Metabolite analysis of *Mycobacterium* species under aerobic and hypoxic conditions reveals common metabolic traits

Margit Drapal,¹ Paul R. Wheeler² and Paul D. Fraser¹

¹School of Biological Sciences, Royal Holloway University of London, Egham, UK
²Tuberculosis Research Group, Veterinary Laboratories Agency Weybridge, New Haw, UK

A metabolite profiling approach has been implemented to elucidate metabolic adaptation at set culture conditions in five *Mycobacterium* species (two fast- and three slow-growing) with the potential to act as model organisms for *Mycobacterium tuberculosis* (*Mtb*). Analysis has been performed over designated growth phases and under representative environments (nutrient and oxygen depletion) experienced by *Mtb* during infection. The procedure was useful in determining a range of metabolites (60–120 compounds) covering nucleotides, amino acids, organic acids, saccharides, fatty acids, glycerols, -esters, -phosphates and isoprenoids. Among these classes of compounds, key biomarker metabolites, which can act as indicators of pathway/process activity, were identified. In numerous cases, common metabolite traits were observed for all five species across the experimental conditions (e.g. uracil indicating DNA repair). Amino acid content, especially glutamic acid, highlighted the different properties between the fast- and slow-growing mycobacteria studied (e.g. nitrogen assimilation). The greatest similarities in metabolite composition between fast- and slow-growing mycobacteria were apparent under hypoxic conditions. A comparison to previously reported transcriptomic data revealed a strong correlation between changes in transcription and metabolite content. Collectively, these data validate the changes in the transcription at the metabolite level, suggesting transcription exists as one of the predominant modes of cellular regulation in *Mycobacterium*. Sectors with restricted correlation between metabolites and transcription (e.g. hypoxic cultivation) warrant further study to elucidate and exploit post-transcriptional modes of regulation. The strong correlation between the laboratory conditions used and data derived from *in vivo* conditions, indicate that the approach applied is a valuable addition to our understanding of cell regulation in these *Mycobacterium* species.

INTRODUCTION

The genus *Mycobacterium* contains a variety of species with different phenotypes (e.g. fast- and slow-growers, chromogens, pathogens and saprophytes) and hence, provides a range of suitable model organisms for *Mycobacterium tuberculosis* (*Mtb*). The suitability of *Mycobacterium* species as model organisms has been extensively discussed highlighting differences/similarities in growth rate, cell envelope chemistry, pathogenicity/biosafety and their phylogenetic relationship compared to *Mtb* (e.g. Barry, 2001). For the purpose of this study, two fast-growing (*M. smegmatis* and *M. phlei*) and three slow-growing (*M. bovis* BCG, *M. avium* and *M. intracellularum*) mycobacteria were chosen to represent a diverse range of *Mycobacterium* species. These mycobacteria were analysed at set growth stages to show adaptation processes upon the induction of abiotic stresses (e.g. nutrient and oxygen limitation through natural depletion of given resources) which are comparable to the microenvironment experienced by *Mtb*. The metabolite levels monitored elucidated metabolic pathways common to the genus *Mycobacterium* [e.g. mycolic acid synthesis (Gago *et al.*, 2011)] and specific to certain phenotypes mentioned above [e.g. poly-glutamine synthesis in slow-growers (Harth & Horwitz, 1999)].
The culture conditions in the present study were based on published in vitro models (Wayne & Hayes, 1996) to represent typical environments experienced by Mtb under physiological conditions. The prevalent stress conditions experienced within the host, including infection stages of active replication in alveolar macrophages and dormancy within granulomas (Chao & Rubin, 2010), involve a gradual depletion of oxygen and nutrients (Russell et al., 2010). To minimize environmental influences on the mycobacterial cells, they were cultivated in a standardized volume of nutrient-rich medium with no additional supplementation over the duration of the experiments, creating a natural depletion of nutrients over the period of batch cultivation. The three culture conditions investigated included growth from lag to stationary phase (Phase I), growth from logarithmic (log) phase for 28 days under aerated (Phase II) conditions and hypoxic (Phase III) conditions. To capture the changes in metabolites occurring under these conditions a quantitative metabolite profiling approach was used (Drapal et al., 2014). The resulting changes at the metabolite level were compared with previous published transcriptomic and proteomic data (e.g. Betts et al., 2002; Hampshire et al., 2004) for a better understanding of cellular regulation in Mycobacterium and its changing chemotype with environmental adaptation. Collectively, these data will enable an assessment of how representative the laboratory conditions used are compared to real-life scenarios.

METHODS

Bacteria. M. smegmatis [National Collection of Type Cultures (NCTC) 8159, Public Health England], M. phlei (NCTC 8151), M. bovis BCG (Pasteur strain, from AHVLA Collection, Weybridge, UK), M. avium (serotype 8, private collection) and M. intracellulare (serotype 7, private collection) were cultivated and prepared as a starting culture as published previously (Drapal et al., 2014). For the following culture conditions five replicates per species were grown in parallel.

For Phase I cultivation, fresh Middlebrook 7H9 supplemented with 10% OADC (oxalic acid-albumin-dextrose-catalase) and 0.4% Tween 80 was inoculated with the starting culture until an initial optical density at 600 nm (OD) of 0.1 or 0.05, for fast- and slow-growing mycobacteria respectively, was reached. The cultures (1.5 times the total volume sampled) were then incubated with shaking (180 rpm, 37°C) under aerated conditions in vent-cap flasks.

For the other two culture conditions, fresh medium (1.5 times the total volume sampled) was inoculated as described for Phase I and incubated with shaking (180 rpm, 37°C) under constant aeration in vent-cap flasks. After 16 h (M. smegmatis), 1 day (M. phlei) or 7 days (M. bovis BCG, M. avium, M. intracellulare), an aliquot (8 ml) of the inoculated medium was sampled, representing the induction point of the two different oxygen conditions. The aerated, shaking condition was maintained for Phase II cultivation and samples (8 ml) were taken at 1, 2 and 28 days after induction for all mycobacteria. For the hypoxic cultivation (Phase III), the cultures were aliquoted (8 ml) at the induction point and all aliquots cultivated without stirring at 37°C until sampled for analysis. The depletion of oxygen in the hypoxic culture was visualized by discoloration of methylene blue (1.5 µg ml⁻¹ cell culture). Aliquots of inoculated medium (8 ml) were sampled following the same time regime as described for Phase II.

RESULTS

Growth properties under aerated and hypoxic cultivation

The growth curves for all three culture conditions were measured by monitoring OD and colony forming units (cfu) (Supplementary File 1, available in the online Supplementary Material). Both these measurements over Phase I showed the typical sigmoid shape for all five mycobacteria in Phase I (Fig. 1). The culture condition in Phase II was characterized by an almost horizontal linear curve at least 2 days after the log phase. Again all five mycobacteria showed similar growth properties (Fig. 1). The OD data were consistent with the cfu measurements and indicated a constant viable count of culturable cells, which is associated with data found for non-replicating persistence (NRP) 1 (Chao & Rubin, 2010; Shi et al., 2010; Bacon et al., 2014). The exception was M. phlei that showed a decline of growth from 1 day to 2 days after the log phase followed by constant values until 28 days suggesting a death phase before the switch to NRP (Bacon et al., 2014). Interestingly, a resurgent increase of cfu values was detected at 28 days (Phase II) only for M. smegmatis, M. avium and M. intracellulare, indicating a reactivation of cells or a second log phase of the remaining active cells. Phase III cultures, contrary to Phase II, showed an immediate stop of replication at the

Sampling and analysis of polar and non-polar metabolites. Aliquots of the cultures were quenched with isotonic 80% (v/v) methanol and centrifuged, and only the resulting cell pellets used for further analysis. The weighed cell pellets were extracted using the methanol/chloroform method followed by analysis with gas chromatography mass spectrometry (GC/MS) and high performance liquid chromatography (HPLC) as previously published (Drapal et al., 2014). The metabolites were identified through a customized library (Drapal et al., 2014). Variation in the number and type of metabolites identified occurred at each sampling point. The GC/MS results were normalized to the internal standard and weight of the cell pellet. The identified compounds within each culture condition were compared to the first time point taken. Statistically significant changes of metabolites were analysed with one-way ANOVA with Dunnett’s post-test and were then plotted over a pathway diagram.

Identification of lipids and proteins of the secreted layer. After 4 days of induction of hypoxia, the secreted layer was carefully removed from the cell pellet and separately analysed for lipid and protein content. For the identification of lipids, the collected secreted layer was dissolved (1:2) in chloroform/methanol/water (10:10:3, v/v/v). The diluted sample was then mixed (1:1) with 2,5-dihydroxybenzoic acid matrix (5 mg ml⁻¹ in acetonitrile with 0.1% (v/v) trifluoroacetic acid) and placed on a 600 µm Anchor chip 384 format MALDI target plate (Bruker Daltonics) before analysis with MALDI–TOF/TOF-MS as described previously (Jones et al., 2013).

For the identification of proteins of the secreted layer, a previously published protocol (Robertson et al., 2012; Mora et al., 2013), which included precipitation of proteins and separation by SDS-PAGE followed by in-gel digestion of the four major protein bands and analysis with nano-LC/MS/MS, was followed. The proteins were identified through the detected peptides as previously published (Nogueira et al., 2013) with SwissProt protein database for taxonomy of M. tuberculosis complex.

http://mic.microbiologyresearch.org
first time point after induction of hypoxic conditions as a result of the removal of agitation (Fig. 1). This was shown through constant values, similar to the induction point (log phase), measured until 28 days and indicate that the cells are capable of rapid detection/adaptation to the change in oxygen concentration. This change in condition was monitored in situ by the reduction of methylene blue in the medium. Discolouration arose 4 h after induction, which was approximately half the duration required for all cells to settle at the bottom of the culture tube and was the same for all five mycobacteria. All samples retained the discolouration throughout Phase III.

The metabolite profile was measured at each set time point and compared to the first time point of the culture condition for each Mycobacterium species separately. The resulting changes of metabolite levels were calculated and their significance evaluated (Supplementary File 2). Key metabolites within the data set were chosen to visualize changes in the nucleotides, the nitrogen and sulfur pathways, TCA cycle, glyoxylate shunt, the biosynthesis of fatty acids and complex lipids and thus, describe the metabolic state over the growth stages.

Metabolite changes occurring at the logarithmic and stationary growth phases (Phase I)

Overall ~70 compounds were detected throughout Phase I for four of the five mycobacteria tested. M. phlei was the exception with 126 metabolites detected. The summarized Phase I data for all five mycobacteria (Fig. 2) highlighted the differences in metabolite levels between the fast-growing and the slow-growing Mycobacterium species. Interestingly, the slow-growers had predominantly decreased metabolite levels, when compared to the lag phase, which suggested that metabolites associated with primary metabolism were either not detectable or rapid utilization occurred. The data on the fast-growers, M. phlei and M. smegmatis, showed increased levels of polar metabolites, suggesting accumulation of the latter. M. bovis BCG, being one of the slow-growing mycobacteria, showed metabolite changes similar to M. avium and M. intracellulare but differed from the latter two as more metabolites were detected in M. bovis BCG including uracil, glycine, fatty acid precursors and intermediates of the TCA cycle.

The common nucleotide detected in M. smegmatis, M. bovis BCG and M. phlei was uracil and showed increased levels from log phase onwards. M. phlei had the most nucleotides detected, which showed the same increasing trends as uracil (Supplementary File 2). No nucleotides were detected for M. avium and M. intracellulare over Phase I, which would be compliant with rapid utilization.

Homocysteine, the key intermediate of the sulfur pathway, can be metabolized via cysteine to mycothiol (Zeng et al., 2013) or converted to methionine (Singhal et al., 2013) leading to reduced levels of the latter as detected throughout Phase I, in four out of five mycobacteria tested. M. phlei was the only Mycobacterium species in this study for which no homocysteine was found, but increased cysteine levels were detected.

Glutamic acid, the preferred nitrogen assimilation product (Amon et al., 2009), showed higher levels at log phase compared to the stationary phase in M. phlei and M. smegmatis. M. intracellulare was the only slow-growing species that showed up-regulation of glutamic acid in the stationary phase. The other two slow-growing species, M. bovis BCG and M. avium, had decreased levels of glutamic acid. In addition, in M. bovis BCG, levels of proline were increased.

The only intermediate of the TCA cycle, which was detected in all five mycobacteria studied throughout Phase I, was succinic acid. This intermediary metabolite connects the TCA cycle, glyoxylate shunt and methylcitrate cycle, which are all involved in fatty acid synthesis and catabolism (Eoh & Rhee, 2013). Succinic acid and odd-chain fatty acids were
Fig. 2. Heat map of metabolite levels measured from lag phase over log and stationary phase. *M. smegmatis*, *M. phlei*, *M. bovis* BCG, *M. avium* and *M. intracellulare* were grown under aerated conditions and sampled at lag, log and stationary phases. The reference point for metabolite levels was the lag phase. Metabolites were grouped as polar (nucleotides, amino acids, organic acids and saccharides) and non-polar (fatty acids, glycerol, -esters, -phosphates and isoprenoids) extracts. Changes are indicated as increase (green), no change (grey), decrease (red) and not detected (white) as shown in the legend. Results were means of five replicates.
Metabolic changes under elongated aerated cultivation (Phase II)

In all five mycobacteria, more compounds were detected over Phase II compared to Phase I. *M. phlei* had the most metabolite changes measured over Phase II, which were mainly lower levels compared to the initial time point of measurement (Fig. 3).

Nucleotide metabolism appeared to be active in all five mycobacteria as a variety of changes in nucleotide constituents were detected throughout Phase II. Amino acid content was unchanged for *M. avium* and *M. intracellulare* at 1 day and 2 days, respectively, and decreased for *M. phlei*. Contrary to this, *M. smegmatis* and *M. bovis* BCG showed an increase in number and levels of amino acids especially at 2 days of Phase II.

Even though the overall trends of amino acid levels differed between the five mycobacteria studied, the amino acids involved in the sulfur and nitrogen pathways were similar between them. Homocysteine/cysteine content showed no change overall and glutamic acid levels showed a decreasing trend throughout Phase II after an initial increase for *M. smegmatis* and *M. intracellulare*. In addition, *M. phlei* had decreased levels of biochemically related consecutive intermediates of glutamic acid (ornithine and citrulline), whereas *M. bovis* BCG and *M. smegmatis* showed increased levels at 1 day or 2 days (proline and ornithine) (Supplementary File 2).

The glyoxylate shunt seemed activated after 1 day for *M. smegmatis* and after 2 days for BCG and *M. avium*, which was indicated by increased levels of glyoxylate and/or glycine. *M. intracellulare* showed decreased levels of glyoxylic acid at 2 days and no change in glycine, whereas, *M. phlei* had decreased levels both glyoxylic acid and glycine throughout Phase II with a further decrease from 1 day to 2 days.

The metabolite profiling data of Phase II showed that trehalose and glycerol contents were related to even-chain fatty acid levels, which are all precursors for the biosynthesis of TDM or triacylglyceride (TAG). In *M. phlei*, fatty acids and trehalose were decreased, whereas in the three slow-growing species no change was detected for both trehalose and fatty acids within the first 2 days of Phase II. Furthermore, glycerol-3-phosphate was increased for *M. bovis* BCG and *M. intracellulare*, and together with glycerol-esters, decreased in *M. avium* and *M. phlei*. Only *M. smegmatis* showed no change of fatty acids, an increase in trehalose and a decrease of glycerol-3-phosphate.

The chromogenic mycobacteria (*M. phlei* and *M. intracellulare*) and *M. smegmatis* had increased levels of isopenoids throughout Phase II and increased levels of MK9 at 1 day except for *M. phlei*, which showed no change in MK9 levels. *M. avium* and *M. bovis* BCG showed no change of MK9 and an additional MK (MK8) was detected for *M. bovis* BCG.

Cultivation of mycobacteria tested over Phase II highlighted differences between the *Mycobacterium* species, especially for *M. phlei*, which showed downregulated metabolite levels...
throughout Phase II and even further decreases at 28 days whereas the other mycobacteria showed a predominantly positive metabolic switch at the last time point. At 28 days, *M. smegmatis* showed increased levels of the glyoxylate shunt, sulfur pathway and fatty acids and *M. bovis BCG* showed increased levels of the glyoxylate shunt, nucleotides and fatty acid precursors, indicating activated energy metabolism and induced activity for cell replication. At the same time, *M. avium* and *M. intracellulare* showed a distinct metabolic activation of all pathways with increased levels except for glycerol-1-phosphate.

---

**Fig. 3.** Heat map of metabolite levels measured over Phase II. *M. smegmatis*, *M. phlei*, *M. bovis BCG*, *M. avium* and *M. intracellulare* were grown under aerated conditions throughout and sampled from log phase onwards over 28 days. The reference point for metabolite levels was the first sampling point at log phase. Metabolites were grouped under polar (nucleotides, amino acids, organic acids and saccharides) and non-polar (fatty acids, glycerol, -esters, -phosphates and isoprenoids) extracts. Changes are indicated as increase (green), no change (grey), decrease (red) and not detected (white) shown in the legend. Results were means of five replicates. d, Day(s).
esters, which were decreased. For \textit{M. smegmatis}, \textit{M. avium} and \textit{M. intracellulare} these metabolic changes at 28 days were also reflected with increased cfu values as described earlier.

**Effects of hypoxic culture conditions on metabolite levels (Phase III)**

Over Phase III, mycobacterial cells were not agitated and became oxygen-depleted, a well-documented effect (Wayne & Sohaskey, 2001). The measured changes of metabolites over Phase III were more similar between the five mycobacteria tested (Fig. 4) compared to the data described for Phase II. In general, fewer metabolites were detected in Phase III (~90) than in Phase II (~110).

The number of nucleotides detected followed this trend with a decrease in amount and number or a general lack of nucleotides detected for \textit{M. smegmatis}, \textit{M. avium} and
M. intracellulare, respectively. In M. bovis BCG uracil showed increased levels after 2 days and in M. phlei the highest number of nucleotides was detected with increased levels of most nucleotides at 1 day (Supplementary File 2).

No change of homocysteine levels was detected for M. bovis BCG throughout Phase III, for M. intracellulare after 1 day and for M. smegmatis and M. avium until 28 days. All three mycobacteria had increased levels of homocysteine at the other time points. As seen in Phase I and II, only cysteine was detected in M. phlei with decreased levels throughout Phase III.

A striking observation was the decrease of glutamic acid in all three slow-growers throughout Phase III whereas the fast-growing species showed increased levels. Only two biochemically related consecutive metabolites, proline and ornithine, were detected in M. smegmatis and M. phlei, respectively, with increased content at 1 day.

The succinic acid levels varied for all five mycobacteria tested. M. smegmatis and M. avium showed decreased levels from 1 day and 2 days, respectively, in M. bovis BCG no change occurred, and M. phlei and M. intracellulare showed increased followed by decreased levels of succinic acid at 1 day and 2 days, respectively. Similar to succinic acid, precursors for lipid and cell wall synthesis (glycerol, fatty acids and saccharides) were expressed with different metabolite levels for all mycobacteria. M. smegmatis and M. avium showed decreased levels of glycerol-3-phosphate, whereas M. phlei and M. intracellulare showed increased levels of glycerol-3-phosphate and -esters, respectively, at 1 day followed by no change from 2 days onwards. M. bovis BCG showed an increase of glycerol, -phosphates and -esters and most fatty acids at 2 days with the exception of decreased levels of C18:0, a fatty acid favoured for first or second position of TAG, throughout Phase III (Walker et al., 1970). Arabinose was detected in M. smegmatis at 1 day and in M. phlei and M. avium at 28 days. Galactose content was mainly unchanged over Phase III apart from decrease in M. smegmatis and increase at 1 day in M. phlei. At 1 day M. phlei also had an increased content of mannose, which was otherwise unchanged for the other four species. Inositol and trehalose were detected with similar trends of levels over Phase III. For M. smegmatis they were increased over the first 2 days and at 2 days, respectively. In M. avium both saccharides were decreased after 1 day and 2 days, respectively. Inositol and trehalose were unchanged in M. bovis BCG until 28 days at which point they were decreased. M. intracellulare also showed unchanged levels of inositol and an increase at 28 days whereas trehalose was increased until 2 days and showed no change at 28 days. In M. phlei, trehalose and inositol were increased at 1 day followed by no change of trehalose and decreased levels of inositol.

MK9 levels showed no change over Phase III for all mycobacteria tested and for M. intracellulare after 1 day. For M. bovis BCG MK8 and MK9 were detected as described for Phase II. A smaller number of carotenoids (less than half) was detected for M. phlei and M. intracellulare over Phase III compared to Phase II. The carotenoids showed no change except for phytoene, which was at an increased level throughout Phase III.

At 28 days of Phase III a renewed change of metabolite levels was detected similar to Phase II but without an increase in cfu number. M. bovis BCG and M. smegmatis showed activation of sulfur and energy metabolism (e.g. glyoxylate shunt, fatty acid metabolism) and an increase of nucleotide levels (Supplementary File 2). M. smegmatis and M. intracellulare had increased contents of almost all fatty acids detected. Furthermore, M. avium and M. intracellulare showed activity for all metabolic pathways as described for Phase II with the exception of increased levels of nucleotides for M. avium.

The most striking property of the hypoxic cultivation was a secreted lipid layer of only the two fast-growing Mycobacterium species (Fig. 5a). At 3–4 days after induction of hypoxic conditions, a translucent layer became visible right above the cell pellets and showed a clear separation from the medium. The control tube, containing bacteria-free medium, showed no such occurrence, indicating that the layer was a product of the bacteria. In the case of the chromogenic M. phlei, the extracellular material was coloured yellow/orange throughout and showed a zone of denser colouration at the border of the cell pellet. Analysis of carotenoids extracted from the secretion did not show any results as the amount of carotenoids was below the level of detection due to the volume of secretion per tube (~50 µl/10 mg cell pellet).

Thus, the concentration of carotenoids could be significant but the total amount of extracellular material precludes adequate extractable amounts.

After collection, the secreted layer was analysed for metabolite and protein composition. The analysis with MALDI showed two series of peaks from 525 to 917 m/z and 1005 to 2035 m/z (Fig. 5b). The fingerprint of the molecular ion peaks was typical for MALDI spectra of TAG as seen to 2035 m/z (Fig. 5b). The fingerprint of the molecular ion was the main compound of the secretion as no other spectra detection of TAGs due to a combination of fatty and mycolic acids with different chain lengths as described for M. smegmatis (Rafidinarivo et al., 2009). The MALDI data suggested that TAG was the main compound of the secretion as no other spectra were detected in the sample. The two series of peaks in the TAG spectrum of M. smegmatis further indicated two different types of TAGs due to a combination of fatty and mycolic acids with different chain lengths as described for M. smegmatis (Rafidinarivo et al., 2009).

For the protein analysis, proteins were extracted from the secreted layer and separated by SDS-PAGE. The same pattern of protein bands was seen for both fast-growing mycobacteria. The two major protein bands of both species were identified as a putative diacylglycerol O-acyltransferase (DGAT, ~63 kDa) from Mycobacterium and acyl-CoA acetyltransferase (ACAT, ~40 kDa). Furthermore, a match for the early secreted antigen target (ESAT)-6-like protein EssB (~11kDa) was found.
DISCUSSION

The metabolome, as the end product of gene expression and protein regulation (Harrigan & Goodacre, 2003; Boshoff & Lun, 2010), can be used to give a mechanistic insight into adaptation processes of an organism. An example in the present study is increasing levels of uracil detected through all culture conditions as part of DNA repair of G+C-rich bacteria in macrophage infections (Venkatesh et al., 2003; Cossu et al., 2012). Difficulties of metabolite profiling methods, including the quick metabolic turn-over and leakage during sampling, were minimized in the approach used (Drapal et al., 2014) and the results reveal snapshots of the intracellular metabolism. Furthermore, the comparison of the metabolic data with transcriptional and translational data elucidates the principal mode of cellular regulation during adaptation to a stress condition.

The identified common properties of all mycobacteria specific to a culture condition (Fig. 6) were consistent with transcriptional and translational data published [e.g. during macrophage infection (Sassetti & Rubin, 2003)]. For Phase I this included an active nucleotide and amino acid metabolism (Wang et al., 2005), which ceased with cell replication over Phase III as reported under in vivo and in vitro conditions (Wayne & Sohaskey, 2001; Betts et al., 2002). In addition, changes in homocysteine levels as a precursor for cell wall maintenance (Dhiman et al., 2009) and for protein and nucleotide synthesis (Singhal et al., 2013) were detected. MK9 and isoprenoids, both involved in the electron transport chain, seemed to play an essential interconnected role over all three conditions tested (Lee et al., 2008; Dhiman et al., 2009). Another important and already well-known compound class for mycobacteria are lipids, which act as a barrier to the environment (e.g. TDM) (Archuleta et al., 2005) and as carbon/energy storage (e.g. TAG) (Cossu et al., 2012). Their precursor metabolites detected included fatty acids, monosaccharides and glycerol derivatives. All of these metabolites displayed an active metabolism during replication cycles for plasma membrane and cell wall (Sassetti et al., 2003; Cossu et al., 2013), as well as part of the adaptation to environmental changes (Arulchand et al., 2005) and the transition to the dormant state in Mtb as reported in mycobacterial infections (Stehr et al., 2013).

One typical mycobacterial feature is the redirection of the carbon flow under reduced oxygen conditions, which results in a switch of the TCA cycle to the glyoxylate shunt (Sassetti & Rubin, 2003; Eoh & Rhee, 2013). Succinic acid and glyoxylate, both products of the isocitrate lyase in the glyoxylate shunt (Eoh & Rhee, 2013), were detected in this study. The detection of both of those metabolites over Phase I suggested that the glyoxylate shunt was already activated during active replication, contrary to published literature (e.g. Wayne & Sohaskey, 2001; Chao & Rubin, 2010). Levels of glyoxylate and related metabolites indicated a far less active glyoxylate shunt over Phase II than that described for a transcriptomic study following progressive nutrient depletion similar to the conditions in the present study (Hampshire et al., 2004).

The main metabolic changes, which showed distinct differences between fast- and slow-growing mycobacteria, were glutamic acid levels and sequestration of TAG over Phase III. Increased levels of glutamic acid in the fast-growing species over Phase I were coherent with nitrogen assimilation under nitrogen excess in the medium (Amon et al., 2009) and suggest that fast-growing species can sense upcoming

---

**Fig. 5.** Lipid secretion of M. smegmatis under hypoxic cultivation. (a) The secretion layer occurred after 3–4 days of hypoxic cultivation of M. smegmatis. The translucent secretion layer (arrow) was collected and analysed with MALDI for metabolite composition. (b) An average MALDI spectrum is presented.
limitation in the surrounding medium and adapt accordingly (Smeulders et al., 1999). Contrary to this, glutamic acid levels over Phase I in the slow-growing species were consistent with utilization of the latter for nucleotide and protein synthesis and transcriptional data for optimal growth (Sassetti et al., 2003). Over Phase III, the lack of nucleotides in combination with decreased levels of glutamic acid in slow-growing species suggested secretion of glutamic acid into the extracellular environment. Pathogenic mycobacteria (e.g. M. bovis and M. tuberculosis) are known to release glutamine synthetase during infection and synthesis poly-L-glutamate/glutamine as an extracellular carbon and nitrogen storage (Harth & Horwitz, 1999). The intracellular metabolic processes are indicated with black arrows and utilization of compound classes for the cell wall (grey circle) with grey arrows. The same changes of compound classes for all mycobacteria tested are highlighted as up- and downregulated (solid and dotted underlined, respectively).

For fast-growing species a release of TAG into the medium was observed a few days after Phase III induction (Fig. 5). Lipid body formation with TAG is a common property of mycobacteria during the hypoxic phase of the infection (e.g. Garton et al., 2002; Low et al., 2009) and M. smegmatis is known to constantly release fatty acids or TAG into the medium (Selishcheva et al., 2012). The proteins detected in the secreted layer suggest simultaneous synthesis of TAG by DGAT similar to mycobacterial infections (Stehr et al., 2013) and β-oxidation of fatty acids by ACAT for butyryl-CoA and acetyl-CoA synthesis (Kanehisa et al., 2006). DGAT was detected in higher amounts than ACAT, resulting in more TAG synthesis compared to β-oxidation and, consequently, the visible TAG layer. Saprophytic mycobacteria usually cannot gain access to lipids originating from a host such as pathogenic mycobacteria (Russell et al., 2010). In the present study, oleic acid was available in the medium in its free form and through hydrolysis of Tween 80. Hence, the production and secretion of TAG with oleic acid might be the adaptation process of choice for non-pathogenic mycobacteria to create an environment similar to foamy macrophages during infection with Mtb (Stehr et al., 2013) and to secure storage of extracellular signalling metabolites (oleic acid) for resuscitation (Selishcheva et al., 2012). Similar metabolic changes related to TAG synthesis were detected over Phase II, and they highlight that TAG synthesis and secretion might be a reaction to stressful conditions including nutrients and/oxygen depletion, leading to an NRP state (Wayne & Sohaskey, 2001). The metabolic changes related to phenotypes suggest a possible genetic
variation between pathogenic and non-pathogenic mycobacteria due to necessities presented by their respective ecological niches.

In the present study, a renewed increase in metabolic activity and growth rate was detected at 28 days of Phase II and III cultivation for all mycobacteria tested. The metabolic activities correlated with gene expression for optimal growth over Phase I (Sassetti et al., 2003), which indicates the presence of active and ‘dormant’ cells in the culture. This supports reports of heterogeneous culture in in vivo and in vitro studies and suggests that this phenomenon is a mycobacterial trait and might provide new insight into NRP cultures (Smeulders et al., 1999; Chao & Rubin, 2010).

Despite the metabolic differences of non-pathogenic and pathogenic mycobacteria, a comparison of their metabolic features provided valuable insight to in vitro studies, as metabolic reactions detected were consistent with results described for mycobacteria under macrophage infection. The present study revealed that all Mycobacterium species maintain an active turn-over of metabolites involved in transcription, translation and other general cellular processes through all three culture conditions. The comparison with published literature highlighted that metabolic changes over a gradually occurring nutrient depletion (Phase I and II) seemed to be more influenced by transcriptional and translational processes, whereas cells experiencing a sudden oxygen reduction (Phase III) showed a more independent metabolic regulation related to a phenotype. This suggested a more complex and diverse regulation of intracellular processes over Phase III for the different phenotypes, contrary to the orderly shift-down previously described (Cunningham & Spreadbury, 1998). This observation emphasizes the importance of integrated data from several levels of cellular regulation to guarantee sufficient data for a more complex understanding of the biological processes as a whole.

In conclusion, all five Mycobacterium species can be considered as model organisms for Mtb in relation to cell wall and MK9 synthesis over the cultures conditions tested, although most other metabolic changes detected over the three culture conditions (e.g. poly-L-glutamate layer over Phase III) showed a divide between fast- and slow-growing mycobacteria. This suggests that for metabolite profiling study purposes Mycobacterium species phenotypically closer to Mtb (e.g. M. bovis BCG and M. avium) should be recommended as model organisms. Given that a chlorof orm/methanol/ water step, lethal to mycobacteria, is used for the extraction of metabolites, the methodology is applicable to use with ACDP3 pathogens such as virulent Mtb. The strong correlation between responses detected in the present laboratory-based study and published data, often acquired under conditions approaching in vivo scenarios, adds support to the metabolomic approach as a means of obtaining conclusive datasets for interpretation into exploitable networks. Thus, a metabolite profiling of at least one Mtb strain should be done to further validate the presented conclusions and lead to a more precise consideration for the choice of model species for metabolic modelling.

ACKNOWLEDGEMENTS

This work was supported by a Royal Holloway University of London studentship to P. D. F. and Animal Health and Veterinary Laboratories Agency, UK to P. R. W. and the EUFP7 Colospor project (P. D. F). We thank Christopher Gerrish for technical support and guidance.

REFERENCES


Edited by: K. Dobos

http://mic.microbiologyresearch.org