxin exposure in order to evaluate if there is a correlation between the membrane electrostatic surface potential and the susceptibility of RBCs to PLY-induced lysis. Figure 8C shows the measured membrane-associated fluorescence intensity as a function of time to lysis. Differences in the fluorescence intensity of FPE are indicative of the degree of natural variations in the magnitude of the surface electrostatic potential of the (negatively charged) RBC membrane. FPE is sensitive to changes in the

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surface potential due to a shift in the protonation-deprotonation equilibrium (61), resulting in higher fluorescence intensities when the magnitude of the potential is lower. From these experiments we conclude that cells exhibiting lower magnitude of the surface potential (hence lower surface density of negative charges) are more susceptible to toxin. Conversely, more negative membranes show increased resistance to lysis.

Correlation between levels of glycated haemoglobin (Hba1c) and susceptibility of RBCs from individuals with diabetes to PLY–Next, we sought to establish whether the response to PLY in RBCs derived from diabetic subjects correlates with levels of glycated haemoglobin (Hba1c), which is elevated in diabetes; the higher the HbA1c levels, the greater the risk of developing diabetes-related complications. We investigated samples from 36 individuals (23 of whom were on metformin therapy, whilst 13 were not) for RBC susceptibility to PLY-induced lysis. Diabetic RBCs were exposed to PLY (118 ng/mL) and the percentage of live cells after exposure to toxin for 30 minutes was plotted against Hba1c levels. For the subset of individuals who were not treated with metformin (Figure 9A), there is a statistically significant positive correlation between the percentage of live cells and Hba1c levels, indicating that RBCs from individuals with diabetes with increased levels of Hba1c are more resistant to PLY. For the other subset (individuals to whom metformin was prescribed), this correlation was much weaker, making the dependence statistically insignificant (Figure 9B).

RBCs from individuals with diabetes show increased resistance to PLY and PFO-The significant positive correlation between Hba1c levels and PLY resistance of RBCs from individuals with diabetes not on metformin therapy motivated us to compare the susceptibility of RBCs from healthy and diabetic individuals to two members of the CDC family of PFTs: PLY and PFO. Fresh RBCs from healthy individuals (n = 17) and individuals with diabetes not on metformin therapy (n = 13) were incubated with purified recombinant PLY (118 ng/mL) or PFO (72 ng/mL) and cell lysis was monitored by phase contrast microscopy. Figure 10 shows the average (± SEM) haemolysis time profiles of the cells treated with the toxins. RBCs from diabetic individuals showed increased resistance to both PLY (Figure 10A) and PFO (Figure 10B), indicated by a right-shift of the haemolysis time profiles relative to healthy RBCs. At the toxin concentrations used, the time required to lyse 50% of the RBCs from individuals with diabetes has increased by approximately 6 minutes (on average) relative to control, healthy cells.

Diabetic RBCs exhibit increased membrane stiffness–In a separate set of experiments, we sought to establish whether the mechanical properties of the RBC plasma membrane are altered in diabetes. Using the micropipette aspiration method, we measured the modulus of shear elasticity of RBCs derived from diabetic subjects (n = 12) neither on insulin nor on metformin treatment compared to healthy, age-matched controls (n = 14). A summary of the measurements is shown in Figure 11, from which the modulus of shear elasticity was evaluated. The average shear modulus for the controls was 5 ± 1 μN/m, whilst for the diabetic group the average value was significantly higher, 12 ± 2 μN/m.

DISCUSSION

Membrane biophysical properties and cell susceptibility to PLY–The results obtained in this study paint a complex landscape of biophysical factors affecting the interaction between PLY and RBCs. Single cell studies carried out to assess the effect of the physical properties of the membrane on cell susceptibility to toxin (Figure 8) revealed that membrane elasticity and electrical properties in healthy RBCs are correlated with their susceptibility to PLY-induced lysis.

Surface charge density (and therefore surface potential) will modify the interactions of the membrane with charged molecules. Whilst the detailed charge distribution on the surface of a PLY monomer is complex (Figure 12), the overall charge of the molecule is -15 (78). This, to the lowest approximation, would explain the observed dependence in Figure 8C, which suggests that cells that naturally possess lower (negative) surface potential are more prone to haemolysis, probably due to the reduced electrostatic repulsion between the molecule of PLY and the RBC membrane. The reason for the marked electronegative potential of PLY in contrast to other CDCs is unclear (33).

The membrane dipole potential has its origins in the alignment of the lipid molecules

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(containing a number of dipoles mainly in the headgroup region) in the plane of the membrane and the orientation of water molecules in the immediate vicinity of the lipid headgroups (79-81). This potential has been reported to affect protein function (59), as well as insertion and secondary structure formation of peptides (76). Here we have shown that healthy RBCs naturally characterised by higher magnitudes of the membrane dipole potential are more susceptible to PLY (Figure 8B) and to the related toxin PFO (data not shown), probably due to increased cholesterol levels in these cells (see below) (59). In a similar trend, cells that exhibit higher bending rigidity of their membranes are easier to lyse by PLY. However, we must emphasise that these two parameters are not the sole and direct determinants of lytic resistance *per se*. This can be seen in comparison with cells pretreated with cumOOH (Figure 5). We have previously shown that treatment of RBCs with cumOOH increased both membrane bending elastic modulus (64) and membrane dipole potential (77), yet these cells are much more resistant to toxin compared to healthy cells, for which higher bending rigidity and dipole potential meant lower resistance to PLY (Figure 8A and B, respectively). Therefore, the origins of the correlations between these two properties and susceptibility to PLY in healthy cells should be sought in a common underpinning factor, such as the variations in molecular composition and supramolecular organisation of the lipid membrane, which may alter the cell resistance to toxin, as well as the membrane physical properties.

Factors affecting cell susceptibility to PLY–One of the likely factors suggested by the cell membrane modification studies (see below) is the age of the individual cells within the population. As a measure of the time spent by the cell in an environment characterised by chemical stresses, cell age is likely to alter the membrane physical properties. Indeed, a number of studies reported that RBC *deformability* decreases with cell age (for a comprehensive summary see (82)). However, many of these measurements are method-dependent and the reported quantities are often ambiguously defined. In addition, changes in the overall cell deformability are generally related to changes in viscosity of the cytoplasm, membrane fluidity and membrane elasticity (82), which is further characterised by bending, shear and area deformations (7). The two parameters we measure in this work, membrane bending modulus and dipole potential, reflect primarily the properties of the lipid bilayer, but to the best of our knowledge there are no comprehensive studies as to how these two properties would change with cell age. As a first approximation to the process of aging, we measured the bending elastic modulus of cells treated with DHEA, but found no significant alterations from untreated cells (data not shown). DHEA inhibits glucose-6-phosphate dehydrogenase (G6PD) activity, and there are contradictory reports on RBC deformability in G6PD-deficient subjects (83-85), but again, the methods used to assess cell deformability did not necessarily mean measuring the membrane bending elastic modulus. A detailed study of the effect of aging on RBC membrane physical properties (bending, shear, area elastic moduli and membrane electrostatic potentials) falls beyond the scope of the present study. Even though the membrane modification studies suggest that cell aging is a factor determining cell susceptibility to toxin, it would be too speculative to also attribute the correlations we established in Figure 8A and B solely and exclusively to RBC age. It is also notable that we found no significant correlation between the age of the healthy donors (a parameter different from individual cell age in the same population) and the susceptibility of their RBCs to PLY (data not shown). Other factors are bound to play a significant role.

One of these factors is likely to be the membrane cholesterol content. It has been established that the presence of membrane cholesterol is an essential condition for successful insertion of PLY into membranes (1) and depletion of membrane cholesterol impairs the haemolytic activity of PLY (52). Natural variation in cholesterol content between different cells could then be responsible for the different binding of PLY to RBCs (Figure 3); our measurements of membrane bending modulus (Figure 8A) and membrane dipole potential (Figure 8B) point in the same direction. It is well known that inclusion of cholesterol in bilayer membranes of lipids with either two saturated chains or one saturated and one monounsaturated chain leads to increase of their bending elastic modulus (86-90). In membranes, cholesterol intercalates between lipid

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chains to form a highly ordered but laterally mobile liquid ordered phase, which is believed to be the basis of the membrane lipid rafts (91). This liquid ordered phase is characterised with higher magnitudes of its membrane dipole potential (59,92). Thus, the fact that stiffer membranes and membranes with higher dipole potential are more susceptible to lysis is likely to reflect higher cholesterol content.

Whilst it is recognised that CDC binding to the lipid membrane requires the presence of cholesterol, it is also clear that its role in this process is complicated (93,94), with significant differences (both quantitative and qualitative) between different CDC toxins. For example, studies using PFO revealed that membrane binding depends on the availability of 'free cholesterol' at the membrane surface and does not correlate with the presence of detergent-resistant domains (93). In contrast, PLY has been reported to bind to cholesterol-rich lipid raft microdomains in corneal epithelial cells (95). Such differences suggest that the composition and organisation (and hence physical properties) of the lipid bilayer itself is likely to be a key regulator of the interaction of CDCs with the membrane.

We also found that cell morphology has an effect on membrane susceptibility to PLY, with discocytes being more resistant than stomatocytes (Figure 4). Interestingly, in a previous study investigating the dependence of the membrane dipole potential in RBCs and ghosts on membrane curvature (77), we found that stomatocytes are characterised with higher membrane dipole potentials compared to discocytes, which could also have an effect on PLY recruitment to the membrane (cf. Figure 8B). Additional imaging experiments with echinocytes revealed that toxin distribution along the surface of the echinocytic cells was non-uniform, with the majority of toxin clustering onto the highly curved membrane projections (Figure 4C). These observations suggest that PLY may have curvature preference when binding to or diffusing along the membrane. Further studies would be necessary to clarify whether PLY has an intrinsic curvature preference or the effect is caused by curvature-driven sorting of lipids in the plasma membrane (96). If this is the case, such spatially restricted distribution may serve to effectively increase the local toxin concentration, leading to shorter diffusion distances and faster formation of oligomers, hence shorter lysis times.

Membrane modification and cell susceptibility to PLY–It has previously been shown that reduction of extracellular calcium strongly enhances the lytic capacity of PLY due to increased membrane binding (97). One of the main findings of this study suggests that cell susceptibility to PLY also critically depends on the oxidative and/or other chemical stress the membrane has been subjected to prior to interaction with the toxin (Figure 5). In addition, it demonstrates non-universality of the effect of different oxidative agents, since the outcome, in terms of cell resistance to toxin, critically depends on the mode of action of each oxidant. This is evident by comparing the effects of the two oxidative agents used, H_2O_2 and cumOOH. H_2O_2 is water-soluble and readily partitions in the cytoplasm once it has crossed the lipid bilayer, where its primary target is haemoglobin. Oxidation and denaturing of haemoglobin leads to the formation of spectrin-globin complexes, changes spectrin network organisation and also causes clustering of the transmembrane protein Band 3 (64,98-101). Although H_2O_2 may affect the molecular organisation in the lipid bilayer (99), the transbilayer lipid distribution is not affected and its overall effect on the lipid bilayer is limited (64,77,99), hence the lack of effect on the susceptibility of RBCs to PLY. On the other hand, direct oxidation of the lipid bilayer membrane with the membrane-bound cumOOH drastically affects the PLY-RBC interactions and makes the membrane much more resistant to toxin. This could be due to the chemical modification of PLY receptors on the membrane surface (40) and/or oxidation of cholesterol that could modulate the conformation of glycans necessary for the successful binding of the toxin to the RBC membrane (102). Direct cholesterol oxidation (103) will also affect the lateral microdomain organisation of the lipid membrane (104-106), which could impair membrane insertion of the toxin, since PLY has been reported to bind to cholesterol-rich lipid raft microdomains (95). As a result, the membrane is rendered more impervious to toxin. Lipid oxidation also has an effect on the physical state of the membrane. We have previously shown that cumOOH leads to tighter in-plane lipid packing as demonstrated by an

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increase in the membrane dipole potential (77), as well as increased membrane bending and shear rigidity (64) (for a discussion of the membrane physical properties see above). Such changes in lipid packing may result in reduced ability of the toxin to insert into the plasma membrane.

In contrast to the effect of cumOOH, aging cells artificially using DHEA leads to lower resistance to PLY. DHEA inhibits glucose-6-phosphate dehydrogenase (G6PD) activity, which results in reduced levels of NADPH, an essential molecule in the cell's antioxidant defence system. Therefore, these cells are characterised with higher exposure to oxidative stress (presumably under conditions more similar to those *in vivo*), yet their response to PLY differs from both H_2O_2 and cumOOH-treated cells. This, once again, demonstrates that the general term 'oxidative stress' is insufficient in describing the effect of oxidative agents on membrane response to toxin and that the mechanism of action of each oxidant should be considered on a case-by-case basis.

The final membrane modification we investigated, lipid scrambling caused by calcium ionophore A23187, led to increased cell resistance to PLY that correlates with impaired toxin binding. We designed this experiment to mimic aspects of eryptosis (the analogue of apoptosis in nucleated cells), which is characterised, amongst other processes, by lipid scrambling and exposure of PS on the outer leaflet of the lipid bilayer (58). Our results show that lipid scrambling is a factor for increased cell resistance to not only PLY (Figure 5) but also to the related toxin PFO (data not shown), which suggests that cells set on the path of programmed death are also less likely to haemolyse under the lytic action of the toxin. This could be understood in terms of the asymmetry of the RBC lipid bilayer membrane. In human RBCs lipid species, such as PS and phosphatidylethanolamine (PE), are much more abundant in the inner, cytoplasmic leaflet, whereas phosphatidylcholine (PC) and sphingomyelin (SM) are found in larger concentrations in the outer leaflet (107). Scrambling of lipids would change the lipid composition in the leaflets as well as their lateral lipid organisation. This will ultimately affect the interaction between the toxin and the membrane (see Figure 7), since the toxin is expected to be attuned to effective interactions with the outer surface of the cell membrane, with which it establishes the first contact.

These observations lead to the conclusion that at least one of the factors for the variability in the response of cells within the same population to toxin is likely to be the chemical and/or oxidative prehistory of each individual cell, which would be determined by the cell age in the circulation and the relevant health status of the individual. Cell modifications as a result of disease (e.g. conditions characterised by high levels of oxidative stress, such as diabetes (108)) may lead to altered susceptibility to virulence factors, consistent with our findings that RBCs from individuals with diabetes show increased resistance to PLY and PFO relative to healthy RBCs (Figure 10). Susceptibility to CDCs may also be altered in diseases that affect the RBC cholesterol content, such as acute coronary syndrome where the cholesterol content of the erythrocyte membranes is increased (109) or in diseases that are characterised by PS externalization, such as sickle cell anaemia (110), sepsis (111) and systemic sclerosis (112).

Susceptibility of RBCs from individuals with diabetes to PLY–Our cell modification studies provide a framework for understanding the diversity of response to PLY in RBCs from individuals with diabetes. We found that RBCs from individuals with higher levels of Hba1c, which presumably have been subjected to higher glucose concentrations or resided in hyperglycaemic milieu for longer periods of time, were more resistant to the toxin's lytic action (Figures 9 and 10A). Increased resistance to PLY in RBCs from individuals with diabetes and higher levels of Hba1c could be understood in terms of elevated oxidative stress, to which the cell membrane is exposed in diabetes, and its consequent biochemical and biophysical modifications. Numerous studies have demonstrated that oxidative stress levels are higher in diabetes and this plays an important role in the progression of the disease and its complications (113,114). This is a consequence of the elevated glucose levels, leading to abundance of free radicals generated through glucose oxidation as well as non-enzymatic glycation of proteins and their subsequent oxidation (114). As discussed above, higher levels of oxidative stress would cause modification of the bilayer lipid membrane

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(including lipids, cholesterol and membrane proteins) and/or PLY receptors on the surface, which in some cases may lead to increased resistance to PLY (cf Figure 5). In this context, Hba1c can be considered as a measure of the oxidative stress levels, which the cells have been exposed to. Further evidence for the altered RBC membrane physical properties in diabetes is presented in Figure 11, showing that for diabetic cells, the membrane shear elastic modulus is more than twice the value of age-matched controls. Such stiffening of the membrane is suggestive of the involvement of oxidative processes, as previously demonstrated (64,99,115), and supports our conclusion that increased haemolytic resistance of RBCs from diabetic individuals is due to oxidative modifications of their membranes.

To the extent that the RBC membrane is representative of plasma membranes of other cell types, our studies on RBCs from individuals with diabetes suggest that the increased association of *S. pneumoniae* with disease in individuals with diabetes may not necessarily be related to the direct and immediate haemolytic action of PLY. It is known that diabetic patients often have impaired immune functions (116) and this may outweigh the increased resistance of cells to the action of the toxin, providing other routes through which the adverse effects of *S. pneumoniae* could occur. Alternatively, the reduced haemolytic activity of PLY in individuals with diabetes may favour the initial survival and proliferation of *S. pneumoniae* in the blood. Such an interpretation is supported by a recent study showing that PLY with low hemolytic activity conferred an early growth advantage to *S. pneumoniae* in the blood compared to strains expressing PLY with full haemolytic activity (117). PLY also has non-cytolytic, complement-activating properties that act independently of its cytolytic activity (118,119).

It is important to note the differences between the two subsets of diabetic individuals investigated in this study (Figure 9A and B). The dependence of the susceptibility of RBCs to PLY on Hba1c appears to be much weaker in individuals treated with metformin (to the point of being statistically insignificant). Metformin is a common anti-hyperglycaemic agent for the treatment of type 2 diabetes and it is thought to help prevent complications by increasing cell sensitivity to insulin (120), thereby providing satisfactory glucose control. However, there is evidence that metformin may offer further benefits by reducing the levels of glyoxal and methylglyoxal and preventing the formation of advanced glycation end products (121,122). Recent studies have also suggested that metformin could reduce the production of reactive oxidative species (120,123). Our previous *in vitro* experiments on RBC membrane elasticity demonstrated that, whilst glycated RBCs are more susceptible to oxidative stress than normal cells, the metformin is able to ameliorate considerably the increased vulnerability of glycated cells to oxidative stress (124). These results suggest that oxidation-induced membrane modifications may be significantly reduced in the presence of metformin, and this could be the main factor explaining the difference in the response of diabetic cells to toxin between the two groups (Figure 9A and B).

Conclusion-In conclusion, our studies indicate that the diversity of response to PLY within a population of RBCs is influenced by the biophysical, biochemical and morphological properties of the plasma membrane and is also correlated to membrane modifications in diabetes. These results are not only relevant to understanding the interactions between pore-forming toxins and RBCs but also (to the extent that the RBC membrane serves as a model of eukaryotic cell membranes) to understanding the behaviour of toxins in tissues. We believe that our findings are relevant to other CDCs and similar methodology can readily be employed for assessing cell susceptibility to a variety of other pore-forming toxins.

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Author contributions: MBB conducted most of the experiments, analysed the results and wrote the paper with PGP. PGP designed research, analysed parts of the results and wrote the paper with MBB. MAK carried out the micropipette experiments. CPW and RWT conceived the idea for the project, coordinated the study and revised the manuscript. CEN prepared Figure 12 and assisted in the preparation of the manuscript. MKM generated, expressed and purified PLY and most of its derivatives. TJM assisted in the preparation of the manuscript and revised the manuscript. ACS, KMG and FC made contributions to the design of the research, recruited participants and acquired samples and data. All authors reviewed the results and approved the final version of the manuscript.

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FOOTNOTES
This work was supported by the Defence Science and Technology Laboratory (DSTLx1000075949), Porton Down, UK.

The abbreviations used are: PFT, pore-forming toxin; PLY, pneumolysin; PFO, perfringolysin O; CDC, cholesterol-dependent cytolysin; RBC, red blood cell; DPBS/BSA, DPBS buffer at pH 7.0-7.2 supplemented with 1 mg/mL bovine serum albumin; cumOOH, cumene hydroperoxide; DHEA, dehydroepiandrosterone; FPE, fluorescein-phosphatidylethanolamine; eGFP, enhanced green fluorescent protein; H_2O_2; hydrogen peroxide; PS, phosphatidylserine; Hba1c, glycated haemoglobin

Ethical approval disclosure
Ethical approval was granted by the NRES South West - Exeter REC committee, reference 10/H0206/67. Human blood samples obtained from the University of Exeter Medical School, NIHR Exeter Clinical Research Facility, Diabetes and Vascular Medicine Centre, Exeter, UK were processed in the NIHR Exeter Clinical Research facility following written informed consent by all participants.

FIGURE LEGENDS

FIGURE 1. Variation of RBC response to PLY. (*A*) Representative phase contrast images of RBCs exposed to PLY. Scale bar, 5 µm. (*B*) Average (± SEM) time course of haemolysis induced by PLY (118 ng/mL) in RBCs from 17 healthy individuals. (*C*) Individual time courses of haemolysis induced by PLY (118 ng/mL) in RBCs from three healthy individuals. (*D*) Dot plot of the percentage of live RBCs 30 minutes after exposure of RBCs from 17 healthy individuals to PLY (118 ng/mL).

FIGURE 2. Time dependence of the normalised contour radii for two cells from the same population exposed to PLY (59 ng/mL). The radii at each time point (R_i) are normalised with respect to the values before the addition of toxin (R_0). Arrows indicate the onset of cell lysis.

FIGURE 3. Human RBCs with prolonged resistance to eGFP-PLY show reduced toxin binding. (*A*) Representative DIC (top) and GFP fluorescence (bottom) images of RBCs incubated with eGFP-PLY (0.67 µg/mL). Lysed cells in the top image are characterised with faint outlines of their membranes. The cell with prolonged resistance to eGFP-PLY appears with a halo around its edge. Scale bar, 5 µm. (*B*) Correlation between GFP fluorescence intensity (hence eGFP-PLY concentration) on the surface of lysed and non-lysed cells. Each image had its background intensity subtracted and the GFP intensities of cells (n = 38) were measured 2 minutes after exposure to toxin using ImageJ software (53). Significant differences are indicated: P = 0.0028 (**), unpaired, two-tailed Student t test.

FIGURE 4. Effect of cell morphology on the susceptibility of human RBCs to PLY. (*A*) RBCs from 17 healthy individuals were incubated with PLY (118 ng/mL) and the percentage of lysed discocytes and stomatocytes in each population was determined after exposure to PLY for 15 minutes. Significant differences are indicated: P = 0.0211 (*), unpaired, two-tailed Mann-Whitney t test. (*B*) GFP fluorescence intensity of stomatocytes (n = 7) and discocytes (n = 7) after exposure to eGFP-Δ6PLY^{L363A} (1.12 µg/mL) for 2 min. Each image had its background intensity subtracted and the GFP intensities of cells were measured using ImageJ software (53). Significant differences are indicated: P = 0.0012 (**), unpaired, two-tailed Mann-Whitney t test. (*C*) Merged DIC and GFP fluorescence images of echinocytes showing the distribution of eGFP-Δ6PLY^{L363A} on the surface of the cell. The fluorescence from eGFP-Δ6PLY^{L363A} is shown in red. Scale bar, 5 µm.

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FIGURE 5. Haemolysis profiles of a population of human RBCs that has undergone different biochemical treatments: (▼) control, (□) H_2O_2, (▲) cumOOH, (○) DHEA, (○) calcium ionophore A23187. One representative experiment out of three is shown.

FIGURE 6. Flow cytometry and phase contrast microscopy analysis of control and calcium ionophore A23187-treated human RBCs labelled with annexin V. (*A*) Dot plots of side-scattered (SSC-A) versus forward-scattered (FSC-A) light. One representative experiment out of three is shown. (*B*) Representative phase contrast microscopy images of control and calcium ionophore A23187-treated RBCs. Scale bar, 5 μm.

FIGURE 7. Flow cytometry analysis of annexin V-labelled control and calcium ionophore A23187-treated RBCs before and after eGFP-Δ6PLY^{L363A} binding. Double fluorescence plots of red ($Ex_{633\ nm}/Em_{650\text{-}670\ nm}$, annexin V) and green fluorescence ($Ex_{488\ nm}/Em_{515\text{-}545\ nm}$, eGFP-Δ6PLY^{L363A}) of (*A*) control - before toxin, (*B*) calcium ionophore A23187 - before toxin, (C) control - after toxin, (*B*) calcium ionophore A23187 - after toxin. Q1 = green, Q2 = green and red, Q3 = red, Q4 = not green and not red.

FIGURE 8. Differences in the membrane physical properties of individual cells within a population of human RBCs are correlated with the susceptibility of cells to PLY. (*A*) Dependence of the red blood cell membrane bending elastic modulus on the time to lysis. Cells (n = 9) were exposed to 59 ng/mL PLY. One representative experiment out of three is shown. Linear regression line, R^2 = 0.52, P = 0.027 (*). (*B*) Dependence of the RBC membrane dipole potential on the time to lysis. Cells (n = 25) were exposed to 5.9 ng/mL PLY. One representative experiment out of three is shown. Linear regression line, R^2 = 0.40, P = 0.002 (**). (*C*) Dependence of the measured fluorescence intensity of FPE-labelled RBCs on the time to lysis. Cells (n = 108) were exposed to 5.9 ng/mL PLY. One representative experiment out of three is shown. Linear regression line, R^2 = 0.52, P = 0.029 (*).

FIGURE 9. Correlation between levels of Hba1c and susceptibility of RBCs from individuals with diabetes to PLY. (*A*) Samples (n = 13) derived from subjects with diabetes not on metformin therapy: R^2 = 0.410, P = 0.018 (*). (*B*) Samples (n = 23) derived from subjects with diabetes on metformin therapy: R^2 = 0.054, P = 0.285 (not significant). RBCs from individuals with diabetes were exposed to PLY (118 ng/mL) and the percentage of live cells after exposure to toxin for 30 minutes was plotted against levels of Hba1c.

FIGURE 10. RBCs from individuals with diabetes (●) show increased resistance to PLY (*A*) and PFO (*B*) relative to RBCs from healthy individuals (◆). Average (± SEM) time course of haemolysis induced by PLY (118 ng/mL) or PFO (72 ng/mL) in RBCs from healthy individuals (n = 17) and individuals with diabetes not on metformin therapy (n = 13). Cell lysis was monitored by phase contrast microscopy for 30 minutes.

FIGURE 11. Dependence of the measured projection length, L, on the applied pressure, ΔP (L and ΔP are scaled according to Equation (1)) for samples derived from subjects with diabetes (●) and from healthy controls (◆). Each point represents an average measurements for each group (n = *12* in the diabetic group and n = 14 in the healthy control group). The modulus of shear elasticity was evaluated from the gradient of the linear fits.

FIGURE 12. Isosurface of PLY monomer. (*A*) Ribbon representation of the PLY peptide backbone with the four domains numbered. The highly conserved tryptophan-rich loop and the cholesterol binding region at the base of domain 4 are shown in stick and ball representations, respectively. The two putative sugar-binding sites, site 1 near the conserved tryptophan-rich loop (in purple) and site 2 at the domain 3-domain 4 interface (grey), are shown in stick representation. (*B*) The corresponding PLY isosurface was

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drawn at -1 (red) and +1 (blue) contour levels as calculated and drawn using the APBS (125,126) add-on to PyMol (127). The field projecting from the PLY monomer is mostly, but not completely, negative.

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FIGURE 1

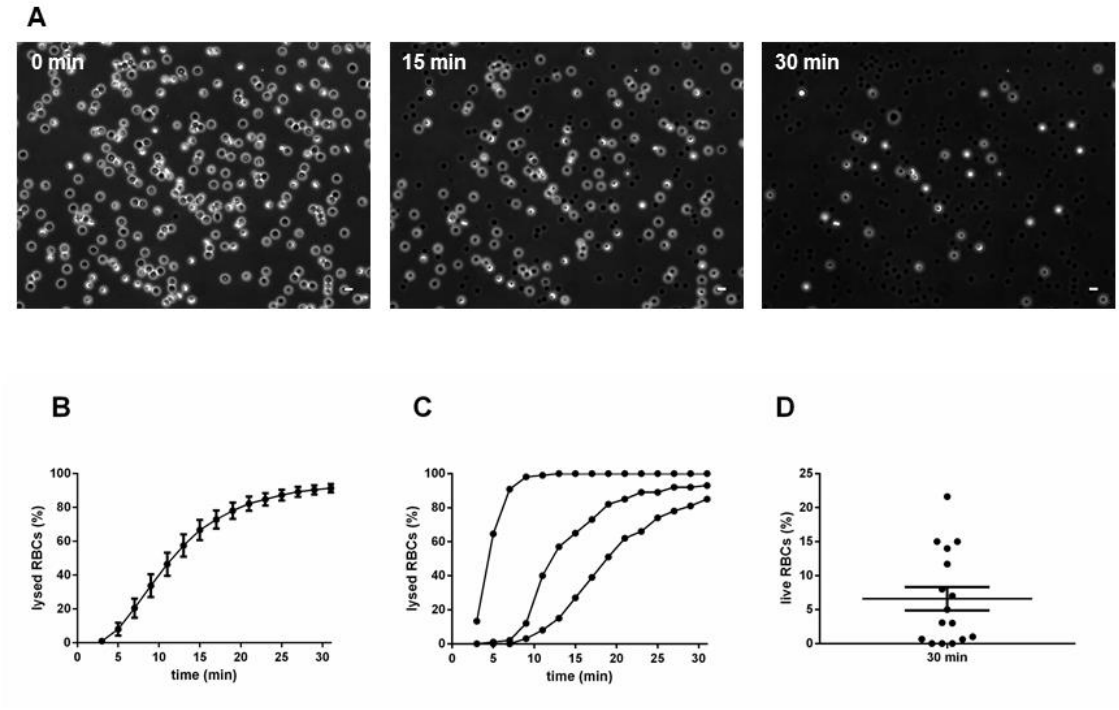

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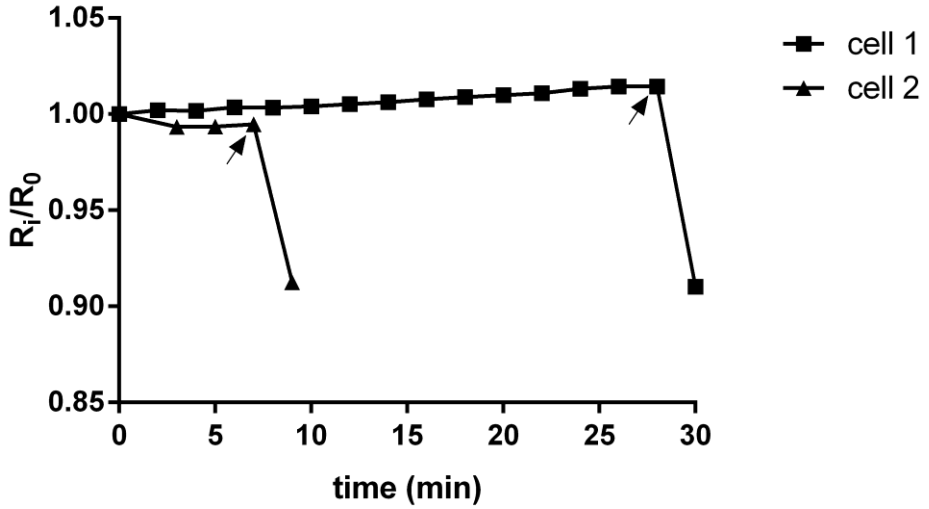
FIGURE 2



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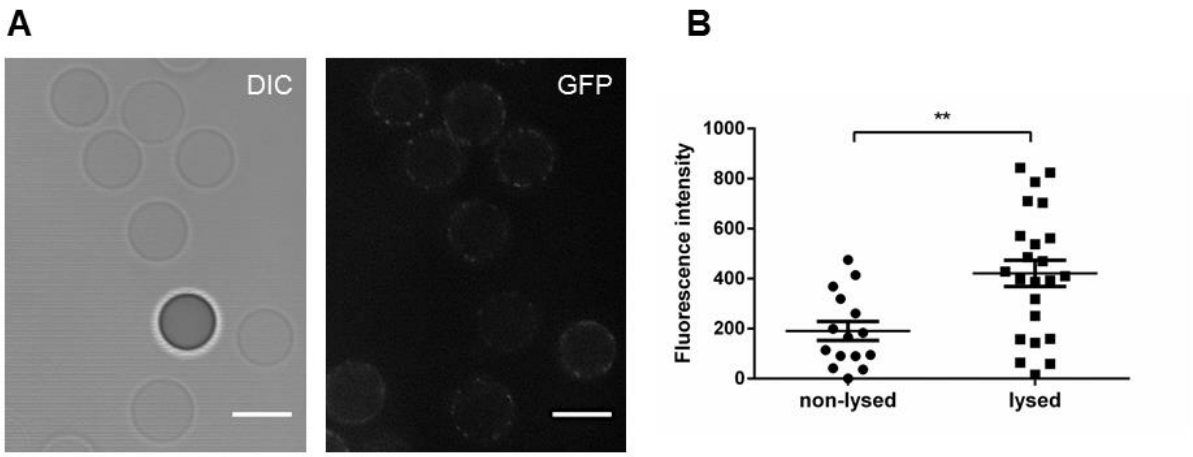

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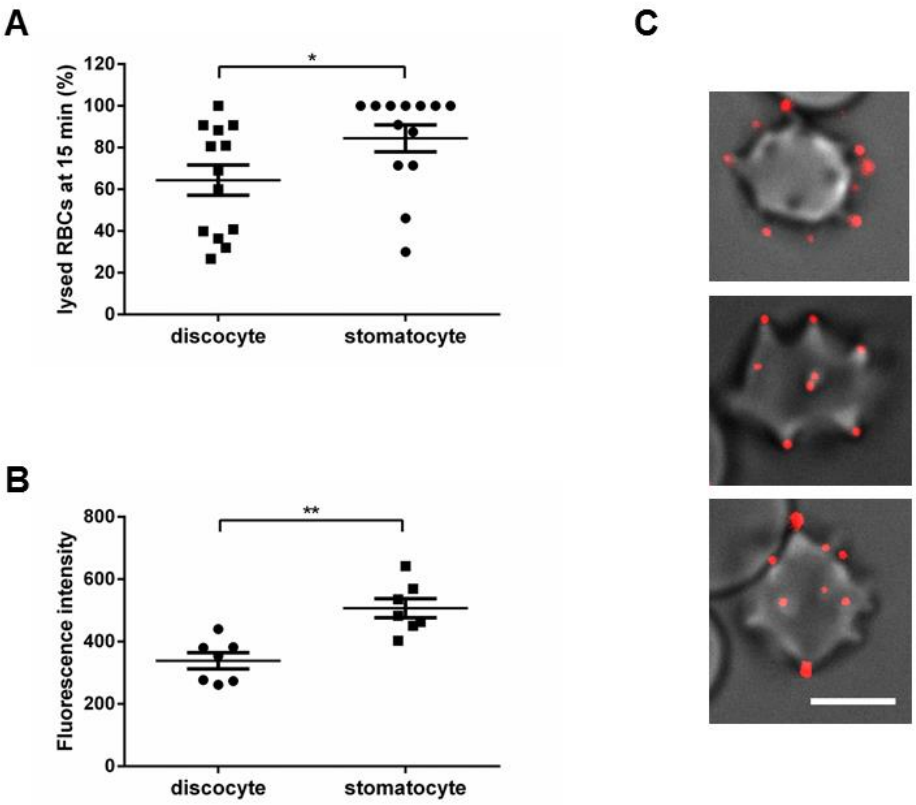

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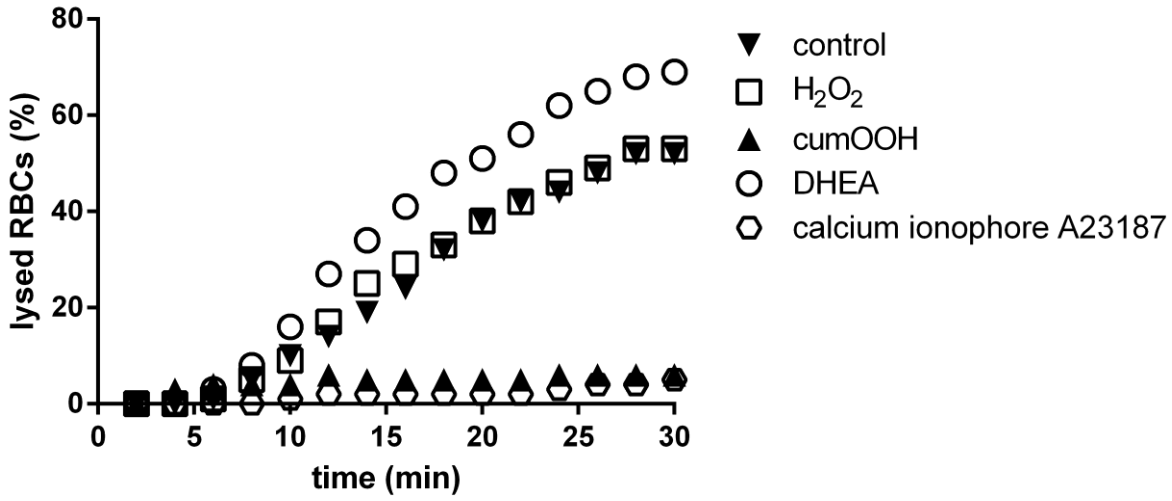
FIGURE 5



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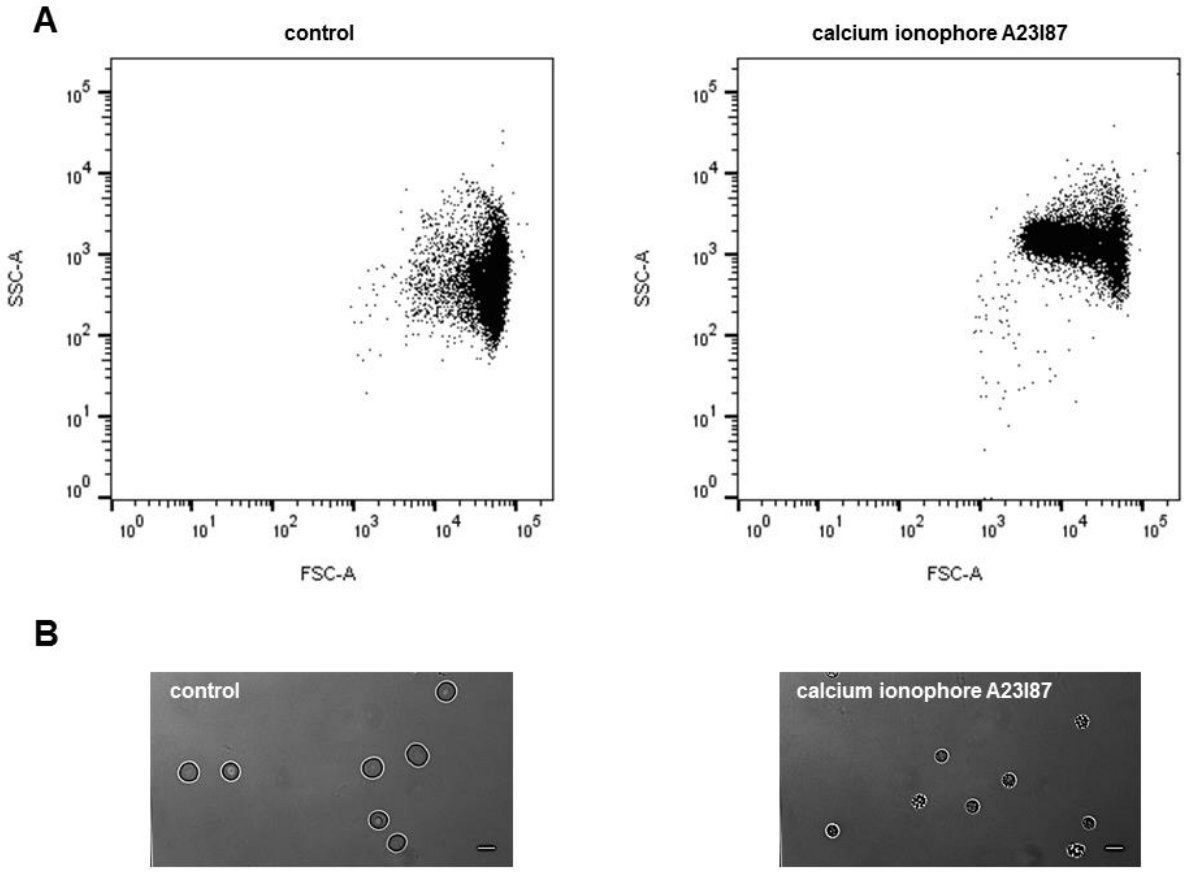

Figure 6

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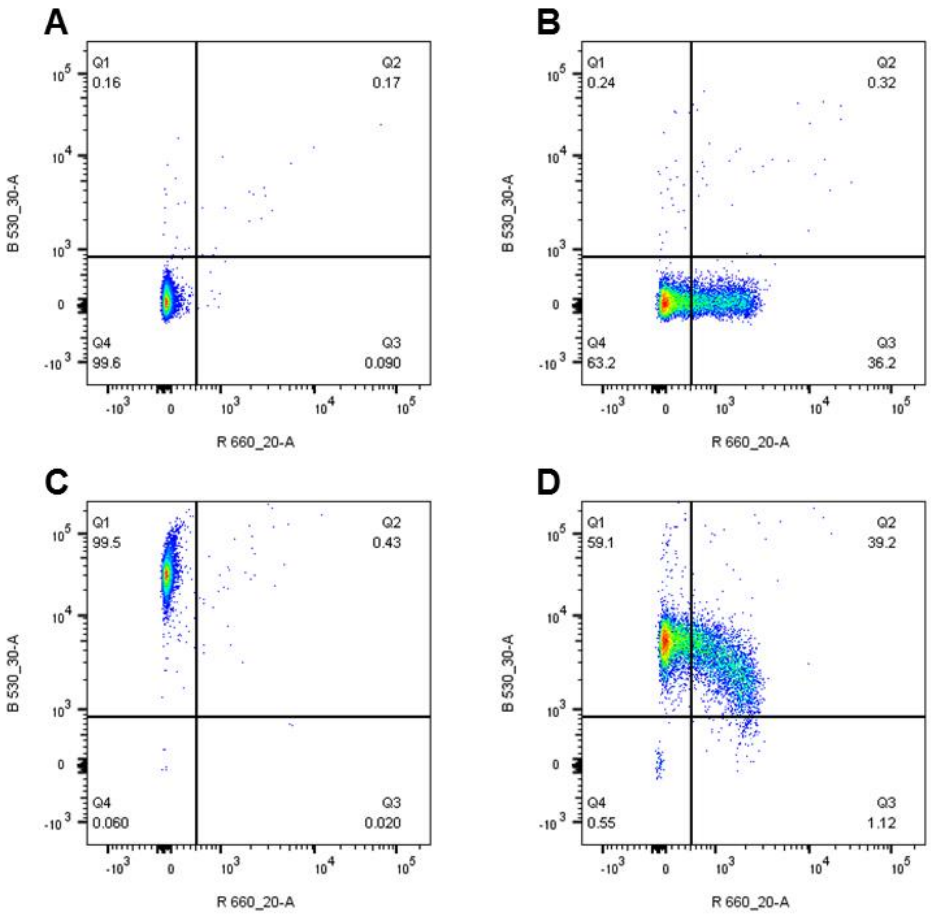

Figure 7

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FIGURE 8

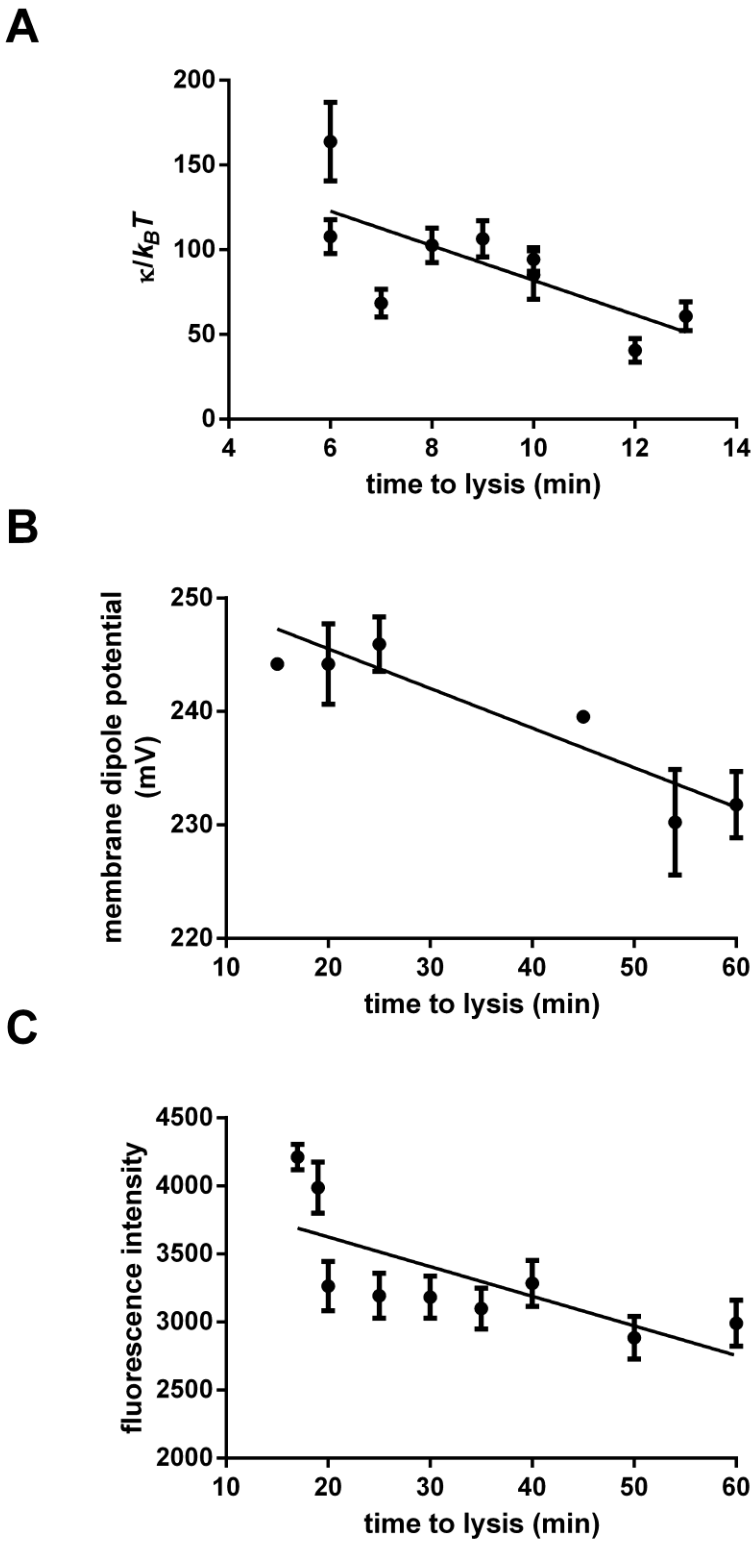

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FIGURE 9

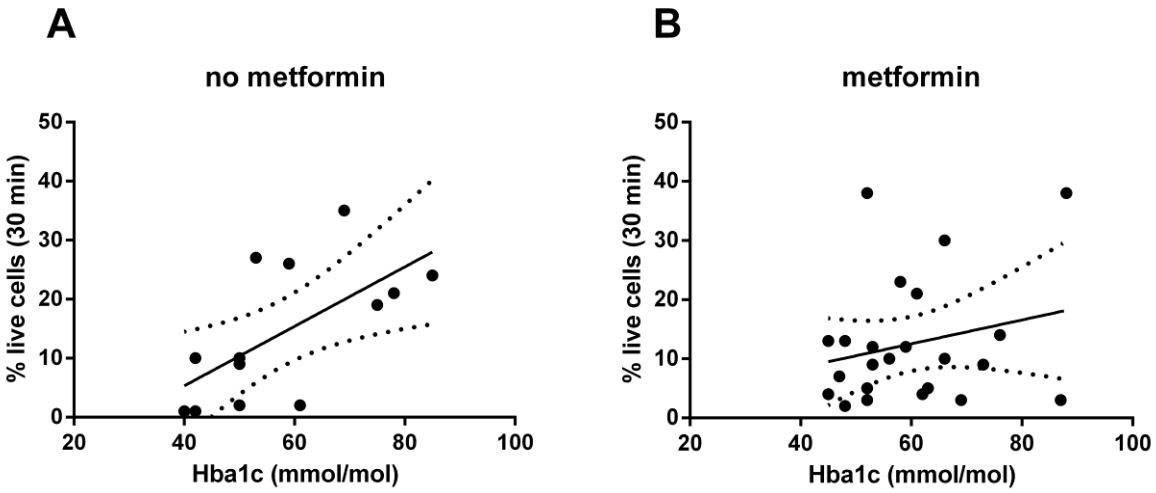

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FIGURE 10

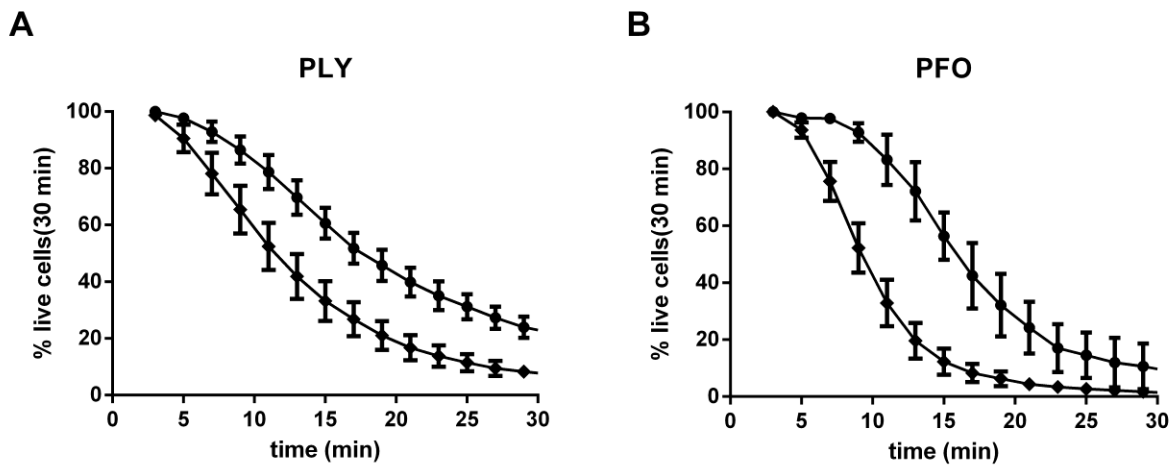

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FIGURE 11

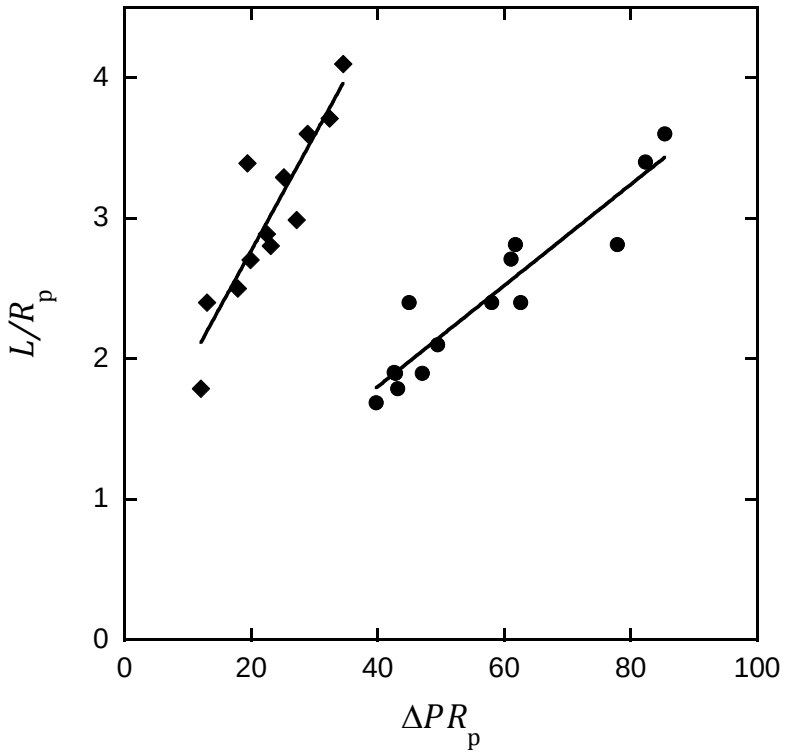

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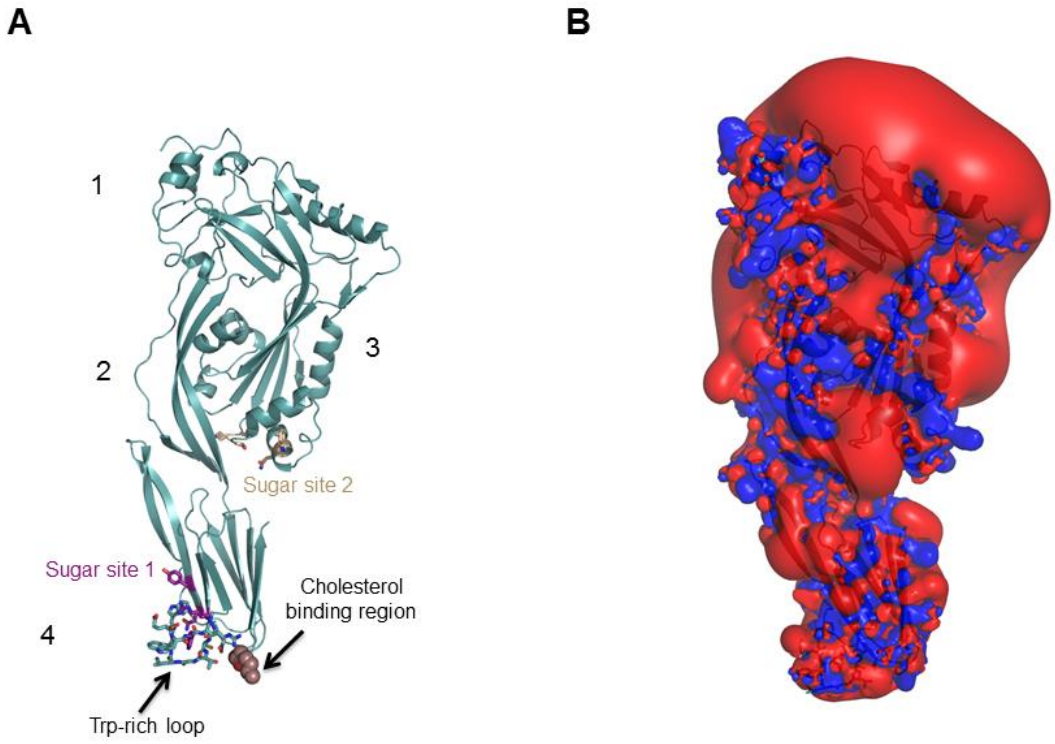
FIGURE 12



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Red Blood Cell Susceptibility to Pneumolysin: Correlation with Membrane Biochemical and Physical Properties

Monika Bokori-Brown, Peter G. Petrov, Mawya A. Khafaji, Muhammad K. Mughal, Claire E. Naylor, Angela C. Shore, Kim M. Gooding, Francesco Casanova, Tim J Mitchell, Richard W. Titball and C. Peter Winlove

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