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Innate Immunity

IgA2 ACPA Drives a Hyper-Inflammatory Phenotype in Macrophages via ATP Synthase and COX2

Luís Almeida[1] | Alice Bacon[2] | Mohan Ghorasaini[3] | Alwin J. van der Ham[1] | René E. M. Toes[2] | Martin Giera[3] | Bart Everts[1]

[1]Centre for Infectious Diseases, Leiden University Medical Centre, Leiden, The Netherlands | [2]Department of Rheumatology, Leiden University Medical Centre, Leiden, The Netherlands | [3]Centre for Proteomics and Metabolomics, Leiden University Medical Centre, The Netherlands

Correspondence: Bart Everts (b.everts@lumc.nl)

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ABSTRACT

IgA can form immune complexes (ICs) and activate myeloid cells via Fc alpha receptor-mediated signalling to secrete pro-inflammatory cytokines. It was previously described that of the two IgA subclasses (IgA1 and IgA2), IgA2 is more inflammatory than IgA1. However, the mechanisms underlying this differential pro-inflammatory potential remain poorly defined. Using anti-citrullinated protein IgA1 and IgA2 antibodies (ACPA) that are commonly found in rheumatoid arthritis (RA) patients and linked to chronic inflammation, we show here that, in macrophages, IgA2-ICs boost TLR-induced TNF and IL6 secretion, COX2 expression, and production of COX2-dependent lipid mediators to a higher level than IgA1-ICs. Metabolically, we found the amplification of TLR-induced cytokine production and COX2 induction by IgA2-ICs to be dependent on mitochondrial ATP synthesis, but not glycolysis. Finally, we found the potentiation of TLR-induced cytokine production by IgA-ICs to be COX2-dependent. Together this work points towards a key role for mitochondrial ATP synthesis in driving COX2 expression and subsequent IgA2-IC-dependent potentiation of TLR-induced cytokine production by macrophages. As such, our work provides new insights into the mechanisms underlying IgA2-induced inflammation in the context of RA. Thus, this may hold novel clues to be explored as therapeutic possibilities to target antibody-driven inflammation in chronic inflammatory diseases.

1 | Introduction

IgA is the most abundant antibody in the human body [1], primarily located in mucosal tissues as a dimer, where it plays an important role in both protection and maintenance of homeostasis [2]. However, IgA is also the second most common circulating antibody, where, unlike in the mucosa, it exists as both a monomer or dimer, lacking the secretory component [3]. This inherent characteristic of circulatory IgA allows it to bind to Fcα-receptor I (FcαRI) expressed by myeloid cells, such as macrophages, which has been linked to inducing pro-inflammatory cytokines, such as TNF and IL-6 [4].

Two subclasses of IgA exist: IgA1 and IgA2. Recent studies have described that IgA2 potentiates TLR-induced inflammatory responses in macrophages, dendritic cells (DCs), monocytes, and

Abbreviations: 12-HETE, 12-hydroxyeicosatetraenoic acid; ACC1, acetyl-CoA carboxylase 1; ACPA, anti-citrullinated protein antibody; AMP, adenosine monophosphate; ATP, adenosine triphosphate; BSA, bovine serum albumin; COX2, cyclooxygenase-2; CPT1A, carnitine palmitoyltransferase 1A; CS, citrate synthase; DC, dendritic cell; FASN, fatty acid synthase; FcR, Fc receptor; FcαR, Fcα receptor; GeoMFI, geometric mean fluorescent intensity; IC, immune complex; IgA, immunoglobulin A; IgG, immunoglobulin G; IL-6, interleukin-6; Indo, indomethacin; LOX, lipoxygenase; mTOR, mammalian target of rapamycin; Oligo, oligomycin; PAM, Pam3CSK4; PBS, phosphate buffer solution; PGE2, prostaglandin E2; PGF2α, prostaglandin F2α; RA, rheumatoid arthritis; SCENITH, single-cell energetic metabolism by profiling translation inhibition; TLR, toll-like receptor; TNF, tumour necrosis factor; TxB2, thromboxane B2.

Luís Almeida and Alice Bacon contributed equally to this work.

neutrophils more strongly than IgA1 [5–9]. However, the mechanisms by which IgA2 achieves this remain to be determined. IgA1 and IgA2 differ in their glycosylation profile and hinge regions. IgA1 has two conserved N-glycosylation sites and a hinge with an O-linked glycosylation-rich structure, while IgA2 has four conserved N-glycosylation sites and no O-linked sites [10, 11]. Although it has been suggested that differences in glycosylation affect IgA-receptor interactions [11, 12], it is still unknown how this translates into altered cellular responses in myeloid cells, leading to different inflammatory outputs.

It has been established that changes in the metabolism of myeloid cells are intimately linked to their function and activation states [13, 14]. In the context of FcR-driven inflammatory responses, it was shown that IgA immune complexes (ICs) enhance the synthesis of pro-inflammatory cytokines in DCs and that this is achieved through glycolytic reprogramming [6, 15]. In a similar fashion, it was demonstrated that IgG boosts TLR-induced cytokine synthesis in macrophages by inducing a switch towards glycolytic metabolism [16].

Moreover, IgG-ICs have been shown to induce prostaglandin E_2 (PGE_2) synthesis in macrophages [16]. It is well known that lipid mediators, such as PGE_2, play an important role in regulating inflammatory responses, including that of macrophages, through autocrine and paracrine signalling [16–20]. However, it is still unknown whether differential metabolic reprogramming or COX2/PGE_2 expression plays a role in the ability of IgA1 and IgA2 to induce distinct inflammatory responses.

Therefore, in this study, we aimed to investigate the difference in inflammatory potential and underlying mechanisms of IgA1 and IgA2 in human monocyte-derived macrophages in the context of TLR co-stimulation. We found that IgA2-ICs synergize more strongly with TLR stimulation than IgA1-ICs, as evidenced by higher levels of TNF and IL-6 induction. Additionally, we show a metabolic link between IgA2 signalling and COX2 induction, whereby ATP synthase is crucial for the aforementioned effects of IgA2, but not IgA1, on macrophage activation. We also show that this IgA2-induced phenotype is associated with increased PGE_2 synthesis and, correspondingly, with an augmented expression of COX2. Finally, we describe that, by targeting COX2 activity with indomethacin, we are able to abrogate the boosting effects of IgA2 in macrophage inflammatory potential, albeit this effect seems to be independent of PGE_2.

In summary, our work links IgA2-induced inflammation, with COX-dependent mediators, and ATP Synthase activity in macrophages.

2 | Results

2.1 | IgA2 Synergizes With TLR1/2 Signalling to Induce a More Inflammatory Phenotype in Macrophages via Syk

We first aimed to assess the inflammatory potential of IgA1 and IgA2 on human macrophages. We decided to focus on IgA ACPAs, which are known to play an important role in the inflammatory response in RA. This disease is characterized by chronic inflammation of the joints, specifically the synovium. One of the hallmarks of this inflammatory environment in the synovium is the crosstalk between macrophages and ACPAs. Importantly, the levels of IgA ACPAs and rheumatoid factor-specific IgA in the synovium are significantly increased in patients with RA and are associated with RA flares [21, 22]. Moreover, higher IgA2:IgA1 ratios have been associated with a worse disease score in RA patients [5], making IgA1 and IgA2 ACPAs highly clinically relevant to the study of this interaction. To do so, we employed an in vitro model whereby we cultured human monocyte-derived macrophages in plates pre-coated with citrullinated antigen (CCP2), and with equal concentrations of either monoclonal IgA1 or IgA2 ACPA (Figure S1A–C)—both having the same patient-derived variable domain sequence—to simulate ACPA-ICs, in the presence or absence of PAM3CSK4 (PAM), a TLR1/2 ligand, since many danger associated molecular patterns associated with RA have been shown to signal via these TLRs [23]. Furthermore, we opted to differentiate macrophages with GM-CSF due to its role in RA in driving macrophage differentiation, M1-polarization, Fcα receptor expression, and subsequent inflammation and cartilage degradation [24–30]. Additionally, GM-CSF has been implicated in regulating macrophage proliferation, glycolysis, lipid metabolism, and mitochondrial function [31, 32]. Therefore, macrophages from a GM-CSF background present themselves as a relevant model to study macrophages in the context of RA and IgA binding, along with their metabolism and inflammatory responses.

Upon dual stimulation with PAM and IgA, we found that IgA2, but not IgA1, synergized with the TLR signalling to induce TNF and IL-6 (Figure 1A,B). In addition, COX-dependent lipid species, including PGE_2, were also more strongly upregulated following IgA2 stimulation (Figure 1C; Figure S2A,B). However, this was not the case for LOX-dependent species (Figure 1D). The increased production in PGE_2 was paralleled by potentiated COX2 expression (Figure 1E). Finally, we found the effect of IgA2 to be dependent on syk, a crucial mediator of FcR-signalling, as syk inhibition abrogated IgA2-driven potentiation of TLR-induced cytokine synthesis and COX2 expression, with no decrease in cell viability (Figure S3A–D).

Together, these data show that IgA2 has a stronger pro-inflammatory effect than IgA1 on macrophages and further suggest that this is syk-dependent.

2.2 | IgA2 and PAM Co-Stimulation Induces Minor Metabolic Changes in the Mitochondrial Compartment

Since IgA has been previously shown to reprogram DCs into a pro-inflammatory phenotype by potentiating glycolysis [15], and since PGE_2 was shown to have an effect on mitochondrial metabolism in macrophages [33], we aimed to explore whether IgA2-driven inflammatory responses were accompanied by, and dependent on, metabolic rewiring. Using a metabolic flux analyser to measure OCR (oxygen consumption rate) (Figure 2A) and ECAR (extracellular acidification rate) (Figure S4A), we found that IgA1 and IgA2 did not promote significant changes in glycolysis (Figure S4B–D), basal respiration (Figure 2B), or ATP synthesis (Figure 2C) 24 h after stimula-

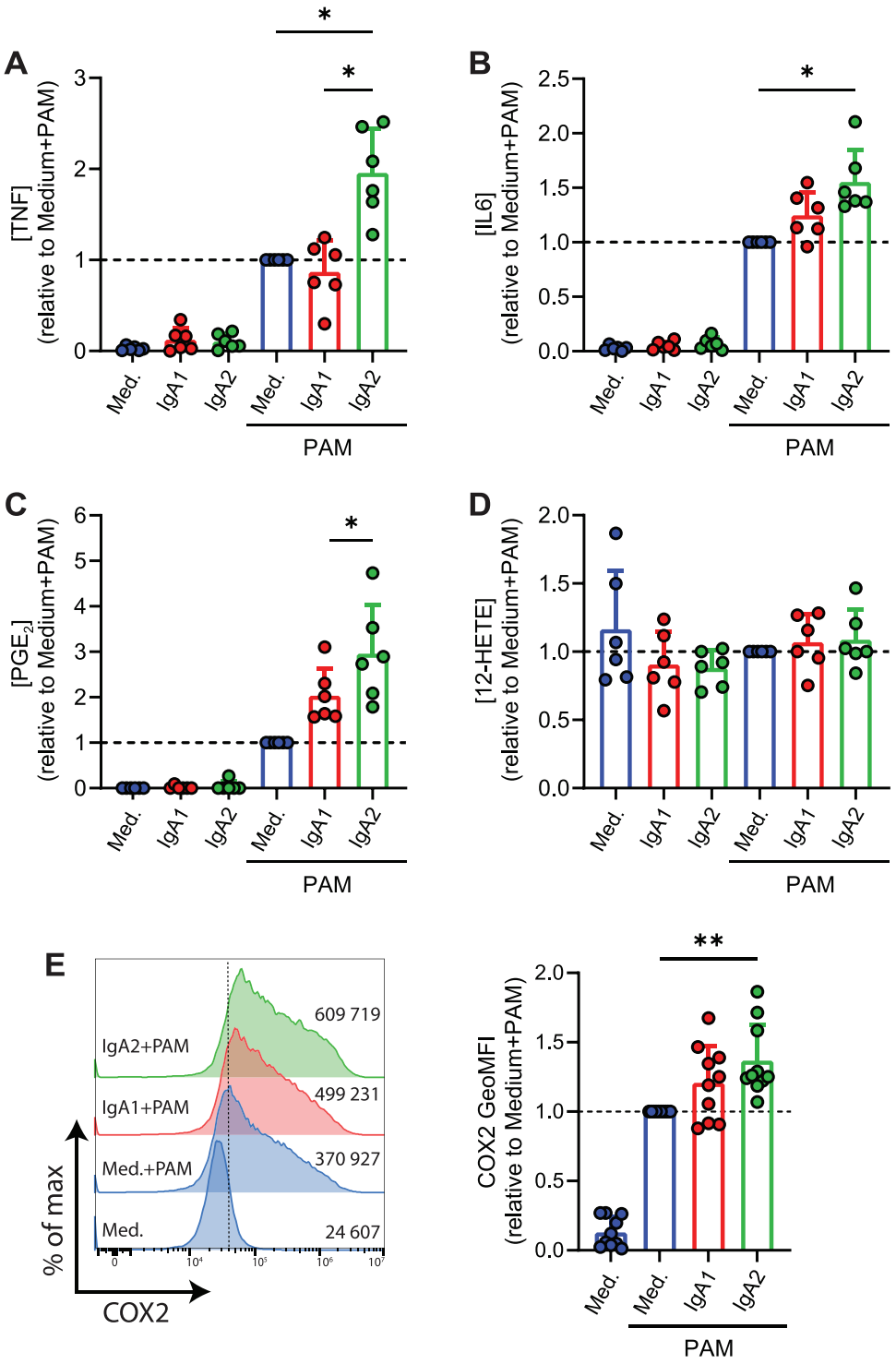

FIGURE 1 | IgA synergizes with PAM to potentiate TLR-induced cytokine production and COX2 expression in macrophages. Levels of (A) TNF, (B) IL-6, (C) PGE_2, and (D) 12-HETE measured in supernatants following stimulation of cells with indicated compounds. Levels of (A) TNF and (B) IL-6 were measured with ELISA as described in materials and methods. (E) Representative histogram of COX2 expression for each indicated stimulus (left); values represent the pooled average raw GeoMFI of all experiments. (Right) Normalized COX2 GeoMFI of cells treated with indicated stimuli. (A)–(D) are representative plots of six donors from two independent experiments (mean ± SD). (E) is a representative plot of 10 donors from five independent experiments (mean ± SD). All data were analysed using a paired one-way ANOVA. $^{*}p < 0.05$, $^{**}p < 0.01$.

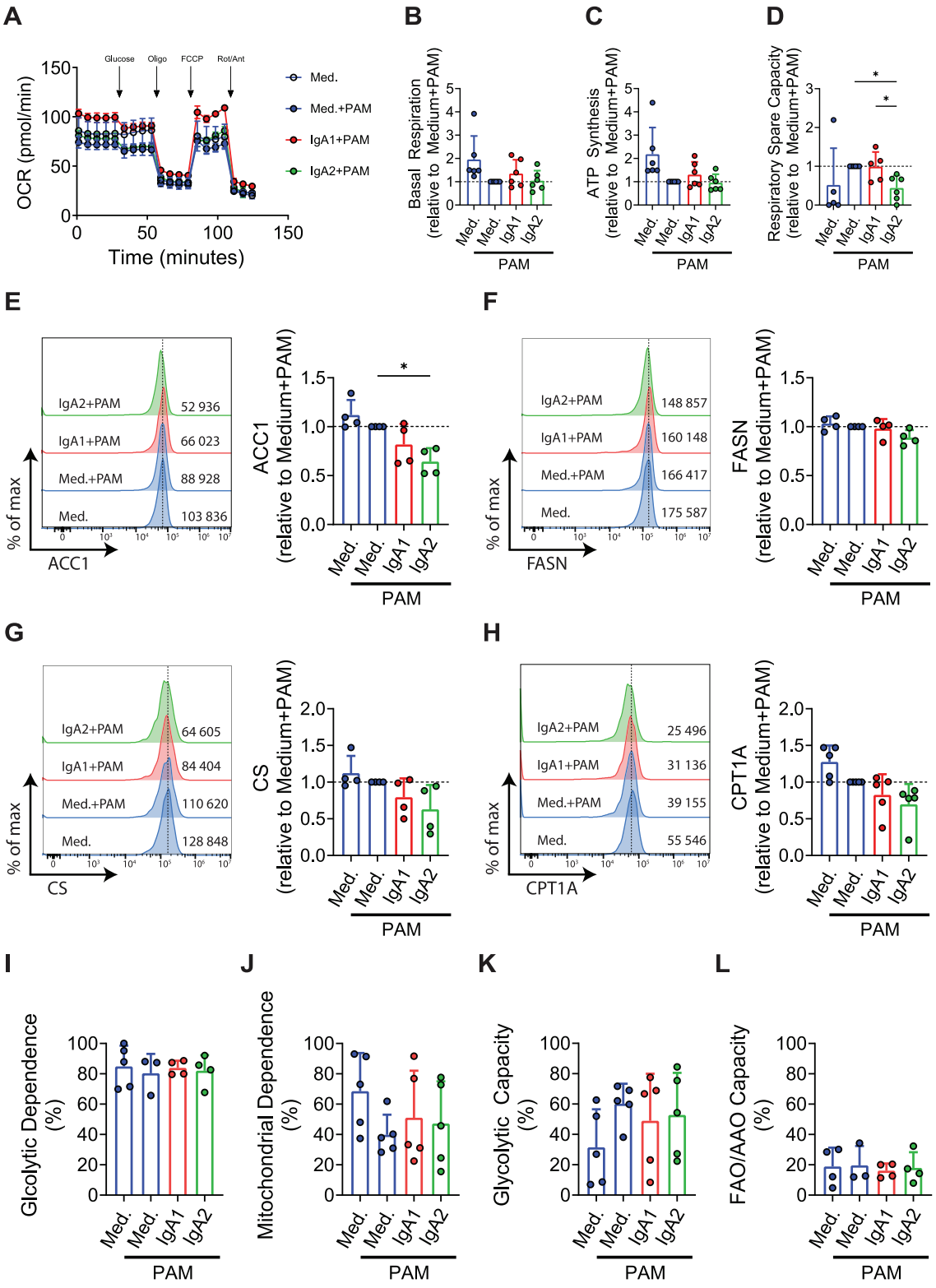

FIGURE 2 | IgA2-PAM co-stimulation induces metabolic changes in the mitochondrial compartment. Representative plots of (A) Oxygen consumption rate, (B) Basal respiration rate, (C) ATP Synthesis, and (D) Respiratory Spare Capacity in cells stimulated for 24 h with indicated stimuli, measured using an extracellular flux analyser (Seahorse). Representative histograms (left) and normalized GeoMFI (right) of (E) ACC1, (F) FASN, (G) CS, and (H) CPT1A measured via FACS following 24 h stimulation of cells with indicated stimuli. Values in histograms represent the pooled average raw GeoMFI of all experiments. (I) Glycolytic dependence, (J) mitochondrial dependence, (K) glycolytic capacity, and (L) fatty acid and amino acid oxidation (FAO/AAO) capacity measured using SCENITH and calculated as described in materials and methods. (A)–(D) are representative plots of six donors from three independent experiments with outliers removed (mean ± SD). (E)–(G) are representative plots of four donors from two independent experiments (mean ± SD). (H) is a representative plot of five donors from three independent experiments (mean ± SD). (I)–(L) are representative plots of five donors from two independent experiments (mean ± SD). All data were analysed using a paired one-way ANOVA. *$p < 0.05$.

tion, although IgA2-stimulated cells appeared to have a lower respiratory spare capacity (Figure 2D). This was also associated with trends towards lower expression of mitochondrial enzymes 24 h following stimulation with IgA2 (Figure 2E–H), albeit no change was observed in mitochondrial membrane potential (Figure S4E). A SCENITH assay to assess the dependence on mitochondrial metabolism and glycolytic metabolism for ATP-dependent translation, revealed no clear differences (Figure 2I–L). Together this indicates that, in human macrophages, IgA1 and IgA2, except for altered mitochondrial respiratory spare capacity, induce minor changes in core metabolic pathways.

2.3 | Inhibition of Mitochondrial Respiration Abrogates the Pro-Inflammatory Effects of IgA2

Next, we evaluated whether the potentiated inflammatory profile induced by IgA2 was dependent on any core metabolic pathway activity, using various inhibitors. While blocking glycolysis with 2-deoxy-D-glucose (2-DG), slightly affected TNF production, blocking glycolysis with 2-DG, or fatty acid oxidation with etomoxir, did not affect the production of IL-6, nor COX2 expression (Figure S5A–C). Interestingly, blocking ATP Synthase with oligomycin abrogated the potentiating effects of IgA2 on both TNF (Figure 3A) and IL-6 (Figure 3B) production. Additionally, oligomycin also prevented the boosting effect of IgA2 on COX2 expression (Figure 3C). Correspondingly, oligomycin, and the general COX inhibitor indomethacin (Indo), but not 2-DG or etomoxir, were able to block IgA2-induced PGE_2 synthesis, and other COX2-dependent mediators (Figure 4A–C). Of note, there were no effects on cellular viability by the inhibitors used, apart from minimal effects by 2-DG (Figure S6). Interestingly, oligomycin showed no effect on IgA1-induced potentiation of COX2-derived products by TLR-stimulated macrophages (Figure 4D–F). Additionally, LOX-dependent mediators were unaffected by oligomycin treatment upon IgA2 or IgA1 stimulation (Figure 4G,H). This together suggests that the effects of IgA2 on TLR-induced cytokine production and COX2 activity are dependent on ATP Synthase activity.

2.4 | The Pro-Inflammatory Effects of IgA2 Are Supported by COX2 Activity

As PGE_2 is a well-known signalling lipid in macrophages [16–20], we wondered if this IgA2-potentiated inflammatory profile was dependent on COX2 induction and subsequent PGE_2 synthesis. To test this, we stimulated cells with IgA in the presence of PAM and indomethacin. Upon inhibiting COX activity, the enhancement of IgA2 on TNF (Figure 5A) and particularly IL-6 (Figure 5B) production was reduced. Furthermore, in a similar fashion as observed with oligomycin (Figure 3B), Indomethacin not only prevented IgA2 potentiation on IL-6 production, but it also decreased the production of IL-6 by PAM in the absence of IgA, thus showing that PAM as well as the potentiated response by IgA2 requires COX2 activity for IL-6 production by these cells.

Since IgA2 was boosting COX2 expression and PGE_2 synthesis, and indomethacin reduced the pro-inflammatory cytokine production by IgA2/PAM co-stimulation, we tested whether we could rescue these effects by adding PGE_2 to the medium of these cells. Interestingly, the addition of PGE_2 had no effect on the synthesis of IL-6 upon inhibition of COX with indomethacin or oligomycin (Figure S7), indicating the synergistic effect of IgA2 and PAM on the pro-inflammatory phenotype of macrophages is dependent on COX, but possibly independent of PGE_2 synthesis.

3 | Discussion

Previous studies have shown that IgA2 drives stronger pro-inflammatory signalling in both macrophages and neutrophils, compared with IgA1 [5]. Correspondingly, higher ratios of IgA2:IgA1 ACPA have been correlated with worse RA scores [5], pointing to a more detrimental role of IgA2 than IgA1 in RA pathology. In our study we have further extended these findings, by showing that, in macrophages, IgA2 ACPA has the ability to induce higher levels of TNF and IL-6, both when compared with TLR1/2 ligation alone or TLR1/2 and IgA1 ACPA co-stimulation. Furthermore, we also found that this increased inflammatory signalling was associated with both higher expression of COX2 and higher levels of COX2-dependent lipid mediators, specifically PGE_2. Interestingly, while no major changes were seen in OCR or glycolysis, IgA2 did show a decrease in respiratory spare capacity. These data align with previous work done by van den Bossche et al. [34] showing that M1-polarized macrophages both present some mitochondrial dysfunction and display a lower metabolic elasticity, unlike M2 which can more easily adapt their metabolism if one pathway is blunted. However, despite a lack of clear reprogramming of core metabolic pathways by these macrophages, we observed a dependence of IgA2 on ATP Synthase for TLR-induced cytokine production, COX2 expression and subsequent PGE_2 levels. We also report that indomethacin, a general COX2 inhibitor, was able to reduce the inflammatory potential of IgA2.

The distinct inflammatory effects of IgA2 and IgA1 have been postulated to be driven by differences in their glycosylation profiles. These differences may alter interaction strength with the FcαR, and thus also downstream signalling pathways, and ultimately TLR-induced cytokine production. IgA has been shown to also signal via MAPK and MyD88 [35, 36], which are known mediators of TLR-driven cytokine responses and COX2 expression [37–42]. This overlap of signalling pathways, together with the recent findings that IgA2 induces stronger binding and activating signalling than IgA1 [5], could explain why IgA2 induces higher expression of COX2 and drives a stronger inflammatory response than IgA1.

We have previously shown that IgA-ICs induce, and depend on, glycolytic reprogramming to render tolerogenic DCs pro-inflammatory [15], with no effect or dependency on mitochondrial metabolism. In contrast, our current observations in macrophages show no role for glycolysis, but instead point to a crucial role for mitochondrial ATP synthase in supporting the pro-inflammatory effects of IgA2. This is in line with other studies that have shown that in an L929 fibrosarcoma cell line, a functional electron transport chain (ETC) is required for proper NFκB activation, and TNF and IL-6 synthesis. Furthermore, tampering with either ETC complexes or ATP Synthase resulted in a reduction of these cytokines in whole blood [43, 44]. An additional

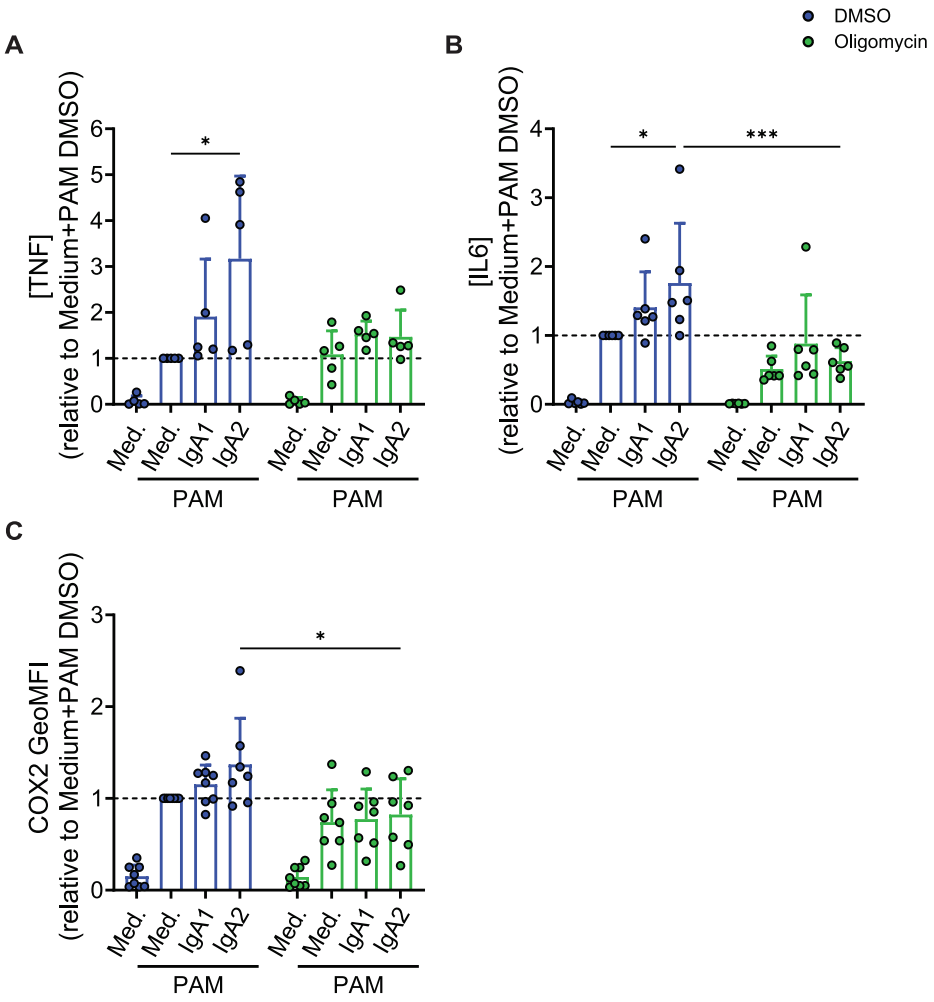

FIGURE 3 | Inhibition of ATP Synthase with oligomycin abrogates the pro-inflammatory potentiation effects of IgA2. Levels of (A) TNF and (B) IL-6 measured in supernatants with ELISA following stimulation of cells with indicated stimuli in the presence of DMSO (blue) or Oligomycin (green). (C) Normalized COX2 GeoMFI of cells treated with indicated stimuli in the presence of DMSO (blue) or Oligomycin (green). (A) is a representative plot of five donors from three independent experiments (mean ± SD). (B) is a representative plot of six donors from three independent experiments (mean ± SD). (C) is a representative plot of eight donors from four independent experiments with outliers removed (mean ± SD). All data were analysed using a paired two-way ANOVA, with matched values both stacked and spread across a row, using Tukey's multiple comparisons test, with a single pooled variance. $^{*}p < 0.05$, $^{***}p < 0.001$.

explanation as to why ATP synthase is required for IgA2-driven inflammatory responses in macrophages may be connected to mTOR and its role in cytokine and COX2 expression, and promotion of inflammation [42, 45]. Since mTOR is inhibited in conditions of low ATP:AMP ratio, it is conceivable that oligomycin, by blocking ATP synthase, decreases the ATP:AMP ratio, leading to mTOR inhibition and thus lower cytokine and COX2 expression. This, however, remains to be explored in future studies.

Additionally, work by Sanin et al. [33] showed an effect of PGE_2 on mitochondrial membrane potential, which in turn affected gene expression in macrophages. However, in our work, we did not find alterations in membrane potential despite high levels of PGE_2 production. This can probably be explained by differences in macrophage models used, as the authors used murine M2-like macrophages from MCSF (macrophage colony-stimulating factor) cultures, while in our study we used human GM-CSF stimulated M1-like macrophages, which have been shown to respond differently to inflammatory signals [46].

Interestingly, it was shown that, in RA synoviocytes, mitochondrial dysfunction increases COX2 expression [47]. In these studies, it was indicated that oligomycin increased ROS (reactive oxygen species) production, which in turn stimulated the expression of COX2, again indicating that different cell types can respond in opposite ways to the same metabolic manipulation [14].

As shown previously for IgG, IgA, and IgE (Immunoglobulin E) stimulation of monocytes [48, 49], we here report that IgA2 synergizes with TLR ligands to promote COX2 and PGE_2 synthesis, and that the former is required for boosting the pro-inflammatory profile of macrophages induced by IgA2. However, how COX2 achieves this, in an apparently PGE_2-independent manner, remains to be determined. Possibly, there is another COX2-dependent mediator responsible for the IgA2-induced inflammation, or the effects of PGE_2 are time- and/or dose-dependent in a way that cannot be mimicked by a single supplementation in culture. This phenomenon has previously

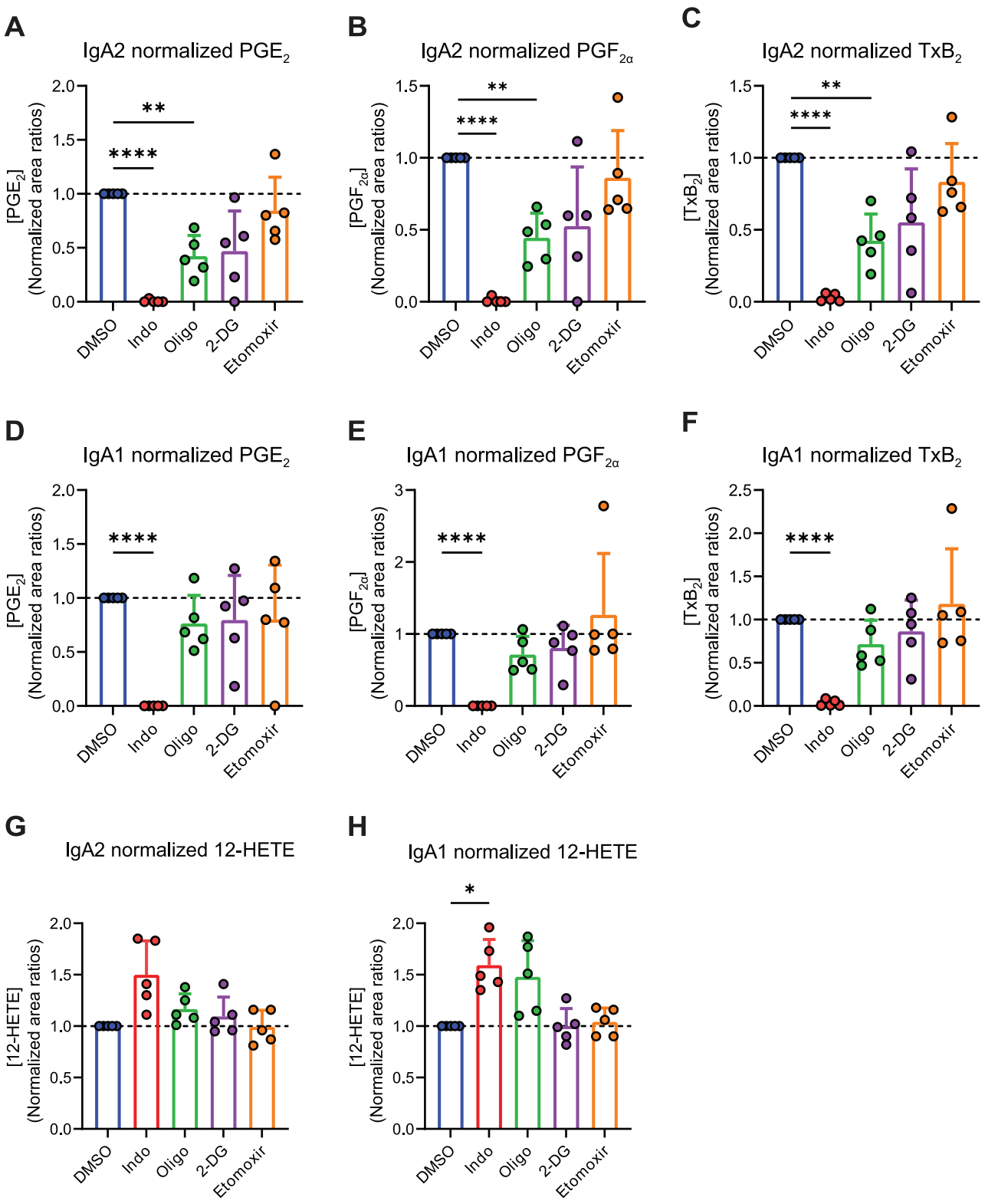

FIGURE 4 | IgA2 requires ATP Synthase for potentiation of PAM-driven synthesis of COX2-dependent lipid mediators. Levels of (A) PGE_2, (B) $PGF_{2\alpha}$, and (C) TxB_2 measured in supernatants of cells co-stimulated with IgA2 and PAM and indicated inhibitors. Levels of (D) PGE_2, (E) $PGF_{2\alpha}$, and (F) TxB_2 measured in supernatants of cells co-stimulated with IgA1 and PAM and indicated inhibitors. Levels of COX2-independent 12-HETE measured in supernatants of cells co-stimulated with PAM and (G) IgA2, or (H) IgA1, and indicated inhibitors. (A)–(H) are representative plots of five donors from two independent experiments (mean ± SD). All data were analysed using a paired one-way ANOVA with Dunnett's post hoc test. The mean of each column was compared with the mean of the control column (DMSO). *$p < 0.05$, **$p < 0.01$, ****$p < 0.0001$.

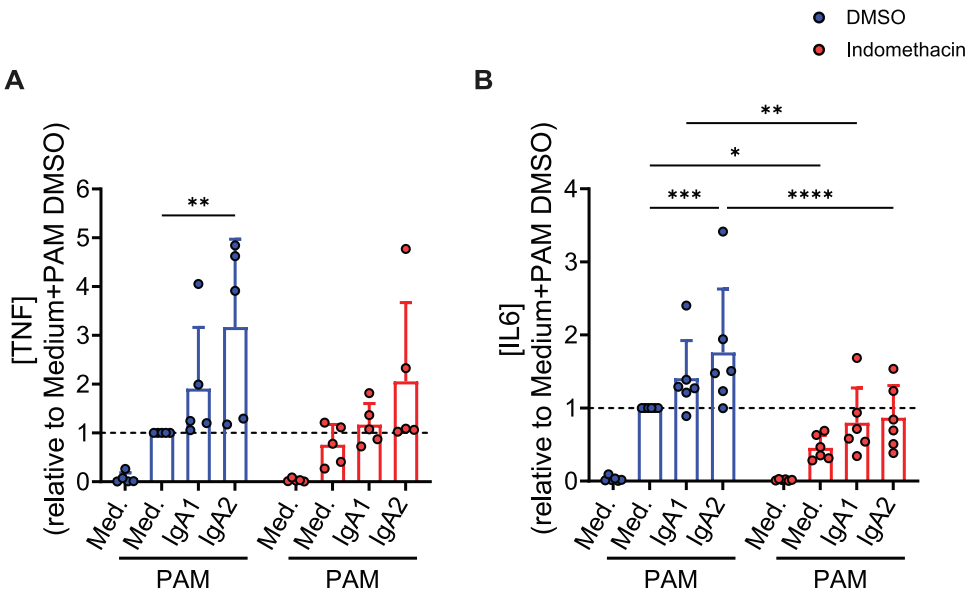

FIGURE 5 | IgA2 requires COX2 activity for potentiation of TLR-induced cytokine production. Levels of (A) TNF and (B) IL-6 measured in supernatants with ELISA following stimulation of cells with indicated stimuli in the presence of DMSO (blue) or Indomethacin (red). (A) is a representative plot of five donors from three independent experiments (mean ± SD). (B) is a representative plot of six donors from three independent experiments (mean ± SD). Respective DMSO controls are the same as the ones shown in Figure 3. All data were analysed using a paired two-way ANOVA, with matched values both stacked and spread across a row, using Tukey's multiple comparisons test, with a single pooled variance. *$p < 0.05$, **$p < 0.01$, ***$p < 0.001$, ****$p < 0.0001$.

been shown in different contexts, where PGE_2 plays distinct roles depending on the concentration and the stimulation time-point [50–53]. Our data also showed $PGF_{2\alpha}$ and TxB_2 to be decreased following oligomycin treatment. As such, one could speculate that one of these plays a role in supporting the pro-inflammatory effect of IgA2. Indeed, it was shown that both $PGF_{2\alpha}$ and Thromboxane A_2 (the active precursor of TxB_2) are present in higher levels in patients with RA compared with either healthy controls or RA patients undergoing treatment [54–56]. Furthermore, previous studies suggest that prostaglandin I_2, another lipid mediator downstream of COX2, plays a role in driving inflammation in the context of RA [57, 58], identifying prostaglandin I_2 as another interesting candidate for further study in the context of IgA2-driven inflammation.

In conclusion, we find a crucial role for mitochondrial ATP synthase-dependent COX2 induction in promoting a pro-inflammatory cytokine response following co-stimulation with PAM and IgA2, revealing a novel interplay between metabolism, lipid mediator production and cytokine expression that shapes the inflammatory profile of macrophages. Thus, our work warrants exploration of the potential of targeted manipulation of macrophage mitochondrial metabolism, as a novel strategy, to dampen IgA-driven inflammation in inflammatory disorders, such as RA.

4 | Materials and Methods

4.1 | Generation of IgA1 ACPA and IgA2 ACPA

All monoclonal antibodies had identical variable domains corresponding to the anti-citrullinated protein antibody (ACPA) clone 1C11. This clone was derived from CCP2 reactive B-cells, isolated by single-cell sorting from an ACPA-positive patient. The heavy and light chain variable domains of the B-cell receptor were sequenced as previously described [59]. The ACPA 1C11 IgA variable gene sequences, linked to the lambda light chain (LC), IgA1 heavy chain (HC), or IgA2m1 HC constant domains, along with the leader peptides MELGLSWVFLVVILEGVQC (for HC) or MAWIPLFLGVLAYCTDIWA (for LC), the Kozak sequence, and BamHI and XhoI restriction sites, were codon-optimized by GeneArt (Life Technologies) and ordered from IDT. The 1C11 IgA HC and LC constructs were cloned into the pcDNA3.1(+) expression vector and co-transfected into FreestyleTM 293-F cells (Gibco) as previously reported [60]. Supernatants from transfected and nontransfected cells (as negative controls) were collected and 0.45 μM filtered 5–6 days later. The supernatants were then diluted to achieve an IgA concentration of 2 μg/mL, as measured by ELISA using a light chain detection antibody to check for equal coating.

4.2 | Coating of Plates With IgA1 ACPA or IgA2 ACPA

For regular culture and stimulation, 96-well streptavidin microplates (Microcoat, Bavaria) were coated with 50 μL of 1 μg/mL biotinylated CCP2 antigen in sterile PBS/0.1% BSA for 1 h at room temperature. After three washes with 150 μL sterile PBS, 50 μL of IgA1, IgA2 or negative control HEK cell supernatant (Med.) were added and incubated for 1 h at 37°C. The plate was washed three times with sterile PBS prior to adding the cells.

For the seahorse and SCENITH experiment, untreated six-well culture plates (Corning) were coated with 1.5 mL of 1 μg/mL

streptavidin (Invitrogen) in sterile coating buffer (0.1 M Na_2CO_3 0.1 M $NaHCO_3$ in H_2O Mili-Q) and incubated overnight at 4°C. After three washes with 2 mL sterile PBS, 1 mL of 1 μg/mL biotinylated CCP2 antigen in sterile PBS/0.1% BSA was added per well. The wells were washed three times with 2 mL sterile PBS and 800 μL of HEK cell supernatant were added for 1 h at 37°C. The wells were washed three more times with sterile PBS prior to cell stimulation.

4.3 | Lambda Light Chain ELISA

Ninety-six-well streptavidin microplates (Microcoat, Baviera) were coated as described above. 50 μL of Sheep anti-lambda-light chain-HRP (polyclonal, Abcam) in PBS/0.05% Tween/1% BSA were added for 1 h at 37°C. The plate was washed 3 times with PBS/0.05% Tween and absorbance was measured at 415 nm using ABTS and H_2O_2 (Figure S1A–C).

4.4 | Human Macrophage Culture and Stimulation

Peripheral blood mononuclear cells were isolated from the venous blood of healthy volunteers by density centrifugation in Ficoll as described before [61]. Monocytes were isolated by positive magnetic cell sorting using CD14-microbeads (Miltenyi Biotech, 130-097-052) and cultured in complete RPMI medium (RPMI containing 10% FCS, 100 U/mL penicillin/streptomycin, and 2 mM L-glutamine) supplemented with 20 ng/mL rGM-CSF (ThermoFisher, PHC2011). On day 2/3, the medium, including supplements, was replaced.

Macrophages were stimulated on day 5 in the presence or absence (if indicated) of 2 μg/mL PAM3CSK4 (InvivoGen, tlrl-pms) in wells previously coated with HEK cell medium, IgA1 or IgA2, along with the indicated reagents: 50 μM Indomethacin (Sigma-Aldrich, I7378), 2 μM Oligomycin (Cayman, 11342), 1 μM 2-DG (Sigma-Aldrich, D8375), 3 μM Etomoxir (Sigma-Aldrich, E1905), 1 μM Entosplenetinib (SelleneckChem, S7523), 10 μM Prostaglandin E_2 (Cayman, 14010).

After 24 h of stimulation, the supernatant was collected and stored at −20°C, if for ELISA, or at −80°C, if for lipidomics. Cells were harvested and stained with the viability dye Zombie NIR (Biolegend, 423106) for 15 min at 4°C in the dark, before being fixed with 2% PFA for 10 min, in the dark, at room temperature.

4.5 | Staining Protocol and Analysis

Fixed cells were washed once in 1× permeabilization buffer (ThermoFisher, 00-5523-00) before staining intracellular targets in 1× permeabilization buffer, containing Fc-block, for 2 h in the dark at room temperature. The expression of intercellular enzymes was determined by flow cytometry (Aurora; Cytek, Amsterdam, the Netherlands) using the following antibodies: COX2 (clone AS67, BD 565125), ACC1, (Abcam, ab272704), FASN (Abcam, ab128870), CPT1A (Abcam, ab235841), and CS (Abcam, ab129088). Only single live cells that were negative for Zombie NIR were included in the analysis. The gating strategy and FMOs can be seen in Figure S8. The acquired samples were unmixed using SpectroFlo version 3 and analysed with FlowJo version 10.10.0.

4.6 | TNF and IL6 Cytokine ELISA

Supernatants from cell cultures stored at -20°C were slowly thawed at 37°C and used to measure the concentration of TNF, with BD OptEIA Human TNF ELISA Set (BD Biosciences, 555212), and IL-6, with BD OptEIA Human IL-6 ELISA Set (BD Biosciences, 555220) according to manufacturer instructions.

4.7 | Measurement of Lipid Mediators

Lipid mediators and polyunsaturated fatty acids (PUFA) were measured using reverse-phase liquid chromatography coupled to tandem mass spectrometry (RPLC-MS/MS) as previously described [62], with some modifications. Briefly, a 2 μL internal standard (IS) mix of deuterated lipid standards consisting of PGE_2-d_4, 15-HETE-d_8, Leukotriene B_4-d_4, DHA-d_5, 8-iso-$PGF_{2\alpha}$-d_4, and 14(15)-EET-d_{11} (50 ng/mL in methanol (MeOH)) was added to 400 μL culture supernatants. Lipids were extracted and purified by solid-phase extraction (SPE) after protein precipitation with 1.2 mL MeOH. The dried extracts were reconstituted in 100 μL 40% MeOH and transferred into a micro-vial glass insert. Furthermore, a 40-μL sample was injected and analysed using a Shimadzu Nexera LC40 system with an autosampler coupled to a QTrap 6500 mass spectrometer (Sciex). Kinetex C18 50 × 2.1 mm, 1.7 μm column, and C8 precolumn (Phenomenex) were used for LC separation. LC-MS/MS chromatograms were integrated manually using Sciex OS (Sciex). The results were reported as the relative peak area of lipids to the internal standards. PGE_2-d_4 IS was used for reporting the area ratios of PGE_2, TxB_2, and $PGF_{2\alpha}$.

4.8 | Extracellular Flux Assay (Seahorse)

5×10^5 macrophages were plated in an XFe96 well Seahorse plate (Agilent) after being stimulated overnight. The medium was replaced, after washing 2× with PBS, with 180 μL XF assay made from base RPMI without HEPES and $NaHCO_3$ (Sigma, R6504) supplemented with 5% FCS and 2 mM L-glutamine, and incubated in a non-CO_2 37°C incubator for 1 h. As cells were incubating, injected compounds were diluted in XF media (without FCS) and added to the hydrated cartridge, after which the cartridge was immediately loaded into the Seahorse for calibration. 10 mM Glucose (Sigma, G8644), 1.5 μM Oligomycin (Cayman, 11342), 3 μM FCCP (Sigma, C2920), 1 μM Rotenone (Sigma, 557368), and 1 μM Antimycin A (Sigma, A8674).

4.9 | Homopropargylglycine Uptake (SCENITH)

5×10^5 macrophages were plated in a 96-well untreated V-bottom plate, washed with PBS, and plated in 90 μL of methionine-free medium (Sigma, R7513) supplemented with 65 mg/L L-cystine dihydrochloride (Sigma, C6727), 2 mM L-glutamine (Sigma, G3126), and 10% dialyzed FCS (ThermoFisher, A3382001). Cells were starved of methionine for 45 min at 37°C, before the addition

of 10 μL of indicated inhibitor(s) (medium, 2 μM Oligomycin, 100 mM 2DG, or 2 μM Oligomycin, and 100 mM 2DG) and subsequently incubated another 15 min at 37°C. Homopropargylglycine (Click Chemistry Tools, 1067) was added at a final concentration of 100 μM and incubated for 30 min at 37°C before being washed 2× with cold PBS, live/dead stain with Zombie NIR at 4°C for 15 min, washed 2× with cold PBS, and fixed with 2% PFA for 10 min.

4.10 | Click Chemistry Reaction

Cells fixed after Homopropargylglycine uptake were permeabilized with PBS containing 1% BSA/0.1% Saponin for 15 min and washed 2× in Click buffer (100 mM Tris-HCl, pH 7.4) before the addition of Click reaction mix. The reaction mix was made by sequential addition of 10 mM Sodium Ascorbate (Sigma, A7631), 2 mM THPTA (Click Chemistry Tools, 1010), 0.5 μM AFdye488 azide plus (Click Chemistry Tools, 1475) and 1× click buffer to $CuSO_4$ (0.5 mM final conc., [Sigma, 209198]). Samples were incubated for 30 min in the dark at room temperature. Cells were washed with FACS buffer and measured on the Aurora. The acquired samples were unmixed using SpectroFlo version 3 and analysed with FlowJo version 10.10.0. Calculations of metabolic capacities and dependences were done as previously described [63].

4.11 | Statistical Analysis

The statistical tests used are indicated in the figure legends. Generally, data were compared using one-way ANOVA for more than two groups or two-way ANOVA for comparing multiple parameters across two or more groups, with Tukey's post hoc test for multiple comparisons. p-values <0.05 were considered significant ($^*p < 0.05$, $^{**}p < 0.01$, $^{***}p < 0.001$, $^{****}p < 0.0001$). All statistical analyses were performed using GraphPad Prism v.10.2.3.

Author Contributions

Luís Almeida: formal analysis, investigation, methodology, visualization, and writing–original draft. Alice Bacon: formal analysis, investigation, methodology, and writing–review & editing. Mohan Ghorasaini: data curation, formal analysis, investigation, methodology, and writing–review & editing. Alwin J. van der Ham: investigation, methodology, and writing–review & editing. René E. M. Toes: conceptualization, resources, supervision, and writing–review & editing. Martin Giera: conceptualization, resources, supervision, and writing–review & editing. Bart Everts: conceptualization, funding acquisition, project administration, supervision, and writing–original draft.

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Ethics Statement

The studies involving humans were approved by the Sanquin National Blood Donation Bank. The studies were conducted in accordance with the local legislation and institutional requirements. The human samples used in this study were acquired from voluntary blood donations to Sanquin Blood Bank. Written informed consent for participation was not required from the participants or the participants' legal guardians/next of kin in accordance with the national legislation and institutional requirements.

Conflicts of Interest

The authors declare no conflicts of interest.

Data Availability Statement

The data that support the findings of this study are available from the corresponding author upon reasonable request.

Peer Review

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Supporting Information

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