High monocyte to lymphocyte ratio is associated with impaired protection after subcutaneous administration of BCG in a mouse model of tuberculosis [version 2; peer review: 2 approved]

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Abstract

Background: The only available tuberculosis (TB) vaccine, Bacillus Calmette-Guérin (BCG), has variable efficacy. New vaccines are therefore urgently needed. Why BCG fails is incompletely understood, and the tools used for early assessment of new vaccine candidates do not account for BCG variability. Taking correlates of risk of TB disease observed in human studies and back-translating them into mice to create models of BCG variability should allow novel vaccine candidates to be tested early in animal models that are more representative of the human populations most at risk. Furthermore, this could help to elucidate the immunological mechanisms leading to BCG failure. We have chosen the monocyte to lymphocyte (ML) ratio as a correlate of risk of TB disease and have back-translated this into a mouse model.

Methods: Four commercially available, inbred mouse strains were chosen. We investigated their baseline ML ratio by flow cytometry; extent of BCG-mediated protection from Mycobacterium tuberculosis infection by experimental challenge; vaccine-induced interferon gamma (IFNγ) response by ELISPOT assay; and tissue distribution of BCG by plating tissue homogenates.

Results: The ML ratio varied significantly between A/J, DBA/2, C57Bl/6 and 129S2 mice. A/J mice showed the highest BCG-mediated protection and lowest ML ratio, while 129S2 mice showed the lowest protection and higher ML ratio. We also found that A/J mice had a lower antigen specific IFNγ response than 129S2 mice. BCG tissue distribution appeared higher in A/J mice, although this was not statistically significant.

Conclusions: These results suggest that the ML ratio has an impact on BCG-mediated protection in mice, in alignment with observations from clinical studies. A/J and 129S2 mice may therefore be useful models of
BCG vaccine variability for early TB vaccine testing. We speculate that failure of BCG to protect from TB disease is linked to poor tissue distribution in a ML high immune environment.

Keywords
Tuberculosis, animal models, BCG, vaccine, ML ratio, mice

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Introduction

Tuberculosis (TB), caused by Mycobacterium tuberculosis (Mtb), is the leading cause of death from a single infectious agent. Multidrug-resistant TB remains a public health crisis, and only one vaccine (the M. bovis-derived Bacillus Calmette-Guérin, BCG) is currently licensed for clinical use. To meet the sustainable development goal of ending the TB epidemic by 2030, new treatments and vaccines are both urgently needed.

BCG efficacy is highly variable\(^2\). The reasons why BCG protects when it does and why it fails when it doesn’t are incompletely understood, but are crucial to the successful design and testing of new vaccines\(^3\). Furthermore, to be able to accurately assess vaccine candidates in models where BCG both protects and does not protect very early on in the vaccine development pipeline would be highly advantageous and de-risk failure in later stage clinical trials. There is however a lack of a broad range of tools that can collectively predict with some confidence whether a vaccine will be protective.

One of the tools for very early testing of TB vaccine candidates is a mouse model. However, in order to obtain meaningful information, new vaccine candidates should be tested in models that are clinically relevant and reflect the breadth and heterogeneity of immune environments and varying BCG efficacy found in human populations. We propose that this could be achieved by back-translating observations from clinical studies, such as correlates of risk of TB disease, into animal models.

A number of correlates of risk of TB disease have recently been identified, including transcriptomic mRNA signatures in blood, T cell activation, and monocyte to lymphocyte (ML) ratio\(^4\), while others are being investigated (reviewed in \(^9\)). We have chosen the ML ratio to provide proof of principle that correlates of risk can be back-translated into the mouse to develop a model for vaccine testing that better reflects the populations most at risk of BCG failure.

Methods

Animals and experiment design

The following mouse strains were used for the experiments reported here (abbreviated names used throughout the manuscript are given in brackets): A/JOlHsd (A/J); DBA/2OlaHsd (DBA/2); C57BL/6JOlHsd (C57Bl/6); 129S2/SvHsd (129S2). Female mice were acquired from Envigo UK at 5–7 weeks of age. Animals were housed in specific pathogen-free individually ventilated cages with environmental enrichment (play tunnel and tapvei block), with 12 hours light / 12 hours dark cycles, at temperatures between 19° – 23°C and relative humidity of 45 – 65%. Mice were fed sterilized diet RM1 and filtered water ad libitum, and were allowed to acclimatize for at least 5 days before the start of any experimental procedure. Mice were allocated to cages as groups of 5 by technical staff not involved in experimental procedures or data analysis, and mice of the same strain were housed together. Each cage was allocated to a treatment in no particular order, but without formal randomisation. Animal welfare was assessed twice every day before and during the study.

Two independent experiments with separate primary outcomes were carried out to obtain the data described in this report. In Experiment 1, 5 naïve mice of each strain (20 mice total) were culled by anaesthetic overdose, and cardiac blood, lungs and spleens were collected for determination of the ML ratio by flow cytometric analysis (see below for details). The primary outcome for this experiment was the ML ratio (Figure 1). In Experiment 2, parallel groups of mice (n=5 per group) were BCG-immunised or left untreated. These were allocated at the start of the study to either an immunogenicity group (IFN\(\gamma\) response and BCG dissemination; 10 mice per strain; 40 mice total; Figure 3 and Figure 4), or an Mtb challenge group (bacterial burden in lung; 10 mice per strain; 40 mice total; Figure 2). Six weeks after immunisation, mice were infected with Mtb or culled for isolation of cells from lung and spleen. In all, a total of 100 mice (25 per strain) was used to obtain all data presented here.

The study was not blinded.

Vaccination

The BCG Pasteur strain was obtained from Aeras (Rockville, MD, USA) as frozen aliquots. These were stored at -80°C until needed. BCG was then thawed at room temperature and diluted to a final concentration of 2×10\(^7\) CFU/ml in physiological saline solution for irrigation (Baxter Healthcare, Newbury, UK). Each animal received a subcutaneous injection of 100 \(\mu\)l BCG containing 2×10\(^7\) CFU BCG (vaccinated groups). BCG dose was confirmed by plating of an aliquot of the prepared vaccine...
Figure 1. The ML ratio differs significantly in four different inbred mouse strains. A Gating strategy for flow cytometric analysis. Cells from naïve animals were fixed, stained and data acquired as described in Materials and Methods. Cell debris was gated out by use of a FSC-SSC gate, followed by gating on single cells (FSC-H and FSC-W). A sequential gating strategy was then applied to determine the frequency of T cells (CD3\(^+\)), B cells (B220\(^+\)), neutrophils (CD11b\(^+\) Ly6G\(^+\)), monocytes/macrophages (CD11b\(^+\) CD11c\(^{low-int}\), red gate) and CD11b\(^{int}\) CD11c\(^+\) cells (blue gate) as a percentage of single cells. Plots shown are from a sample of a C57Bl/6 spleen. B–D The ML ratio was calculated by dividing the percentage of monocytes/macrophages by the sum of the percentages of B and T cells. ML ratio was analysed in blood (B), lung (C) and spleen (D) of four different mouse strains. E Percentage of CD11b\(^{int}\) CD11c\(^+\) cells in the lung of four different mouse strains, likely to be enriched in alveolar macrophages. Each symbol represents one animal; box plots represent the median (middle line), 25\(^{th}\) to 75\(^{th}\) percentile (box) and minimum to maximum value (error bars). Data sets are presented in order of decreasing protection. \(p\) values were determined using ordinary ANOVA with Holm-Sidak test for multiple comparisons. Multiplicity adjusted \(p\) values are reported. A \(p\) value <0.05 was considered statistically significant.
Figure 2. Protection from Mtb infection varies after BCG vaccination in ML high and low mouse strains. A Mice of each strain were immunised s.c. with 2x10^5 CFU BCG Pasteur (open circles) or left untreated (filled circle), and infected i.n. with 30 CFU Mtb Erdmann 6 weeks later. Bacterial burden in the lungs of all animals was enumerated 7 weeks after challenge. Each symbol represents one animal. Bacterial numbers are given as log10 CFU per whole organ. No bacteria were detected in one of the C57Bl/6 samples; this value was set to zero. ∆ indicates the difference in bacterial burden between naïve and BCG immunised mice. p values were determined by Kruskal-Wallis test with Dunn’s post-test for multiple comparisons between naïve groups, and multiplicity adjusted p values are reported. Individual Mann-Whitney tests to compare naïve with BCG immunised groups of each mouse strain. p<0.05 was considered statistically significant. Error bars represent the median and interquartile range. LoD: limit of detection. B ML ratio in comparison to protection in the lung of ML high and low mice. The median ML ratio in lung (red; as in Figure 1) is plotted together with protection expressed as the median % decrease in CFU (blue; as in A).

Figure 3. Antigen-specific interferon gamma response varies in splenocytes of ML high and ML low mouse strains. Splenocytes were isolated from BCG-immunised or control mice at the time of Mtb challenge (6 weeks after immunisation), and restimulated with PPD. The number of IFNγ producing cells were enumerated using an ELISPOT assay (presented as spot forming units [SFU] per 10^6 cells). Non-specific background measured in unstimulated duplicate wells was removed. Data sets are presented in order of decreasing protection. Each symbol represents one animal. p values were determined by using one-way ANOVA and Dunn’s post test for multiple comparisons. Error bars represent the median and interquartile range. Multiplicity adjusted p values are reported. p<0.05 was considered statistically significant.
suspension on 7H11 agar plates. Colonies were counted after 12–14 days of incubation at 37°C. Animals were then rested for 6 weeks before either infection with *Mtb*, or sacrifice for cell isolation.

**BCG enumeration in tissues**

Approximately half of each spleen and the right-hand side lobes of the lungs from mice in the immunogenicity group were used to determine the number of viable BCG bacteria in each organ six weeks after vaccination. Tissues were removed aseptically in a microbiological safety cabinet and placed in sterile 2 ml screwcap vials containing 500 μl PBS + 0.05% Tween80 and Precellys 1.4mm ceramic beads (CK14; Peqlab, Sarisbury Green, UK). A Precellys 24 homogeniser (Peqlab) was used to homogenise tissues for 15 s at 5000 rpm before plating. Each entire homogenate was plated onto two 7H11 agar plates containing 10% OADC supplement (Yorlab, York, UK) and 0.5% glycerol. Colonies were counted after 3 weeks of incubation at 37°C.

**Infection with *M. tuberculosis***

Mice were infected intranasally with *M. tuberculosis* Erdman (BEI Resources, Manassas, VA, USA) 6 weeks after vaccination of ML high and ML low mice. Approximately half of each lung (A) and spleen (B) was homogenised at the time of Mtb challenge (6 weeks after immunisation) and plated on 7H11 agar plates to determine viable BCG bacteria. Total CFU per organ are reported. Data sets are presented in order of decreasing protection. Each symbol represents one animal. In some instances, bacteria could not be detected and values were set to zero. *p* values were determined by using Kruskal-Wallis test and Dunn’s post test for multiple comparisons. Error bars represent the median and interquartile range. Multiplicity adjusted *p* values are reported. *p*<0.05 was considered statistically significant.

**Figure 4.** BCG distribution varies between lung and spleen after vaccination of ML high and ML low mice. Approximately half of each lung (A) and spleen (B) was homogenised at the time of Mtb challenge (6 weeks after immunisation) and plated on 7H11 agar plates to determine viable BCG bacteria. Total CFU per organ are reported. Data sets are presented in order of decreasing protection. Each symbol represents one animal. In some instances, bacteria could not be detected and values were set to zero. *p* values were determined by using Kruskal-Wallis test and Dunn’s post test for multiple comparisons. Error bars represent the median and interquartile range. Multiplicity adjusted *p* values are reported. *p*<0.05 was considered statistically significant.
BCG immunization and kept in isolators under CL-3 containment. Frozen aliquots of Mtb Erdman were thawed at room temperature, and diluted in saline. Mice were anaesthetized by an intraperitoneal injection of a combination of Ketamine (50 mg/kg; Ketalar Pfizer Ltd, Kent, UK) and Xylazine (10 mg/kg; Rompun; Berkshire, UK) in saline. Each animal then received 50 μl of the inoculum, estimated to contain 30 CFU. The number of bacteria in the inoculum was confirmed by plating aliquots on 7H11 agar plates containing 10 % OADC and 0.5 % glycerol.

Seven weeks after infection, animals were killed by cervical dislocation. Lungs and spleens were removed aseptically and homogenized by mechanical disruption in sterile PBS, using the plunger of a 5 ml syringe and a 100 μm cell strainer. A series of 10-fold dilutions of tissue homogenates in PBS with 0.05 % Tween 80 were plated onto 7H11 agar plates with 10 % OADC supplement and 0.5 % glycerol. Plates were incubated at 37 °C and colonies counted after 3 weeks.

Protection is expressed by the percent reduction of median CFU/lung in the BCG group compared to the control group for each mouse strain.

**Flow cytometry**

Single cell suspensions from spleens were prepared in RPMI-1640 media (Sigma-Aldrich, Dorset, UK) containing 10% heat-inactivated FBS (Labtech International Ltd, Uckfield, UK) and 2 mM L-Glutamine (Fisher Scientific, Loughborough, UK) as soon as possible after sacrifice. Spleens were mechanically disrupted by mashing through a 100μm cell strainer using the rubber end of the plunger from a 5ml syringe. Lungs were disrupted by mashing through a 100μm cell strainer using the remaining spleen samples from the immunogenicity group as a positive control. After lysis of red blood cells, single cell suspensions were made up in RPMI-1640 media containing 10% heat-inactivated FBS and 2 mM L-Glutamine. 96-well microtiter ELISPOT plates (MAIPS4510, Millipore, Watford, UK) were coated with 10 μg/ml rat anti-mouse IFN-γ (clone AN18, Mabtech, Nacka Strand, Sweden). Free binding sites were blocked with RPMI-1640 supplemented with 10% heat-inactivated FBS and 2 mM L-Glutamine. 2x10^4 of total splenoocytes were added and incubated in duplicate with PPD (10 μg/ml), supplemented RPMI as a negative control, or Phorbol myristate acetate (PMA) (0.1 μg/ml, Sigma-Aldrich) and Phytohemagglutinin (PHA) (1 μg/ml, Sigma-Aldrich) as a positive control. After overnight incubation at 37°C in 5% CO₂, IFN-γ was detected with 1 μg/ml biotin labelled rat anti-mouse antibody (clone R4-6A2, Mabtech) and 1 μg/ml alkaline phosphatase-conjugated streptavidin (Mabtech). The enzyme reaction was developed with BCIP/NBT substrate (5-Bromo-4-chloro-3-indolyl phosphate/Nitro blue tetrazolium) (MP Biochemicals, UK) and stopped by washing the plates with tap water when individual spots could be visually detected (up to 5min). ELISPOT plates were analysed using an automatic plate reader. IFN-γ-specific cells are expressed as number of spot-forming units (SFU) per million spleen cells after non-specific background was subtracted using negative control wells.

**Statistical analysis**

Groups of animals were compared, and a p value of <0.05 was considered statistically significant. Statistical analysis was carried out using GraphPad Prism version 6. The specific test used for each analysis is described in the figure legends.

**Results**

Four commercially available inbred mouse strains were chosen to investigate the impact of the baseline ML ratio on BCG vaccine efficacy. A/J, DBA/2, C57Bl/6 and 129S2 mice were selected to represent varying monocyte frequencies and a range of BCG-mediated protection based on available data (Jax Phenome Database https://phenome.jax.org/). To allow the direct comparison of the ML ratio between strains, animals were age and sex matched and all samples were processed at the same time, stained with aliquots of the same antibody cocktail, and using the automatic function in FlowJo version 10.4. Compensation matrices were manually checked and adjusted where necessary.

Analysis was carried out using FlowJo version 10.4.
data acquired as a batch. All animals used in this experiment were included in the analysis.

We found significant differences between mouse strains in their baseline ML ratio in blood, spleen, and lung (Figure 1). Across all tissues, A/J mice showed the lowest ML ratio (Figure 1 B–D). In spleen and blood, the ML ratio of DBA/2, C57Bl/6 and 129S2 mice was higher than A/J, but only minor differences were found between those three strains (Figure 1 B and D). In the lung, differences between all strains were more apparent (Figure 1C). 129S2 mice had the highest ML ratio, with DBA/2 and C57Bl/6 showing intermediate levels. These differences in ML ratio were mostly driven by differing frequencies in monocytes/macrophages, with minor differences in B and T cell frequencies between mouse strains (Figure S1–S3).

To assess the impact of these differences in ML ratio on BCG efficacy in our model, we infected mice of all strains with virulent Mtb Erdmann.

Mouse strains with varying ML ratios are differentially protected from Mtb infection by BCG

Mice of each strain were vaccinated s.c. with BCG, or left untreated, and infected with Mtb Erdmann six weeks later. The extent of protection by BCG was measured by determining the bacterial burden in lung and spleen of vaccinated and control mice (Figure 2). All mice were immunised with the same inoculum of BCG and infected using the same inoculum of Mtb, so that results of the different strains are directly comparable. All animals were included in the analysis and no unexpected adverse events were observed. No more than 10% weight loss was recorded over the duration of the experiment. We found varying degrees of protection (Figure 2A). A/J mice were the most protected with a difference in median CFU (Δ) between vaccinated and control groups of 1.41 log_{10}, followed by DBA/2 (Δ0.81 log_{10}) and C57Bl/6 (Δ0.54 log_{10}), and 129S2 mice were the least protected (Δ0.37 log_{10}). Interestingly, the mouse strain with the highest ML ratio in the lung showed the lowest protection (129S2), and the strain with the lowest ML ratio showed the highest protection (A/J; Figure 2B). Some differences were also observed in the innate susceptibility between strains, most notably C57Bl/6 mice were significantly less susceptible than DBA/2 (Δ1.16 log_{10} CFU) or A/J mice (Δ1.41 log_{10} CFU). Alveolar macrophages play an important role in the defence against respiratory pathogens, however they are not included in the gate used here to quantify monocytes/macrophages (Figure 2A). While we did not include specific markers for this cell population, they carry a CD11b intermediate (CD11bint), CD11c+ phenotype. We found that the frequency of CD11bint CD11c+ cells was significantly higher in C57Bl/6 mice compared to the other mouse strains (Figure 2E).

Next, to investigate whether differential BCG-mediated protection from Mtb infection was associated with a differential immune response, we carried out an IFNγ ELISPOT assay.

A differential antigen-specific IFNγ response is associated with differential protection

To assess the immune response to mycobacterial antigens in the differentially protected mouse strains, splenocytes from mice vaccinated with BCG were stimulated with PPD, and the number of IFNγ-producing cells was measured by ELISPOT (Figure 3). IFNγ is a cytokine associated with control of infection in mice and reduced risk of TB disease in humans. We found that there were significantly more antigen-specific IFNγ producing splenocytes in 129S2 mice than in A/J or DBA/2 mice, both of which were better protected by BCG from Mtb challenge than 129S2 mice.

Since BCG is a live mycobacterium, and monocytes and macrophages are the natural host cells for these organisms, it was plausible that a high ML ratio and high IFNγ production in 129S2 mice impair BCG survival and dissemination to and/or persistence in tissues, and thus prevent the formation of a protective immune response in the lung.

BCG dissemination to lung and spleen is impaired in ML high mice

To determine the extent to which BCG is found in lungs and spleens after s.c. administration, we plated organ homogenates onto 7H11 agar plates and enumerated viable BCG after 3 weeks of culture (Figure 4). We generally found low numbers of bacteria per organ, especially in the lung, where the bacterial count did not exceed 80 CFU/lung in any sample. Moderate differences were detected between mouse strains. Most notably, the most protected ML low A/J mice had the highest number of BCG in the lung, while no BCG was detectable in the lung of the least protected ML high 129S2 mice.

These data led us to speculate that certain host immune-environments, such as a high ML ratio, can influence BCG dissemination and/or persistence, which in turn could impact BCG efficacy.

The data presented here are from one experiment as detailed in the Methods section. To ensure reproducibility, we have endeavoured to include as much experimental detail as possible to allow others to repeat the study and confirm the results. Groups of animals of all strains received the same treatments at the same time to
minimise technical variation. We are therefore confident that the major differences between strains are true biological differences.

Dataset 4. BCG distribution raw data
http://dx.doi.org/10.5256/f1000research.14239.d197137

This file contains the raw data as colony forming units (CFU) for the graph shown in Figure 4.

Discussion

The varying efficacy of BCG has long been a concern for the control of the TB epidemic. Numerous factors have been discussed as contributors to this, such as population differences, different BCG strains, vaccination schedules, exposure to environmental mycobacteria, co-infections with viruses and/or parasites, and geographical location. While BCG works in some populations and protects children from pulmonary and extra-pulmonary disease, new vaccines are urgently needed for the populations where BCG fails to protect, such as adolescents and adults in endemic areas. The incomplete understanding of the mechanisms behind BCG failure, together with limited tools for early assessment of vaccine efficacy, are hampering the development of new vaccines. In order to allow early vaccine testing in a model that better represents the populations most at risk of TB disease, we have taken a correlate of risk observed in human studies and back-translated it into a mouse model. The monocyte to lymphocyte (ML) ratio is a non-specific marker of inflammation and has been shown to be associated with risk of TB disease in several populations, including pregnant HIV infected women, people starting anti-retroviral therapy, BCG vaccinated infants and latently Mtb infected adolescents. This may point towards an involvement of host factors, as the influence of environmental factors would be limited so early in life. On the one hand, Scriba et al. show a cascade of inflammatory events as adolescents progress towards disease, which appears to start with increased Type I/II IFN signalling, followed by an increase in monocytes and a decrease in lymphocytes. An increased risk of TB disease in BCG vaccinated individuals with a high ML ratio indicates that BCG is failing in those populations.

In order to provide proof of principle that the ML ratio, and observations from human studies more generally, can be back-translated to develop more clinically relevant mouse models, we chose to use commercially available, genetically tractable inbred mouse strains. We could show that these have highly varying ML ratios in blood, spleen, and lung, and that these differences, particularly in the lung, were associated with varying BCG-mediated protection from Mtb infection. Using mouse strains with genetically different backgrounds means that there are likely other confounding factors that could impact vaccine efficacy. This is exemplified by the DBA/2 mice, which are well protected despite having a relatively high ML ratio across all tissues. This could be due to the fact that they have a higher neutrophil frequency than some of the other strains (data not shown). Although confounding factors may be at play here, this would also be the case in a clinical setting since an altered ML ratio can have different underlying causes. An increased ML ratio is an indicator for inflammation, likely driven by monocyotosis during inflammation. Some factors that are thought to influence BCG efficacy also drive inflammation, such as co-infection with viruses or parasites, malnutrition, or exposure to environmental mycobacteria. However, as manipulation of ML ratio in vitro impacts on ability to control mycobacterial growth, it is likely that ML ratio itself is contributing to TB risk, independent of the factor driving inflammation. It is also possible that host genetic factors determine baseline inflammation and ML ratio. If this is the case in TB endemic populations, inbred mouse strains with naturally varying ML ratios may be a useful model for BCG vaccine variability.

There are genetic differences between the inbred mouse strains used in this study, some of which have been well described, while others are likely to be unknown. Among the most well described genetic factors is the mutation of the interleukin-3 (IL-3) receptor alpha subunit gene in A/J mice, which leads to impaired IL-3 signalling and reduced proliferation of haematopoietic stem cells and their differentiation into myeloid precursors. This is likely to play a role in the low ML ratio observed in these mice. A/J mice additionally carry a defect in the gene for Naip5, an intracellular pattern recognition receptor involved in control of proliferation of intracellular pathogens. It may thus have an effect on BCG persistence and dissemination. C57Bl/6 mice carry a polymorphism in the slc11a1 (formerly nramp1) gene, which has been shown to determine susceptibility or resistance to intravenous infection with BCG as defined by BCG load in the spleen. It does not seem to determine susceptibility to primary Mtb infection in mice, and the effect on BCG efficacy is not well studied. In addition, different inbred mouse strains carry different MHC haplotypes. For the strains used in this study, they are as follows: 129S2, H2b; C57Bl/6, H2b; A/J, H2d; DBA/2, H2d. Each one confers the ability to recognise a slightly different range of epitopes, although there is overlap. This may also impact BCG-mediated immunity.

It is currently unclear what the relative contributions are of genetic and environmental factors to a change in ML ratio. Does a naturally high ML ratio in an individual make them more prone to TB disease, or do other factors including Mtb itself drive up the ML ratio, causing BCG to fail? Does a naturally high ML ratio in an individual exacerbate an inflammatory response initiated by environmental factors? There is striking heterogeneity in the immune response to BCG in infants vaccinated at birth, including in the ML ratio and cytokine responses. This points towards an involvement of host factors, as the influence of environmental factors would be limited so early in life. On the other hand, Scriba et al. observe increases in inflammation and ML ratio over time in adolescents as an individual progresses towards active TB disease and diagnosis. This may point towards the pathogen itself as the cause of an altered immune environment.

Interestingly, we found a higher number of antigen-specific IFNγ-producing splenocytes in unprotected 129S2 mice compared to protected A/J mice at the time of Mtb challenge. This seemed counterintuitive at first, but is in line with recent findings showing that a sub-population of BCG-vaccinated infants with an increased ML ratio showed increased
phages or T cells in this study, although it is likely that this plays a role. In particular, inflammatory monocytes might lead to killing of BCG. It will be interesting in future to investigate this, as well as comparing the ML ratio and immune cell phenotypes before and after BCG vaccination in the different mouse strains and locations.

We found a significantly higher proportion of CD11b+ CD11c+ cells in the lungs of C57Bl/6 mice, which are likely to be enriched in alveolar macrophages. Interestingly, C57Bl/6 mice are also the strain least susceptible to Mtb infection without BCG vaccination. While the frequency of this population does not seem to be associated with BCG-mediated protection after subcutaneous administration of the vaccine, it could play a role after intranasal vaccination. Alveolar macrophages are located on the luminal side of the epithelium, therefore encountering antigens and pathogens taken up from environmental air. The monocyte/macrophage population included in our ML ratio on the other hand is likely to be of interstitial nature, residing on the basal side of the epithelium and encountering antigens from the blood stream.

While our data on the susceptibility of naïve mouse strains to Mtb infection agrees with other studies30, we found some discrepancies between the data presented here and previously published data on BCG-mediated protection. A study using DBA/2 mice has shown that these mice are not protected by s.c. administration of BCG, but control infection with Mtb better when vaccinated i.n.31 This is in contrast to our finding that DBA/2 mice are protected from Mtb challenge after s.c. vaccination. However, there are some differences between these two studies that may explain the different findings: a different source of mice was used; protection was assessed at 8 weeks vs 6 weeks after vaccination; the BCG strain and Mtb strain differed; and the Mtb dose used for challenge was three times higher in the study by Aguilo and colleagues compared to ours. Another report detailing the susceptibility of different mouse strains to Mtb challenge shows that A/J mice are notably less protected than C57Bl/6 mice, while in our hands the opposite is the case. There are important differences between the two studies, including the age and sex of mice used, the time point after vaccination at which protection was measured, and the use of different BCG and Mtb strains. In combination, these factors may lead to a differing extent of protection. With particular relevance to this study, the immune cell frequency between male and female animals differ in A/J mice. For example, dataset Donahue5 on the Jackson Laboratory Mouse Phenome Database indicates a higher percentage of monocytes in blood for males compared to females, while T cells are less frequent in males, leading to a higher ML ratio in males37.

In conclusion, the back-translation of a correlate of risk of TB disease, the ML ratio, into an animal model is a step forward for better tools to study the immune mechanisms behind BCG vaccine failure and to test vaccines in a model more relevant to populations most at risk. Hopefully other risk factors can also be back-translated in the future to obtain a more complete picture of vaccine efficacy at very early stages of testing. We would encourage the use of more diverse mouse models in TB vaccine testing and development to reflect the heterogeneity of immune environments found in human populations.
Data availability

**Dataset 1:** Flow cytometry raw data – This file contains the data underlying the analysis of the ML ratio and cell subsets in blood, spleen, and lung shown in Figure 1, Figure 2B, Figure S1, Figure S2, and Figure S3. 10.5256/f1000research.14239.d207942

**Dataset 2:** Mtb challenge CFU raw data – This file contains the raw data as colony forming units (CFU) of the graphs in Figure 2. 10.5256/f1000research.14239.d197118

**Dataset 3:** ELISPOT raw data – This file contains the raw data for the graph shown in Figure 3. 10.5256/f1000research.14239.d197136

**Dataset 4:** BCG distribution raw data – This file contains the raw data as colony forming units (CFU) for the graph shown in Figure 4. 10.5256/f1000research.14239.d197137

Competing interests

No competing interests were disclosed.

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Supplementary material

**Figure S1:** The frequency of T cells varies in tissues of ML high and ML low mouse strains. T cell (CD3+ frequencies were determined in blood (A), lung (B) and spleen (C) of four different mouse strains using the gating strategy described in Figure 2A. The ML ratio was calculated using these data. Each symbol represents one animal; box plots represent the median (middle line), 25th to 75th percentile (box) and minimum to maximum value (error bars). Data sets are presented in order of decreasing protection. p values were determined using ordinary ANOVA with Holm-Sidak test for multiple comparisons. Multiplicity adjusted p values are reported. A p value <0.05 was considered statistically significant. Click here to access the data.

**Figure S2:** The frequency of B cells varies in tissues of ML high and ML low mouse strains. B cell frequencies (B220+) were determined in blood (A), lung (B) and spleen (C) of four different mouse strains using the gating strategy described in Figure 2A. The ML ratio was calculated using these data. Each symbol represents one animal; box plots represent the median (middle line), 25th to 75th percentile (box) and minimum to maximum value (error bars). Data sets are presented in order of decreasing protection. p values were determined using ordinary ANOVA with Holm-Sidak test for multiple comparisons. Multiplicity adjusted p values are reported. A p value <0.05 was considered statistically significant. Click here to access the data.

**Figure S3:** The frequency of monocytes/macrophages varies in tissues of ML high and ML low mouse strains. Monocyte/macrophage (CD11b+ CD11clow-int) frequencies were determined in blood (A), lung (B) and spleen (C) of four different mouse strains using the gating strategy described in Figure 2A. The ML ratio was calculated using these data. Each symbol represents one animal; box plots represent the median (middle line), 25th to 75th percentile (box) and minimum to maximum value (error bars). Data sets are presented in order of decreasing protection. p values were determined using ordinary ANOVA with Holm-Sidak test for multiple comparisons. Multiplicity adjusted p values are reported. A p value <0.05 was considered statistically significant. Click here to access the data.

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Version 2

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Nacho Aguilo
Department of Microbiology, Preventive Medicine, and Public Health, University of Zaragoza, Zaragoza, Spain

I am satisfied with the answers given to my comments and therefore I recommend the indexing of the study.

Competing Interests: No competing interests were disclosed.

Reviewer Expertise: tuberculosis vaccines immunology

I confirm that I have read this submission and believe that I have an appropriate level of expertise to confirm that it is of an acceptable scientific standard.

Version 1

Reviewer Report 20 April 2018

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Maximiliano G Gutierrez
Host-Pathogen Interactions in Tuberculosis Laboratory, Francis Crick Institute, London, USA

The work from Zelmer and collaborators is very interesting, timely, well executed and clearly written. I anticipate a great interest in the tuberculosis vaccine field.
I have only minor comments and suggestions:

Regarding introduction and/or discussion, it would be important the authors discuss what are the main genetic differences between the 4 mouse strains selected for this study.

In Figure 4, it is right to state that colonies vary in tissues but only 2 tissues were analysed here so it would be more appropriate to state "between lung and spleen". Moreover, would it be possible to get the data in lymph nodes as well? Lymph nodes are critical for the responses to vaccination.

The variation in CFU/organ seem to be higher in animals that have high levels of protection in this study (e.g. A/J mice). Could the authors comment on this? Is it possible to know the ML ratio in the 2 mice showing high CFU/lung from Fig 4A?

Not sure if the authors have the samples available, but it would have been interesting to see the profiles of Type I/II IFN in tissue at least by qPCR. This information could be of great interest for the tuberculosis field.

The authors should discuss the limitations of a relatively low number of biological experiments in this work.

Is the work clearly and accurately presented and does it cite the current literature?
Yes

Is the study design appropriate and is the work technically sound?
Yes

Are sufficient details of methods and analysis provided to allow replication by others?
Yes

If applicable, is the statistical analysis and its interpretation appropriate?
I cannot comment. A qualified statistician is required.

Are all the source data underlying the results available to ensure full reproducibility?
Yes

Are the conclusions drawn adequately supported by the results?
Yes

**Competing Interests:** No competing interests were disclosed.

I confirm that I have read this submission and believe that I have an appropriate level of expertise to confirm that it is of an acceptable scientific standard.

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**Author Response 19 Jun 2018**

**Andrea Zelmer**, Department of Immunology and Infection, Keppel Street, UK

Dear Dr Gutierrez

We would like to thank you for taking the time to review our manuscript, and for the thoughtful feedback provided. We address your individual comments below.
The work from Zelmer and collaborators is very interesting, timely, well executed and clearly written. I anticipate a great interest in the tuberculosis vaccine field. I have only minor comments and suggestions:

Regarding introduction and/or discussion, it would be important the authors discuss what are the main genetic differences between the 4 mouse strains selected for this study.

We have now included a paragraph in the Discussion to address this.

In Figure 4, it is right to state that colonies vary in tissues but only 2 tissues were analysed here so it would be more appropriate to state "between lung and spleen". Moreover, would it be possible to get the data in lymph nodes as well? Lymph nodes are critical for the responses to vaccination.

We have now specified “lung and spleen” in the legend to Fig. 4 and also in the sub-heading in the results section.

It would be very interesting to look at tissue distribution to lymph nodes, and this is a point both reviewers have brought up. Unfortunately, we do not have the samples available and no additional funding is available at the moment to repeat this study. Furthermore, we believe it would be difficult to justify the use of further animals solely for this purpose; however, we will investigate this in future experiments and thank you for the suggestion.

The variation in CFU/organ seem to be higher in animals that have high levels of protection in this study (e.g. A/J mice). Could the authors comment on this? Is it possible to know the ML ratio in the 2 mice showing high CFU/lung from Fig 4A?

Since a different set of animals was used for flow cytometry and BCG distribution studies (outlined in the Methods section), it is not possible to directly compare the ML ratio and BCG CFU of individual animals.

With regards to variation in Fig. 4, we believe this is likely to be a technical effect – we detected very few bacilli in general, and especially in the lung, we did not detect any bacteria in some samples from lesser protected animals. This does not mean there are non – it just means that we were not able to detect them with the method used. As such, it is difficult to interpret the real variation within those mouse strains.

Not sure if the authors have the samples available, but it would have been interesting to see the profiles of Type I/II IFN in tissue at least by qPCR. This information could be of great interest for the tuberculosis field.

Unfortunately we do not have those samples available. It is an important point, and would indeed be very relevant. We plan to investigate this in future studies.

The authors should discuss the limitations of a relatively low number of biological experiments in this work.
We have added a comment to this effect at the end of the results section.

Competing Interests: No competing interests were disclosed.
The study by Zelmer et al. evaluates in different mouse genetic backgrounds whether the ratio of monocytes/macrophages vs T lymphocytes could affect BCG-induced protection. This study results are highly interesting as it evaluates in an animal model data derived from a previous vaccine efficacy trial. In addition, it highlights a critical question in the field of vaccine evaluation in mice, which is the genetic heterogeneity among inbred mouse strains. This issue is of particular importance when we are assessing vaccines which aim to be moved to humans. During the reading of the manuscript I have found some minor questions that I think should be amended to improve the quality of the study.

1. I think that the gating criteria used to enclose the monocyte/macrophage population (CD11b+CD11cint cells) is excluding myeloid populations that could be highly informative for the outcome of the study. This is particularly important in the case of the lungs, where naïve alveolar macrophages have a phenotype CD11bintCD11c+. Alveolar macrophages represent a first-line defense against respiratory pathogens, and therefore results could be very informative to know which is the status of these cells in the different strains used. More even if we consider that authors compare directly data from BCG-induced protection with the ML ratio in the lungs (Figure 2B).

2. I suggest to make the comparison between ML ratio and protection using a linear regression, so statistical significance of the shown data could be assessed.

3. I find highly interesting the data showing the differences in BCG persistence among the four strains, more even considering the influence of vaccine persistence in protective efficacy. This result evidences that live vaccine persistence does not only depends on the vaccine itself, but also on the host, and this is a question that should be considered in the future to study novel tuberculosis vaccines. My question is whether the authors could provide some data of BCG persistence in the local draining lymph nodes (in addition to lungs and spleen), as they are the primary sites of BCG biodistribution following subcutaneous/intradermal vaccination.

**Is the work clearly and accurately presented and does it cite the current literature?**
Yes

**Is the study design appropriate and is the work technically sound?**
Yes

**Are sufficient details of methods and analysis provided to allow replication by others?**
Yes

If applicable, is the statistical analysis and its interpretation appropriate?
Partly

Are all the source data underlying the results available to ensure full reproducibility?
Yes

Are the conclusions drawn adequately supported by the results?
Partly

**Competing Interests:** No competing interests were disclosed.

**Reviewer Expertise:** tuberculosis vaccines immunology

I confirm that I have read this submission and believe that I have an appropriate level of expertise to confirm that it is of an acceptable scientific standard, however I have significant reservations, as outlined above.

Author Response 19 Jun 2018

Andrea Zelmer, Department of Immunology and Infection, Keppel Street, UK

Dear Dr Aguilo
Thank you for reviewing our manuscript, and for providing timely and helpful comments and feedback. We discuss your individual points below.

The study by Zelmer et al. evaluates in different mouse genetic backgrounds whether the ratio of monocytes/macrophages vs T lymphocytes could affect BCG-induced protection. This study results are highly interesting as it evaluates in an animal model data derived from a previous vaccine efficacy trial. In addition, it highlights a critical question in the field of vaccine evaluation in mice, which is the genetic heterogeneity among inbred mouse strains. This issue is of particular importance when we are assessing vaccines which aim to be moved to humans. During the reading of the manuscript I have found some minor questions that I think should be amended to improve the quality of the study.

1. I think that the gating criteria used to enclose the monocyte/macrophage population (CD11b$^+$CD11c$^{int}$ cells) is excluding myeloid populations that could be highly informative for the outcome of the study. This is particularly important in the case of the lungs, where naïve alveolar macrophages have a phenotype CD11b$^{int}$CD11c$^+$. Alveolar macrophages represent a first-line defense against respiratory pathogens, and therefore results could be very informative to know which is the status of these cells in the different strains used. More even if we consider that authors compare directly data from BCG-induced protection with the ML ratio in the lungs (Figure 2B).

We have analysed the frequency of CD11b$^{int}$CD11c$^+$cells in the lungs of the four different mouse strains, and have added Fig. 1E, as well as described the data in the Results section and discussed it in the Discussion. In brief, the frequency of this population is significantly higher in C57Bl/6 mice, and seems to be associated with susceptibility of naïve mice, but not BCG-mediated protection.
2. I suggest to make the comparison between ML ratio and protection using a linear regression, so statistical significance of the shown data could be assessed. This would indeed be an informative analysis; however, our experimental design does not allow it here. Since the data shown from flow cytometry and protection studies were acquired from two different sets of mice (see Methods section), the data are not paired, and it would not be appropriate to link them in a linear regression.

3. I find highly interesting the data showing the differences in BCG persistence among the four strains, more even considering the influence of vaccine persistence in protective efficacy. This result evidences that live vaccine persistence does not only depend on the vaccine itself, but also on the host, and this is a question that should be considered in the future to study novel tuberculosis vaccines. My question is whether the authors could provide some data of BCG persistence in the local draining lymph nodes (in addition to lungs and spleen), as they are the primary sites of BCG biodistribution following subcutaneous/intradermal vaccination.

This is an important point, and was also raised by Dr Gutierrez, the other reviewer. As you will see from our response to Dr Gutierrez’ comments, we unfortunately do not have the samples available and no additional funding is available at the moment to repeat this study. Furthermore, we believe it would be difficult to justify the use of further animals solely for this purpose; however, we are very interested to investigate the role of BCG distribution in vaccine efficacy in more detail in the future, and thank you for the suggestion.

**Competing Interests:** No competing interests were disclosed.