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TNFα inhibitors exacerbate Mycobacterium paratuberculosis infection in tissue culture: a rationale for poor response of patients with Crohn's disease to current approved therapy

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Burnett School of Biomedical Sciences, Division of Molecular Microbiology, College of Medicine, University of Central Florida, Orlando, Florida, USA

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Dr Saleh A Naser; Saleh.Naser@ucf.edu ABSTRACT Background The role of *Mycobacteriumavium* subspecies paratuberculosis (MAP) in Crohn's disease (CD) is

paratuberculosis (MAP) in Crohn's disease (CD) is increasingly accepted as evident by detection of the bacteria in the blood and intestinal tissue from patients with CD, and by supporting data from several open-label anti-MAP treatment studies. Tumour necrosis factor alpha (TNF α) monoclonal antibodies (anti-TNF α) have been widely used for CD treatment. Despite the shortterm benefit of anti-TNF α in controlling CD symptoms, most patients suffer from detrimental adverse effects, including higher susceptibility to mycobacterial infections. Methods We investigated the effect of recombinant cytokines and anti-TNF α therapeutics on macrophages infected with clinical MAP strain isolated from CD patient blood. MAP viability was measured in macrophages pulsed with PEGylated and non-PEGylated anti-TNF α monoclonal antibodies at concentrations 0 to 50 µg/ mL and with rTNF α , rlL-6, rlL-12, rlL-23 and IFN γ at a final concentration of 1000 U/mL. Expression of proinflammatory cytokines was measured by RT-PCR following MAP infection.

Results Both PEGylated and non-PEGylated forms of anti-TNF α increased MAP viability by nearly 1.5 logs. rlL-6 and rlL-12 induced MAP viability at 5.42±0.25 and 4.79±0.14 log CFU/mL, respectively. In contrast, rTNF α reduced MAP survival in infected macrophages by 2.63 logs. Expression of *TNF\alpha*, *IL*-6 and *IL*-12 was upregulated threefold following MAP or *M. tuberculosis* infection compared with other bacterial strains (p<0.05), while expression of *IL*-23 and *IFN* γ was not significant after MAP infection.

Conclusion The data indicate MAP-positive patients with CD receiving anti-TNF α treatment could result in favourable conditions for MAP infection, which explains the poor response of many patients with CD to anti-TNF α therapy.

INTRODUCTION

Crohn's disease (CD) is described as a complex idiopathic inflammation, which can affect any part of the digestive tract. Patients diagnosed with this chronic form

Summary box

What is already known about this subject?

- Mycobacterium avium subspecies paratuberculosis (MAP) is among the most investigated pathogens associated with Crohn's disease (CD).
- Although the standard CD therapy has shifted from general immunosuppressants towards more specific targets including tumour necrosis factor alpha (TNFα), patients are often unable to reach full remission to this treatment.
- Antagonizing TNFα have several adverse effects, including higher risk for multiple infections especially mycobacterial infections such as *Mycobacterium tuberculosis*, a closely related micro-organism to MAP.

What are the new findings?

- Anti-TNFα therapeutics unexpectedly demonstrated similar cytotoxic effects to recombinant TNFα on uninfected macrophages.
- Anti-TNFα therapeutics induce MAP survival in infected macrophages, which is a serious issue for CD patients who have MAP infection.
- MAP induces expression of TNFα, IL-6 and IL-12 in infected macrophages.
- Unlike rTNFα, rIL-6 induced MAP survival in infected macrophages, suggesting that IL-6 in MAP-infected patients with CD might be a better drug target.

of inflammatory bowel disease suffer from persistent diarrhoea, abdominal pain and malnutrition.¹ The prevalence of CD in western countries increased recently, which carries a huge economic burden on health-care cost, since 50% of patients with CD require surgical intervention within 10 years of diagnosis.^{1–3}

The aetiology of CD involves various components including genetic susceptibility, altered microbiota and environmental triggers.⁴ One of the most investigated pathogens associated with CD is *Mycobacterium*

Summary box

How might it impact on clinical practice in the foreseeable future?

- MAP is accepted to be a serious pathogen in some patients with CD.
- We have demonstrated that TNFα is the essential cytokine required for containment and eradication of MAP. It is, therefore, alarming for patients with CD who are infected with MAP to receive anti-TN-Fα therapeutics. Alternative CD therapeutic drug targets should be considered instead.
- Higher expression of *TNFα*, *IL-6* and *IL-12* following MAP infection in vitro shows that the elevated level of these cytokines in patients with CD might be due to MAP infection.
- Eradicating MAP infection with anti-MAP antibiotics is highly expected to suppress expression of proinflammatory cytokines.
- ► The positive effects of recombinant IL-6 and IL-12 on MAP survival (unlike TNF α) directs the attention to novel therapeutic targets with dual effects on suppressing the immune response and MAP infection.

avium subspecies *paratuberculosis* (MAP).⁵ ⁶ However, current treatment guidelines do not consider this bacterial infection as a source of inflammation. Although the standard CD therapy has shifted from general immunosuppressants such as corticosteroids and thiopurines towards more specific targets including tumour necrosis factor alpha (TNF α), patients are usually unable to reach full remission or at least maintain a sustainable clinical response to this kind of therapeutic approach.⁷⁻⁹

Introducing anti-TNF α biologics (infliximab, adalimumab, certolizumab pegol) to CD treatment has shown that targeting a specific cytokine could be helpful to control CD symptoms and reduce flare-ups.⁷ Unfortunately, sustainable remission is very limited to a small group of patients.⁹ It has been reported that 10%–30% of patients with CD have no initial response to anti-TNF α therapeutics, and over 50% of initial responders lose their response to treatment over time.¹⁰ Additionally, about 40% of patients with CD are at risk of disease relapse after anti-TNF α treatment discontinuation.¹¹

Moreover, blocking TNF α carries several adverse effects, including higher risk for malignancy, heart failure and multiple infections.⁴ There is a well-established evidence supporting the role of anti-TNFa therapeutics in increasing the incidence for mycobacterial infections including Mycobacterium tuberculosis, which is due to the importance of TNFa in granuloma formation and containment of M. tuberculosis.¹² Since MAP and M. tuberculosis share molecular similarities and they both avoid phagosome-lysosome fusion in infected macrophages, $^{13-15}$ TNF α remains the essential cytokine required for containment and eradication of MAP. It is, therefore, alarming for patients with CD who are infected with MAP to receive anti-TNFa therapeutics, and an extensive search for alternative CD therapeutic drug targets is required. Nevertheless, anti-TNFa treatment might still be considered for patients with CD who

do not have MAP infection and who are genetically more likely to respond to this treatment.¹⁶

For refractory cases of CD, there are a few current medications with a novel therapeutic pathway known as integrin inhibitors, such as natalizumab (Tysabri) and vedolizumab (Entyvio). Although these two medications have shown a clinical efficacy in CD treatment, however, they increased the risk for progressive multifocal leucoencephalopathy in multiple clinical trials.¹⁷⁻¹⁹ Besides, several proinflammatory cytokines are emerging as possible therapeutic targets for CD such as IL-6, IL-12 and IL-23.²⁰ However, the effect of these medications on mycobacterial infection is unknown. Additionally, the effect of MAP infection on upregulating proinflammatory cytokines in CD needs further investigation.

In this study, we focused on elucidating the effects of non-PEGylated and PEGylated anti-TNF α monoclonal antibodies on MAP survival in infected human-derived macrophages. We also evaluated the ability of recombinant cytokines (TNF α , IL-6, IL-12, IL-23 and IFN γ) to modulate MAP survival in vitro. Finally, we evaluated the effects of MAP infection on the gene expression level of these proinflammatory cytokines.

MATERIALS AND METHODS

Effect of anti-TNF α monoclonal antibodies and recombinant TNF α on MAP in culture

BD Bactec MGIT Para-TB medium (Becton Dickinson, Sparks, Maryland, USA) system was used to determine the bactericidal effects of anti-TNFa therapeutics against clinical MAP strain (UCF4; isolated from intestinal biopsy of a patient with CD) and other micro-organisms as controls. MGIT-para media with supplements were used to culture mycobacteria as described previously.²¹ For other micro-organisms, nutrient broth media replaced MGIT-para media in MGIT tubes. All tubes contained a fluorescent molecule embedded in an oxygen-sensitive silicone, where fluorescence is detected in the presence of active respiring bacteria. Anti-TNFa therapeutics were tested in concentrations between 0 and 200 μ g/mL. Recombinant TNF α (rTNF α) was obtained as sterile filtered lyophilised powder (Gemini), where each 1.0µg of powder had 2500 U. Then, 50µg was dissolved in 500 µL of sterile water in order to prepare $0.1 \,\mathrm{mg/mL}$ stock solution, which was stored at -20° C. Then, rTNF α was added to bacterial cultures at final concentrations between 0 and 1000 U/mL. The micro-organisms included in this study are MAP UCF4, Listeria monocytogenes ATCC 19112, Klebsiella pneumoniae ATCC 13883 and recombinant Escherichia coli. All culture tubes were incubated in BD Bactec MGIT 320 Analyzer at 37 C. Mycobacterial cultures were read weekly whereas other micro-organism cultures were read daily. Bacterial growth was visualised under the UV by using Andromeda BioSens SC 645 UV illuminator.

Effect of anti-TNF α monoclonal antibodies and recombinant TNF α on THP-1 cell viability and measurement of apoptosis THP-1 cells (ATCC TIB-202) were cultured in RPMI-1640 medium containing 9.8% fetal bovine serum (FBS) (Sigma Life Science) and 0.09% 2-mercaptoethanol (BME) (Gibco Life Technologies), while maintained in a humidified 5% CO₉ incubator at 37°C. Cells were grown until confluency in tissue culture plates was reached. Then, cells were distributed in 1 mL aliquots in a 24-well tissue culture plate. THP-1 cells were then treated with recombinant TNFa or anti-TNFa monoclonal antibodies at final concentrations between 0 and $50 \mu g/$ mL, followed by incubation of 24, 48 and 72 hours. Cell viability was determined by trypan blue exclusion assay. Briefly, 10 µL of cell suspension was mixed with 10 µL of 0.4% trypan blue solution. Following 5min of incubation at room temperature, 10 µL of mixture was injected on a haemocytometer, and the percentage of stained (viable) cells was counted by binocular microscope. The apoptotic activities of recombinant TNFa and anti-TNFa monoclonal antibodies were determined by caspase-3 colorimetric assay (Abcam). At each time point, 500 µL of each cell suspension was mixed with 50 µL of chilled lysis buffer and incubated on ice for 10 min. Mixture was centrifuged for 1 min at 10000g. The cytosolic extract was transferred to another tube and protein concentration was measured and adjusted to 100 µg per 50 µL of samples. Caspase reaction mix was prepared by mixing $50\,\mu\text{L}$ of reaction buffer with $0.5\,\mu\text{L}$ of 1,4-dithiothreitol for each reaction in duplicates. Each sample was mixed with 50µL of reaction buffer and 5µL of 4mM DEVDp-NA substrate on a 96-well microplate. Following 90 min of incubation at 37°C, the output was measured at 405 nm wavelength by using a microplate reader. Fold increase in caspase-3 activity was determined by comparing treated samples with the untreated control.

Infection of monocyte-derived macrophages with MAP

THP-1 cells (ATCC TIB-202) were cultured as described earlier, then they were differentiated into monocyte-derived macrophages by adding 50 ng/mL of phorbol 12-myristate 13-acetate (PMA) (Sigma-Aldrich) for 24 hours of incubation. Monocyte-derived macrophages were then infected with 1×10^7 bacteria/mL. Micro-organisms used include viable *M. tuberculosis* HR237, *MAP* UCF4 and *M. smegmatis* ATCC 27199, and heat-inactivated *M. tuberculosis* HR237, *MAP* UCF4 and *M. smegmatis* ATCC 27199. Non-mycobacterial micro-organisms included *L. monocytogenes* ATCC 19112, *K. pneumoniae* ATCC 13883 and recombinant *E. coli*. All micro-organisms were used at a final concentration of 1×10^7 viable bacteria/mL, while maintained at the same conditions for 24 hours.

Measurement of *TNFa*, *IL-6*, *IL-12*, *IL-23* and *IFN* γ expression in infected macrophages

RNA was isolated from 1.0 mL of each sample suspension after 24 hours of infection and used for cDNA synthesis in order to analyse expression of *TNFα*, *IL-6*, *IL-12*, *IL-23*

and *IFN* γ via RT-PCR. Briefly, cells were centrifuged at 100g for 5 min. Pellets were suspended in 1.0 mL of TRIzol reagent (Invitrogen) for 15 min and then mixed with 0.2 mL of chloroform. Following 3 min of incubation at room temperature, samples were then centrifuged at 12 100g for 15 min at 4°C. The RNA was transferred from the upper aqueous colourless part into a new 2.0 mL microcentrifuge tube. Each sample was mixed with 0.5 mL of 100% isopropanol following 10 min of incubation at room temperature. Then, each sample was centrifuged at 12 100g for 10 min at 4°C and mixed with 1.0 mL of 75% ethanol, followed by centrifugation at 7000g for 5 min at 4°C. After RNA pellets were air-dried for 15 min, samples were suspended in 20 µL of RNase-free water and finally heated at 60°C for 10 min.

A total amount of 600 ng of each RNA sample was added to 0.2 mL of PCR reaction, 4 µL of iScript Reverse Transcription (Bio-Rad) and up to 20 µL RNase-free water for cDNA synthesis. All samples were transferred to a thermal cycler (MyGene Series Peltier Thermal Cycler), where reaction was performed for 5 min at 25°C, 20 min at 46°C and 1 min at 95°C. A total volume of 1 µL of cDNA $(30 \text{ ng/}\mu\text{L})$ was mixed with $10 \mu\text{L}$ of Fast SYBR Green Mastermix (Thermo Fisher Scientific), 1µL of either IL-6, IL-12, IL-23 or IFNy PrimePCR SYBR Green Assay mix (Bio-Rad), in addition to 8µL of molecular biological grade sterile water in a 96-well microamp RT-PCR reaction plate. The 18s RNA gene oligonucleotide primers (forward primer: 5'-GTA ACC CGT TGA ACC CCA TT-3'; reverse primer: 5'-CCA TCC AAT CGG TAG TAG CG-3') were used as controls to get baseline CT values. The RT-PCR reaction was performed using 7500 Fast Real-Time PCR System (Applied Biosystems). Relative mRNA expression levels were calculated by using the equation $(2^{(-\Delta CT)} \times 1000)$, where ΔCT =sample RT-PCR CT value-18s CT baseline value.

Modulating MAP viability in infected macrophages pulsed with exogenous recombinant cytokines and anti-TNF α monoclonal antibodies

Recombinant cytokines (rTNF α , rIL-6, rIL-12, rIL-23 and rIFN γ) were obtained as sterile filtered lyophilised powders (Gemini), where each 1.0 µg of powder had 2500 U. Then, 50 µg of each powder was dissolved in 500 µL of sterile water in order to prepare 0.1 mg/mL stock solution, which was stored at -20°C. Recombinant cytokines at final concentrations between 0 and 1000 U/mL were added to monocyte-derived macrophages infected with MAP strain UCF4. Similarly, two anti-TNF α monoclonal antibodies (PEGylated and non- PEGylated forms) at final concentrations between 0 and 50 µg/mL were also evaluated. Then, MAP viability was tested after 24, 48 and 72 hours.

Measurement of bacterial viability in infected macrophages

After infecting monocyte-derived macrophages with MAP for 24 hours, cells were washed to remove extracel-lular bacilli, and then recombinant cytokines/anti-TNF α



Figure 1 Direct bactericidal activity of non-PEGylated anti-TNF α (1) and PEGylated anti-TNF α (2) therapeutics against MAP growth in MGIT fluorescence system at 200 µg/mL, following 14 days of incubation. (P) indicates positive control (0µg/mL) and (N) is a negative control.

monoclonal antibodies were added to the culture accordingly. Monocyte-derived macrophages were collected at three time points (24, 48 and 72 hours) and lysed with 200 µL of M-PER Mammalian reagent (Thermo Scientific) for bacterial viability detection using Live/Dead Baclight (Thermo Fisher Scientific). Briefly, five different proportions of live and dead MAP were prepared (0:100, 10:90, 50:50, 90:10, 100:0), then 100 µL of each bacterial suspension was pipetted in triplicates into separate wells of 96-well flat-bottom microplate and mixed 100 µL of staining reagent mixture. Following 15 min of incubation at room temperature in the dark, fluorescence intensity was measured at 530 nm, which indicates live bacteria reading (green), and again at 630 nm for the dead bacteria reading (red). Data were analysed by dividing the fluorescence intensity of the stained bacterial suspensions (ratio=emission 1 (green)/emission 2 (red)). The least-squares fit line was generated and the equation was used to calculate the bacterial viability from the infected cells post-treatment.



Figure 2 Direct bactericidal activity of non-PEGylated anti-TNF α (A) and PEGylated anti-TNF α (B) therapeutics against bacterial growth in MGIT fluorescence system at 200 µg/mL, following 72 hours of incubation. (1): *S. aureus*, (2): recombinant *E. coli*, (3): *K. pneumoniae* and (4): *L. monocytogenes*. (P) indicates positive control (0 µg/mL) and (N) is a negative control.

Statistical analysis

Data are expressed as mean \pm SE of the mean by using GraphPad Prism V.7.02 (GraphPad, La Jolla, California, USA). Two-tailed Student's t-test was used. The difference between samples and controls was considered statistically significant at a level of p <0.05.

RESULTS

Anti-TNF α therapeutics and recombinant TNF α have no direct bactericidal activity against MAP or other tested micro-organisms

In order to rule out the direct bactericidal effects of anti-TNFα monoclonal antibodies and rTNFα, we tested them in supratherapeutic levels against MAP and non-mycobacterial MGIT cultures. Both PEGylated and non-PEGylated anti-TNFa monoclonal antibodies have demonstrated no direct bactericidal activity when they were tested against MAP in addition to three non-mycobacteria strains (L. monocytogenes ATCC 19112, K. pneumoniae ATCC 13883 and recombinant E. coli). All bacterial strains we tested showed resistance to anti-TNF α treatment at concentrations as high as $200 \,\mu\text{g/mL}$ (4× C_{max}). Similarly, all strains we tested were resistant to rTNFa treatment at concentrations as high as 1000 U/mL. Figure 1 shows the growth florescence of MGIT tubes incubated with MAP after 14 days of exposure to anti-TNF α , while figure 2 shows the growth fluorescence of MGIT tubes incubated with non-mycobacteria strains following 72 hours of anti-TNFα exposure.

Anti-TNF α therapeutics demonstrate similar cytotoxic effects to recombinant TNF α on uninfected macrophages

To further establish the cytotoxic role of $TNF\alpha$ and anti-TNFα monoclonal antibodies on monocyte apoptosis and whether these alone are able to modulate monocyte apoptosis independently of MAP infection, we treated uninfected THP-1 cells with different concentrations of exogenous rTNFa and therapeutic levels of anti-TNFa antibodies. Following 24 hours of incubation with 250 U/ mL of rTNFa, THP-1 cell viability has decreased from 100% to 77.2%, which continued to decline over time until it reached 63.7% after 72 hours. In a concentration-dependent manner, 500 U/mL of rTNF α led to a decrease in THP-1 cell viability from 100% to 52.6%, while it reached 45.9% with 1000U/mL, following 72 hours of incubation (p<0.05) (figure 3A). Caspase-3 activity has confirmed these findings since it has shown higher activity in THP-1 cells treated with rTNFa. At 250U/mL, caspase-3 activity was 2.47-fold higher than control, while it was 6.49-fold and 8.92-fold higher in cells treated with 500 and 1000 U/mL of rTNFa following 72 hours of incubation, respectively (p<0.05) (figure 4A). Surprisingly, anti-TNFa monoclonal antibodies showed similar cytotoxic effects as rTNFa in a dose-dependent manner. The viability of THP-1 cells treated with 5µg/ mL of non-PEGylated anti-TNFa started to decrease over 72 hours of incubation, when it reached 70.6%.



Figure 3 Cytotoxicity of rTNF α (A), non-PEGylated anti-TNF α (B) and PEGylated anti-TNF α (C) therapeutics determined by Trypan blue exclusion assay, following 24, 48 and 72 hours of incubation. *P<0.05.

Higher concentrations have shown further decline in cell viability, when it reached 62.8%, 57% and 48% following 72 hours of incubation with 10, 20 and 50 ug/mL, respectively (p<0.05) (figure 3B). The PEGylated form of anti-TNF α was less cytotoxic, but it still demonstrated decline in THP-1 cell viability following 72 hours of incubation, when cell viability was 74.7%, 68.8%, 62.6% and 57.9%, treated with 5, 10, 20 and 50 µg/mL, respectively (p<0.05) (figure 3C). Similarly, caspase-3 activity was 4.9-fold and 4.4-fold higher than control following 72 hours of treatment with 50 µg/mL of non-PEGylated and PEGylated anti-TNF α therapeutics, respectively (p<0.05) (figure 4B,C).

6

MAP induces expression of $TNF\alpha$, *IL-6* and *IL-12* in infected macrophages

We have found that MAP and M. tuberculosis induce TNFa expression in infected macrophages significantly (3.2±0.23 and 2.8±0.13, respectively) compared with M. smegmatis (0.8 ± 0.17) and other non-mycobacteria species following 24 hours of infection (figure 5A). Similarly, we found that MAP and M. tuberculosis both had about two times higher IL-6 expression (2.9±0.41 and 2.6±0.19, respectively) compared with M. smegmatis (1.3 ± 0.12) or other non-mycobacterial pathogens (p<0.05). Furthermore, when M. tuberculosis and MAP were both heat inactivated (80°C for 20 min), they have lost their activity to induce IL-6 expression (0.35±0.14 and 0.29±0.11, respectively) (p<0.05) (figure 5B). Additionally, IL-12 expression was also significantly higher in MAP or M. tuberculosis infected macrophages $(1.6\pm0.36 \text{ and } 1.5\pm0.29, \text{ respectively}),$ but only in comparison to non-mycobacteria species (p<0.05) (figure 5C). However, the expression of other proinflammatory cytokines (IFNy and IL-23) was not significantly higher in MAP or *M. tuberculosis* infected macrophages (figure 5D,E).

Recombinant TNF α decreases MAP survival in infected macrophages

First, we tested the effects of adding exogenous rTNF α into MAP infected macrophages at different concentrations between 0 and 1000 U/mL. We found that MAP viability drops with time significantly in a concentration-dependent manner. At 500 U/mL, MAP viability has declined from 7.0 (log CFU/mL) to 3.95±0.22, 3.31±0.34 and 2.11±0.17, following 24, 48 and 72 hours of incubation, respectively (p<0.05) (figure 6A). At the maximum concentration we have tested, adding rTNF α at 1000 U/mL to MAP infected macrophages had decreased MAP viability from 7.0 (log CFU/mL) to 1.50±0.15, following 72 hours of incubation (p<0.05) (figure 6A).

Anti-TNF α therapeutics increase MAP survival in infected macrophages

In contrast, treating MAP infected macrophages with anti-TNF α monoclonal antibodies increases MAP survival in a dose-dependent manner. The non-PEGylated form of anti-TNF α at 50 µg/mL had MAP viability of 5.09±0.11 (log CFU/mL), while the untreated control had 4.02±0.16 (log CFU/mL) (p<0.05) (figure 6B). Similarly, the PEGylated anti-TNF α had increased MAP viability up to 5.63±0.14 (log CFU/mL) at 50 µg/mL following 72 hours of incubation (p<0.05) (figure 6C).

Recombinant IL-6 promotes MAP survival in infected macrophages

Since we found that MAP modulates some proinflammatory cytokine gene expression in infected macrophages, it was worthy to test the effects of exogenous recombinant cytokines on MAP survival. We tested rIL-6







Figure 5 Expression of $TNF\alpha$ (A), IL-6 (B), IL-12 (C), IL-23 (D) and $IFN\gamma$ (E) in monocyte-derived macrophages following 24 hours of bacterial infection. Bacterial strains presented in the X-axis are 1: control (without infection), 2: *M. tuberculosis* (heat inactivated), 3: *MAP* UCF4 (heat inactivated), 4: *M. tuberculosis*, 5: *MAP* UCF4, 6: *M. smegmatis*, 7: *K. pneumoniae*, 8: *L. monocytogenes*, 9: recombinant *E. coli*. *P<0.05.

at different concentrations between 0 and 1000 U/mL. Interestingly, rIL-6 has promoted MAP survival significantly in a concentration-dependent manner. Following 72 hours of incubation, MAP viability was 3.42±0.39, 4.25±0.23, 4.82±0.19 and 5.42±0.25 (log CFU/mL), at 0, 250, 500 and 1000 U/mL of rIL-6, respectively (p<0.05) (figure 7A). Similarly, rIL-12 had some positive effect on MAP viability in infected macrophages; however, it was only significant at a concentration of 1000 U/mL, when MAP viability was 4.79±0.14 compared with 3.73±0.33 (log CFU/mL), following 72 hours of incubation (p<0.05) (figure 7B). On the other hand, both rIL-23 and rIFNy had similar effects to $rTNF\alpha$, where they had detrimental effects on MAP survival. MAP viability has declined from 7.0 to 2.76±0.16 and 2.95±0.19 (log CFU/mL), following 72 hours of incubation with 1000 U/mL of rIL-23 and rIFN γ , respectively (figure 7C,D).

DISCUSSION

Macrophages exhibit several mechanisms in order to eradicate intracellular pathogens, such as releasing reactive oxygen intermediates, changing phagolysosomal acidity and production of proinflammatory cytokines.²² TNF α is one of those cytokines, which has a prominent role during mycobacterial infection, resulting in a formation of a complex circuit of other cytokines able to modulate T cells and macrophages response to infection and granuloma formation.²³ Consequently, blocking TNF α function in animal models induced mycobacterial proliferation and reduced granuloma formation, indicating that $TNF\alpha$ is a primary cytokine for protection against mycobacterial infection.²⁴⁻²⁶ However, current treatment guidelines for many inflammatory disorders of supposed non-infectious origin recommend blocking TNFa



Figure 6 Mycobacterium avium subspecies paratuberculosis (MAP) viability in monocyte-derived infected macrophages pulsed with rTNF α (A), non-PEGylated anti-TNF α (B) and PEGylated anti-TNF α (C) therapeutics, following 24, 48 and 72 hours of infection. *P<0.05.



Figure 7 MAP viability in monocyte-derived infected macrophages pulsed with recombinant IL-6 (A), IL-12 (B), IL-23 (C) and IFN- γ (D), following 24, 48 and 72 hours of infection. *P<0.05.

pathway in order to suppress the hyperactive immune response and inflammation.²⁷

Although there is a strong evidence demonstrating the involvement of MAP in CD, there is no recommendation of using antibiotics for CD treatment so far.²¹ On the contrary, the clinical use of anti-TNF α therapeutics has increased the risk for multiple infections including tuberculosis.^{28–30} Thus, assessment of latent tuberculosis infection status is highly recommended in order to determine if any patient intended to initiate anti-TNF α therapy has a risk for development of active disease.³¹

This study was concerned with identifying the detrimental ability of recombinant TNFa, IL-6, IL-12, IL-23 and IFNy on MAP survival in infected macrophages and if blocking TNFα function by anti-TNFα monoclonal antibodies modulates MAP viability in vitro. Additionally, our goal was to identify which proinflammatory cytokines are highly expressed by macrophages following MAP infection. A recent study has reported that infliximab treatment increases MAP viability in infected macrophages from patients with CD by predominant induction of MAP dormant form.³² Our data show that both PEGylated and non-PEGylated forms of anti-TNFa therapeutics do not have any direct bactericidal effects against MAP or other non-mycobacterial strains at supratherapeutic concentrations (>200 mg/mL). However, these medications increased MAP survival in infected macrophages in a dose-dependent manner, which indicates that patients with CD receiving such treatment are at a higher risk for MAP growth if they had MAP infection before initiation

of therapy. In contrast, MAP viability declined in infected macrophages pulsed with exogenous rTNF α in a concentration-dependent manner, which shows that TNF α plays a significant role in protection against MAP infection.

Furthermore, anti-TNFa therapeutics demonstrated similar cytotoxicity level to rTNFa at therapeutic concentrations, which explains why these medications increase the risk for infections once they induce apoptosis in macrophages. In addition, we measured expression level of TNFa, IL-6, IL-12, IL-23 and IFNy in infected macrophages following 24 hours. We found that TNFa, IL-6 and IL-12 are also expressed significantly in MAP or M. tuberculosis infected macrophages, which shows that a high level of these cytokines in patients with CD could be a result of MAP infection. Interestingly, MAP survival was induced significantly when exogenous rIL-6 was added to infected macrophages in a concentration-dependent manner. However, rIL-23 and IFNy had a similar effect to rTNF α , where they reduced MAP viability significantly with higher concentrations.

Newly emerging monoclonal antibodies indicated for CD treatment have shifted from targeting TNF α into more selective targets such as anti-IL-6 (PF-04236921), anti-IL-23 (AMG-139) and anti-IL-12/IL-23 (ustekinumab).²⁰ Indeed, IL-6 is highly expressed in patients with CD.^{33–35} Therefore, blocking IL-6 pathway is anticipated to reduce the hyperactive immune response among patients with CD. Moreover, our data suggest that IL-6 promotes MAP survival in infected macrophages. Thus, specifically targeting this cytokine will lead to a decline

in MAP viability, which could replace anti-TNF α treatment eventually. Additionally, in *M. tuberculosis* infected macrophages, IL-6 was found to inhibit IFN γ responsive genes at the transcriptional level selectively, which also results in inhibition of major histocompatibility complex (MHC) class II induction.³⁶ Clinical studies are needed to offer a proof of principle for this new CD drug target with dual effect on MAP infection and inflammation.

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Contributors AQ is the primary author who performed all experiments, collected data and participated in writing the manuscript. SAN is the leading investigator in the laboratory and has supervised all aspects of the study including writing and editing of the manuscript.

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