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**Mycobacterium tuberculosis** programs mesenchymal stem cells to establish dormancy and persistence

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Tuberculosis (TB) remains a major infectious disease worldwide. TB treatment displays a biphasic bacterial clearance, in which the majority of bacteria clear within the first month of treatment, but residual bacteria remain nonresponsive to treatment and eventually may become resistant. Here, we have shown that *Mycobacterium tuberculosis* was taken up by mesenchymal stem cells (MSCs), where it established dormancy and became highly nonresponsive to isoniazid, a major constituent of directly observed treatment short course (DOTS). Dormant *M. tuberculosis* induced quiescence in MSCs and promoted their long-term survival. Unlike macrophages, where *M. tuberculosis* resides in early-phagosomal compartments, in MSCs the majority of bacilli were found in the cytosol, where they promoted rapid lipid synthesis, hiding within lipid droplets. Inhibition of lipid synthesis prevented dormancy and sensitized the organisms to isoniazid. Thus, we have established that *M. tuberculosis* gains dormancy in MSCs, which thus serve as a long-term natural reservoir of dormant *M. tuberculosis*. Interestingly, in the murine model of TB, induction of autophagy eliminated *M. tuberculosis* from MSCs and consequently, the addition of rapamycin to an isoniazid treatment regimen successfully attained sterile clearance and prevented disease reactivation.

**Introduction**

Tuberculosis (TB), caused by the obligate intracellular organism *Mycobacterium tuberculosis*, is the oldest known infectious disease in humans. Current therapy for TB consists of multiple antibiotics, is lengthy, and causes toxicity. However, the majority of the bacteria are cleared within 3–4 weeks of treatment, and patients start feeling better and often discontinue treatment, which may promote the generation of drug-resistant variants of *M. tuberculosis* (1). The remaining small numbers of organisms are highly nonresponsive to antibiotic treatment and continue to persist (2). Incomplete treatment may lead to disease reactivation, often associated with drug-resistant variants (3, 4). Therefore, a therapeutic strategy that eliminates persistent bacteria is urgently needed. Addition of such therapeutics along with conventional antibiotics should dramatically reduce the treatment length, and thereby reduce the generation of drug-resistant variants.

The reasons for the unresponsiveness of these persisting organisms to antibiotics remains incompletely understood. Current antibiotic therapy is mostly focused on eliminating replicating *M. tuberculosis*. The natural host for *M. tuberculosis* is macrophages, in which they replicate and survive by employing a variety of host-evasion mechanisms that include inhibition of phagolysosome fusion (5, 6), deacidification of lysosomal compartments (7), and translocation to the cytosol (8). These bacteria respond to antibiotics and are readily cleared. However, nonreplicating bacteria survive within granulomatous structures containing mesenchymal stem cells (MSCs), with limited accessibility to therapeutics (9). Recently, we and others have shown that *M. tuberculosis* infects MSCs (9, 10). In some cases *M. tuberculosis* was detected in patients who had completed directly observed treatment short course (DOTS) (11). MSCs express high levels of ABC transporter efflux pumps, which expel a variety of drugs employed to treat TB (12). Thus, MSCs represent a hiding place for *M. tuberculosis*. The mechanisms by which *M. tuberculosis* adapts to MSCs and the targets in MSCs that allow persistence of *M. tuberculosis* remain unknown.

*M. tuberculosis* within macrophages generally respond to the conventional antibiotic, isoniazid (INH). In contrast, dormant forms of the bacteria generally do not respond to antibiotics, and where and how they evade drugs and detection is incompletely understood. Nevertheless, studies, including our previously published data, have indicated that MSCs represent a major niche for dormant TB (9, 10, 13). Based on these considerations, we hypothesized that *M. tuberculosis* acquires dormancy and thereby drug nonresponsiveness in MSCs.

Here, we show that MSCs are a natural host for dormant *M. tuberculosis*. Upon uptake by MSCs, *M. tuberculosis* induces the expression of dormancy-related genes and promotes quiescence in MSCs. In contrast, *M. tuberculosis* residing in macrophages continues to replicate and causes macrophage necrosis. INH does not affect *M. tuberculosis* survival in MSCs but successfully eliminates bacteria from macrophages. In macrophages, most of the organisms are found in early-phagosomal compartments, but in MSCs:

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Results and Discussion

Previously, we and others have shown that MSCs are associated with nonreplicating *M. tuberculosis* (9, 10, 13). Therefore, we sought to determine whether MSCs are a natural reservoir for *M. tuberculosis* and dormancy that renders nonresponsiveness to antibiotic treatment. We infected human MSCs and peripheral blood mononuclear cell-derived (PBMC-derived) macrophages with *M. tuberculosis* (Supplemental Figure 1; supplemental material available online with this article; https://doi.org/10.1172/JCI128043DS1). We found that, to attain a saturation of infection in macrophages, 4 hours of infection at 1:10 multiplicity of infection (MOI) was required, whereas 6 hours at 1:50 MOI attained saturation of infection in MSCs. Under these conditions, similar numbers of bacilli were taken up by these 2 cell types (Figure 1, A and B). Thus, it appears that MSCs are less permissive than macrophages for *M. tuberculosis* infection, which might be evolutionarily related to latency of *M. tuberculosis* in MSCs.

With the progression of time, *M. tuberculosis* continued to replicate and macrophages became necrotic by 96 hours of infection (Supplemental Figure 2, A–E). Strikingly, *M. tuberculosis* numbers gradually decreased in MSCs, reached a plateau by 72 hours, and remained there in a viable form for an extended time period. To understand this differential behavior of *M. tuberculosis* in macrophages and MSCs, we examined the expression of replication- and dormancy-related genes in *M. tuberculosis* isolated from infected macrophages and MSCs. We found sustained expression of dormancy-related devR/dosR regulon genes in *M. tuberculosis* isolated from MSCs (Figure 1C and Supplemental Figure 3). However, genes that are involved in various steps of *M. tuberculosis* replication were enriched in *M. tuberculosis* isolated from infected macrophages (Figure 1D).

To explore the in vivo relevance, we sorted CD45 Sca1+ MSCs from the bone marrow and CD45+CD11b+ macrophages from the lungs of *M. tuberculosis*-infected mice. Consistent with the in vitro data, we found that *M. tuberculosis* in MSCs express dormancy-related genes, whereas *M. tuberculosis* that are in macrophages express replication-related genes (Figure 1, E and F). Taken together, these observations strongly suggested that macrophages and MSCs are differentially programmed for supporting active and dormant infection, respectively.

Our findings showed that MSCs are less permissive to *M. tuberculosis* infection and allow the bacteria to establish dormancy. It will be interesting to determine if other nonpermissive cells such as hepatocytes or fibroblasts similarly allow *M. tuberculosis* to establish dormancy. Although it has been reported that *M. tuberculosis* can infect and replicate in fibroblasts (14, 15), we were unable to infect fibroblasts.

Next, we explored whether *M. tuberculosis* infection affects MSC replication and found that *M. tuberculosis* inhibits MSC replication in a time-dependent fashion. Therefore, we measured expression of quiescence markers characteristic of stem cells (16, 17). RNA sequencing (RNA-Seq) analysis revealed upregulation of several quiescence markers and downregulation of cell cycle progression markers in human MSCs infected with *M. tuberculosis* (Figure 1G). This was confirmed by quantitative PCR (qPCR) of selected quiescence markers such as FOXO3a, NOTCH1, and SOX9, which were upregulated in MSCs as compared with macrophages (Figure 1H). In contrast, the cellular proliferation markers S-phase kinase 2 (SKP2) and CCNA1 (encoding cyclin A1) were highly upregulated in macrophages (Figure 1H). Western blot analysis confirmed enhanced expression of NOTCH1, FOXO3a, and p-FOXO3α at Ser318/Ser321 (Figure 1I and Supplemental Figure 4), suggesting that these quiescence markers might play a prominent role in attaining a quiescent state in MSCs. This observation implied that upon infection *M. tuberculosis* acquires dormancy, whereas MSCs enter into a quiescent state. This dual strategy may assist *M. tuberculosis* to better shield itself from the host immune system and drugs used for treatment.

It is intriguing that macrophages, which are equipped with phagolysosomal killing mechanisms, are permissive to *M. tuberculosis* replication, whereas MSCs, which lack a well-defined phagosomal system compared with macrophages, restrict *M. tuberculosis* growth (7, 8). To obtain insight into this apparent paradox of *M. tuberculosis* infection, we determined the intracellular localization of GFP-labeled *M. tuberculosis* in human macrophages and MSCs. To determine endosomal localization of *M. tuberculosis*, we employed an antibody directed against the early-endosomal marker, Rab5, whereas for cytosolic localization, we employed phalloidin, which selectively binds F-actin (19). We observed that in macrophages, most of the *M. tuberculosis* localized to early endosomes immediately after infection, whereas the majority of bacilli in MSCs were found in the cytosol (Figure 2, A and B, and Supplemental Figures 5 and 6). Interestingly, we also observed abnormal lipid droplets in MSCs, which became prevalent over time (Figure 2C and Supplemental Figure 7). *M. tuberculosis* colocalized with these lipid droplets (Figure 2, C and D, and Supplemental Figure 8) and their intensity was significantly higher in MSCs than in macrophages (Figure 2E). Electron microscopy data revealed that *M. tuberculosis* hides within the lipid droplets (Figure 2F). This result is consistent with previous reports that *M. tuberculosis* uses lipids as a carbon source (20, 21). To further investigate the pathway of lipid synthesis in MSCs and to explore it will be interesting to determine if other nonpermissive cells such as hepatocytes or fibroblasts similarly allow *M. tuberculosis*
The molecular mechanism of *M. tuberculosis* adaptation, we performed RNA-Seq analyses of infected MSCs. We found that lipid synthesis pathways, especially genes involved in sphingolipid synthesis, were highly upregulated in infected MSCs (Figure 2G). To examine the relationship between lipid synthesis and dormancy, we employed the lipid synthesis inhibitor, triacsin C. Triacsin C is a potent inhibitor of fatty acyl-CoA synthetase that strongly interferes with lipid metabolism by blocking the de novo synthesis of diacylglycerols, triacylglycerols, and cholesterol (22). Inhibition of lipid synthesis resulted in profound downregulation of dormancy-related gene expression in *M. tuberculosis* (Figure 2H), with significant alteration in the expression of replicative genes (Figure 2I). These results imply that *M. tuberculosis* organisms induce lipid synthesis in MSCs and compartmentalize themselves within oleophilic droplets, hence thwarting antimicrobial host defense mechanisms.
were more significant than on macrophages (Figure 3, B and C). This observation indicated that autophagy can eliminate both active and dormant *M. tuberculosis* residing in macrophages and MSCs, respectively. Next, we investigated the status of dormancy and replicative gene expression in bacilli from bone marrow and lungs of *M. tuberculosis*-infected mice that were untreated or treated with INH. We found that the bacilli residing in bone marrow of the INH-treated mice were enriched with dormancy-related genes and expressed fewer replication-related genes (Figure 3, D and E). We also observed similar trends in the lung (Figure 3, F and G).

To decipher the mechanism by which MSCs provide a niche for dormancy of *M. tuberculosis*, we analyzed RNA-Seq data and found that MSCs strongly induce the expression of autophagy-related genes (Figure 3A). Inhibition of autophagy is one of the most widely adopted host-evasion mechanisms used by virulent strains of *M. tuberculosis* (23, 24). Therefore, we tested if induction of autophagy by rapamycin can eliminate *M. tuberculosis* in MSCs. We treated infected human macrophages and MSCs with INH, rapamycin, or a combination of both and assessed the viability of *M. tuberculosis* thereafter. Interestingly, we observed that addition of rapamycin reduced bacterial loads in both macrophages and MSCs in a time-dependent manner. However, effects on MSCs were more significant than on macrophages (Figure 3, B and C). This observation indicated that autophagy can eliminate both active and dormant *M. tuberculosis* residing in macrophages and MSCs, respectively. Next, we investigated the status of dormancy and replicative gene expression in bacilli from bone marrow and lungs of *M. tuberculosis*-infected mice that were untreated or treated with INH. We found that the bacilli residing in bone marrow of the INH-treated mice were enriched with dormancy-related genes and expressed fewer replication-related genes (Figure 3, D and E). We also observed similar trends in the lung (Figure 3, F and G). We made attempts to culture these bacteria but we were unable to culture them consistently (Supplemental Figure 9, A and B), which
Rapamycin is known to induce autophagy by inhibiting the mTOR pathway (26). To further test if addition of rapamycin along with antibiotics indeed attains sterile cure, we employed dexamethasone to suppress immunity in animals that were previously treated with INH or with the combination of INH and rapamycin. Suppression of the immune response with dexamethasone reactivated TB disease in INH-treated animals but not in animals treated with the combination of INH and rapamycin, in agreement with previous reports that dormant M. tuberculosis are difficult to culture on solid media (25). As our ex vivo data indicated that INH eliminates replicating bacteria in macrophages, whereas induction of autophagy by rapamycin kills nonreplicating M. tuberculosis in MSCs, we validated these observations in a mouse model of TB. As expected, addition of rapamycin along with antibiotics was able to achieve sterile cure of TB (Figure 3H), as compared with INH treatment alone (Figure 3I and Supplementary Figure 9A). Rapamycin is known to induce autophagy by inhibiting the mTOR pathway (26). To further test if addition of rapamycin along with antibiotics indeed attains sterile cure, we employed dexamethasone to suppress immunity in animals that were previously treated with INH or with the combination of INH and rapamycin. Suppression of the immune response with dexamethasone reactivated TB disease in INH-treated animals but not in animals treated with the combination of INH and rapamycin.
as measured by CFU in the lung (Figure 3J). To our surprise, treatment with INH reduced bacterial burden less efficiently in bone marrow than in lung (compare Figure 3I and Supplemental Figure 9A). Furthermore, dexamethasone did not efficiently reactivate *M. tuberculosis* in bone marrow (compare Supplemental Figure 9, A and B). These apparent differences between lung and bone marrow might be due to differential drug penetration in these organs. In future studies we will seek to identify TB drugs that effectively penetrate bone marrow. Interestingly, dexamethasone treatment strikingly upregulated replicative genes in the harbored *M. tuberculosis*. *M. tuberculosis* acquires dormancy in MSCs, which in turn induces MSCs to acquire quiescence. *M. tuberculosis* induces synthesis of lipid droplets, which are employed by the organism to hide from host defense mechanisms. Successful treatment of TB requires elimination of both replicating and dormant bacteria. Dormant bacteria do not respond to conventional antibiotics but can be eliminated by inducing autophagy. Therefore, a combination of antibiotics and inducers of autophagy provides the opportunity for the successful treatment of TB.

Our data indicate that MSCs are a natural reservoir for latent *M. tuberculosis* infection, whereas macrophages support the replicating form of *M. tuberculosis*. *M. tuberculosis* acquires dormancy in MSCs, which in turn induces MSCs to acquire quiescence. *M. tuberculosis* induces synthesis of lipid droplets, which are employed by the organism to hide from host defense mechanisms. Successful treatment of TB requires elimination of both replicating and dormant bacteria. Dormant bacteria do not respond to conventional antibiotics but can be eliminated by inducing autophagy. Therefore, a combination of antibiotics and inducers of autophagy provides the opportunity for the successful treatment of TB.

**Methods**

This study was ethically approved by the Institutional Committee for Stem Cell Research, All India Institute of Medical Sciences, New Delhi, India [reference number: IC-SCR/47/16(R)]. Detailed information regarding materials and methods can be found in Supplemental Methods.

**Author contributions**

SF, SSK, VPD, DB, and SK performed the experiments and analyzed data. GD conceived the hypothesis and both GD and SM supervised the experiments. SF, VPD, AR, LVK, and GD wrote the manuscript.

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We thank the Director of the Council of Scientific and Industrial Research Institute of Genomics and Integrative Biology (CSIR-IGIB) and Manish Kumar for assistance with confocal imaging. The authors also thank the National Institute of Biomedical Genomics (NIBMG), India and Partha P. Majumder for help with the RNA-Seq studies. SF is supported by a University Grants Commission Senior Research Fellowship (UGC-SRF). SSK is a recipient of a National Post Doctoral Fellowship (NPDF) from the Science and Engineering Research Board–Department of Science and Technology (SERB-DST). VPD is a DST-INSPIRE faculty awardee. DB is supported by CSIR-Senior Research Associate. We thank the International Centre For Genetic Engineering and Biotechnology (ICGEB) at Delhi University, All India Institute of Medical Sciences, and IGB for generously providing BSL-3 facilities. This work was supported by grants from the Department of Biotechnology (BT/PR24544/MED/29/1217/2017), Department of Science and Technology (SERB/F/4821/2017-18), and the Indian Council of Medical Research (Special Centre for Molecular Medicine is funded by ICMR).

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