**Increased Toll-like Receptor-2 Expression on Nonclassic CD16+ Monocytes from Patients with Inflammatory Stage of Eales’ Disease**

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**PURPOSE.** To identify the distribution, differential Toll-like receptor (TLR) expression, and functional contribution of monocyte subpopulations in the inflammatory stage of Eales’ disease (ED).

**METHODS.** Peripheral blood mononuclear cells were isolated from nine patients during the inflammatory stage of ED and nine age- and sex-matched healthy controls. The expression of CD14, CD16, TLR-2, and TLR-4 on monocytes was measured by flow cytometry. The CD14⁺, CD16⁺, and CD16⁻ monocyte populations were sorted on the basis of magnetic-activated cell-sorting methodology, and levels of cytokines were measured by ELISA.

**RESULTS.** In ED patients, the number of circulating monocytes was significantly expanded compared with that in controls (P = 0.01), with a marked increase in the nonclassic CD16⁺ subset, which showed an activated phenotype in patients that correlated with levels of serum proinflammatory cytokines and clinical progression. A higher expression of cell surface TLR-2 (P = 0.02), but not TLR-4, was found in monocytes of patients with ED. Furthermore, TLR-2 was expressed at higher levels on CD16⁺ monocytes than on CD16⁻ monocytes in patients, whereas no significant variation was found in TLR-4 expression on different monocyte subsets. Peptidoglycan-induced TNF-α expression correlated with TLR-2 expression in monocytes isolated from controls (r = 0.85, P = 0.0061), but not in monocytes isolated from ED patients (r = 0.555, P = 0.1328).

**CONCLUSIONS.** These results indicate that in the pathogenesis of ED, TLR activation and increased numbers of nonclassic CD16⁺ monocytes are crucial regulators, along with the secretion of proinflammatory cytokines that perpetuate the inflammatory process in the retina. *(Invest Ophthalmol Vis Sci. 2011; 52:6940–6948)* DOI:10.1167/iovs.11-7834

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nents, such as peptidoglycan (PGN), whereas an undefined heat-labile cell-associated mycobacterial factor has been found to be the ligand for TLR-4—hence, the relevance of studying TLR-2 and-4 in this respect.

Monocytes, too, are crucial for the immune and inflammatory response, and by using the PRRs, they produce a large number of functionally distinct host cytokines. Research interest in monocyte heterogeneity has gained strong thrust in the last decade past decade, as a subset-specific contribution of monocytes to immune stimuli has been postulated. Presently, three human monocyte subsets are defined, by virtue of differential surface expression of LPS receptor CD14 and FcγRII receptor CD16—namely, CD14+/CD16− (monocytes expressing CD14 but not CD16), CD14+/CD16+ (monocytes expressing CD14 and CD16), and CD14−/CD16+ (monocytes expressing CD16 and low CD14) cells, of which the latter two subsets are summarized as CD16+ monocytes and have been found to be a minor monocyte population in healthy individuals.

Although, TLR expression is known to differ among classic and minor monocyte populations in peripheral blood, no study to date has documented any alteration of the monocyte subpopulations and the mechanisms underpinning changes in blood monocyte TLR expression in the pathogenesis of ED. Therefore, the present study was conducted to identify the distribution, differential TLR expression, and functional contribution of monocyte subpopulations, as well as the cytokine production pattern of isolated monocytes after interaction of a clinically relevant bacterial antigen with TLR in the inflammatory stage of ED.

METHODS

Study Subjects

Nine (eight men, one woman) patients, who received a diagnosis of ED were recruited from the retina research clinic at the Regional Institute of Ophthalmology, Kolkata, India, from 2007 through 2010. All nine patients were in the active stage of ED, as characterized by acute inflammation with macular edema. The patients received no medication before sample collection.

Diagnosis was made for all patients by digital color fundus photography and fluorescein angiography, slit lamp biomicroscopy, and direct and indirect ophthalmoscopy, with a three-mirror lens, stereoscopic color fundus photography, and fluorescein angiography. Differential TLR expression and functional contribution of monocyte subpopulations, as well as the cytokine production pattern of isolated monocytes after interaction of a clinically relevant bacterial antigen with TLR in the inflammatory stage of ED.

Flow Cytometry

Four-color flow cytometry was performed on freshly isolated PBMCs, to investigate the cell surface expression of CD14, CD16, TLR-2, and TLR-4, on monocytes of patients with ED and healthy controls. Briefly, PBMCs were washed twice with phosphate-buffered saline (PBS; 0.02 M, pH 7.2) and resuspended in PBS containing 2% heat-inactivated fetal bovine serum (FBS). Fifty microliters of PBMC suspension (1 × 10^6 cells/mL) was incubated with primary antibodies for 30 minutes at room temperature: fluorescein isothiocyanate (FITC)-conjugated anti-CD14 (clone 61D3, eBioscience, San Diego, CA), phycoerythrin (PE)-conjugated anti-CD16 (clone 3G8, Biologic, San Diego, CA), and allophycocyanin (APC)-conjugated anti-TLR-2 (clone TL2.1; eBioscience), and phycoerythrin (PE)-conjugated anti-TLR-4 (clone HTA125, eBioscience), along with isotype-matched antibody controls. After they were washed with PBS, the cells were resuspended in 400 μL PBS containing 2% FBS, and counts were acquired on a four-parameter flow cytometer (FACSCalibur; BD Biosciences, San Diego, CA). The monocytes were gated on the basis of parameters of forward and side light scatter, and acquisition was performed on 5000 gated events. Data analysis was performed with system-associated software (CellQuest Pro; BD Biosciences). The absolute count of monocytes was obtained with a hemocytometer counting chamber, and the monocyte subpopulation counts were calculated with the percentage distribution obtained from flow cytometry. To measure TLR fluorescence in monocytes, the cells were plotted on the basis of their characteristic linear forward and side scatter and further gated with CD14+ and/or CD16+ positivity, and then TLR fluorescence was measured on a logarithmic scale in the FL2 channel (TLR-4) and FL4 channel (TLR-2). The mean channel fluorescence intensity (MFI) derived from the fluorescence histogram was used to determine the extent of cell surface TLR expression and expressed as the MFI of specific subtracted from the MFI of respective isotype control (i.e., MFI-specific staining minus MFI isotype).

Monocyte Separation and Culture

After isolation of PBMCs from healthy controls and ED patients by density gradient separation, the monocytes were isolated from the PBMCs by incubation with magnetic-activated cell sorting (MACS) beads coated with a monoclonal antibody against human CD14 (Miltenyi Biotec, Bergisch Gladbach, Germany). Immunomagnetic separation was performed according to the manufacturer’s instructions. Purity >90% was confirmed by flow cytometry. The cells were adjusted to 1 × 10^6 monocytes/mL and cultured in RPMI supplemented with 100 U/mL penicillin/100 μg/mL streptomycin and 10% FBS for 18 hours at 37°C in 5% CO2, with or without stimulation by 5 μg/mL PGN of Staphylococcus aureus (InvivoGen, San Diego, CA), and the cell supernatants containing TLR-2 and-4 in this respect.16,19
were collected and stored at −20°C until used for detection of cytokines.

**Separation and Culture of Monocyte Subpopulation**

CD14⁺CD16⁻ and CD14⁺CD16⁺ monocytes were selectively isolated from purified CD14⁺ monocytes (isolated by CD14 microbead and MACS methodology) of three ED patients by using a CD16⁺ monocyte isolation kit (Miltenyi Biotec) and MACS methodology, according to the manufacturer’s instructions. Purity >90% was confirmed by flow cytometry analysis. CD14⁺CD16⁻ and CD14⁺CD16⁺ monocytes were separately cultured in RPMI supplemented with 100 U/mL penicillin/100 µg/mL streptomycin and 10% FBS for 48 hours at 37°C in 5% CO₂ without any stimulation, and the cell supernatants were collected and stored at −20°C until used for cytokine detection.

**Measurement of Cytokines**

The presence of cytokines in the culture supernatants and serum was measured by enzyme-linked immunosorbent assay (ELISAs for TNF-α, IL-6, IFN-γ, and IL-10; ImmunoTools, Friesoythe, Germany; for IL-1β and TGF-β; R&D System, Inc., Minneapolis, MN). Measurements were performed in duplicate with 100-µL sample volume, according to the manufacturer’s instructions.

**Inhibition of TLR-2 Expression by siRNA**

Human TLR-2-specific or nonspecific control siRNA was transfected at 10 to 80 nM, with the transfection reagent (Lipofectamine 2000; Invitrogen), according to the protocol of the manufacturer. Briefly, the purified monocytes (0.5 × 10⁶ cells/mL) were plated in a 24-well plate and incubated at 37°C, 5% CO₂ for 24 hours. Before the transfection, cultures were washed, and medium was replaced by 400 µL/well of serum-free RPMI1640 medium (without antibiotics). Serial dilutions of siRNA were transfected at 10 to 80 nM, with the transfection reagent (1 µL/mL). The transfection reactions were supplemented with 100 µL of FBS after 8 hours and changed to fresh culture medium containing 10% FBS in the next morning. After 48 hours of transfection, cells from some wells were harvested and examined for surface TLR-2 expression by flow cytometry. The remaining cells were stimulated with PGN (5 µg/mL) for 18 hours, and cell culture supernatants were collected to measure TNF-α by ELISA.

**Statistical Analysis**

Age and sex differences between the patients and control subjects were investigated by Student’s t test and χ² test, respectively. The significance of differences of measured parameters between corresponding groups of observations was evaluated by the Mann-Whitney U test, and all values are expressed as the mean ± SD. To examine correlations, we used Spearman’s rank correlation coefficient on the logged data (Graph-Pad, San Jose, CA). Acceptable significance was recorded when values reached P < 0.05. To determine the minimum number of patients, yet appropriate sample sizes for our experiments, we undertook power analysis calculations (PS Power and Sample Size Calculation software version 3.0.34; http://biostat.mc.vanderbilt.edu/wiki/Main/PowerSampleSize; open source software developed by William DuPont and Walton Plummer, Jr., Department of Biostatistics, Vanderbilt University, Nashville, TN). First, based on our previous studies, we estimated the effect size among different experimental units. Therefore, the sample size was set to nine per group to reject the null hypothesis at a 5% significance level, ensuring at least 80% power for each experiment.

**RESULTS**

Nine patients with the inflammatory stage of ED satisfying the inclusion and exclusion criteria were studied and compared with nine healthy age- and sex-matched controls. Demographic and clinical characteristics indicative of disease progression are summarized in Table 1.

**Increase in Total Circulating Monocytes in Patients with the Inflammatory Stage of ED, along with a Shift toward the Nonclassic CD16⁺ Monocyte Subset**

Monocytes were analyzed after exclusion of other peripheral mononuclear cells shortly after the isolation by side scatter and forward scatter (Fig. 1A); a higher number of circulating blood monocytes were found in patients with the inflammatory stage of ED than were found in healthy controls (Figs. 1B, 1C). CD14⁺CD16⁻ (R1), CD14⁺⁺CD16⁺ (R2), and CD14⁺CD16⁺ (R3) monocytes were distinguished by the surface expression pattern of the LPS receptor CD14 and the FcyRIll receptor CD16 (Fig. 1D). In healthy controls, CD14⁺CD16⁺ monocytes (R1) constituted the major population (69.96% in the representative subject shown), whereas CD14⁺⁺CD16⁺ (R2) and CD14⁺CD16⁺ (R3) were the minor populations (Fig. 1D). However, in a

**Table 1. Demographic and Clinical Characteristics of the Study Participants**

<table>
<thead>
<tr>
<th>Characteristics</th>
<th>Patients with ED in Inflammatory Stage</th>
<th>Healthy Controls</th>
<th>P</th>
</tr>
</thead>
<tbody>
<tr>
<td>Ratio of men to women</td>
<td>8.1</td>
<td>7.2</td>
<td>NS</td>
</tr>
<tr>
<td>Age, y</td>
<td>30.2 ± 3.8</td>
<td>30.4 ± 8.6</td>
<td>NS</td>
</tr>
<tr>
<td>IL-6, pg/mL</td>
<td>36.15 ± 18.46</td>
<td>6.28 ± 1.71</td>
<td>0.0004</td>
</tr>
<tr>
<td>TNF-α, pg/mL</td>
<td>21.06 ± 6.72</td>
<td>9.09 ± 1.01</td>
<td>&lt;0.0001</td>
</tr>
<tr>
<td>hsCRP, mg/L</td>
<td>2.89 ± 0.65</td>
<td>0.89 ± 0.19</td>
<td>&lt;0.0001</td>
</tr>
<tr>
<td>Total leukocytes, cells/μL</td>
<td>8679 ± 2405</td>
<td>5772 ± 1130</td>
<td>0.03</td>
</tr>
<tr>
<td>Lymphocyte count, cells/μL</td>
<td>1843 ± 395</td>
<td>2150 ± 538</td>
<td>NS</td>
</tr>
<tr>
<td>ESR, mm/h</td>
<td>38 ± 12</td>
<td>21 ± 14</td>
<td>0.013</td>
</tr>
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</table>

Data are expressed as the mean ± SD.
patient with ED, CD14⁺CD16⁺ (R2) was predominant, being 57.55% versus 7.12% in the control (Fig. 1D).

On average, the percentage of CD14⁺CD16⁻ and CD14⁺CD16⁺ monocytes was increased in patients compared with healthy controls (3.99% vs. 0.84% vs. 2.38% vs. 0.83%; \( P \leq 0.0004 \), respectively). In contrast, the proportion of CD14⁺CD16⁻ monocytes significantly decreased in ED patients compared with controls (27.09% ± 3.26% vs. 69.06% ± 4.47%; \( P \leq 0.0001 \); Fig. 1E). Significant increases in the CD14⁺CD16⁻ (\( P \leq 0.0001 \)) and CD14⁺CD16⁺ (\( P = 0.0008 \)) monocyte subsets were also observed for absolute cell counts, along with a decrease in CD14⁺CD16⁻ monocytes (\( P = 0.0004 \)) when compared with the count in the healthy subjects (Fig. 1F).

When the absolute number of total monocytes and different subsets were related to demographic data, serum inflammatory cytokine levels, serum hsCRP level, total leukocyte count, lymphocyte count, and ESR, the CD14⁺CD16⁺ monocyte subset showed a significant correlation with serum CRP (\( r = 0.95; \ P = 0.0004 \)) and ESR (\( r = 0.52; \ P \leq 0.001 \)), which are accepted clinical indicators of the disease. The CD14⁺CD16⁻ and CD14⁺CD16⁺ monocyte subsets also correlated with serum TNF-\( \alpha \) (\( r = 0.784; \ P = 0.003 \) and \( r = 0.4692; \ P = 0.009 \), respectively), but not with age, sex, and other studied parameters, whereas the CD14⁺⁺CD16⁻ monocytes showed an inverse correlation with these markers (Table 2).

### Increased Expression of TLR-2 on Isolated Total Monocytes and CD16⁺ Monocyte Subsets in Patients with ED

The intensity of TLR-2 and -4 expression in total and different subsets of the monocyte population was measured shortly after isolation. Figure 2A shows a representative histogram profile of

| Table 2. Correlation Analyses between the Absolute Number of Total Monocytes or the Subpopulation of Monocytes and Demographic Data, Inflammatory Cytokine Levels, and Other Blood Cells |
|-----------------|-----------------|-----------------|-----------------|-----------------|
|                 | Total Monocytes | CD14⁺⁺CD16⁺ Monocytes | CD14⁺CD16⁺ Monocytes | CD14⁺⁺CD16⁻ Monocytes |
| Age, y          | -               | -               | -               | -               |
| Sex             | -               | -               | -               | -               |
| IL-6, pg/mL     | 0.961 <0.001    | -               | -               | -               |
| TNF-\( \alpha \), pg/mL | 0.894 <0.001 | 0.784 0.003 | 0.4692 0.009 | -0.618 0.001 |
| hsCRP, mg/L     | 0.85            | 0.0061          | 0.95 0.0004     | 0.374 NS        |
| Total leukocytes, cells/\( \mu \)L | 0.9667 0.0002 | -               | -               | -               |
| Lymphocyte count, cells/\( \mu \)L | -0.8167 0.0108 | -               | -               | -               |
| ESR, mm/h       | 0.462 0.0006   | 0.52 <0.001     | -               | -               |
TLR-2 expression on gated monocytes and the different cell subsets from healthy controls and patients with ED. A significantly higher level of TLR-2 expression, as measured by MFI, was observed on the total monocytes of patients in the active stage of ED, compared with age- and sex-matched healthy controls ($P < 0.02$; Fig. 2B). When comparison was made between different monocyte subsets in patients, the average MFI of TLR-2 on CD14$^+$CD16$^+$ and CD14$^+$CD16$^+$ monocytes were significantly higher than that of CD14$^+$CD16$^+$ monocytes in patients with ED ($P = 0.028$ and $P = 0.0132$, respectively; Fig. 2C). Conversely, in healthy controls, a higher TLR-2 expression was found in CD14$^+$CD16$^+$ monocytes, but the difference in TLR-2 intensity in the different subsets was statistically nonsignificant (Fig. 2C).

In contrast to TLR-2, staining for TLR-4 revealed low fluorescence intensity in both study groups, and no statistically significant intergroup differences and intragroup monocyte-subset-specific differences were found (Figs. 2D–F).

In addition, in patients with ED, the intensity of TLR-2 expression in total monocytes showed a positive correlation with serum hsCRP level ($r = 0.843; P = 0.007$), whereas no such correlation was found in expression of TLR-4 on total monocytes and serum hsCRP ($r = 0.414; P = 0.21$; data not shown).

Increased TLR-2 Induced Cytokine Production by Monocytes Isolated from ED and Differential Cytokine Secretion in the Monocyte Subsets

The increased baseline TLR-2 expression on monocytes from patients with ED may be due to a previous contact with endotoxin. Hence, we investigated whether TLR-2 engagement results in increased cytokine production. We isolated circulating monocytes by human CD14-coated microbeads via MACS methodology in cells from patients and healthy controls, and then pro- and anti-inflammatory cytokine production was determined after cells were cultured with or without PGN.

In the absence of stimulation, monocytes from ED patients had increased mean levels of proinflammatory (TNF-$\alpha$, IL-6, IFN-$\gamma$, and IL-1$\beta$) and anti-inflammatory (IL-10 and TGF-$\beta$) cytokines compared with monocytes isolated from healthy controls (Fig. 3A). After activation with PGN, mean levels of all cytokines increased in both groups compared with unstimulated cells, within each group, but no statistically significant differences were observed after PGN induction, when the two groups were compared (Fig. 3B).

Because of the marked accumulation of CD16$^+$ monocytes in inflammatory phases of ED, we further sought to define the likely function of this subset in the pathogenesis of this disease.
FIGURE 3. Monocytes were functionally active in patients with a differential release of distinct cytokines by monocyte subpopulation. (A) Cytokine release of isolated monocytes from healthy controls and patients with ED (18-hour culture) without stimulation and (B) after stimulation with 5 μg/ml PGN for 18 hours. (C) Cytokine release by purified monocyte subsets after 48-hour culture without stimulation. 

CD16- and CD16+ monocytes were isolated from three patients by MACS methodology, and baseline cytokine secretion was measured after 48 hours of culture without any stimulation. The CD16+ monocytes were the major producers of TNF-α, IL-6, and IFN-γ, compared with the CD16- subgroup (P≤0.0001, P=0.008, and P=0.0006, respectively). CD16+ monocytes, on the other hand, were the main producers of IL-1β (P=0.03) and TGF-β (P=0.04). Moreover CD16+, but not CD16-, monocytes were the only producers of the anti-inflammatory cytokine IL-10 (Fig. 3C).

Relationship between TLR-2 Expression and Ligand-Induced Cytokine Production

Spearman’s rank correlation analysis was performed to determine the relationship between surface TLR-2 expression on total isolated circulating monocytes and response to the TLR-2 ligand. A significant positive correlation was noted between cell surface TLR-2 expression and PGN-induced TNF-α production (r=0.85; P=0.0061; Fig. 4A) by monocytes isolated from healthy controls. However, no significant correlation was found between TLR-2 expression and PGN-induced TNF-α production (r=0.553; P=0.1328; Fig. 4B) by total monocytes isolated from ED patients.

Diminished Activation by PGN Resulting from Forced Reduction of TLR-2 Expression

Since the relationship of TLR-2 expression on monocytes and activation by PGN was not consistent between healthy controls and ED patients, experiments were performed to directly determine the effects of forced reduction of TLR-2 expression on PGN-induced activation. Forty-eight hours after introducing siRNA into monocytes isolated from four different healthy controls, cell surface TLR-2 expression was significantly reduced by TLR-2-specific siRNA (P=0.003 at concentration of siRNA 20 nM, P=0.002 at concentration of siRNA 40 nM, and P≤0.001 at concentration of siRNA ≥60 nM, when compared with nontransfected controls), but not by control siRNA (Fig. 4C). PGN induced TNF-α production demonstrated a significant dose-dependent reduction (P=0.0016 at concentration of siRNA 20 nM and P≤0.001 at a concentration of siRNA ≥40 nM when compared with nontransfected controls) after the introduction of TLR-2-specific siRNA into monocytes isolated from healthy controls, but no reduction was detected in the nonspecific control siRNA (Fig. 4D). These results demonstrate that the forced reduction of TLR-2 expression in monocytes resulted in diminished PGN mediated secretion of TNF-α.

DISCUSSION

The notion that inflammatory mechanisms play an important role in the progression of the pathologic angiogenesis, including retinal neovascularization, has emerged as a major paradigm shift in our understanding of disease pathogenesis. In an effort to eliminate invading pathogens, inflammation is usually the final common pathway used, and both innate and adaptive immune responses are known to trigger inflammation. Considering the significant impact of ED, including visual disability and blindness, investigation of the basic mechanisms underlying the ocular inflammation linked with this disease is warranted. Association of systemic inflammation with the inflammatory stage of ED has been established by the presence of elevated levels of C-reactive protein9 or circulating IL-6 as a marker.25 However, the findings of association between systemic and local inflammation in ED is limited. Only one study has described the association between increased levels of TNF-α with severity of retinal periphlebitis in patients with ED.26 In concurrence, we also noted that high levels of systemic inflammatory markers correlated with an increased severity of retinal inflammation in patients with ED (data not shown). However, inflammation is not only a phenomenon of plasma acute-phase proteins but also of alteration in circulating pools of blood immune cells, including monocytes.

In this study, we demonstrated that number of monocytes are increased in circulation during the active stage of ED; strikingly, we observed a strong shift toward the CD16+ monocytes, particularly the CD14+CD16+ monocyte subset. These CD16+ cells have a distinct phenotype and are efficient producers of proinflammatory cytokines on TLR engagement, whereas they weakly secrete the anti-inflammatory cytokine IL-10.28 They also have high endothelial affinity conferred by...
their surface expression of chemokine receptors and adhesion molecules such as CX3CR1, CCR5, VLA-4, and ICAM-1.29 –31 Furthermore, the “patrolling” behavior of the mouse counterpart of CD16/H11001 monocytes has been described by investigators, who found that these monocytes crawl along the endothelium and, on inflammatory stimulation, rapidly gain access to the endothelium and home to sites of endothelial activation in a CX3CR1-dependent manner. There, they secrete MMP-9, CCL-2, and IL-6 with the ability to propagate further vascular damage through the recruitment of T-lymphocytes and additional monocytes.32,33

Endothelial dysfunction, a concomitant effect of endothelial cell activation, is the ultimate fate of many vasoproliferative retinal disorders, including ED.54 The evidence makes a good case for a probable role of CD16+ monocytes in this disease. Although, the involvement of MMP-9,55 and inflammatory cytokines60 has been established in the pathogenesis of ED, no previous reports have confirmed the involvement of cell adhesion molecules. Keeping in mind their important role in inflammatory ocular neovascularization events,37 participation of these adhesion molecules with immunopathogenesis of ED cannot be ruled out and is a subject of ongoing research for better understanding of the pathologic course of these diseases. The associated data from the present study (i.e., relative abundance of CD16+ monocytes) correlated with circulating proinflammatory cytokines and parameters indicative of disease progression, whereas CD14+ CD16+ monocytes showed an inverse correlation with these markers, and in view of the endothelial activation capability of these minor subsets, support the relevance of CD16+ monocytes to the inflammatory stage and may be suggested to be stimulators of endothelial damage in the advanced stage of ED.

In addition, elevated levels of cell surface TLR-2 expression on systemic circulating monocytes, but not TLR-4, was found in the inflammatory stage of ED. Interestingly, expression of TLR-2 on various subsets of monocytes from ED patients was different from that of healthy controls. TLR2 expression was significantly higher in CD16+ compared with CD16− monocytes in ED patients. In contrast, the intensity of TLR-4 was similar in both monocyte subsets from ED patients and healthy controls. In addition, the intensity of the TLR-2, but not the intensity of the TLR-4, expressed on total monocytes was found to correlate with serum CRP level in ED patients. Taken together, the data suggest that TLR-2 expression may be enhanced during CD16+ monocyte maturation in vivo in association with disease activity, but TLR-4 expression remained unchanged. These observations further support the proposed concept of M. tuberculosis association and suggest involvement of TLR-2 activation by respective microbial products or their PAMPs in the pathogenesis of ED.

Because we assumed that the increased TLR-2 expression on monocytes isolated from patients was a result of previous contact, we proceeded to determine whether TLR-2 engagement results in increased cytokine expression by monocytes. We also wanted to determine the functional contribution of different monocyte subsets in the pathogenesis of ocular inflammation in ED. Accordingly, cytokine production was mea-

![Figure 4](image-url)
sured in total monocytes, isolated from patients and matched controls, with and without PGN stimulation, and in monocyte subsets in ED patients without PGN stimulation.

At baseline, total monocytes from ED patients secreted significantly higher amounts of inflammatory mediators than healthy subjects. These findings are in good agreement with the hypothesis that increased productions of inflammatory cytokines are a crucial mechanism in development of periretinal neovascularization and worsen outcome of ED. Further dissecting the diverse functional capacities of both monocyte subsets in vitro confirmed that the CD16+ monocyte subset is the main source of proinflammatory mediators, thereby perpetuating the chronic inflammatory response in the retina. This conclusion is corroborated by correlating between circulating CD16+ monocyte counts and levels of serum TNF-α in ED patients.

After PGN stimulation, cytokine production by monocytes increased in all study groups, and no significant intragroup differences were found. It is thought that monocytes isolated from patients are inherently more responsive than those obtained from healthy controls, due to the possibility that the cell surface expression of TLR controls the ligand-induced downstream response. Forced diminution of TLR-2 expression on monocytes in our study resulted in a decreased response to PGN, also supporting the hypothesis that increased expression of TLR-2 results in an enhanced response to TLR-2 ligand. Conversely, when we examined the relationship of surface expression of TLR-2 on monocytes with the levels of cytokines induced by stimulation with TLR-2 ligand, a significant positive association was found in monocytes isolated from healthy controls but not in monocytes from patients. The data revealed that the PGN-induced responses of monocytes isolated from patients, although increased compared with those of unstimulated monocytes in vitro, were less than would have been expected of monocytes isolated from healthy controls at comparable levels of cell surface TLR-2.

These findings are of relevance, given the further evidence supporting the role of a microbial trigger and, in particular, Gram-positive bacteria in the development of ED. As all study patients had active inflammation at the time of sampling, it is feasible that prior in vivo exposure to potential endogenous TLR-2 ligands induced tolerance to repeat stimulation, possibly accounting for the lack of association between TLR-2 expression and response to TLR-2 ligand in ED patients. The existence of TLR-2 ligand in ocular tissue of ED patients has not yet been established. Analysis of vitreous collected from ED patients at the time of vitrectomy by molecular biology techniques has detected the presence of Mycobacterium DNA suggesting the existence of Mycobacterium-derived ligands. However, reduced response to PGN is a transient state, and the present study did not demonstrate a dynamic change in TLR-2 expression and response to TLR-2 ligand in ED patients.

In summary, the findings of the present study indicate that nonclassic CD16+ monocytes are crucial regulators in the pathogenesis of ED and act by secreting an abundance of cytokines perpetuating the retinal inflammatory process. Furthermore, this study also implies a role for TLR-2 activation in the pathogenic outcome of ED. Demonstration of increased TLR-2 expression on systemic immune cells in ED together with a functional state of reduced TLR-2 ligand response provides further evidence of the role of Mycobacterium in the development of Eales’ disease.

References


