An evolutionary recent IFN-IL-6-CEBP axis is linked to monocyte expansion and tuberculosis severity in humans

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Running title
\textit{M. tuberculosis} exploits an IFN/IL6/CEBP axis linked to monocyte expansion
Abstract
Monocyte counts are increased during human tuberculosis (TB) but it has not been
determined whether *Mycobacterium tuberculosis* (*Mtb*) directly regulates myeloid
commitment. We demonstrated that exposure to *Mtb* directs primary human CD34+ cells
to differentiate into monocytes/macrophages. In vitro myeloid conversion did not require
type I or type II IFN signaling. In contrast, *Mtb* enhanced IL-6 responses by CD34+ cell
cultures and IL-6R neutralization inhibited myeloid differentiation and decreased
mycobacterial growth in vitro. Integrated systems biology analysis of transcriptomic,
proteomic and genomic data of large data sets of healthy controls and TB patients
established the existence of a myeloid IL-6/IL6R/CEBP gene module associated with
disease severity. Furthermore, genetic and functional analysis revealed the
*IL6/IL6R/CEBP* gene module has undergone recent evolutionary selection, including
Neanderthal introgression and human pathogen adaptation, connected to systemic
monocyte counts. These results suggest *Mtb* co-opts an evolutionary recent IFN-IL6-
CEBP feed-forward loop, increasing myeloid differentiation linked to severe TB in
humans.
Hematopoiesis, the development of different blood cell lineages from hematopoietic stem cells (HSCs), is a fundamental physiological process in vertebrates. HSCs give rise to lineage-restricted progenitors that gradually differentiate into mature cells. Following cellular differentiation, single-lineage elements including erythrocytes, megakaryocytes, lymphocytes as well as myeloid cells such as monocytes and granulocytes circulate throughout the body performing diverse functions. While HSC development towards cellular lineages during homeostasis has been extensively studied (Hoggatt, Kfoury, & Scadden, 2016), the mechanisms by which how progenitors give rise to mature cells during stress responses are less comprehended. For instance, certain pathogens regulate production of blood cells by the bone marrow and it has been shown that fine-tuned regulation of cytokine-induced signals is required for differentiation of HSC into mature cell types (Kleppe et al., 2017; Mirantes, Passegue, & Pietras, 2014; C. C. Zhang & Lodish, 2008). For example, the protozoan parasite that causes kalazar, *Leishmania donovani*, inhabits the bone marrow of humans (Kumar & Nylen, 2012), targets bone marrow stromal macrophages (Cotterell, Engwerda, & Kaye, 2000) and induces differentiation of myeloid cells at the expense of lymphoid progenitors (Abidin, Hammami, Stager, & Heinonen, 2017; Cotterell et al., 2000). In the same line of evidence, after experimental exposure to Gram-negative bacteria, mice display increased amounts of bone marrow-derived neutrophils, through a G-CSF–C/EBPα dependent mechanism (Boettcher et al., 2014). Moreover, infection by intracellular bacteria has been shown to modulate production of circulating leukocytes involving IFN-γ-mediated pathways (Baldridge, King, Boles, Weksberg, & Goodell, 2010; MacNamara et al., 2011; Murray, Young, & Daley, 1998). Altogether, these studies indicate vertebrate hosts respond to infection by ‘remodeling’ cell lineage production, which are highly dependent upon the interplay of cytokine-induced hematopoiesis triggered during...
infection. Interestingly, recent reports have demonstrated hematopoietic stem/progenitor
cells (HSPCs) may be infected by different classes of infectious agents such as viruses
and bacteria, albeit at low efficiency (Carter et al., 2011; Kolb-Maurer, Wilhelm,
Weissinger, Brocker, & Goebel, 2002). Therefore, since many pathogens may reach the
bone marrow and provide microbial-HSC interactions, it is possible that, in addition to
cytokines, pathogen recognition by progenitor cells directly regulate cell lineage
commitment providing an anti-microbial defense system. In contrast, the Red Queen
hypothesis (Van Valen, 1973) predicts such pathogens would benefit from cell lineage
commitment to establish themselves into the host.

The human pathogen *Mycobacterium tuberculosis* (*Mtb*) has been recently
detected in circulating HSCs (Lin-CD34+) from latent TB individuals (Tornack et al.,
2017). Since *Mtb* can also gain access to the bone marrow during extra-pulmonary (Mert
et al., 2001) as well as active pulmonary TB (Das et al., 2013), it has been suggested
that the human bone marrow is a niche/reservoir for this bacterium during natural
pathogen infection. However, whether interactions between *Mtb* and human CD34+ cells
drive cellular differentiation has not been formally demonstrated. Interestingly, earlier
(Rogers, 1928; Schmitt, Meuret, & Stix, 1977) and recent (Berry et al., 2010; Zak et al.,
2016) studies have reported major changes in the peripheral myeloid cells such as
increased blood counts and dysregulated “interferon transcriptional signature” during
active TB. More specifically, several “interferon-stimulated genes” (ISGs) are modulated
in circulating mature neutrophils and monocytes in active TB patients, which calls forth a
possible role of such genes in TB pathogenesis (Berry et al., 2010; Dos Santos et al.,
2018; Zak et al., 2016). In contrast, lymphocyte compartments were recently
demonstrated to be contracted during progression from latent to active TB in humans
(Scriba et al., 2017). Therefore, the observed changes in blood leukocytes could be a
consequence of the interactions between *Mtb* and the bone marrow cellular
environment. Thus, we hypothesized that \textit{Mtb} regulates cellular differentiation of human HSPCs. By employing in vitro functional assays and integrated systems biology analysis of published available cohorts of healthy controls and TB patients, our study suggest that \textit{Mtb} co-opts an evolutionarily recent IFN/IL-6/CEBP axis linking monocyte differentiation and disease severity.

\textbf{Results}

1. \textit{Mt}b H37Rv replicates in primary human CD34$^+$ cell cultures. To investigate the dynamics of \textit{Mt}b infection by HSPCs, we have exposed peripheral blood mononuclear cells (PBMCs) from healthy donors to H37Rv \textit{Mt}b (multiplicity of infection, MOI3) and measured bacterial infectivity by CD34$^+$ cells. First, by using a fluorescent dye (syto-24) which does not influence bacteria infectivity (data not shown), flow cytometry experiments demonstrated that \textit{Mt}b were associated with CD34$^+$ cells following 4h exposure to mycobacteria (Figure 1a,b and Figure 1-figure supplement 1a). At that time point, we observed ~69% of CD34$^+$ and ~79% of CD14$^+$ associated with \textit{Mt}b (Figure 1c). When compared to CD14$^+$ cells, which are highly phagocytic cells, the MFI measurements within the CD34$^+$ cell population were found to be ~4x lower (Figure 1d). These data suggest that PBMC CD34$^+$ cells may be permissive to \textit{Mt}b infection in vitro. Similarly, purified cord blood derived CD34$^+$ cells display comparable \% and MFI as those seen in PBMC CD34$^+$ cells (Figure 1-figure supplement 1b). Confocal microscopy analysis confirmed the presence of sparse intracellular mycobacteria in purified cord blood derived CD34$^+$ cells at 4h post-infection (pi) (Figure 1-figure supplement 1c).

These findings raise the possibility that although human primary Lin$^-$CD34$^+$ cells can be infected by \textit{Mt}b in vitro and in vivo (Tornack et al., 2017), this cell population may display intrinsic resistance to \textit{Mt}b infection as it has been reported for other bacterial species (Kolb-Maurer et al., 2002). Next, we employed a purified cell culture system to
investigate whether H37RV *Mtb* replicates in CD34+ cells in different time points. When sorted purified cord-blood CD34+ cells were exposed to *Mtb* H37Rv (MOI3) and cultivated in StemSpan™ SFEM II (Bodine, Crosier, & Clark, 1991; Keller, Ortiz, & Ruscetti, 1995), bacilli numbers exhibited a ~1.5-log growth at 5 days post infection (dpi) (Figure 1e). As a control, purified CD14+ cells displayed higher bacterial proliferation than purified CD34+ cells over time (Figure 1-figure 1 supplement 1d). Together, these findings demonstrate that *Mtb* infects and replicates in primary human CD34+ cell cultures in vitro. While at 1 dpi bacilli were more associated with the surface of round cells (Figure 1f), at 5 dpi intracellular bacteria were associated with cells with abundant cytoplasm (Figure 1f), suggesting that *Mtb*-exposed cultures displayed increased frequencies of cells exhibiting morphological alterations over time (Figure 1f, right panel). Indeed, Giemsa staining (Figure 1g, arrows) presented higher frequency of cytoplasm richer cells in bacteria-exposed vs uninfected cell cultures (Figure 1g, right panel), thus suggesting that *Mtb* infection enhances cellular differentiation by CD34+ cells in vitro.

2. Live *Mtb* induces CD34+ cells towards myeloid differentiation and monocyte output. Next, to investigate whether *Mtb* triggered cellular differentiation by human CD34+ cells, we evaluated differential expression of 180 transcription factors (TFs) associated with differentiation of distinct hematopoietic cells (Novershtern et al., 2011) in RNA-seq samples of *Mtb*-exposed purified cells (Figure 1-figure supplement 1e – Figure 2-source data 1). Interestingly, *Mtb* infection increased the expression of lineage-specific regulators of myeloid (GRAN/MONO) (*SPI1, CEBPB, CEBPA, EGR2 and STAT2*), but not lymphoid (B and T CELL) (*GABPA, SOX5, TCF3, GATA3, LEF1, RORA and LMO7*) or megakaryoid/erythroid (EARLY/LATE ERY) (*GATA1, FOXO3, NFE2, TAL1*) differentiation (Figure 2a – Figure 2-source data 1). Similarly, CellRouter (Lummertz da Rocha et al., 2018) signature score of the GRAN/MONO gene set was found to be
increased in *Mtb* vs uninfected samples in all time points studied (Figure 2b - Figure 2-source data 1). Next, we applied a network biology-built computational platform (Cahan et al., 2014) which, based on classification scores, can assess the extent to which a given population resembles mature cell types. Figure 2c (Figure 2-source data 1) shows that mRNA samples from *Mtb*-exposed CD34+ cells presented enrichment of monocyte/macrophage profiles, but not other mature cell populations such as lymphocytes or dendritic cells. Additionally, at 5 dpi, CD34+ cell cultures displayed increased frequencies of cells positive for CD11b (Figure 2d), a surface molecule expressed during myeloid differentiation (Hickstein, Back, & Collins, 1989; Rosmarin et al., 1989). Together, these data suggest that *Mtb* drives human primary CD34+ cells towards myeloid differentiation. We next employed flow cytometry to measure cell surface molecules previously associated with myeloid differentiation of human CD34+ cells (Cimato, Furlage, Conway, & Wallace, 2016; Gorczyca et al., 2011; Kawamura et al., 2017; Manz, Miyamoto, Akashi, & Weissman, 2002; Olweus, Lund-Johansen, & Terstappen, 1995). More specifically, we gated on CD34+ events and quantified % CD64+CD4+ cells. Corroborating our hypothesis, *Mtb* enhanced the frequency of CD64+CD4+CD34+ cells (Figure 2e-h) at 5 dpi, but not CD10+CD34+ (lymphoid) or CD41a+CD34+ (megakaryoid) progenitors (Figure 2-figure supplement 1a). Similarly, Lin− CD34+ cells from PBMC (Figure 2-figure supplement 1b) samples from healthy donors exposed to *Mtb* displayed increased frequency of CD4+CD64+CD34+ cells and augmented levels of CD38 and HLA-DR (Figure 2-figure supplement 1b,c), two molecules associated with advanced stage of cellular differentiation (Cimato et al., 2016; De Bruyn et al., 1995; Terstappen, Huang, Safford, Lansdorp, & Loken, 1991). When compared to their base line levels, we also observed an increased % CD4+CD64+CD34+ cells in *Mtb*-exposed bulk bone marrow samples from 2 healthy individuals (Figure 2-figure supplement 1c, p = 0.08). In addition, frequencies of CD4+CD64+CD34+ cells were
higher in cultures infected to live H37Rv \textit{Mtb} than those exposed to heat-killed (HK) bacteria (Figure 2f,g). These results suggest that the observed cellular phenotype was mostly due to the activities of live pathogen and only partially to mycobacterial PAMPs such as TLR2 (Ara-LAM) or TLR9 (\textit{Mtb} gDNA) agonists (Bafica et al., 2005; Underhill, Ozinsky, Smith, & Aderem, 1999), which induced CD38 and HLA-DR, but not CD4 and CD64 expression in CD34$^+$ cells (Figure 2-figure supplement 1d). Importantly, increased frequency of CD4$^+$CD64$^+$CD34$^+$ cells was also observed when cell cultures were exposed to a clinical isolate of \textit{Mtb} (Figure 2h), ruling out a possible genetic factor associated with the laboratory strain H37Rv (Brites & Gagneux, 2015). Furthermore, CD34$^+$ cell death was not enhanced by \textit{Mtb} infection as demonstrated by the use of a live-and-dead probe and lactate dehydrogenase (LDH) quantification in cell culture supernatants (Figure 2-figure supplement 1e,f). Together, these data indicate live \textit{Mtb} directs primary human CD34$^+$ cells towards myeloid differentiation in vitro.

Next, to investigate whether \textit{Mtb} enhanced HSPC differentiation into mature myeloid populations (Kawamura et al., 2017; Lee et al., 2015; Manz et al., 2002), purified CD34$^+$ cells were exposed to \textit{Mtb} and 10d later, surface molecules were measured by flow cytometry. Live H37Rv (Figure 3a,e) or clinical isolate \textit{Mtb}, (Figure 3-figure supplement 1a) but not \textit{Leishmania infantum} promastigotes (data not shown), enhanced expression of the monocyte surface molecule CD14, confirming the observed monocyte/macrophage output enrichment by CellNet analysis (Figure 2c). Interestingly, in this in vitro culture system, CD14$^+$ cells started to emerge at low levels at day 3 in both uninfected and \textit{Mtb}-exposed cell cultures, while enhancement in monocyte frequency was observed in \textit{Mtb}-stimulated cells at later time points, i.e. at 7 and 10 dpi. (Figure 3-figure supplement 1b). Compared to control cell cultures, CD14$^+$ cells induced by \textit{Mtb} displayed similar MFI expression of CD11b, HLA-DR, CD64 and CD16 surface molecules (Figure 3i) and most, but not all experiments presented increased frequency
of CD14^+CD16^+ monocytes (Figure 3j), which were previously associated with severe pulmonary TB (Balboa et al., 2011). Moreover, albeit not statistically significant, *Mtb* enhanced the frequency of CD16^+CD66b^+ neutrophils in the majority but not all samples tested (Figure 3b,f). In contrast, HK *Mtb* did not stimulate monocyte or neutrophil output (Figure 3e,f). As expected (Figure 2-figure supplement 1a), megakaryoid/platelet-(Figure 3c,g), dendritic cell- (Figure 3d,h) or erythroid- (Figure 3-figure supplement 1c) associated markers were unchanged after exposure to live or HK *Mtb*. Altogether, these results suggest *Mtb* selectively favors the generation of monocytes and, to a lesser extent, neutrophils, by human CD34^+ cells in vitro.

### 3. In vitro *Mtb*-enhanced myeloid differentiation is mediated by IL-6R, but not type I or type II IFN signaling.

Cytokines are important triggers of Lin^CD34^+ differentiation in vivo and in vitro (Endele, Etzrodt, & Schroeder, 2014; Hoggatt et al., 2016; C. C. Zhang & Lodish, 2008) and Reactome pathway analysis of genes differentially expressed between *Mtb*-infected versus uninfected conditions displayed enrichment of “cytokine signaling in immune system” (Figure 3-figure supplement 1d; n=3 donors, 2 independent experiments - Figure 2-source data 1). Among several genes, we observed a significant enrichment of *IL6* (Supplementary File 1 - Figure 2-source data 1), a key HSPC-derived regulator of myeloid differentiation in mouse and human models (Jansen et al., 1992; Zhao et al., 2014) which was confirmed in our system by the addition of exogenous IL-6 to CD34^+ cells (Figure 4-figure supplement 1a). Moreover, cytokine receptors, including *IL6R*, as well as their cytokine partners, containing *IL6*, were enriched in *Mtb*-exposed CD34^+ cell cultures (Figure 4a,b and Figure 4-figure supplement 1b - Figure 2-source data 1). Similarly, increased *IL6* expression was confirmed by qPCR (Figure 4-figure supplement 1c). In addition, “interferon signaling” and “interferon alpha/beta” pathways were significantly enriched in *Mtb*-exposed CD34^+ cells (Figure 3-figure supplement 1d
and Supplementary File 1 - Figure 2-source data 1). This was confirmed in 5 donors, which displayed increased levels of *IFNA2*, *IFNB* and *IFNG* transcripts, albeit at a lower level relative to *IL6* mRNA (Figure 4-figure supplement 1c). Importantly, interferon-stimulated genes (ISGs) such as *MX1*, *ISG15* and *IFI16* as well as IL-6R-stimulated genes such as *IL1RA*, *GRB2* and *CXCL8* were enhanced in *Mtb*-stimulated CD34+ cells from 5 different donors (Figure 4-figure supplement 1d), suggesting IL-6 and IFN signaling are active in these cells. Corroborating previous findings showing that HSPCs produce IL-6 following microbial stimuli (Allakhverdi & Delespesse, 2012), live *Mtb* also induced intracellular IL-6 production in Lin-CD34+ cells from bacteria-exposed PBMC 1d cultures (Figure 4c). This was confirmed in 1d culture supernatants of purified CD34+ cells exposed to live *Mtb* which presented augmented levels of IL-6, but not IFN-γ, IL-1β or TNF (Figure 4-figure supplement 1e). Interestingly, while HK *Mtb* also stimulated production of IL-6 (Figure 4c), dead bacteria did not induce CD38, CD4 and CD64 expression in PBMC Lin-CD34+ cells as seen in cell cultures exposed to live *Mtb* (Figure 4-figure supplement 1f). When compared to the live pathogen, qPCR experiments with HK *Mtb*-exposed purified CD34+ cells did not show induction of ISG *STAT1* (Figure 4-figure supplement 1g), suggesting the existence of cross talking regulatory pathways between live *Mtb*, IL-6 and IFN signaling to boost myeloid differentiation in vitro. Since these data pointed that IL-6 and IFN signaling are potential pathways involved in *Mtb*-enhanced myeloid differentiation by CD34+ cells, we employed neutralizing monoclonal antibodies as a tool to investigate this possibility. While type I IFN signaling was necessary for *Mtb*-stimulated ISGs such as *STAT1* and *MX1* transcription (Figure 4-figure supplement 1h), neither type I nor type II IFN signaling pathways were required for *Mtb*-enhanced monocyte/granulocyte conversion (Figure 4d,e and Figure 4-figure supplement 1i). In contrast, neutralizing anti-IL-6Ra antibody (α-IL-6R) inhibited
background levels of CD14⁺ monocytes and CD66b⁺ granulocytes, as well as Mtb-enhanced myeloid differentiation by CD34⁺ cell cultures (Figure 4f-h) but not transcription of STAT1 and MX1 (Figure 4-figure supplement 1h). In addition, megakaryoid, erythroid- or dendritic cell-associated surface molecules were unaltered in α-IL-6R-treated cell cultures (Figure 4-figure supplement 1j-l). Interestingly, Mtb-exposed CD34⁺ cell cultures treated with α-IL-6R (Figure 4i) presented significantly lower CFU counts when compared with infected untreated control cell cultures, while α-IFNAR2 (Figure 4j) or α-IFN-γ (Figure 4k) did not affect CFU counts. Together, these results suggest live Mtb enhances IL-6R-mediated myeloid differentiation by human CD34⁺ cells in vitro.

4. An IL6/IL6R/CEBPB gene module is enriched in the active TB transcriptome and proteome. To investigate whether IL-6R signaling correlates with monocyte expansion and TB-associated pathology in vivo, we performed a comprehensive systems biology analysis integrating several large transcriptomic and proteomic data sets from published cohorts of healthy controls and patients with latent, active and disseminated TB (Berry et al., 2010; Hecker et al., 2013; Naranbhai et al., 2015; Novikov et al., 2011; Scriba et al., 2017) (Supplementary File 2). First, we used Ingenuity Pathway analysis (IPA) to determine IL-6/IL-6R upstream regulators in transcriptomes from publicly available CD14⁺ monocytes of active TB patients (Berry et al., 2010). As shown in Figure 5a (top panel), IL6, IL6ST, IL6R and STAT3 were significantly enriched in transcriptomes of active TB monocytes, when compared to cells from healthy controls. As reported previously (Berry et al., 2010; Mayer-Barber et al., 2011; Novikov et al., 2011), STAT1 and IL1B were also confirmed as upstream regulators in active TB monocytes (Figure 5a, top panel). We next examined potential genes share between IL6/IL6R and type I
IFN signaling pathways in active TB monocytes. Strikingly, the two top upstream regulators in TB monocytes, *IRF1* and *STAT1* (Figure 5a, top panel), were the only genes in common between the TB monocyte gene signature (Berry et al., 2010), the “IL6/STAT3 pathway” and the “in vivo IFN-β” signature (Figure 5a, Venn diagram, bottom panel), suggesting these genes might be regulated by both IL-6 and type I IFN during active TB in vivo. Since type I IFN and IL-6 share the ability to induce phosphorylation of both STAT1 and STAT3 (Ho & Ivashkiv, 2006), we ran gene set enrichment analysis (GSEA) (Subramanian et al., 2005) to identify potential overlapping downstream target genes in the whole blood “Berry TB” disease signature (Berry et al., 2010). In addition to the previously demonstrated type I IFN/STAT1 signature (Berry et al., 2010), the “IL6/STAT3” pathway was significantly enriched in this data set (FDR-corrected p<10^{-4}, Supplementary File 2). Next, we defined protein signatures by overlapping the “Berry TB”, the “IL6/STAT3” pathway with a published plasma proteome defining disease progression from latent to active TB (Scriba et al., 2017) (“Scriba Plasma TB”, Figure 5b, Venn Diagram top panel). STRING network analysis of protein-protein interactions confirmed two clusters (Figure 5b, bottom panel), which comprised three signatures: “CD34/myeloid”, “IL6/STAT3” and “IFN/IL6-shared” pathways. Reanalysis of the published “Scriba Plasma TB” proteome set (Scriba et al., 2017) confirmed increased IL-6/STAT3 protein levels and changes in CD34/CD38 homeostasis, which were found to be early events in TB pathogenesis (Figure 5c, top panel). “IL6/STAT3” pathway-associated proteins such as PLA2G2A, CRP, STAT3, IL-6 and CFB increased around 12 months before TB diagnosis (Figure 5c,d, top panels - orange circles and bars), which was concomitant with significant changes in the “IFN/IL6-shared” plasma markers CXCL10, IFNAR1 and MMP9 (Figure 5c,d top panels - blue circles and bars). The “IL6/STAT3” and “IFN/IL6-shared” pathways were also significantly enriched in a gene set recently linked to monocyte expansion in vivo, measured as monocyte:lymphocyte...
(ML) ratio (Naranbhai et al., 2015) (Supplementary File 2), and positively correlated with mycobacterial growth in vitro, thus connecting monocyte expansion and increased Mtb survival. Interestingly, the changes found in both the “IL6/STAT3” and “IFN/IL6-shared” pathways during development of TB disease preceded enrichment of the “ML ratio” gene set (Naranbhai et al., 2015) (6 months before diagnosis, p<0.05, Figure 5c, bottom panel and Figure 5d, top panel, gray bar) and reduction of the CD34/CD38 gene markers, in agreement with our in vitro model of Mtb-enhanced CD34+ differentiation (CD34+ → CD34+CD38+ → CD14+). Moreover, fold changes were higher for “IL6/STAT3” pathway genes than for “IFN/IL6-shared” genes, and significantly higher than “ML ratio” genes (p<0.05) or “CD34/myeloid” differentiation genes (p<0.01) (Figure 5d bottom panel). Together, these data suggest sequential activation of IL-6/IL-6R and IFN signaling pathways before monocyte expansion during TB disease progression in vivo, raising a possible link between these two events in disease pathogenesis. In support of this idea, CD34+ cells exposed to Mtb in vitro displayed increased levels of pSTAT1 as well as C/EBPβ (and a slight enhancement of C/EBPα), which are key TF regulators of ISGs and myeloid differentiation genes, respectively (Figure 5-figure supplement 1a). Interestingly, qPCR experiments from HK Mtb-exposed CD34+ cells did not show induction of myeloid differentiation TFs CEBPA and CEBPB (Figure 4-figure supplement 1g). Furthermore, we observed that CEBPB, CEBPD and STAT3 as well as IRF1, STAT1 and ICSBP/IRF8 TFs were significantly enriched in Mtb-infected CD34+ transcriptomes (Figure 5e and Figure 5-figure supplement 1b - Figure 2-source data 1), which were associated with increased mycobacterial replication in vitro (Figure 1e). These results suggest that Mtb infection activates a gene module shared by both type I IFN and IL-6, linking downstream ISGs and CEBPs.
5. An *IL6/IL6R/CEBP* gene module correlates with monocyte expansion and TB severity. TB pathogenesis is a convoluted process which interconnects mycobacterial dissemination, host inflammatory responses and systemic tissue pathology. To further investigate a potential link between this gene module (*IL6/IL6R/CEBP*) with disease severity and monocyte expansion in vivo, we first examined large transcriptomic data sets of “disseminated TB”, which includes extrapulmonary and lymph node TB (GSE63548). The “IL6/STAT3” pathway was found to be significantly enriched among differentially expressed genes in both extrapulmonary (FDR $p=10^{-3}$) and lymph node TB (FDR $p=10^{-4}$, Supplementary File 2). Furthermore, downstream targets of *STAT3*, *CEBPB, CEBPD, SPI1/PU1, ICSBP/IRF8*, which are TF regulators of myeloid differentiation, were enriched in “disseminated TB” and in the “ML ratio” gene sets (Supplementary File 2), suggesting these TFs are activated during severe disease and associated to monocyte expansion in vivo. In contrast, ISRE (STAT1/STAT2) and IRF1 motifs, the major upstream regulators observed in TB monocyte transcriptome (Figure 5a top panel) and shared between IL-6 and IFN signaling (Figure 5b), were not enriched in the “ML ratio” gene set (Supplementary File 2). Of note, only *CEBPB* targets were significantly enriched in the “ML ratio” gene set in healthy subjects (Supplementary File 2), supporting its link with myeloid differentiation during homeostasis. Since the *IL6/IL6R/CEBP* gene module was correlated with both systemic disease dissemination and monocyte expansion, two processes associated with TB disease (Rogers, 1928; Schmitt et al., 1977), we next examined whether these genes might be connected to disease severity in a published cohort with detailed clinical parameters and transcriptome data (Berry et al., 2010). When compared to latent TB subjects, we observed that both the monocyte counts and ML ratio were significantly increased in active TB patients (Figure 5f). *CEBPB* transcripts positively correlated with ML ratio levels (Figure 5g), *IL6R* transcripts (Figure 5h), *STAT3* (Figure 5i) as well as
inflammatory biomarkers such as C-reactive protein (CRP) and erythrocyte sedimentation rate (ESR) (Figure 5—figure supplement 1c). In addition, CEBPB mRNA levels were significantly higher in *Mtb*-positive vs. *Mtb*-negative sputum smears (Figure 5j), and positively correlated to tissue damage, total symptom counts as well as ISG15 levels (Figure 5—figure supplement 1c), in agreement with our previous findings (Dos Santos et al., 2018). Taken together, these results indicate that the IL6/IL6R/CEBP gene module is a hub correlated with monocyte expansion during *Mtb* infection in vivo and is amplified in severe pulmonary and systemic disease.

6. Recent mammalian/primate genetic changes link an IFN/IL-6/IL-6R/CEBP axis to monocyte expansion and TB pathogenesis in humans. The “type I IFN” signature found in active TB (Berry et al., 2010), shared with the IL-6/IL-6R-regulated gene set (Figure 5), comprises a number of well-characterized ISGs with cross-species antiviral activity such as IRF1 and OAS. It has been reported that these ISGs have been undergoing strong purifying selection during primate evolution (Manry et al., 2011; Shaw et al., 2017), including recent Neanderthal introgression (Enard & Petrov, 2018; Quach et al., 2016). We thus undertook an evolutionary approach to investigate whether the IL6/IL6R/CEBP gene module and its partial overlap with type I IFN signaling is linked to monocyte expansion and TB severity. To do so, we performed a stepwise analysis, starting from early mammalian emergence (>100 million years ago (mya), over primate (>50 mya) and hominid evolution (>15 mya). We have also examined the recent human evolution including Neanderthal introgression (<100,000 years ago) and human pathogen adaptation (15,000-1,500 years ago), up to extant human genetic variation through analysis of large genome wide association studies (GWAS).

First, STRING network measurements of amino acid conservation and gene co-occurrence across mammalian and primate evolution revealed that IL-6, IL-6R and
C/EBP family members C/EBPα, C/EBPβ and C/EBPδ differ substantially throughout primate evolution and even among closely related hominins (Pan troglodytes and Gorilla gorilla) (Figure 6a, heat map). In contrast, matched control molecules in the same STRING network (KLF5/NFKB1/MAPK1//STAT1/STAT3) remained largely conserved in most mammals, and even in birds and reptiles (Figure 6a, heat map and Figure 5-figure supplement 1d). Next, to investigate the biological consequence of the evolutionary differences in overlapping IL-6/IFN signaling, we reanalyzed cross-species type I IFN regulation from the ‘mammalian interferome’ database (Shaw et al., 2017). As expected, the conserved “IFN/IL6-shared” genes CXCL10/CXCL9/STAT1/STAT2 displayed higher fold-changes upon type I IFN treatment across all 10 species (from chicken to human, Figure 6b, top panel). Interestingly, the “IL-6/STAT3” pathway genes IL6, STAT3 and SOCS3 were also significantly upregulated while IL6R was significantly down-regulated (Figure 6b, top panel) in the same experimental setting. Among CD34/myeloid differentiation genes, ICSBP/IRF8 and CD38 were strongly upregulated, but only in 4/10 and 2/10 species, respectively, while ELF1 was homogeneously and significantly upregulated in 9/10 species (Figure 6b, top panel). These results suggest that type I IFN consistently regulates expression of IL-6 signaling and myeloid-associated genes in different species. However, among the entire IL6/IL6R/CEBP myeloid gene set, CEBPB was the topmost variable ISG across mammalian evolution (CV >1000%, Figure 6b, bottom panel). Remarkably, type I IFN-induced upregulation of both CEBPB and CEBPD, previously identified as NF-IL6 and NF-IL6β, respectively (Ramji & Foka, 2002) was present only in humans and lacking in all other mammals investigated (Figure 6b, bottom panel, inset). Mechanistically, ChipSeq analysis of IFN-treated human CD14+ monocytes corresponding to regions with active chromatin (DNase Hypersensitivity Sites, DHS and H3K27 acetylation, not shown) confirmed the existence of functional
STAT1 peaks in CEBPB and CEBPD (Figure 6c, top and middle panels, denoted by vertical blue lines). These peaks correlated with increased downstream transcription in CD14+ cells, as compared to purified CD34+ cells (Figure 6c, RNA-seq). In agreement with our findings (represented in Figure 6b, bottom panel, inset), only 3 out of 11 (27%) STAT1 binding peaks in CEBPB and CEBPD were found in conserved regions (Conservation Birds-Mammals line, Figure 6c), while 6 out of 7 (86%) STAT1 peaks were conserved in CXCL9 and CXCL10 genes (Figure 6c, bottom panel). Interestingly, transcriptional regulation of CEBPB and CEBPD in humans and macaques, but not mouse cells stimulated with double-stranded RNA, which mimics a viral infection (Figure 6-figure supplement 1a), were also observed in an independent data set (Hagai et al., 2018). As expected, CXCL9 and CXCL10 responses are conserved in dsRNA-stimulated cells from humans, macaques and mouse (Figure 6-figure supplement 1a).

Thus, transcriptional induction of CEBPB and CEBPD controlled by IL-6- and type I IFN-signaling appears as a relatively recent event in mammalian and primate evolution.

7. Genome-wide association studies (GWAS) connect the IL6/IL6R/CEBP gene module with monocyte expansion in TB disease.

Since genetic susceptibility and transcriptional responses to intracellular pathogens have shown significant links to Neanderthal introgression in populations of European and Asian descent (Dannemann, Prufer, & Kelso, 2017; Quach et al., 2016), we next explored enrichment for introgression in the IL6/IL6R/CEBP and “ML ratio” gene sets. As shown in Figure 6d (Figure 2-source data 1), eleven genes with Neanderthal introgression were significantly upregulated in our Mtb-exposed CD34+ cells transcriptome (enrichment p<0.0001). Of those, OAS1, OAS2 and MT2A transcripts had significantly higher effect sizes upon ML ratios, as compared to other introgressed genes (p<0.05) and to all other genes shown to regulate ML ratio in vivo (p<0.001, Figure 6d).
This finding was confirmed in a recently published data set (n=198) of purified microbial-exposed CD14+ monocytes from a Belgian cohort of European (EUB) and African (AFB) descendance, with documented presence or absence of Neanderthal introgression, respectively (Quach et al., 2016). Strikingly, 9 out of 11 introgressed genes enriched during Mtb-triggered monocyte differentiation (Figure 6d, Venn diagram) were significantly upregulated in TLR1/TLR2-stimulated (Figure 6d, right panel), but not unstimulated monocytes (not shown). These findings suggest pathogen exposure may enhance gene pathways recently selected during hominid evolution linked to monocyte expansion.

We next interrogated whether the IL6/IL6R/CEBP gene module was linked with monocyte expansion in several large published data sets of standing human variation. Two large GWAS studies (Astle et al., 2016; Kanai et al., 2018) containing >230,000 individuals have identified single-nucleotide polymorphisms (SNPs) in or adjacent to IL6R, CEBPA-CEBPD-CEBPE and ICSBP/IRF8 genes as significantly associated to blood monocyte counts (Supplementary File 2 and ranked in Figure 7a as monocyte count GWAS). Moreover, gene-specific z-scores for human polygenic adaptation to pathogens in 51 different populations worldwide (Daub et al., 2013) were positive, representing higher levels of population differentiation, for all genes in our proposed IL6/IL6R/CEBP myeloid differentiation module (except CXCL10, Figure 7a and Supplementary File 3). Lastly, we examined whether myeloid differentiation genes identified in this study are found in GWAS TB susceptibility genes. A significant enrichment (p<0.0001) for differentially expressed genes from our Mtb-exposed CD34+ transcriptome and TB susceptibility GWAS/candidate genes (18 out of 172 genes, including IL6, STAT1 and CD14) was also observed (Figure 6-figure supplement 1b). Similarly, a significant (p<0.0001) overlap was found for the IL6/IL6R/CEPB module and
TB genetic susceptibility (6 shared genes CD14, CXCL10, IL6, IL6R, IRF1 and STAT1, Figure 6-figure supplement 1b).

As ranked in Figure 7a, 24 out of 28 members of this gene module display a genome-wide, transcriptomic, proteomic or functional association to human TB, being strongest for IL6 and its downstream signaling TFs CEBPB and CEBPD, demonstrated in 5-6 independent data sets each. Collectively, our multi-level-based evidence suggests Mtb exploits an evolutionary recent IFN/IL-6/IL-6R/CEBP axis linked to monocyte expansion and human TB disease.

Discussion

Emerging evidence has suggested that Mtb establishes an infectious niche in the human bone marrow during active TB, which is associated with altered numbers of leukocytes in the periphery (Das et al., 2013; Mert et al., 2001; Naranbhai et al., 2015; Rogers, 1928; Schmitt et al., 1977; Tornack et al., 2017; Wang et al., 2015). In the present study, we observed that Mtb consistently stimulated myeloid differentiation molecules in CD34+ cell cultures from three different human tissues, namely: bone marrow, peripheral blood or cord blood samples. Employing a purified cord-blood derived CD34+ culture cell system, we observed that Mtb enhances IL-6R-mediated myeloid differentiation by human primary CD34+ cells in vitro. Importantly, IL-6/IL-6R downstream molecules such as C/EBPβ, C/EBPδ, STAT3 and their targets were significantly enriched in cell transcriptomes from active TB patients as well as were positively correlated with disease severity. Therefore, our data expands previous studies and raise a scenario in which Mtb skews myeloid development, mediated by IL-6/IL-6R signaling, as a key step in human TB pathogenesis.

While Mtb enhanced IL6 expression in purified CD34+ cell cultures from all donors, IFNA and IFNB mRNA were detected in some but not all donors. However, ISGs
were highly enriched in the bacteria-exposed samples suggesting that although low/undetectable amounts of type I IFN were produced in infected cell cultures (Rodero et al., 2017), these cytokines were present in the cell culture (Figure 4-figure supplement 1h). Furthermore, our results show that live Mtb is a potent stimulus to induce ISGs (Figure 6-figure supplement 1c - Figure 2-source data 1) and myeloid differentiation in primary human CD34+ cells. However, while heat killed mycobacteria induced IL-6 production by CD34+ cells, it poorly stimulated STAT1, CEBPB and differentiation cell surface molecules by progenitor cells as well as CD14+ monocyte levels. Interestingly, although IL-6R signaling was involved in both myeloid differentiation and Mtb growth by CD34+ cell cultures, type I or type II IFN signaling were not. These results suggest that monocyte maturation is connected to Mtb proliferation in vitro and could explain why the effects of anti-IL6R antibodies on cellular differentiation inhibited bacteria growth (Figure 4f-i). Although the ISG gene set was enriched in Mtb-exposed CD34+ cells, our data suggest type I or type II IFN signaling appear not to mediate Mtb-enhanced monocyte development in vitro. Collectively, this evidence suggests that unknown activities of live pathogen infection regulate myeloid differentiation involving an IL-6R-mediated process and implies cross-talking of regulatory pathways between live Mtb, IL-6 and IFN signaling to boost myeloid differentiation of CD34+ cells. At the molecular level, it has been reported that IFN-induced C/EBPβ triggers gamma-activated transcriptional elements (GATE) sequences independent of STAT1 (Li, Gade, Xiao, & Kalvakolanu, 2007), suggesting the existence of cooperative and/or redundant roles of IL-6 and IFN signaling in different molecular settings. The mechanisms by which endogenous IL-6, IFN-α/β and live Mtb interplay to enhance C/EBP-mediated myeloid differentiation of HSPCs require further investigation. Of note, in our previously characterized cohort of multiple sclerosis patients (Menezes et al., 2014; Van Weyenbergh, Wietzerbin,
Rouillard, Barral-Netto, & Liblau, 2001), IFN-β therapy in vivo did not significantly change monocyte or lymphocyte counts, nor did it increase the ML ratio after three months of treatment in patients with documented clinical response (data not shown), supporting the idea that type I IFN by itself is not sufficient to cause monocyte expansion in vivo.

It has not been determined how mature myeloid cell populations from active TB patients acquire the “ISG” signature. While monocytes and other cells may encounter Mtb-associated inflammatory stimuli in infected tissues (e.g. lungs and liver), our data suggest the possibility that Mtb may activate these cells during their development in the bone marrow. We have not directly addressed whether circulating monocytes/granulocytes acquire their phenotype in the bone marrow, during development of myeloid progenitors in vivo. Nevertheless, a recent study by Norris and Ernst (Norris & Ernst, 2018) demonstrated increased monocyte egress from the bone marrow in a murine model of Mtb infection. Considering mycobacteria (Arts et al., 2018; Das et al., 2013; Joosten et al., 2018; Mert et al., 2001; Mitroulis et al., 2018) can access the bone marrow and stimulate IL-6, it is possible that individuals draining higher amounts of Mtb into the bone marrow display increased inflammatory alterations including IL-6R-mediated myelopoiesis, upregulation of IFN-stimulated responses and amplified disease severity. Likewise, we found that enrichment of the IL6/IL6R/CEBP axis positively correlated with systemic disease such as lymph node and extrapulmonary TB (Figure 5f,g).

Several independent studies have also indicated a detrimental role of “IFN and IFN-induced genes” during Mtb infection in human TB (Berry et al., 2010; Bustamante, Boisson-Dupuis, Abel, & Casanova, 2014; Dos Santos et al., 2018; Novikov et al., 2011; Scriba et al., 2017; G. Zhang et al., 2018) and murine models (Antonelli et al., 2010; Manca et al., 2001). Our results expand these previous studies, revealing a novel IL6/IL6R/CEBP gene module and its link to monocyte development, mycobacterial
dissemination and TB disease severity. Furthermore, as evidenced by Scriba et al. (Scriba et al., 2017) and re-analyzed in the present study (Figure 5c,d), both IFN and IL6 pathways are early events in TB pathogenesis, detectable in the plasma proteome >6 months before diagnosis. Nevertheless, a pivotal role for IL6/IL6R signaling has not been evident from previous “omics” approaches. While IL-6 signaling partially overlaps with type I IFN responses (Figure 5a,b), possibly due to their shared ability to activate STAT1 and STAT3 (Ho & Ivashkiv, 2006), whole blood transcriptomic analyses in TB are predominated by an “IFN-inducible neutrophil signature” (Berry et al., 2010). Therefore, the high numbers of neutrophils in the blood possibly mask differential expression of other gene sets in less frequent populations, such as monocytes, monocyte subsets and, in particular, Lin'CD34+ cells.

Most ISGs present in the whole blood Berry TB signature (Berry et al., 2010), the Scriba TB plasma proteome (Scriba et al., 2017) and the Naranbhai et al. ML ratio gene set (Naranbhai et al., 2015) displayed cross-species type I IFN-induction throughout mammalian evolution (Figure 6b). Despite a shared STAT1/STAT3 activation by type I IFN and IL-6, homeostatic activation of C/EBPβ is mostly IL-6-specific, as evidenced by data mining and STRING analysis (Figure 6a), in keeping with its original description as NF-IL6 (Akira et al., 1990). Across species, CEBPB and CEBPD are among the highly variable ISG of the entire IFN/IL-6/CD34/myeloid gene set (Figure 6b). Likewise, although type I IFN-induced IL6 and STAT3 transcription are conserved in all mammalian species studied, IFN-inducibility of CEBPB and CEBPD mRNA appeared to be recently acquired in primate evolution. In line with our observations, IL6, CEBPB and SPI1/PU1 genetic polymorphisms have been previously associated with TB susceptibility (G. Zhang et al., 2014; G. Zhang et al., 2012). In addition, a recently identified trans eQTL (rs5743618) (Quach et al., 2016) in TLR1, a gene with peak Neanderthal
introgression (Dannemann et al., 2017; Enard & Petrov, 2018; Hagai et al., 2018; Quach et al., 2016) has been associated to TB susceptibility in several populations worldwide (Barletta-Naveca et al., 2018; Naderi, Hashemi, Mirshekari, Bahari, & Taheri, 2016; Qi et al., 2015). Biological pathway analysis of genes significantly regulated in trans of rs5743618 revealed a significant enrichment of IL-6/STAT3 signaling and IL6 as the most connected gene (data not shown). In agreement, Mtb-induced macrophage IL-6 production, among other cytokines, can be predicted on the basis of strong genetic components as recently reported by (Bakker et al., 2018) in a large GWAS/immunophenotyping cohort study. By employing a data-driven multi-level analysis from large cohorts, we expand these previous observations and revealed significant genetic links shared between IL-6/IL-6R/CEBP signaling, CD34+ myeloid differentiation, monocyte homeostasis and TB susceptibility (compiled in Figure 7a). Together, these findings favor the hypothesis that such genetic changes have undergone stepwise mammalian, primate and recent human selection, including Neanderthal introgression and worldwide population-specific pathogen adaptation.

In summary, our observations suggest that Mtb boosts myeloid differentiation by exploiting a feed-forward loop between IL-6 and type I IFN molecular networks, bridged by C/EBPβ (and C/EBPδ) (Figure 7b). Yet, further experiments will define the precise mechanisms of crosstalk between IFN, IL-6 and CEBP family members, specifically CEBPβ and CEBPδ, during natural Mtb infection. While this question merits direct investigation, nonetheless, the use of IL-6R blockade as an adjunct therapy to treat multi-drug resistant severe TB has been proposed (Okada et al., 2011; Zumla, Rao, Dodoo, & Maeurer, 2016). Thus, the present study provides evidence of a novel host-directed target for therapeutic intervention in a major human disease.
### Material and methods

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**Reagents.** *Mtb* Ara-LAM was obtained from BEI Resources and used at 5 µg/mL. *Mtb* H37Rv genomic DNA was obtained from 28 days colonies growing in Löwenstein– Jensen medium by CTAB method as previously described (Yamashiro et al., 2016).
Recombinant human (rh) IL-6 was purchased from Immunotools. Anti-IFNAR2A (clone MMHAR-2, PBL) and anti-IFN-γ (clone B27, Immunotools) neutralizing antibodies were used at 1 and 10 µg/mL, respectively and anti-IL-6R (Tocilizumab, Roche) was used at 1 µg/mL. Fluorescent dye Syto24 was obtained from Thermo Fisher Scientific.

**Mycobacteria cultures.** The virulent laboratory H37Rv *Mtb* strain and the clinical *Mtb* isolate (Mtbc-267) were maintained in safety containment facilities at LACEN and UFSC as described elsewhere (Yamashiro et al., 2016). Briefly, *Mtb* was cultured in Löwenstein-Jensen medium (Laborclin) and incubated for 4 weeks at 37ºC. Prior to use, bacterial suspensions were prepared by disruption in saline solution using sterile glass beads. Bacterial concentration was determined by a number 1 McFarland scale, corresponding to $3 \times 10^8$ bacteria/mL.

**Subjects samples, cells and *Mtb* infections.** This study was approved by the institutional review boards of Universidade Federal de Santa Catarina and The University Hospital Prof. Polydoro Ernani de São Thiago (IRB# 89894417.8.0000.0121). Informed consent was obtained from all subjects. Peripheral blood and bone marrow mononuclear cells were obtained using Ficoll-Paque (GE) in accordance with the manufacturer’s instructions. Briefly, blood collected in lithium-heparin containing tubes was further diluted in saline solution 1:1 and added over one volume of Ficoll-Paque reagent. The gradient was centrifuged for 40 min at 400 x $g$, 20ºC. The top serum fraction was carefully removed, the mononuclear fraction was harvested and washed once in a final volume of 50 mL of saline solution for 10 min at 400 x $g$, 20ºC. Subsequently, cell pellet was suspended and washed twice with 20 mL of saline solution for 10 min at 200 x $g$, 20ºC, to remove platelets. Cells were then suspended to the desired concentration in RPMI 1640 (Life Technologies) supplemented with 1% fresh complement inactivated (30 min at 56ºC) autologous serum, 2 mM *L*-glutamine (Life Technologies), 1 mM sodium pyruvate (Life Technologies) and 25mM HEPES (Life
Technologies). Human Cord Blood (CB) purified CD34+ cells from 5 different donors were obtained from STEMCELL Technologies and resuspended in StemSpan Expansion Media – SFEM II (STEMCELL Technologies) according to manufacturer’s instruction. Optimal cell density for replication was $5 \times 10^4$ CD34+ cell/mL. In a set of experiments, CD34+ cells were further enriched using a cell sorter (FACSMelody, BD). Following 4 days of expansion, cells were washed and diluted in SFEM II media without cytokine cocktail to the desired concentration. Culture purity was assessed by FACS and showed more than 90% of CD34+ events after expansion. For in vitro infection experiments, 1 McFarland scale was diluted in media to fit the desired multiplicity of infection (MOI). For each experiment, bacteria solution was plated in Middlebrook 7H10 agar (BD Biosciences) supplemented with 10% Oleic Acid Albumin Dextrose Complex (OADC) and incubated at 37°C to confirm initial bacteria input. In a set of experiments, 1 McFarland scale was incubated with 500 nM of Syto24 dye as described previously (Yamashiro et al., 2016). In some experiments, H37Rv Mtb was heat killed (HK) at 100°C for 30 min. *Leishmania infantum* promastigotes were kindly provide by Ms. Karime Mansur/UFSC and Dr. Patrícia Stoco/UFSC and used at MOI=3. In cytokine/cytokine neutralizing experiments, cells were pretreated with anti-IFNAR2 (1 µg/mL), anti-IFN-γ (10 µg/mL) or anti-IL-6R (1 µg/mL) for 1h and exposed to Mtb (MOI3). Following different time points post-infection, cells were harvest and centrifuged at 400 x g for 10 min, 20°C. Supernatants were then stored at -20°C, cells washed once in sterile saline solution and lysed by using 200 µL of 0.05% Tween 80 solution (Vetec) in sterile saline. Cell lysates were diluted in several concentrations ($10^{-1}$ to $10^{-5}$), plated onto Middlebrook 7H10 agar (BD Biosciences) supplemented with OADC 10% and incubated at 37°C. After 28 days, colony-forming units (CFU) were counted and the results were expressed graphically as CFU/mL.
**Microscopy experiments.** After different time points post-infection, cells were washed and fixed with PFA 2% overnight at 4°C. Subsequently, cells were washed with sterile water solution and adhered into coverslips by cytopsin centrifugation. Samples were then fixed with methanol for 5 min, washed with sterile water and stained with carbol-fuchsin (Sigma) for 2 min. Samples were washed once with sterile water and counterstaining was done with methylene blue dye (Sigma) for 30 sec. Coverslips were fixed in slides with Permount mounting medium (Sigma) and examined using Olympus BX40 microscope and digital camera Olympus DP72. Quantification was performed by enumeration of number of infected cells or “cytoplasm rich cells, defined as cells bigger than 10 um and with approximately 2:1 cytoplasm/nucleus ratio. Cells were counted in at least 10 fields from 2 different experiments and plotted as % of events. Syto24-stained *Mtb* was visualized in CD34+ cells by using confocal fluorescence-equipped inverted phase contrast microscope and photographed with a digital imaging system camera. Briefly, 1 x 10^5 CD34+ cells were seeded in 24-well plate and infected with *Mtb* syto24, MOI3, for 4 h. Further, cells were washed, fixed with PFA 2% and adhered into coverslip by cytopsin centrifugation. For nucleus visualization, cells were stained with Hoechst 33342 (Immunochrome technology) for 2h. Cells were after washed and mounted for analysis in Leica DMI6000 B confocal microscope.

**Immunoblotting.** CD34+ cells were seeded at 3 x 10^5 cells in 24-well plate and infected with *Mtb* (MOI3). After 5 days of infection, cells were centrifuged at 4°C, pellet was lysed using M-PER lysis buffer (Thermo Fisher Scientific) containing protease inhibitors (Complete, Mini Protease Inhibitor Tablets, Roche) and protein extracts were prepared according to manufacturer’s instructions. For Western blot, 15 µg of total protein were separated and transferred to nitrocellulose difluoride 0.22 µm blotting membranes. Membranes were blocked for 1h with TBST containing 5% w/v BSA and subsequently washed three times with TBST for 5 min each wash. Further, membranes were then
probed with anti-pSTAT1 Y701 1:1000 (M135 – Abcam), anti-STAT1 1:1000 (SM1 – Abcam), anti-C/EBPβ 1:250 (sc-150 – Santa Cruz) or anti-β-actin 1:5000 (8226 – Abcam) primary antibodies diluted in 5% w/v BSA, 0.1% tween 20 in TBS, at 4ºC with gentle shaking overnight. Membranes were washed with TBST, incubated in secondary HRP-linked Ab for 2h at room temperature, washed and chemiluminescence developed using ECL substrate (Pierce). Relative expression was normalized with β-actin control and pixel area was calculated using ImageJ software.

**Flow cytometry.** PBMC and bone marrow mononuclear cells were seeded at 5 x 10^5 cells per well in a final volume of 200 µL. After 4h of resting at 37ºC with 5% CO₂, cells were infected with *Mtb* (MOI3) for 72h, unless indicated otherwise. Cells were detached from the plate by vigorous pipetting, centrifuged at 450 x g for 10 min and washed twice in saline solution and stained with fixable viability stain FVS V450 (BD Biosciences) at the concentration 1:1000 for 15 min at room temperature. Cells were then washed with FACS buffer (PBS supplemented with 1% BSA and 0.1% sodium azide) and incubated with 10% pooled AB human serum at 4ºC for 15 min. The following antibodies were used in different combinations for staining:

**Staining of human CD34⁺ in PBMC:** anti-Lin1(CD3, CD14, CD16, CD19, CD20,CD56) (FITC, clones MφP9, NCAM 16, 3G8, SK7, L27, SJ25-C1), anti-CD34 (PE, PE, clone 581), anti-CD34 (FITC, 8G12), anti-CD34 (PerCP, clone 581), anti-HLA-DR (PE-Cy7, clone L243), anti-HLA-DR (Bv510, clone G46-6), anti-CD38 (APC, clone HIT2), anti-CD4 (APC-Cy7,GK1.5), anti-CD64 (Bv421, clone 10.1), anti-CD10 (FITC, clone HI10A), anti-CD14 (V450, clone MoP9), anti-CD14 (Alexa488, clone M5E2) were added at titrated determined concentration and incubated for 40 min at 4ºC.

**Staining of CB CD34⁺ cells:** anti-CD34 (PE, clone 581), anti-CD11b (APCCy7,clone M1/70), anti-CD4 (APC-Cy7, clone GK1.5), anti-CD64, (Bv421, MoP9), anti-CD14 (V450, clone MoP9) anti-CD14 (Alexa488, clone M5E2), anti-CD66b (PE, clone G10F5),
anti-BDCA1 (APC-Cy7, clone L161), anti-CD41a (FITC, clone 6C9), anti-BDCA2 (APC, clone 201A), anti-BDCA3 (Bv510, clone 1A4), anti-Clec9A (A700, clone FAB6049P), anti-CD123 (PE, clone 7G3), anti-CD16 (APC, clone 3G8) were added at titrated determined concentrations and incubated for 40 min at 4°C. In a set of experiments, PBMCs were exposed to live Mtb, HK Mtb or LPS (100 ng/mL) for 24h and the Golgi Plug protein transport inhibitor (BD Biosciences) was added for the last 6h according to manufacturer's instructions. Then, cells were surface stained with FITC-Lin (FITC-anti-CD3, Alexa Fluor 488-anti-CD14, FITC-anti-CD16, FITC-anti-CD19, FITC-anti-CD56) and PerCP/Cy5.5-anti-CD34, followed by permeabilization and PE-anti-IL-6 (clone 8C9) staining. All cells were subsequently washed with FACS buffer and resuspended in 2% PFA. Cells were acquired on BD FACS Verse with FACSuite software. Analysis were performed using FlowJo software v. 10.1 (TreeStar).

**Real-time quantitative PCR.** Total RNA was extracted from CD34+ cells exposed or not with *Mtb*. RNA was extracted after 1, 3 and 5 days of infection using TRIzol reagent (Thermo) according to manufacturer's instruction. Using 1 µg of RNA, cDNA was produced with a High-Capacity cDNA Reverse Transcription Kit (Applied Biosystems) and 2 µL of 1:8 diluted product was used to the quantitative PCR reaction in a final volume of 10 µL. qPCR reactions were performed using the primers for: IFNA2A F: 5'-TTGACCTTTGCTTTACTGGT-3', R: 5'-CACAAGGGCTGTATTTCT TC-3'. *IL6* F: 5'-CCACACAGACAGCCACTCAC-3', R: 5'-AGGTTGTTTTTCTGCCAGTG-3'. *IFNB* F: 5'-AAACTCATGAGCAGTCTGCA-3', R: 5'-AGGAGATCTTCAGTTTCGGAGG-3'. *IFNG* F: 5'-TCAGCTCTGCATCGTTTTGG-3', R: 5'-GTTTCCATTATCCGCTACATCTGAA-3'. *IFI16* F: 5'-ACGTAGCAGTCTGCA-3', R: 5'-AGGAGATCTCTCAGTTTCCAG-3'. *MX1* F: 5'-ACTCAGCCAGCAACAGGCATTGA-3', R: 5'-TTCAGCTCTGCATCGTTTTGG-3'. *ISG15* F: 5'-AGGAGATCTCTCAGTTTCCAG-3'. *CXCL8* F: 5'-GAGGTGATTGAGGTGGA-3'.
3', R: 5'-CACACCTCTGCACCCAGTTT-3'. *IL1RA* F: 5'

ATGGAGGGAAGATGTGCCTGTC-3', R: 5'-GTCTCTTCTGTCTGCTTCGCTC-

3'. *GRB2* F: 5'-GAAATGCTTAGCAACAGCGGA-3', R: 5'

TCCACTTCGGAGCACCTTGAG-3'. *STAT1* F: 5'-ATGGCAGTCTGGCGGCTGAATT-

3', R: 5'-CCAAACCAGGCTGGCACAATTG-3'. *CEBPA* F: 5'

TGGACAAGAACAGCAACGAGTA-3', R: 5'-ATTGTCAGTGTCAGCTCCAG-

3'. *CEBPB* F: 5'-TGGGCCAACCAGCATGTCTC-3', R: 5'-TCCGCCTCGTAGTAGAAGTTG-

3'.

**RNA isolation and sequencing.** Total RNA from purified CB CD34+ cells exposed to *Mtb* in vitro was isolated using TRIzol LS (Invitrogen; 10296010). RNA-seq libraries were prepared using the Nugen Ovation Trio low input RNA Library Systems V2 (Nugen; 0507-08) according to the manufacturer’s instructions by the Nucleomics Platform (VIB, Leuven, Belgium). Pooled libraries were sequenced as 150 bp, paired-end reads on an Illumina HiSeq 2500 using v4 chemistry.

**RNA-seq data quality assessment and differential expression analyses.** Illumina sequencing adapters and reads with Phred quality scores lower than 20 were removed with Trimmmomatic (0.36). Trimmed reads were aligned to *H. sapiens* reference genome (hg38) by STAR (2.6.0c). Aligned reads were mapped to genes using feature Counts from the Subread package (1.6.1). Genes with reads of less than 3 were removed. Library based normalization was used to transform raw counts to RPKM and further normalized using the edgeR TMM normalization (3.10.0). Data were then transformed using the limma voom function (3.36.2), prior to batch correction using ComBat (sva 3.28.0). Negative binomial and linear model-based methods were used for differential expression analysis, using packages edgeR and limma packages. Differentially expressed genes (DEGs) were calculated with t-statistics, moderated F-statistic, and
log-odds of differential expression by empirical Bayes moderation of the standard errors (Supplementary File 4).

**CellNet and CellRouter analysis.** We applied CellNet to classify RNA-seq samples as previously described (Cahan et al., 2014). Raw RNA sequencing data files were used for CellNet analysis. We used R version 3.4.1, CellNet version 0.0.0.9000, Salmon (Patro, Duggal, Love, Irizarry, & Kingsford, 2017) version 0.8.2 and the corresponding index downloaded from the CellNet website. We used CellRouter (Lummertz da Rocha et al., 2018) to calculate signature scores for each sample based on cell-type specific transcriptional factors collected from literature. Specifically, for this analysis, we normalized raw counts by library size as implemented in the R package DESeq2 (Love, Huber, & Anders, 2014). We then plotted the distributions of signature scores across experimental conditions. Moreover, we used CellRouter to identify genes preferentially expressed in each experimental condition and used those genes for Reactome pathways enrichment analysis using the Enrichr package version 1.0.

**Systems biology analysis.** Ingenuity Pathway Analysis (IPA) software was used to perform the initial pathway/function level analysis on genes determined to be differentially expressed in transcriptomic analysis (Ingenuity Systems, Red Wood City, CA). Uncorrected p-values and absolute fold-changes were used with cut-offs of p<0.05 (monocyte transcriptomes from active TB patients) or p<0.01 (differentially expressed genes in Mtb-exposed CD34+ cells and all publicly available datasets from GEO). Differentially expressed genes were sorted into gene networks and canonical pathways, and significantly overrepresented pathways and upstream regulators were identified. Additional pathway, GO (Gene Ontology) and transcription factor target enrichment analysis was performed using GSEA (Gene Set Enrichment Analysis, Broad Institute Molecular Signatures Database (MSigDB)) and WebGestalt (WEB-based GEne SeT AnaLysis Toolkit). Gene sets from GO, Hallmark, KEGG pathways, WikiPathways and
Pathway Commons databases, as well as transcription factor motifs, were considered overrepresented if their FDR-corrected p-value was <0.05. To validate our compiled IL6/IL6R/CEBP and CD34+ myeloid differentiation gene modules, we used STRING (version 10.5) protein-protein interaction enrichment analysis (www.string-db.org), using the whole human genome as background. Principal component analysis, correlation matrices, unsupervised hierarchical (Euclidean distance) clustering were performed using XLSTAT and visualized using MORPHEUS (https://software.broadinstitute.org/morpheus/). Chipseq, active chromatin and transcriptional (RNAseq) data of CD14 and CD34+ cells were downloaded from ENCODE (https://genome.ucsc.edu/ENCODE/) and visualized using the UCSC browser (Haeussler et al., 2019).

**Data processing and statistical analyses.** Data derived from in vitro experiments was processed using GraphPad Prism 6 software and analyzed using unpaired t test, one-way ANOVA or two-way ANOVA according to the experimental settings. Data from experiments performed in triplicate are expressed as mean ± SEM. Non-parametric tests (Mann-Whitney, Spearman correlation) were used for clinical data (sputum bacillar load, modal X-ray grade, symptom count) and molecular data that were not normally distributed, Pearson correlation was used for molecular data with a normal distribution. A list of the statistics analysis methods used in each figure is available a supplementary file (Supplementary File 4). Statistical significance was expressed as follows: *p ≤0.05, **p ≤0.01 and ***p ≤0.001.

**Acknowledgments**
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References


in tuberculosis: efficient APC in pleural effusion but also mark disease severity in blood. *J Leukoc Biol*, 90(1), 69-75. doi:10.1189/jlb.1010577


**Figure legends**

**Fig. 1** | *Mtb* H37Rv infects human CD34*+* cells and proliferates in cell cultures in *vitro*. PBMC from healthy donors were exposed to syto24-labeled *Mtb* H37Rv (MOI3, Figure 1-figure supplement 1a) for 4h. **a,** Representative flow cytometry contour plots of gating strategy to analyze *Mtb* syto24 association in FVS-negative (live) CD34*+* events and CD14*+* events. **b,** Live CD34*Lin*− events gated in a were analyzed for *Mtb*-Syto24 MFI. Black line: Uninfected control. Blue, orange and purple lines represent samples from three different donors. **c,** Frequencies and **d,** MFI of *Mtb* syto24*+* events in CD34*+* or CD14*+* events gates from uninfected or *Mtb* syto24-exposed bulk PBMCs. Results are means ± SEM of data pooled from 3 independent experiments, n = 10 healthy donors. ***p≤0.001 between *Mtb* syto24 CD34*+* vs CD14*+* groups. **e,** Purified cord blood-derived CD34*+* cells were exposed to *Mtb* H37Rv (MOI3) for different time points and CFUs from cell culture lysates were enumerated in 7H10 media. Results are means ± SEM of data pooled from 5 independent experiments, ***p≤0.001 between 5d vs 4h groups. **f,** Kinyoun staining of CD34*+* cells after 1d and 5d of infection and quantification, as described in the methodology section, shown in the right panel. Arrows indicate cells associated with bacilli. Experiments shown are representative of two performed. **g,** Representative Giemsa staining of CD34*+* cells of 5d-cultures and quantification, as described in the methodology section, shown in the right panel. Arrow indicates cytoplasm-rich cells in *Mtb*-infected cultures and uninfected cultures. Experiments shown are representative of two performed. *p≤0.05 between *Mtb* vs uninfected groups.

**Fig. 2** | *Live Mtb* induces human CD34*+* cells towards myeloid differentiation in *vitro*. Purified CD34*+* cells from healthy donors (n=3) were exposed to *Mtb* H37Rv (MOI3) for different time points and mRNA-seq was performed as described in...
methodology section. a, Heatmap of the mRNA expression (z-score) of transcription factors involved in cell lineage commitment (Novershtern et al., 2011). b, Signature score of data from a by employing CellRouter analysis. c, Heatmap from mRNA data of uninfected vs Mtb infected cultures analyzed by CellNet. d, Purified CD34+ cells were exposed to Mtb H37Rv (MOI3) for 5 days and flow cytometry was performed. Graph represents frequencies of CD11b+ events in uninfected (open circles) vs Mtb-infected cultures (blue circles) from four independent experiments. ** p≤0.01 between Mtb and uninfected groups. e, Purified CD34+ cells were exposed to Mtb H37Rv, Heat-killed (HK) Mtb H37Rv or Mtb clinical isolate 267 (Mtb-CS267) (MOI3) for 5 days and flow cytometry with the gating strategy was performed. f, Representative contour plots show frequencies of CD4+CD64+ events in CD34+ events. CD34+CD4+CD64+ events of pooled data from f were plotted to generate bar graphs (g) and (h). Results are means ± SEM of data pooled from 4 independent experiments (g) and 2 independent experiments (h). g, ** indicates p≤0.01 between H37Rv vs uninfected or HK H37RV groups. h, * indicates p≤0.05 between Mtb-CS267 vs uninfected groups.

**Fig. 3 | Mtb infection increases monocyte output from CD34+ cells in vitro.** Purified CD34+ cells were exposed to live Mtb H37Rv or HK Mtb H37Rv (MOI3) for 10 days and flow cytometry was employed to determine the mature cell frequencies in the cell cultures. Representative dot plots of a, monocytes (CD14+), b, neutrophils (CD16+CD66b+), c, megakaryocytes/platelets (CD41a+) and d, classical myeloid dendritic cells (BDCA1+CD14low) in uninfected and Mtb-infected CD34+ cell cultures. Graphs show frequencies of e, CD14+, f, CD16+CD66b+, g, CD41a+ and h, BDCA1+CD14low events in uninfected (open circles), live Mtb-infected (blue diamonds) or HK Mtb-exposed (red diamonds) cell cultures at day 10. Each symbol represents one individual experiment. Results are means ± SEM of data pooled from 3-9 independent
experiments. ** p≤0.01 between Mtb vs uninfected or HK Mtb groups. i, Histograms show the expression of CD11b, HLA-DR, CD64 and CD16 in CD14+ events from a. Black dashed lines: Uninfected control. Blue solid lines: Mtb-infected group. Data representative of 5 independent experiments. j, Frequency of CD14+CD16+ events in Mtb-exposed cell cultures after 10d. Contour dot plot of CD14+CD16+ frequencies from one representative donor. Open circles: Uninfected control. Blue circles: Mtb-infected group. Each symbol represents an individual experiment. Pooled data of eight independent experiments, n = 5 different donors. p=0.076 between Mtb vs uninfected groups.

**Fig. 4 | Mtb enhances IL-6R-mediated myeloid differentiation in vitro.** Purified CD34+ cells were exposed to Mtb H37Rv (MOI3) for different time points and mRNA-seq was performed as described in the methodology section. a, Heatmap (z-score) of differentially expressed cytokine receptor genes. b, Heatmap (z-score) of differentially expressed cytokine genes. Shown is the average mRNA expression of three different donors from two independent experiments. c, PBMC from healthy donors were exposed to Mtb H37Rv, HK Mtb or LPS (100 ng/mL) for 24h and intracellular IL-6 was detected by flow cytometry. Live CD34+Lin- events gated as in Fig. 1a were analyzed for IL-6 MFI. Representative histogram from 2 independent experiments. Purified CD34+ cells were treated with d, α-IFNAR2 (1 µg/ml) or e, α-IFN-γ (10 µg/ml) and then exposed to Mtb H37Rv (MOI3) during 10d for determination of CD14+ monocyte frequencies. Results are means ± SEM of data pooled from 2 independent experiments. * p≤0.05 between Mtb, α-IFNAR2 or α-IFN-γ vs uninfected groups. f, Representative contour plots of CD14+ monocytes in CD34+ cell cultures exposed to Mtb, in the presence or absence of α-IL6R (Tocilizumab, 1 µg/ml) for 10d. g, Results shown are means ± SEM of data pooled from
3 independent experiments from f. **p≤0.01 between Mtb vs uninfected groups and
#p≤0.05 between Mtb and Mtb+α-IL6R-treated groups. h, Results shown are means ±
SEM of data pooled from 3 independent experiments showing frequency of CD66+CD16+
neutrophils in Mtb-infected cell cultures in the presence or absence of α-IL6R. Purified
CD34+ cell cultures were treated as in (d-f) with i, α-IL6R, j, α-IFNAR2 and k, α-IFN-γ
and then exposed to Mtb (MOI3) for different time points and CFU enumerated as
described in the methodology section. Results are means ± SEM of data pooled from 4
independent experiments. **p≤0.01 between Mtb and Mtb+ α-IL6R at 7d.

Fig. 5 | IL6/IL6R/CEBPB gene module is enriched in active TB transcriptome and
proteome and correlates with monocyte expansion. a, Top panel: upstream
regulators significantly enriched by causal Ingenuity Pathway Analysis (IPA) in monocyte
transcriptomes from patients with active TB (GSE19443), ranked by activation z-score,
p-values are corrected for genome-wide testing (FDR). Bottom panel: IRF1 and STAT1
are the top upstream regulators shared between the “Berry TB” disease signature (Berry
et al., 2010) (GSE19435, GSE19439, GSE19444), the “IL6/STAT3” pathway (Hallmark
GSEA) and the human “in vivo IFN-β” signature (GSEA HECKER_IFNB1_TARGETS). b,
Top panel: overlap between the “Berry TB” disease signature, the “IL6/STAT3” pathway
and the “Scriba plasma TB” proteomic signature (Scriba et al., 2017) identified “IFN/IL6-
shared” and “IL6/STAT3-specific” signatures. Bottom panel: significant STRING protein-
protein interaction network (p<10^{-16}) for “IFN/IL6-shared” genes (green marbles) and
“IL6/STAT3” genes (red marbles), clustering separately by k-means. c, Top panel:
significant linear increase over time before active TB diagnosis in plasma proteome
(Scriba et al., 2017) for “CD34/myeloid” (yellow), “IL6/STAT3” (orange) and “IFN/IL6-
shared” (blue) clusters found in (b). Bottom panel: monocyte/lymphocyte (ML) ratio gene
set members defined by Naranbhai et al. (Naranbhai et al., 2015) over time before active TB diagnosis in plasma proteome (Scriba et al., 2017). d, Top panel: increased "IL6/STAT3" cluster protein expression precedes monocyte expansion markers (ML ratio gene set) in the TB plasma proteome. Bottom panel: data as in d shows significant higher fold-changes for "IL6/STAT3" vs. "ML ratio" or "CD34/myeloid" cluster members. *p-value<0.05, ** p-value<0.01. e, Transcription factor enrichment analysis (GSEA) of differentially expressed genes determined by RNA-seq in Mtb-exposed CD34+ cells in vitro (n = 3 donors). f, monocyte count and ML ratio in samples from latent vs active TB patients from (Berry et al., 2010) reanalysis. *p-value<0.05, ** p-value<0.01 between active TB vs latent TB groups. Transcriptional data of whole blood reanalysis from Berry et al (Berry et al., 2010) shows a significant correlation of CEBPB transcripts with g, M/L ratio; h, IL6R; i, STAT3 transcript levels, and j, mycobacterial positivity in sputum smears in patients with active TB. ** p-value<0.01 between positive vs negative groups.

**Fig. 6 | Evolutionary recent and human-specific genetic adaptation link**

**IL6/IL6R/CEBP** gene module with monocyte expansion and TB pathogenesis. a, Heat map showing CEBPB network generated by STRING co-occurrence protein conservation scores across primates, mammals, birds and reptiles. Note only CEBPB and CEBPA differ strongly among hominids, while CEBPA/CEBPB/CEBPD vary significantly throughout primate and mammalian evolution, as compared to highly conserved STAT1/STAT3 (Figure 5-figure supplement 1d). b, Top panel: Highly conserved type I IFN upregulation of “IFN/IL6-shared” genes from humans to birds (derived from [http://isg.data.cvr.ac.uk/](http://isg.data.cvr.ac.uk/)) (Shaw et al., 2017), as compared to “IL6/STAT3” and “CD34/myeloid differentiation” genes. Bottom panel: CEBPB and CEBPD displays highest variation, and CXCL10 the lowest variation in type I IFN transcriptional regulation across human-mammalian-bird evolution. Inset, CEBPB and CEBPD selectively
acquired type I IFN upregulation in humans (filled circles); ** p-value<0.01 and * p-value<0.05 represent CEGBP and CEBPD values, respectively for humans versus the other species. **ChipSeq analysis of STAT1-binding peaks in CEBPD (top panel), CEBPB (middle panel), CXCL9 and CXCL10 (bottom panel) in IFN-stimulated human monocytes, corresponding to regions with active chromatin (DNase Hypersensitivity Sites, DHS) and correlating with increased downstream transcription in CD14+ monocytes, as compared to purified CD34+ cells. Conservation analysis among >40 vertebrates (phyloP (Pollard, Hubisz, Rosenbloom, & Siepel, 2010), from chicken to human, analogous to Figure 5b) indicates STAT1 peaks are mostly conserved in CXCL9/CXCL10 (6/7) but not in CEBPD/CEBPB (3/11). d, Top panel: overlap between human genes with significant Neanderthal introgression (Enard & Petrov, 2018; Quach et al., 2016), genes differentially expressed in Mtb-exposed CD34+ cells (CD34+ Mtb UP) and the “ML ratio” gene set. Bottom left panel: OAS1, OAS2 and MT2A transcripts presented significantly higher effect sizes upon ML ratios, corresponding to monocyte expansion, as compared to other introgressed genes (p<0.05) and to all other genes shown to regulate ML ratio in vivo (p<0.001). Bottom right panel: normalized expression of introgressed genes found in CD34+Mtb UP (Venn diagram) in TLR1/2 agonist-treated monocytes from a cohort of matched Belgian individuals of European (EUB) vs. African (AFB) descendence, with documented presence or absence of Neanderthal introgression (Quach et al., 2016), respectively. p-value<0.05, ** p-value<0.01, *** p-value<0.001, **** p-value<0.0001.

**Fig. 7. Compiled multi-level evidence for an IL6/IL6R/CEBP gene module linking CD34+ myeloid differentiation to TB pathogenesis and disease severity.** a, Ranks and scores were determined as 0-1 (presence-absence in data set) or 0-1-2-3, according to enrichment analysis or differential gene expression (quartiles); z-scores
were obtained from Daub et al.\textsuperscript{55} b, Proposed model for C/EBP\(\beta\) and C/EBP\(\delta\) acting as a bridge in the type I IFN and IL-6 feed-forward loop exploited by \textit{Mtb} to induce monocyte differentiation and TB disease severity (details in the text).

\textbf{Legends of the figure supplements}

\textbf{Figure 1-figure supplement 1 – \textit{Mtb}-CD34\(^+\) interactions and signaling pathways associated with HSPC differentiation.} a, representative histogram of median fluorescence intensity (MFI) from H37Rv stained or not with syto24 (FL1 channel). PBMC or cord-blood derived purified CD34\(^+\) cells from healthy donors were exposed to syto24-labeled \textit{Mtb} H37Rv (MOI3) for 4h. b, Frequencies (left panel) and MFI (right panel) of \textit{Mtb} syto24\(^+\) events in CD34\(^+\) cells from PBMC vs purified CD34\(^+\) cell cultures. Results are means \(\pm\) SEM of data pooled from 3 independent experiments. c, Confocal microscopy showing a CD34\(^+\) cell infected with Syto24-stained \textit{Mtb} H37Rv. Nuclei = DAPI/blue. \textit{Mtb} = Syto24/green. d, Purified CD14\(^+\) or purified CD34\(^+\) cells were exposed to \textit{Mtb} H37Rv (MOI3) for different time points and CFUs from cell culture lysates were enumerated in 7H10 media. Results are means \(\pm\) SEM of data pooled from 5 independent experiments, \(*p \leq 0.01\) between CD14\(^+\) vs. CD34\(^+\) groups 5d. e, Heat map showing z-score values of 180 transcription factors (Novershtern et al., 2011) expressed by CD34\(^+\) cells exposed to \textit{Mtb} (MOI3) at days 1,3 and 5 post-infection.

\textbf{Figure 2-figure supplement 1 – Myeloid differentiation by PBMC or bone marrow CD34\(^+\) cells exposed to \textit{Mtb}, mycobacterial ligands and cell death analysis in vitro.} a, Frequencies of CD10\(^+\)CD34\(^+\) and CD41a\(^+\)CD34\(^+\) cells in uninfected vs \textit{Mtb}-infected cell cultures. Representative dot plots of b, peripheral blood samples from 4 healthy individuals and c, bone marrow obtained from 2 healthy subjects showing frequencies of CD4\(^+\)CD64\(^+\)CD34\(^+\) and CD38\(^+\)HLADR\(^+\)CD34\(^+\) cells in uninfected vs \textit{Mtb}-infected cell cultures. \(***p \leq 0.0001\) between \textit{Mtb} vs uninfected groups. d, Purified CD34\(^+\)
cells were exposed to AraLam (10 μg/ml) or gDNA (10 μg/ml) and 5 days later, CD38, HLADR, CD4 and CD64 MFI calculated within CD34+ events. Cell death analysis by means of e, frequencies of cell permeability dye (FVS+) and f, LDH quantities detected in the supernatants from uninfected or Mtb-exposed CD34+ cell cultures 5 dpi. **p≤0.001 and ***p≤0.0001 between mycobacterial ligands vs control groups.

**Figure 3-figure supplement 1** – Monocyte differentiation and reactome pathways associated to Mtb-exposed CD34+ cells in vitro. a, Frequencies of CD14+ cells during 10-day exposure to a clinical isolate of Mtb. *p≤0.05 between Mtb-CS267 vs uninfected groups. b, Purified CD34+ cells were exposed to Mtb H37Rv for 1, 3, 5, 7 and 10 days and flow cytometry was employed to determine the CD14+ monocyte frequency. c, The erythroid cell marker CD235a was measured by flow cytometry in Mtb-exposed and uninfected purified CD34+ cells at 10 dpi. Results shown are representative from 2 experiments. d, Enrichment of Reactome pathways based on gene signatures derived from each experimental condition. Gene signatures were composed by genes with log2 fold change > 0.75 when comparing one experimental condition versus all others. The size and color of the circles are proportional to -log10 of the adjusted p-value.

**Figure 4-figure supplement 1** – Gene expression and cytokine production during myeloid differentiation in vitro. a, CD34+ cells were stimulated with or without recombinant IL-6 (20 ng/mL) for 5 days and frequency of CD4+CD64+CD34+ cells were measured by flow cytometry. b, normalized counts from RNA-seq data as determined by library size normalization. Results are means ± SEM of data pooled from 2 independent experiments (8 replicates). *** p≤0.001 between Mtb vs uninfected groups at different time points. CD34+ cells were exposed to Mtb (MOI3) and at days 1, 3 and 5 p.i. qPCR was performed for quantification of c, IL6/IFN cytokines and d, ISGs and IL-6-induced genes. e, IL-6, IFN-γ, IL-1β and TNF measurements from unexposed or Mtb-exposed purified CD34+ cell culture supernatants at day 1 and 5 p.i. Open circle: uninfected
control. Blue circle: *Mtb*-infected group. Results are means ± SEM of data pooled from 6-8 independent experiments. *p≤0.05 between 1d Mtb vs uninfected groups.

f, purified CD34+ cells were exposed to live or HK-Mtb (MOI3) and 5 days later, CD38, HLADR, CD4 and CD64 MFI calculated within CD34+ events. Results are means ± SEM of data pooled from 5 independent experiments. **p≤0.001; ***p≤0.0001 between Mtb or HK Mtb vs uninfected groups.

g, CD34+ cells were exposed to live or HK-*Mtb* (MOI3) and at days 5 p.i., qPCR was performed for quantification of *STAT1*, *CEBPA* and *CEBPB*. Results are means ± SEM of data pooled from 3 independent experiments. *p≤0.05 between *Mtb* vs HK *Mtb* groups.

h, CD34+ cells were exposed to live *Mtb* (MOI3) in the presence or absence of α-IFNAR2 or α-IL-6R and at day 5 p.i., qPCR was performed for quantification of *STAT1* and *MX1*. **p≤0.001 between *Mtb* vs *Mtb*+αIFNAR2 groups.

CD66b+CD16+ neutrophil frequencies in 10-day culture of *Mtb*-exposed CD34+ treated with i, α-IFNAR2 (1 µg/ml) or α-IFN-γ (10 µg/ml) blocking antibodies.

j, CD41+ megakaryocytes; k, CD235+ erythrocytes and l, BDCA1+CD14low myeloid DC frequencies in 10-day culture of *Mtb*-exposed CD34+ treated with α-IL-6R blocking or control antibodies.

**Figure 5-figure supplement 1 – Gene expression and protein conservation of the IFN/IL6/CEBP gene module and correlation analysis to TB disease.**

a, Western blotting for pSTAT1 (Y701), total STAT1, C/EBPα, C/EBPβ and actin from uninfected or *Mtb*-infected CD34+ cells for 5 days as described in the materials and methods.

b, Heat maps showing z-score values of *CEBP* family members and e ISGs expressed by CD34+ cells exposed to *Mtb* (MOI3) at different time points.

c, Cluster dendrogram and heatmap of Spearman correlation coefficients between molecular and clinical data from a UK cohort of patients with latent and active TB (Berry et al., 2010) (n=30, raw data were obtained from GXB, sputum smear only available for active TB patients).

d, Heat map showing *IL6* network generated by STRING co-occurrence protein conservation
scores across primates, mammals, birds and reptiles. Note highly conserved
STAT1/STAT3 and other molecules found in the network (depicted in Figure 6a,
STRING) throughout primate and mammalian evolution.

Figure 6-figure supplement 1 – TB susceptibility genes of the IFN/IL6/CEBP gene
module and ISG induction during myeloid differentiation in vitro. a, Primary dermal
fibroblasts from humans, macaques and mice were stimulated for 8h in vitro with dsRNA
analog (polyI:C) and CEBP family members, CXCL9 and CXCL10 transcript levels were
quantified by RNA-seq (expressed as fold-change over unstimulated cells). Raw data
obtained from Hagai et al. (Hagai et al., 2018) (https://scb.sanger.ac.uk/#/base/main). b,
Significant overlap (hypergeometric test p<0.0001) between TB susceptibility genes
(identified by GWAS or candidate gene studies) and differentially expressed genes
(DEG) in CD34+ cells exposed to Mtb (left panel) as well as the IL6/IL6R/CEBP gene
module (right panel). c, Purified CD34+ cells were exposed to Mtb H37Rv (MOI3) for
different time points. Heat map shows z-score values of ISGs expressed by CD34+ cells
exposed to Mtb (MOI3) at different time points.

Additional Files
Supplementary File 1 – Reactome Pathways analysis of Mtb-exposed and control
CD34+ cell transcriptomes.
Supplementary File 2 - Systems analysis (Ingenuity Pathway Analysis and Gene Set
Enrichment Analysis) of cohorts of healthy controls, patients with latent TB, active TB,
disseminated TB, overlap with IL6/STAT3 signaling and myeloid development.
Supplementary File 3 - Human adaptation z-scores for IL6/IL6R/CEBP CD34 myeloid
gene module and Gene set enrichment of Top500 human adaptation genes.
Supplementary File 4 - List of statistical methods used in the manuscript.
Figure 1-source data 1 – raw data from figure 1.

Figure 2-source data 1 – raw data from figure 2.

Figure 2-source data 2 – Counts matrix of RNAseq data of *Mtb*-exposed and control CD34+ cell transcriptomes.

Figure 3-source data 1 – raw data from figure 3.

Figure 4-source data 1 – raw data from figure 4.

Figure 5-source data 1 – raw data from figure 5.

Figure 6-source data 1 – raw data from figure 6.

Figure 7-source data 1 – raw data from figure 7.

Figure 1-figure supplement 1-source data 1 – raw data from figure 1-figure supplement 1.

Figure 2-figure supplement 1-source data 1 – raw data from figure 2-figure supplement 1.

Figure 3-figure supplement 1-source data 1 – raw data from figure 3-figure supplement 1.

Figure 4-figure supplement 1-source data 1 – raw data from figure 4-figure supplement 1.

Figure 6-figure supplement 1-source data 1 – raw data from figure 6-figure supplement 1.
Figure 1. Mtb H37Rv infects human CD34+ cells and proliferates in cell cultures in vitro

(a) Flow cytometry gating on singlets and live cells.

(b) Gated on CD14-CD34+ cells.

(c) Mtb syto24 positivity in CD34+ and CD14+ cells.

(d) Mtb syto24 MFI in uninfected and infected cells.

(e) CFU/mL over time (4h, 1d, 3d, 5d).

(f) Microscopy images of infected cells at 1d and 5d.

(g) Uninfected vs infected cells, showing cytoplasm richness.

Legend:
- Mtb: M. tuberculosis
- Syto24: Fluorescent dye
- CFU: Colony forming units
- Uninf.: Uninfected

N.T.: Not Tested
**: p < 0.01
***: p < 0.001
n.s.: Not significant
Figure 2. Live Mtb induces human CD34+ cells towards myeloid differentiation in vitro

(a) Heatmap showing gene expression changes in CD34+ cells over time (1d, 3d, 5d) under different conditions (Uninf., Mtb).

(b) Box plot showing signature score for different cell types (B cell, Gran/Mono, HSC/Ery, Late Ery, T cell) across different conditions (Uninf. 1d, Mtb 1d, Uninf. 3d, Mtb 3d, Uninf. 5d, Mtb 5d).

(c) Flow cytometry analysis showing HSPCs and Mtb interaction over time (1d, 3d, 5d).

(d) CD11b% expression levels in HSPCs, T cells, B cells, Dendritic cells, and Monocytes/Macrophages under different conditions (Uninf., Mtb).

(e) Flow cytometry dot plots for SSC-A, FSC-H, FSC-A, FVS, and CD34.

(f) Gating strategy for CD34+ and CD64 expression under control (Uninf.) and Mtb (H37Rv) conditions.

(g) Bar graph showing CD4+CD64+ cell percentage change under different conditions.

(h) Bar graph showing CD4+CD34+ cell percentage change under different conditions.
Figure 3. Mtb infection increases monocyte output from CD34+ cells in vitro
Figure 4. Mtb enhances IL-6R-mediated myeloid differentiation in vitro

(a) Heatmap showing gene expression levels of various cytokines and receptors in uninfected (Uninf.) and Mtb-infected samples at 1, 3, and 5 days post-infection.

(b) Heatmap showing gene expression levels of cytokines in uninfected (Uninf.) and Mtb-infected samples at 1, 3, and 5 days post-infection.

(c) Flow cytometry analysis of CD14+ cells in uninfected (Uninf.), Mtb-infected (Mtb), HK Mtb-infected (HK Mtb), and LPS-treated samples.

(d) Bar graph showing the percentage of CD14+ cells in uninfected (Uninf.), Mtb-infected (Mtb), and Mtb-infected with anti-IL-6R antibody (Mtb + αIL-6R) samples.

(e) Bar graph showing the percentage of CD14+ cells in uninfected (Uninf.), Mtb-infected, and Mtb-infected with anti-IFN-γ antibody (Mtb + αIFN-γ) samples.

(f) Flow cytometry analysis of CD16+CD14+ cells in uninfected (Uninf.), Mtb-infected (Mtb), and Mtb-infected with anti-IL-6R antibody (Mtb + αIL-6R) samples.

(g) Bar graph showing the percentage of CD16+CD14+ cells in uninfected (Uninf.), Mtb-infected, and Mtb-infected with anti-IL-6R antibody (Mtb + αIL-6R) samples.

(h) Bar graph showing the percentage of CD16+CD14+ cells in uninfected (Uninf.), Mtb-infected, and Mtb-infected with anti-IL-6R antibody (Mtb + αIL-6R) samples.

(i) Bar graph showing the CFU/mL levels of Mtb and Mtb + αIL-6R at 3, 5, and 7 days post-infection.

(j) Bar graph showing the CFU/mL levels of Mtb and Mtb + αIFN-2 at 3, 5, and 7 days post-infection.

(k) Bar graph showing the CFU/mL levels of Mtb and Mtb + αIFN-γ at 3, 5, and 7 days post-infection.
Figure 5. IL6/IL6R/CEBPB gene module is enriched in active TB transcriptome and proteome and correlates with monocyte expansion.
Figure 6. Evolutionary recent and human-specific genetic adaptation link IL6/IL6R/CEBP gene module with monocyte expansion and TB pathogenesis

(a) Phylogenetic tree showing the evolution of Homo sapiens along with other species.

(b) Heatmap depicting the expression levels of IFN-induced log(FC) across 10 species.

(c) Gene expression heatmap showing the regulation of IFN genes across species.

(d) Venn diagram illustrating the overlap of genes associated with CD34 and CD14+ monocytes.

(e) Bar graph showing the ratio of effect sizes and normalized expression levels.

(f) Scatter plot comparing the effect sizes of CD34 and CD14+ genes with Neanderthal introgression.
Figure 7. Compiled multi-level evidence for an IL6/IL6R/CEBP gene module linking CD34+ myeloid differentiation to TB pathogenesis and disease severity

(a) Genes ranked by rank/z-score

(b) steady state vs active TB
Figure 1-figure supplement 1. Mtb-CD34+ interactions and signaling pathways associated with HSPC differentiation

(a) FL-1

(b) Mtb syto24 (%)

(c) MERGE/DIC

(d) CFU/mL [log10]

(e) Heatmap
Figure 2-figure supplement 1. Myeloid differentiation by PBMC or bone marrow CD34+ cells exposed to Mtb, mycobacterial ligands and cell death analysis in vitro

a) Gated on CD34+ cells exposed to Mtb

Uninf. Mtb

SSC-A

CD10

19.9 12.7

SSC-A

1.49 1.55

CD41a

1.3

b) Peripheral blood

Lin1

0.18

CD4

CD34

CD64

CD38

CD38+HLA-DR+/CD34+ (%)

Uninf. Mtb

***

[Graphs showing distribution and quantification of various cell markers and phenotypes]

c) Bone marrow

Uninf. Mtb

SSC-A

CD64

CD34

CD4

HLA-DR

CD38

CD38+HLA-DR+/CD34+ (%)

Uninf. Mtb

***

[Graphs showing distribution and quantification of various cell markers and phenotypes]

d) 

[Graphs showing flow cytometry data for various cell markers and phenotypes in bone marrow samples exposed to different conditions]

e) Gated on singlets

SSC-A

FVS

FVS+ cells (%)

Uninf. Mtb HK Mtb

n.s n.s

[Graph showing LDH release (O.D. 490nm) for various conditions]

f) LDH release (O.D. 490nm)

Uninf. Mtb

n.s
Figure 3-figure supplement 1. Monocyte differentiation and reaetome pathways associated to Mtb-exposed CD34+ cells in vitro

(a) Uninf. vs Mtb-CS267 for SSC-A and CD14.

(b) CD14+ cells (%).

(c) Uninf. vs Mtb for SSC-A and CD235a.

(d) Reactome pathways.

- Downstream signal transduction
- Signaling by FGF1
- Signaling by PDGF
- NGF signaling via TRKA from the plasma membrane
- Signaling by FGF2
- Downstream signaling of activated FGF1
- Signaling by FGF3
- Downstream signaling of activated FGF2
- Downstream signaling of activated FGF3
- Phospholipase C-mediated cascade, FGR
- Signaling by Type 1 Insulin-like Growth Factor 1 Receptor (IGF1R)
- IRS-related events triggered by IGF1R
- IGF1R signaling cascade
- Interaction between L1 and A2yA5
- EPAC-mediated growth cone collapse
- Negative regulation of FGR signaling
- SHC-mediated cascade FGR4
- Atonin guidance
- FGF4/gp binding and activation
- Cell surface interactions at the vascular wall
- Adherens junction interactions
- C-linked glycosylation
- G alpha (i) signaling events
- Neutrophil System
- Transmission across Chemical Synapses
- O-glycosylation of TSR domain-containing proteins
- Preterm activation, signaling and aggregation
- Defective B3GALTL causes Peter’s plus syndrome (PWS)
- RIG–IMDA5 mediated induction of IFN–alpha/beta pathways
- Negative regulators of RIG–IMDA5 signaling
- ISG15 antisense mechanism
- Antiviral mechanism by IFN–stimulated genes
- Interferongamma signaling
- Interferon beta signaling
- Interferon signaling
- Synthesis of pyrophosphate in the Cytosol
- Class B2 (Secretin family receptors)
- Intracellular transport
- Bacterial transport
- Tocopherol Maintenance
- Inositol phosphate metabolism
- Extension of Tenoblast
- O2/C2 exchange in erythrocytes
- Erythrocytes take up carbon dioxide and release oxygen
- Erythrocytes take up oxygen and release carbon dioxide
- Immune System
- Collagen formation
- Immunoregulatory interactions between a Lymphoid and a non-Lymphoid cell
- Chemokine receptors bind chemokines
- GPCR (G protein-coupled receptor)
- Peptide ligand-binding receptors
- Extracellular matrix organization
- Class A1 (Rhodopsin-like receptors)
- Cytokine signaling in immune system

-log10 (p-value)
- 5
- 10
- 15

1d 3d 5d
Figure 4-figure supplement 1. Gene expression and cytokine production during myeloid differentiation in vitro

(a) Gated on CD34+ cells and CD4+ cells.

(b) Normalized count (IL-6).

(c) Fold increase over uninfected controls.

(d) Fold increase over uninfected controls.

(e) IL-6 (pg/mL).

(f) CD38 MFI/CD34+.

(g) STAT1 expression over uninfected controls.

(h) STAT1 expression over uninfected controls.

(i) Neutrophils (%).

(j) BDCA1+CD14low cells (%).

(k) CD235A+ cells (%).
Figure 5-figure supplement 1.

Gene expression and protein conservation of the IFN/IL6/CEBP gene module and correlation analysis to TB disease

(a) Uninf. Mtb

100kD
75kD
100kD
75kD
50kD

pSTAT1
Y701
STAT1
β-actin

Uninf. Mtb

42kD
50kD
50kD

C/EBPα
C/EBPβ
β-actin

(b) Heatmap showing gene expression levels over time (1d, 3d, 5d) for different conditions (Uninf., Mtb).

(c) Flowchart or diagram showing gene expression relationships.

(d) Heatmap or heatmap showing percentage of sequence conservation across different genes.
Figure 6-figure supplement 1. TB susceptibility genes of the IFN/IL6/CEBP gene module and ISG induction during myeloid differentiation in vitro

(a) 

CD34+ + Mtb DEG

366

154

18

TB susceptibility genes (GWAS+ candidate genes)

166

23

TB susceptibility genes (GWAS+ candidate genes)

IL6/IL6R/CEBP gene module

(b) 

Fold change

Fold change

(c) 

1d 3d 5d