Comparative Analysis of *Mycobacterium tuberculosis* pe and *ppe* Genes Reveals High Sequence Variation and an Apparent Absence of Selective Constraints

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**Abstract**

*Mycobacterium tuberculosis* complex (MTBC) genomes contain 2 large gene families termed *pe* and *ppe*. The function of *pe*/*ppe* proteins remains enigmatic but studies suggest that they are secreted or cell surface associated and are involved in bacterial virulence. Previous studies have also shown that some *pe/ppe* genes are polymorphic, a finding that suggests involvement in antigenic variation. Using comparative sequence analysis of 18 publicly available MTBC whole genome sequences, we have performed alignments of 33 *pe* (excluding *pe_pgrs*) and 66 *ppe* genes in order to detect the frequency and nature of genetic variation. This work has been supplemented by whole gene sequencing of 14 *pe/ppe* (including 5 *pe_pgrs*) genes in a cohort of 40 diverse and well defined clinical isolates covering all the main lineages of the *M. tuberculosis* phylogenetic tree. We show that nsSNP’s in *pe* (excluding *pgrs*) and *ppe* genes are 3.0 and 3.3 times higher than in non-*pe/ppe* genes respectively and that numerous other mutation types are also present at a high frequency. It has previously been shown that non-*pe/ppe* *M. tuberculosis* genes display a remarkably low level of purifying selection. Here, we also show that compared to these genes those of the *pe/ppe* families show a further reduction of selection pressure that suggests neutral evolution. This is inconsistent with the positive selection pressure of “classical” antigenic variation. Finally, by analyzing such a large number of genes we were able to detect large differences in mutation type and frequency between both individual genes and gene sub-families. The high variation rates and absence of selective constraints provides valuable insights into potential *pe/ppe* function. Since *pe/ppe* proteins are highly antigenic and have been studied as potential vaccine components these results should also prove informative for aspects of *M. tuberculosis* vaccine design.

**Introduction**

*Mycobacterium tuberculosis*, the main causative agent of tuberculosis in humans, is a member of the *M. tuberculosis* complex (MTBC), a closely related group of slow-growing pathogenic mycobacteria. Recent studies of MTBC evolution have revealed that the *M. tuberculosis* genome appears to be a composite genome created by frequent horizontal gene transfer events in a broad, genetically diverse, progenitor species prior to an evolutionary bottleneck or selective sweep around 35,000 years ago [1]. Divergence of the rare, smooth colony forming tubercle bacilli *M. canetti* seems to immediately predate this bottleneck/selective sweep while all other members of the MTBC are the result of the clonal expansion of a small number of surviving bacteria. This recent clonal expansion with the concurrent absence of horizontal gene transfer explains the relatively high degree of genetic homogeneity (99.9%) observed between MTBC members despite differences in their phenotypic characteristics and host ranges [2,3,4]. Whole genome sequencing of several *M. tuberculosis* strains, along with *M. bovis* and *M. africanum*, has confirmed this genetic homogeneity and revealed many other interesting biological aspects [5,6,7].

One of the surprises emerging from the analysis of the first sequenced *M. tuberculosis* genome (the laboratory strain H37Rv) was the discovery of two large gene families, designated *pe* and *ppe*, that in H37Rv comprise 99 and 69 members respectively and that numerous other mutation types are also present at a high frequency. It has previously been shown that non-*pe/ppe* *M. tuberculosis* genes display a remarkably low level of purifying selection. Here, we also show that compared to these genes those of the *pe/ppe* families show a further reduction of selection pressure that suggests neutral evolution. This is inconsistent with the positive selection pressure of “classical” antigenic variation. Finally, by analyzing such a large number of genes we were able to detect large differences in mutation type and frequency between both individual genes and gene sub-families. The high variation rates and absence of selective constraints provides valuable insights into potential *pe/ppe* function. Since *pe/ppe* proteins are highly antigenic and have been studied as potential vaccine components these results should also prove informative for aspects of *M. tuberculosis* vaccine design.
glutamic acid (ppe) at positions 7–9 in a highly conserved N-terminal domain of approximately 180 amino acids. The C-terminal domains of both pe and ppe protein families are highly variable in both size and sequence and often contain repetitive DNA sequences that differ in copy number between genes [5]. The pe and ppe gene families can be divided into sub-families based on similarities in their N-terminal regions and the phylogenetic relationships between each gene sub-family have been previously described, demonstrating that their evolutionary expansions are linked to the duplications of the ESAT-6 (esx) gene clusters [8].

The pe and ppe gene families can be divided into sub-families based on similarities in their N-terminal domains and the phylogenetic relationships between each gene sub-family have been previously described, demonstrating that their evolutionary expansions are linked to the duplications of the ESAT-6 (esx) gene clusters [8]. Ppe genes can be subdivided into 5 sub-families, the most numerous of which are the ppe_svp (24 members) and the ppe_mptr (major polymorphic tandem repeat) subfamilies (Fig. 1a). Pe genes can also be divided into 5 sub-families, the largest of which, the polymorphic GC-rich-repetitive sequence (pe_pgrs), comprises 65 members in H37Rv (Fig. 1b). This sub-family is characterised by a C-terminal domain that contains multiple tandem repeats of a glycine-glycine-alanine (Gly-Gly-Ala) or a glycine-glycine-asparagine (Gly-Gly-Asn) motif. Phylogenetic analysis indicates that the emergence of the large pe_pgrs and ppe_mptr subfamilies is a recent evolutionary event, with their presence being restricted to members of the MTBC and close relatives such as M. marinum and M. ulcerans [8].

The high pe/ppe gene content of the MTBC suggests an important biological role for their respective proteins. However, their precise function is unknown although recent studies have provided some intriguing clues. In pathogenic organisms it is generally found that proteins that are directly exposed to host immune surveillance show higher levels of polymorphism than that found in general housekeeping proteins [9]. This is thought to reflect their involvement in antigenic variation and immune evasion. Many pe/ppe proteins have been found to be highly
immunogenic and several groups have investigated this aspect of their biology with regard to vaccine production (for example, [10,11]). Persuasive evidence now exists that many *M. tuberculosis* pe/ppe proteins are cell surface located [12,13,14,15] and that others are probably secreted [16,17] and this, in conjunction with their immunogenicity and the well established polymorphic nature of their C-terminal repeats, has led to the suggestion that they may well be involved in antigen variation and immune evasion [5]. Indeed, several studies have revealed varying degrees of pe/ppe sequence polymorphism between *M. tuberculosis* clinical isolates. Talarico and colleagues have reported a high degree of polymorphism within the *pe_pgrs33, pe_pgs16* and *pe_pgs26* genes [18,19,20]. Similar results have also been found for *ppe18* [21].

Less sensitive analysis based on the size of DNA repeats in the C-terminal region of *ppe34* and *ppe38* have also revealed a high frequency of polymorphism [12,22]. In addition, some *pe/ppe* genes have been reported to display elevated levels of IS6110 integration [23,24,25,26,27,28] and homologous recombination [26,29,30,31]. However, sequence analysis of 4 *pe* (*pe5, pe11, pe18* and *pe31*) and 4 *ppe* (*ppe9, ppe27, ppe41* and *ppe50*) genes found polymorphism to be limited or absent [32]. Along with sequence variation, gene expression alterations may contribute to antigenic variation and these have also been noted in *pe/ppe* genes from different *M. tuberculosis* strains [33,34,35]. For example, *ppe44* shows limited sequence diversity between strains (only isolates of the Beijing genotype were found to be polymorphic) whereas transcript levels of the gene are highly variable [35]. Numerous other reports have documented variation in *pe/ppe* transcription levels under different environmental and experimental conditions [36,37,38,39]. Furthermore, there does not appear to be a global regulator of *pe/ppe* expression [36,40], suggesting a complex regulatory network and a high degree of plasticity in their expression repertoire.

It has been proposed that *pe/ppe* proteins can aid *M. tuberculosis* pathogenesis by negatively influencing host immunity [5] and recently Toll-like receptor 2 (TLR2) has assumed a prominent role in this theory. For example, Basu et al showed that *pe_pgs33* is able to enhance the expression of tumour necrosis factor alpha (TNFα) in a TLR2-dependent manner leading to macrophage apoptosis [41]. Interestingly, deletions within the PGRS domain (as is often seen in clinical isolates) inhibited this ability. Ppe proteins have also been shown to function in a TLR2-dependent manner. Nair et al demonstrated that ppe18 binds to TLR2 which stimulates IL-10 production in macrophages [42]. This leads to an anti-inflammatory Th2 type immune response. Evidence also exists to suggest that *pe_pgrs* proteins may be able to inhibit antigen processing and/or presentation [43] and it has been proposed that the Gly-Ala repeats in the C-terminal PGRS domain are able to inhibit protosomerial degradation of the N-terminal PE domain [44] thus inhibiting antigen processing by CD8+ T cells in a manner similar to that seen in Epstein–Barr virus nuclear antigen 1 [45]. Several other lines of evidence also suggest a major role for *pe/ppe* proteins in mycobacterial pathogenesis. For example, recent work has shown that *pe_pgs33* localises to host cell mitochondria where it is able to induce apoptosis and primary necrosis [46]. Studies demonstrating increased mycobacterial growth in macrophages and subsequent macrophage necrosis of *pe_pgs33* expressing strains (as oppose to *pe_pgs33* negative strains) have also been reported [47,48] and other studies have documented an attenuated phenotype with the knockout of specific *pe/ppe* genes [49,50] or the upregulation of specific *pe/ppe* genes upon infection [38,31].

Evidence for other diverse alternative or additional *pe/ppe* functions also exists. In *silo* analysis of PGRS protein sequences reveal that at least 56 *pe_pgrs* members contain multiple non-peptide repeats (GXXGXD/NXXUX, where X = any amino acid and U = a large non-polar hydrophobic residue) that are predicted to be calcium binding motifs [52]. The authors suggest that these motifs might be involved in the initial attachment of *M. tuberculosis* to host alveolar macrophages. PGRS domains have also been implicated in cellular structure and colony morphology [14] and in the binding of fibronectin [53]. A possible role in iron uptake has also been proposed for *ppe37* following the finding that it is upregulated under low iron conditions [34]. It is also notable that *pe/ppe* genes are often found paired within operons with the *pe* gene located upstream of the *ppe* gene. *Pe/ppe* genes within these operons are cotranscribed and physically interact with each other and transcription of both is required for correct cellular localization [55,56]. This is emphasised by the findings of Strong and colleagues who failed in numerous attempts to determine the crystal structures of individual *pe* and *ppe* proteins. Co-expression and copurification of the proteins coded by the linked genes Rs2431c (*ppe25*) and Rs2430c (*ppe41*) was successful, however, and the crystal structure revealed a 1:1 pe25/ppe41 protein dimer where helices from each protein are predicted to interact and form a stable complex. The structure implies a docking site for an additional protein and suggests a role in signal transduction [56].

Here, we have used recently acquired whole genome sequence data from 18 isolates representing a broad spectrum of the MTBC phylogeny to investigate variation in 33 *pe* (excluding *pe_pgs*) and 66 *ppe* genes. We have supplemented this data by selecting 14 *pe* and *ppe* genes (including 5 *pe_pgs*) and performing whole gene sequencing on a cohort of 40 clinical isolates representing a broad and well characterised spectrum of the *M. tuberculosis* phylogeny. We hypothesise that if *pe/ppe* proteins are involved in immune evasion and antigenic variation their genes will have undergone rapid evolutionary change, as demonstrated by high levels of DNA sequence polymorphism and evidence for diversifying selection compared to other *M. tuberculosis* genes. Previous work on this theme [12,18,19,20,21,22,32] has produced conflicting results that may be due to the lack of sensitivity of the analysis technique, the decision to examine genes that belong to a particular *pe* or *ppe* sub-family that might show abnormal variation levels, or the decision to examine clinical isolates that are too closely related to reveal polymorphic differences. The resultant comparative gene analysis presented here provides new insights into the variation and evolution of these genes along with their potential role in providing the pathogen with a source of antigenic variation.

**Results**

**Comparative gene analysis using whole genome sequences**

A total of 66 *ppe* and 33 *pe* genes were analysed. Unfortunately, due to the extensive repetitiveness of their C-terminal regions and the inherent difficulties encountered in sequencing through repetitive regions using the third generation short read sequencing techniques, the *pe_pgrs* genes of most publicly available whole genome sequences were incomplete or of low sequence quality and could not be included in this analysis. Variability estimates for *ppe38*/*71* and *ppe30* could not be determined due to the difficulty in obtaining a reference sequence. *Ppe38*/*71* are completely homologous in most cases and are located in a hypervariable region that is prone to homologous recombination, gene conversion, IS6110 integration and large deletion events [26]. *Ppe30* is also highly variable and displays numerous different sequence types.
due to large deletions and other sequence variations [32]. Due to
the exclusion of genes with notations suggesting potential sequence
effects, an average of 15.2 and 16.5 genomes (from a possible
maximum of 18) were analysed for each ppe and pe gene
respectively. Full details of all variations detected can be seen in
tables S1, S2, S3.

Confirmation of whole genome sequence accuracy

In order to ascertain the accuracy of the whole genome se-
quencing used in our analysis we obtained the original DNA used in
the sequencing process to determine the F11, CPHL_A, K85, T17
and T92 sequences. A total of 40 variations observed in the pe/ppe
genes of these 5 isolates were reanalysed by amplifying the sur-
rounding region by PCR and using standard Sanger sequencing
methodology to sequence the amplicons. A variety of variations
were chosen for analysis and these comprised sSNP’s, nsSNP’s,
frameshifts, and an in-frame deletion. We also ensured that some
of the variations detected in the large ppe_mpfr genes, ppe35/6 and
ppe7/18, were analysed since it could be suggested that mistakes are
more likely to be made here due to the highly repetitive nature of
their C-terminal domains. Table S4 lists the variations, primer
details and results of our analysis. Four of the 40 variations (10%) were
found to be erroneous in the publicly available whole genome
sequences. One of these (T17, ppe20) appears to be due to an
assembly error while another (CPHL_A, ppe13) involves a long
poly C region at the 3’ end of the gene. The other 2 errors include
a SNP or single bp deletion. The 10 variations that were checked in
the ppe35/6 and 7/18 genes were all confirmed indicating that the
large ppe_mpfr genes were not more likely to produce sequencing
errors than the smaller less complex genes.

Number of structural protein variants

Various aspects of genetic variation between the homologous
genes may be analysed. First we wished to determine the number of
predicted different structural variants of each pe/ppe protein,
based on the observed genetic variations, as a proportion of the
total number of isolates analysed. Thus, sSNP’s were ignored,
variations that were specific to multiple isolates from a single
lineage were counted as a single variant and single isolates that
contained more than 1 variation were still counted as a single
variant. Results for the ppe gene analysis are shown in Fig. 2a.
They reveal a high level of variation across all subfamilies, with
only one gene (ppe51) showing no variation in all genomes
analysed. Subfamily V (the MPTR subfamily) shows many genes
with extreme levels of variation. By distinguishing between
different types of mutation it is notable that certain genes display
alternate mechanisms of variation. For example, homologous re-
combination events, particularly between closely related ppe genes
in close physical proximity, are shown to be responsible for a high
degree of variation within certain genes (ppe57/58/59 and ppe18/19/60).
Other macromutational events (whole or partial gene
deletions and IS6110 integrations) were found to be responsible for
a significant proportion of the variation in several genes. Also
notable is the finding that macromutational events do not con-
tribute to variation in the most hypervariable genes of the MPTR
subfamily. Six genes in particular (ppe3/6, 7/18, 24, 34, 54 and 55)
show extreme variation and 5 of these have a variation index of 1
(indicating that each isolate had a unique sequence). These 6 genes
are all large (between approximately 3.1 and 10.0 kb) and reveal
mutations including nsSNP’s, frameshifts and in-frame indels.
The sequences of these 6 hypervariable genes were further compared
between 3 closely related genomes, KZN 1435, KZN 605 and
KZN 4207 [57] in order to ascertain whether they were evolving at
a rate that would enable us to distinguish even between

extremely closely related isolates. For each gene the sequence in
all 3 genomes was identical. The sequences of four of the hyper-
variable ppe genes (ppe24, 34, 54 and 55) were also compared
between the index case and 2 transmission chain endpoint isolates
of the Harlingen cluster [50,59]. An average of 84% of the coding
region for each of these genes was available for analysis. No
variations were observed. These results indicate that while these
ppe genes are hypervariable across the full phylogeny of M.
tuberculosis, they do not evolve at a rate fast enough to distinguish
between extremely closely related isolates.

A similar analysis of the ppe (excluding pe_pgrs) genes revealed
again lower level of variation with many of the genes showing
no variation across the analysed genomes (Fig. 2b). Macro-
mutational events, including homologous recombination, were rare.

Pe/ppe variation levels in comparison with other M.
tuberculosis genes

In order to ascertain whether the variation levels of the pe
and ppe genes differed from other M. tuberculosis genes we compared our
results to those obtained by Herschberg and colleagues who
identified the SNP’s present in 89 non-pe/ppe genes comprising
65,829 bp, from 107 MTBC isolates [60]. This study identified a
total of 231 nsSNP’s, which when divided by the total number of
nucleotides multiplied by the number of isolates gives a nsSNP
frequency of 231/(65,829×107) = 0.327×10^{-4} nsSNP’s per nu-
cleotide. Similar calculations using our ppe data required the
exclusion of several genes. Ppe38/71 and ppe50, which exhibit
extreme levels of macro-mutational variation, were excluded.
Ppe18, 19, 24, 34, 54, 55, 57, 58, 59 and 60 were also excluded
because of extreme variability or frequent homologous recombina-
tion events which resulted in difficulty in determining the
consensus sequence of the gene. The remaining 54 ppe genes
comprise 100,657 bp and contain 163 nsSNP’s and the average
number of isolates analysed per gene was 15.17. This results in a
nsSNP frequency of 163/(100,657×15.17) = 1.067×10^{-4} nsSNP’s
per nucleotide. This value is approximately 3.3-fold greater than
that found in the non-pe/ppe MTBC genes [60] despite the
exclusion of the most variable ppe genes. Similarly, the 33 pe
(excluding pgrs) genes comprised 21,726 bp and contained
35 nsSNP’s with an average isolate number per gene of 16.5,
resulting in a nsSNP frequency of 35/(21,726×16.5) = 0.976×
10^{-4} nsSNP’s per nucleotide. This value is approximately 3.0-fold
higher than that found in non-pe/ppe MTBC genes [60]. These
results confirm that nsSNP’s occur at a far higher frequency in pe/
ppe genes than in non-pe/ppe genes.

Whole gene sequencing results of 14 pe and ppe genes

Complete results for all variations found from whole gene
sequencing of 14 pe and ppe genes from 40 phylogenetically diverse
clinical isolates covering the whole M. tuberculosis phylogenetic tree
(PGG1, 2 and 3 strains including members of all the main lineages
EAI, CAS, Beijing, LAM, Haarlem, LCC and T) are shown in
Table S5. Our sequencing of 3 pe genes (pe35, 11 and 3) and 6 ppe
genes (ppe68, 2, 44, 10, 42 and 62) confirmed the results found for
these genes in our in silico gene analysis. In each case lineage
specific variations were consistent between the 2 different analyses.
Interestingly, our 3 EAI samples failed to show the ppe62 G1690A
SNP which was present in 2 (T17 and T46) of the 4 EAI samples
analysed in silico. This suggests that our EAI isolates are relatively
closely related and do not reflect the large genetic diversity
observed within this group [60].

Particular interest lies in our analysis of the 5 pe_pgrs genes since the
pgrs subfamily could not be analysed using in silico methods.
Three of these genes (pe_pgrs 16, 26 and 33) have previously been
analysed for their variation [18,19,20]. Our replication of this work (using better defined *M. tuberculosis* lineages) confirms that all analysed sequences were unique. Average number of genomes analysed per gene = 15.2. Genes have been grouped together according to their subfamily [8] by colour and subfamilies are also separated by dotted lines. Each vertical bar is subdivided into micromutations (nsSNP’s, frameshifts, small in-frame indels) in dark shading and macromutations (homologous recombination, IS6110 integration, partial and whole gene deletions) in light shading. *Ppe38* and *ppe50* were not included due to hypervariability at the macromutational level [26,30] and the difficulty in establishing a consensus sequence. For details of all variations detected see Tables S1 and S2. B. Calculations of sequence variation in 33 *pe* (excluding *pgrs*) genes. Synonymous variations have been ignored. Average number of isolates analysed per gene = 16.5. The genes from subfamily V (*pgrs* subfamily, yellow) are those which are classified as members of this subfamily by their N-terminal amino acid sequences [8] but that do not include the long PGRS C-terminal region. For details of all variations detected see Tables S1 and S3.

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Figure 2. Sequence variation levels in *ppe* and *pe* genes. A. Calculations of sequence variation in 64 *ppe* genes. Synonymous variations have been ignored. The Y axis shows the proportion of sequences that show variation predicted to result in amino acid changes. A value of 1 indicates that all analysed sequences were unique. Average number of genomes analysed per gene = 15.2. Genes have been grouped together according to their subfamily [8] by colour and subfamilies are also separated by dotted lines. Each vertical bar is subdivided into micromutations (nsSNP’s, frameshifts, small in-frame indels) in dark shading and macromutations (homologous recombination, IS6110 integration, partial and whole gene deletions) in light shading. *Ppe38* and *ppe50* were not included due to hypervariability at the macromutational level [26,30] and the difficulty in establishing a consensus sequence. For details of all variations detected see Tables S1 and S2. B. Calculations of sequence variation in 33 *pe* (excluding *pgrs*) genes. Synonymous variations have been ignored. Average number of isolates analysed per gene = 16.5. The genes from subfamily V (*pgrs* subfamily, yellow) are those which are classified as members of this subfamily by their N-terminal amino acid sequences [8] but that do not include the long PGRS C-terminal region. For details of all variations detected see Tables S1 and S3.

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istics of pe_pgrs62 have not previously been reported. Results for this gene were surprising because despite being the same size as most of the other analysed pe_pgrs genes it showed very little variation and no in-frame indels were observed (Table S5). Additional in silico analysis of this gene in M. bovis confirmed its invariant nature. A closer inspection of the gene’s predicted amino acid sequence revealed that it does not possess the C-terminal multiple tandem repeats of Gly-Gly-Ala and Gly-Gly-Xaa typical of pgrs proteins. Taken together, our results suggest that pe_pgrs genes generally display high variation levels with in-frame indels making a large proportion of mutations. However, mutational mechanisms and levels of variation can differ greatly between individual genes implying functional variation within this subfamily.

The 252 bp deletion identified in the pe_pgrs16 gene of isolate SAWC 2185 (Haarlem, F2) (Table S5) was further analysed in order to determine how variable this mutation was within both the F2 family and other members of the same cluster as SAWC 2185. Isolates from 36 different F2 clusters as well as 4 isolates from the same cluster were examined. All other members of the cluster to which isolate SAWC 2185 belongs, along with 27 of the additional F2 clusters, were found to contain this mutation. However, isolates representing the remaining F2 clusters lacked the mutation confirming the presence of within-family variation for this mutation.

Analysis of selective constraints in pe/ppe genes

One of the major findings of the MTBC genetic diversity study of Hershberg and colleagues [60] was the low level of purifying selection compared to other bacteria, as assessed by the ratio of nonsynonymous to synonymous SNP’s (dN/dS) in 89 non-pe/ppe genes. A dN/dS ratio of <1 is considered to indicate purifying selection, dN/dS = 1 suggests an absence of selection (i.e. neutral evolution) and dN/dS > 1 indicates positive or diversifying selection. In our analysis of 54 ppe genes (excluding the genes described above) we discovered a total of 220 SNP’s, of which 163 (74%) were nonsynonymous (Table S2). The average pairwise dN/dS ratio for the concatenated ppe genes was 1.045. This is substantially higher than the already extremely high value of 0.57 reported for the non-pe/ppe M. tuberculosis genes [60] and suggests an absence of selection pressure. Similarly, in our analysis of 33 pb genes we detected a total of 47 SNPs, of which 35 (74%) were nonsynonymous (Table S3). The average pairwise dN/dS ratio for the concatenated pb genes was 1.000, again far higher than the value previously obtained for non-pe/ppe genes [60] and again suggesting an absence of selection pressure. We also calculated the dN/dS value for the 3 pe_pgrs genes that show a “typical” pgrs variation profile (pe_pgrs16, 26 and 33 – see above) using the SNP’s identified in our current study in addition to those detected previously [18,19,20]. A total of 63 SNP’s were found in these 3 genes of which 43 (68%) were nonsynonymous. The average pairwise dN/dS ratio for the 3 concatenated pe_pgrs genes was 0.369, a value once again close to that indicating neutral evolution.

Discussion

Although polymorphisms in certain M. tuberculosis pe and ppe genes have been previously documented, this study is the first to make use of publicly available MTBC whole genome sequences, as well as a comprehensive set of 40 clinical isolates covering the known M. tuberculosis phylogenetic tree and all major M. tuberculosis strain lineages including EAI, CAS, Beijing, Haarlem, LAM, LCC and T, to produce an extensive analysis of pe/ppe gene variation. Unfortunately, the large pe/pgrs subfamily was not able to be analysed using these methods due to a lack of sequencing accuracy but our own sequencing analysis of selected pe_pgrs genes, in conjunction with those of previous investigators, also provides important insights into genetic variation within this subfamily.

The first important observation made was the confirmation that pe and ppe genes display a high frequency of variation (Fig. 2) and that this variation exceeds that seen in other MTBC genes. Hershberg and colleagues previously analysed MTBC genetic diversity by sequencing 89 non-pe/ppe genes (classified as either “housekeeping”, “virulence” or “surface”) in 107 MTBC isolates [60]. Compared to these genes, the nsSNP frequency in the ppe and pe (excluding pe_pgrs) genes in our analysis was approximately 3.3 and 3.0 times greater, respectively. Several qualifying points should be emphasised when considering these values. Our quality assurance analysis of 40 selected SNP’s from the whole genome sequences revealed that 4 were incorrect (Table S4), indicating an overestimation of variation frequency of approximately 10%. However, it should also be noted that our ppe variation values were obtained without the inclusion of the 12 most variable ppe genes which were excluded from the analysis due to the difficulty in determining a consensus sequence. The inclusion of these genes would undoubtedly result in a significant increase in observed ppe variation. In addition, many of the ppe genes that were included in our analysis displayed high levels of variation that were not due to nsSNP’s. Indeed, the mutational spectrum seen in ppe genes was extensive. The most common mutations observed were nsSNP’s and frameshifts caused by small indels. However, many large ppe genes of the mptr subfamily often display in-frame indels, certain groups of genes undergo frequent homologous recombination events and, as previously reported, ppe39 and ppe40 are particularly susceptible to IS6110 insertions [27]. Figure 2a reveals that members of the ppe_mptr subfamily have a generally higher frequency of mutation but this does not apply consistently to all members of this group.

Interestingly, although the pe (excluding pgrs) genes revealed far lower variation than the ppe’s (Fig. 2), the frequency of nsSNP’s was similar to that of the ppe’s and was found to be approximately triple that of the non-pe/ppe genes analysed previously [60]. Protein changes in these genes were generally due to nsSNP’s and small indels leading to frame shifts. In-frame indels and macromutations (whole or partial gene deletions and IS6110 integrations) were rare. The lower variation in these genes probably reflects a strong functional constraint of the pe protein. It has previously been shown that pe proteins and the pe domain of pe_pgrs proteins are responsible for cell wall localisation [15]. This is presumably essential for optimal protein function and mutations that hinder this process would therefore be subject to strong negative selection pressures.

Our own sequencing analysis of 5 pe_pgrs genes showed that, in general, variation within the pe_pgrs subfamily exists at far higher levels than in non-pgrs pe members and that this increase in variation is largely caused by a higher frequency of in-frame indels within the C-terminal pgrs region. These results support the findings of Talarico and colleagues who have previously reported analysis of genetic polymorphism in pe_pgrs33, 16 and 26 [18,19,20]. We show that the deletions in these 3 genes are often large (for example, in EAI isolates 666 bp has been deleted from pe_pgrs16, Table S3). The fact that large deletions were often found in multiple isolates from the same lineage suggests that these mutations are not subjected to strong purifying selection forces. The phenotypic consequences of these deletions may include a reduction in macrophage apoptosis caused by a decrease in TNFα production [41] and, at an epidemiological and clinical level, be associated with clustering and a lack of lung cavitations [19]. Our analysis of pe_pgrs18 and 62 has provided additional interesting information relating to pe_pgrs variation since neither of these
genes displayed the “typical” variation pattern seen in \( \text{pe}_pgrs35 \), 16 and 26 (Table S5). Variation in \( \text{pe}_pgrs18 \) was found to be largely caused by gene conversion with \( \text{pe}_pgrs17 \). These genes are in close physical proximity, have high sequence homology, and are presumably the result of a recent duplication event. A previous study has documented homologous recombination between these genes and has identified a polymorphism present in one or both of these genes and used it to infer details of the evolution and clonal expansion of the MTBC [30]. Genetic variation in \( \text{pe}_pgrs62 \) has not been reported previously and we chose this gene for analysis because studies have shown that it is a T cell antigen with vaccine potential [61,62,63] and that its PGRS domain is able to elicit a strong antibody response [64]. The PGRS domain of \( \text{pe}_pgrs62 \) is atypical as it lacks the Gly-Gly-Ala or Gly-Gly-Asn repeats found in most members of this subfamily. Interestingly, the amount of variation seen in this gene was far less than in the more typical \( \text{pe}_pgrs \) genes with only 4 SNPs (of which only 2 were non-synonymous) seen in our 40 clinical isolates. This lack of genetic variation is especially interesting since \( \text{pe}_pgrs62 \) can stimulate both cell-medicated and humoral host immunity and might therefore be expected to undergo significant levels of antigenic variation. Taken together, these results reveal that while variation in \( \text{pe}_pgrs \) genes is generally very high, this variation, along with the dominant type of mutational mechanism, can differ greatly between genes. The finding of low variation in a highly immunogenic \( \text{pe}_pgrs \) member lacking the typical PGRS domain also implies functional variation in certain members of this sub-family.

Another major finding of this study was that selection appears to be absent in \( \text{pe}/\text{ppe} \) genes. Most genomic regions in all organisms are subjected to strong purifying selection pressures. Within the Actinobacteria, for example, pairwise genome-wide comparisons result in a general dN/dS value of 0.15–0.20 [60]. This value appears to be fairly typical of both prokaryotic and eukaryotic organisms [65]. The recent comparative sequence analysis of 89 genes in 107 MTBC isolates [60] found an average pairwise dN/dS ratio of 0.57, a value far higher than that found in other bacteria and an indication that purifying selection is severely reduced in the MTBC on a general genomic level. In \( \text{pe}/\text{ppe} \) genes specifically, a high ratio of nonsynonymous to synonymous SNP’s has previously been noted [6,20] and it has also been shown that these genes are under greater selection for amino acid substitutions than other \( M. \, \text{tuberculosis} \) genes [66]. Our pairwise dN/dS ratio calculations for 54 \( \text{ppe} \) and 33 \( \text{pe} \) genes were 1.045 and 1.000 respectively, suggesting that selection pressure on these genes is extremely limited or altogether absent. Although our analysis of \( \text{pe}_pgrs \) genes was numerically limited, the pairwise dN/dS ratio was also close to 1 (0.869), again indicating a selection pressure close to neutral. This result is surprising because \( \text{pe}/\text{ppe} \) proteins are thought to provide antigenic variation and therefore be subjected to positive, rather than neutral, selection pressure. Thus, our results indicate that variation in these proteins is inconsistent with “classical” antigenic variation. It should be noted, however, that these results are an average of the gene families as a whole and that individual genes might be subjected to greater or lesser selective pressures. Evidence that \( \text{pe}/\text{ppe} \) genes are the major targets of positive selection in \( M. \, \text{tuberculosis} \) comes from a recent paper that examined the genomes of \( H37Rv \) and \( H37Ra \) [67]. Of the 12 genes that were found to be positively selected in these strains 6 were from the \( \text{pe} \) or \( \text{pe}_pgrs \) families. Our results also need to be interpreted in light of the report of Comas and colleagues [68] who found that the antigenic epitopes (excluding pe and ppe proteins) of \( M. \, \text{tuberculosis} \) are highly conserved and that there appears to be a strong selection pressure against sequence diversity in these regions. This finding was unexpected and is also inconsistent with the classical model of an evolutionary immunological arms race between pathogen and host and the authors favour the explanation that the host immune response is, paradoxically, beneficial to the pathogen. Despite the fact that our \( \text{pe} \) and \( \text{ppe} \) dN/dS values were far higher than those found for \( M. \, \text{tuberculosis} \) antigens in the Comas study, this explanation may also apply (to a lesser extent) to \( \text{pe} \) and \( \text{ppe} \) proteins and explain why their dN/dS values were less than those of typical antigens in other organisms.

Although our results suggest that \( \text{pe}/\text{ppe} \) proteins do not act as typical antigenic variants it is also important to consider the impact of population genetics on dN/dS values. The dN/dS ratio is a popular measure of selection pressure not only because it is simple and robust but also because of the simple interpretation of dN/dS<1 as negative selection, dN/dS=1 as neutral selection and dN/dS>1 as positive selection. This analysis was originally designed for comparisons between sequences from divergent lineages or species and it has recently been shown that the standard signature of positive selection (dN/dS>1) does not hold for comparisons within a population [69]. It can sometimes be difficult to determine the appropriate evolutionary time-scale (distinct lineages/species versus numerous isolates from a single population) associated with a dataset of microbial sequences and it is possible that some of the more closely related sequences in our dataset have not diverged sufficiently for this analysis to be appropriate. If this is the case it is unlikely that our dN/dS values would alter drastically. We would, however, predict that our values are underestimates and therefore conclude that a mild positive selection pressure is acting upon these genes. Many of the \( \text{pe}/\text{ppe} \) genes present within the MTBC have homologues in the closely related, but phylogenetically distinct, species \( M. \, \text{marinum} \) [70] and we suggest that a comparison between these genes could provide a more accurate estimate of the evolutionary pressures they have been subjected to.

We hope that our results will allow for a more directed approach towards the use of \( \text{pe}/\text{ppe} \) proteins as vaccine components since it is possible that the high levels of polymorphism observed in certain members of these protein families could limit their effectiveness in some cases. This has been highlighted in a recent mathematical modelling analysis that has predicted the negative impact on vaccine efficacy that may occur when mycobacterial strain diversity is not considered [71]. For example, the MtB72F vaccine comprises the 2 recombinant proteins pepA (Rv0125) and ppe18 (Rv1196). MtB72F has been shown to have a protective effect against challenges with two \( M. \, \text{tuberculosis} \) laboratory reference strains (\( H37Rv \) and Erdmann) in numerous animal models, including a primate model [72,73,74,75]. However, a recent study has shown that over 20% of \( M. \, \text{tuberculosis} \) strains taken from 2 geographical regions contain mutations that alter at least 1 amino acid in the ppe18 protein, many of which are in regions predicted to be T cell epitopes [21]. Our study confirms a high rate of ppe18 variation and shows that it is predominantly due to homologous recombination between ppe18, ppe19 and ppe60, which have extremely high sequence similarity. These results suggest that the MtB72F vaccine could have limitations in a clinical setting and that, in hindsight, a pe/ppe protein that displays higher sequence conservation across many strains may have been a more effective vaccine candidate. An example of this is \( \text{pe}_pgrs62 \) which has also been investigated for its vaccine potential with promising results [61,62]. This highly immunogenic, atypical pgrs protein showed extremely limited sequence variation across our cohort of isolates (Table S3) and might be expected to provide more consistent protection against a variety of \( M. \, \text{tuberculosis} \) strains. The data available for immunogenicity at the pe/ppe epitope level is limited.
however and it should be noted that variable regions of pe/ppe genes may be less immunogenic and less important for an immune response. It should also be noted that pe/ppe proteins probably have functional variation and that some may have a limited role in immune function.

The exact nature of pe/ppe function in the host cell is yet to be determined. However, our results also provide some additional insights and allow us to speculate on potential mechanisms of action for these proteins. When the high levels of pe/ppe sequence variation are considered in conjunction with the high inter-strain expression profiles [33,34,35] it is apparent that there is likely to be a huge diversity of pe/ppe expression and functional variation across the MTBC. This would lead to a situation where only extremely closely related isolates have identical functional and expression profiles across the entire pe/ppe spectrum. We note that this situation has parallels to the classical MHC class I and II systems where highly polymorphic MHC loci produce multiple alleles which, despite their structural and functional similarities, are distinct with regards to the antigenic peptides they present to CD4+ and 8+ T cells. It may be speculated that the large number of polymorphic pe/ppe proteins have evolved in response to the multiple MHC alleles expressed by host populations and that specific pe/ppe proteins are adapted to preferentially coexist alongside specific MHC alleles. The absence of selection exerted on pe/ppe genes may be interpreted as both a result of immune pressure selecting for antigenic variants and an adaptation for these proteins to function alongside new or rare MHC alleles that have not previously been encountered in the bacteria’s evolutionary history. Although purely speculative, this theory is consistent with the large pe/ppe expansion within the MTBC (and in the closely related species M. marinum which is a natural pathogen of fish), it’s functional and expression variability, and the finding that some pe/ppe proteins appear to interfere with antigen processing [43,44]. The true nature of pe/ppe function remains one of the great mysteries of M. tuberculosis pathogenesis however and many additional functional studies will probably be required.

Table 1. Details of 18 whole genome sequence isolates used for in silico comparative gene analysis.

<table>
<thead>
<tr>
<th>Isolate</th>
<th>Lineage</th>
<th>Reference</th>
</tr>
</thead>
<tbody>
<tr>
<td>T92</td>
<td>Lineage 1. PGG1, EAI family</td>
<td>[57]</td>
</tr>
<tr>
<td>T17</td>
<td>Lineage 1. PGG1, EAI family</td>
<td>[57]</td>
</tr>
<tr>
<td>T46</td>
<td>Lineage 1. PGG1, EAI family</td>
<td>[57]</td>
</tr>
<tr>
<td>EA5054</td>
<td>Lineage 1. PGG1, EAI family</td>
<td>[57]</td>
</tr>
<tr>
<td>94_M4241A</td>
<td>Lineage 2. PGG1, Beijing family</td>
<td>[57]</td>
</tr>
<tr>
<td>02_1987</td>
<td>Lineage 2. PGG1, Beijing family</td>
<td>[57]</td>
</tr>
<tr>
<td>T85</td>
<td>Lineage 2. PGG1, Beijing family</td>
<td>[57]</td>
</tr>
<tr>
<td>C strain</td>
<td>Lineage 4. PGG2, low copy clade</td>
<td>[57]</td>
</tr>
<tr>
<td>CDC1551</td>
<td>Lineage 4. PGG2, low copy clade</td>
<td>[6]</td>
</tr>
<tr>
<td>Haarlem</td>
<td>Lineage 4. PGG2, Haarlem family</td>
<td>[57]</td>
</tr>
<tr>
<td>F11</td>
<td>Lineage 4. PGG2, LAM family</td>
<td>[57]</td>
</tr>
<tr>
<td>GM1503</td>
<td>Lineage 4. PGG2, LAM family</td>
<td>[57]</td>
</tr>
<tr>
<td>KZN1435</td>
<td>Lineage 4. PGG2, LAM family</td>
<td>[57]</td>
</tr>
<tr>
<td>98-R604_INH-RIF-EM</td>
<td>Lineage 4. PGG2, LAM family</td>
<td>[57]</td>
</tr>
<tr>
<td>H37Rv</td>
<td>Lineage 4. PGG3</td>
<td>[5,77]</td>
</tr>
<tr>
<td>CPHL_A</td>
<td>Lineage 5. PGG1, West Africa-1 (M. africanum)</td>
<td>[57]</td>
</tr>
<tr>
<td>K85</td>
<td>Lineage 6. PGG1, West Africa-2 (M. africanum)</td>
<td>[57]</td>
</tr>
<tr>
<td>M. bovis AF2122/97</td>
<td>Animal lineage</td>
<td>[76]</td>
</tr>
</tbody>
</table>

Each analysed genome sequence is listed along with its lineage number [78], Principal Genetic Group (PGG) [2] and family group.

doi:10.1371/journal.pone.0030593.t001

Table 2. Details of clinical isolates used in this study.

<table>
<thead>
<tr>
<th>Isolate</th>
<th>Lineage</th>
<th>South African IS6110 Lineage [84]</th>
</tr>
</thead>
<tbody>
<tr>
<td>SAWC 1659</td>
<td>1, PGG1, EAI</td>
<td>-</td>
</tr>
<tr>
<td>SAWC 2493</td>
<td>1, PGG1, EAI</td>
<td>-</td>
</tr>
<tr>
<td>SAWC 4981</td>
<td>1, PGG1, EAI</td>
<td>-</td>
</tr>
<tr>
<td>SAWC 2803</td>
<td>3, PGG1, CAS</td>
<td>F34</td>
</tr>
<tr>
<td>SAWC 2240</td>
<td>3, PGG1, CAS</td>
<td>F20</td>
</tr>
<tr>
<td>SAWC 2666</td>
<td>3, PGG1, CAS</td>
<td>F33</td>
</tr>
<tr>
<td>SAWC 974</td>
<td>3, PGG1, CAS</td>
<td>F25</td>
</tr>
<tr>
<td>SAWC 2088</td>
<td>2, PGG1, Atypical Beijing</td>
<td>F31</td>
</tr>
<tr>
<td>SAWC 2701</td>
<td>2, PGG1, Atypical Beijing</td>
<td>F27</td>
</tr>
<tr>
<td>SAWC 2076</td>
<td>2, PGG1, Typical Beijing</td>
<td>F29</td>
</tr>
<tr>
<td>SAWC 1430</td>
<td>4, PGG2</td>
<td>F3</td>
</tr>
<tr>
<td>SAWC 3656</td>
<td>4, PGG2, LAM</td>
<td>F26</td>
</tr>
<tr>
<td>SAWC 2576</td>
<td>4, PGG2, LAM</td>
<td>F15</td>
</tr>
<tr>
<td>SAWC 2525</td>
<td>4, PGG2, LAM</td>
<td>F9</td>
</tr>
<tr>
<td>SAWC 1815</td>
<td>4, PGG2, LAM</td>
<td>F11</td>
</tr>
<tr>
<td>SAWC 1733</td>
<td>4, PGG2, LAM</td>
<td>F13</td>
</tr>
<tr>
<td>SAWC 3100</td>
<td>4, PGG2, LAM</td>
<td>F14</td>
</tr>
<tr>
<td>SAWC 1595</td>
<td>4, PGG2, Quebec/S</td>
<td>F28</td>
</tr>
<tr>
<td>SAWC 198</td>
<td>4, PGG2, “1 bander”</td>
<td>F110</td>
</tr>
<tr>
<td>SAWC 2073</td>
<td>4, PGG2, LCC – “2 bander”</td>
<td>F120</td>
</tr>
<tr>
<td>SAWC 233</td>
<td>4, PGG2, LCC – “3 bander”</td>
<td>F130</td>
</tr>
<tr>
<td>SAWC 861</td>
<td>4, PGG2, LCC – “4 bander”</td>
<td>F140</td>
</tr>
<tr>
<td>SAWC 1162</td>
<td>4, PGG2, LCC – “5 bander”</td>
<td>F150</td>
</tr>
<tr>
<td>SAWC 716</td>
<td>4, PGG2, Pre-Haarlem</td>
<td>F19</td>
</tr>
<tr>
<td>SAWC 1748</td>
<td>4, PGG2, Pre-Haarlem</td>
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</tr>
<tr>
<td>SAWC 1127</td>
<td>4, PGG2, Haarlem-like</td>
<td>F6</td>
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<tr>
<td>SAWC 103</td>
<td>4, PGG2, Haarlem-like</td>
<td>F7</td>
</tr>
<tr>
<td>SAWC 386</td>
<td>4, PGG2, Haarlem</td>
<td>F1</td>
</tr>
<tr>
<td>SAWC 1645</td>
<td>4, PGG2, Haarlem</td>
<td>F10</td>
</tr>
<tr>
<td>SAWC 1841</td>
<td>4, PGG2, Haarlem</td>
<td>F4</td>
</tr>
<tr>
<td>SAWC 2185</td>
<td>4, PGG2, Haarlem</td>
<td>F2</td>
</tr>
<tr>
<td>SAWC 239</td>
<td>4, PGG3, T</td>
<td>F22</td>
</tr>
<tr>
<td>SAWC 2901</td>
<td>4, PGG3, T</td>
<td>F16</td>
</tr>
<tr>
<td>SAWC 1608</td>
<td>4, PGG3, T</td>
<td>F5</td>
</tr>
<tr>
<td>SAWC 1109</td>
<td>4, PGG3, T</td>
<td>F23</td>
</tr>
<tr>
<td>SAWC 4302</td>
<td>4, PGG3, T</td>
<td>F18</td>
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<tr>
<td>SAWC 1956</td>
<td>4, PGG3, T</td>
<td>F17</td>
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<tr>
<td>SAWC 1290</td>
<td>4, PGG3, T</td>
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<td>SAWC 300</td>
<td>4, PGG3, T</td>
<td>F12</td>
</tr>
<tr>
<td>SAWC 1870</td>
<td>4, PGG3, T</td>
<td>F8</td>
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</table>

Each clinical isolate along with its lineage number [78], PGG group [2], spoligotype family group status [88] and South African IS6110 lineage [84] is listed.

doi:10.1371/journal.pone.0030593.t002
Table 3. Details of the pe and ppe genes examined by whole gene sequencing.

<table>
<thead>
<tr>
<th>Gene</th>
<th>Rv number</th>
<th>Size in H37Rv (bp)</th>
<th>Sublineage*</th>
<th>Variability in literature</th>
<th>Comments</th>
</tr>
</thead>
<tbody>
<tr>
<td>pe35</td>
<td>Rv3872</td>
<td>300</td>
<td>I</td>
<td>No data.</td>
<td>Ancestral pe protein. Present in RD1 region. Highly immunogenic, eg [89].</td>
</tr>
<tr>
<td>pe11, lipX</td>
<td>Rv1169c</td>
<td>303</td>
<td>IV</td>
<td>Invariable [32].</td>
<td>B cell responses in subgroups of patients [90]. Putative lipase [77].</td>
</tr>
<tr>
<td>pe_pgrs16</td>
<td>Rv0977</td>
<td>2772</td>
<td>V</td>
<td>(PGRS subfamily)</td>
<td>Upregulated in mouse model [39,91].</td>
</tr>
<tr>
<td>pe_pgrs18</td>
<td>Rv9980c</td>
<td>1374</td>
<td>V</td>
<td>(PGRS subfamily)</td>
<td>Known to undergo homologous recombination with pe_pgrs17 [30]. Highly upregulated during the early stages of M. tuberculosis invasion of the blood-brain barrier [91]. High sequence identity to pe_pgrs17 implying recent duplication event [30].</td>
</tr>
<tr>
<td>pe_pgrs26</td>
<td>Rv1441c</td>
<td>1476</td>
<td>V</td>
<td>(PGRS subfamily)</td>
<td>Downregulated in mouse model [39].</td>
</tr>
<tr>
<td>pe_pgrs33</td>
<td>Rv1818c</td>
<td>1497</td>
<td>V</td>
<td>(PGRS subfamily)</td>
<td>Localised in cell wall [14] and surface exposed [15]. SigA-mediated transcription downregulated during stationary phase and under stress conditions [92]. Implicated in pathogenicity and host immune responses [43,47,46,61,90,93,94]. Possible inhibitor of antigen processing [44].</td>
</tr>
<tr>
<td>pe_pgrs62</td>
<td>Rv3812</td>
<td>1515</td>
<td>V</td>
<td>(PGRS subfamily)</td>
<td>Elicits strong antibody response [64]. T cell antigen [61,62].</td>
</tr>
<tr>
<td>ppe68</td>
<td>Rv3873</td>
<td>1107</td>
<td>I</td>
<td>No data.</td>
<td>Ancestral ppe protein.</td>
</tr>
<tr>
<td>ppe2</td>
<td>Rv0255c</td>
<td>1671</td>
<td>II</td>
<td>(PPW subfamily)</td>
<td>PPW subfamily.</td>
</tr>
<tr>
<td>ppe44</td>
<td>Rv2770c</td>
<td>1149</td>
<td>IV</td>
<td>(SVP subfamily)</td>
<td>Limited diversity. Alteration in Beijing isolates [35]. Variable expression in clinical isolates [35]. Expressed during subcutaneous and intravenous infection by M. bovis BCG in BALB/c mice [95].</td>
</tr>
<tr>
<td>ppe10</td>
<td>Rv0442c</td>
<td>1464</td>
<td>V</td>
<td>(MPTR subfamily)</td>
<td>Ancestral ppe MPTR protein.</td>
</tr>
<tr>
<td>ppe42</td>
<td>Rv2608</td>
<td>1743</td>
<td>V</td>
<td>(MPTR subfamily)</td>
<td>Variable in clinical isolates [96]. Elicits a high humoral and low T cell response [96].</td>
</tr>
<tr>
<td>ppe62</td>
<td>Rv3533c</td>
<td>1749</td>
<td>V</td>
<td>(MPTR subfamily)</td>
<td>MPTR protein.</td>
</tr>
</tbody>
</table>

*As defined in reference [8].

Each gene sequenced in this study is listed along with its phylogenetic position within its family and any additional information regarding its protein’s function available in the literature.

doi:10.1371/journal.pone.0030593.t003

before we are able to gain a more complete understanding of their role.

Materials and Methods

Ethics statement

We recovered sputum specimens from the National Health Laboratory Service (NHLS) after routine processing. None of the authors were directly involved in sputum collection. This study was approved by the Stellenbosch University Health Research Ethics Committee (approval reference number N10/04/126). Informed consent was not required as we received samples from the NHLS after routine processing. This was approved by the Stellenbosch University IRB.

In silico whole genome sequence analysis

Sequence selection details. Analysis of pe and ppe genes from the following 19 fully sequenced MTBC genomes was conducted: M. bovis strain AF2122/97 [76], H37Rv [77], CDC1551 [6], CPHL A (M. africanum), K05 (M. africanum), T92, T46, T48, 54S054, 94M4241A, 02_1907, T63, C strain, Haarlem, F11, GM1503, KZN 1435 and 98-R604 INH-RIF-EM [57]. Details of the phylogenetic placements of each isolate are shown in Table 1. At least 1 representative from all 7 major MTBC lineages (including the animal lineage) [78] are included in this study apart from lineage 3 (CAS lineage). ppe genes from the fully sequenced isolates KZN 605 and KZN 4207 [57] as well as the Harlingen transmission chain [58] were also analysed in specific instances. Orthologues of each gene were located by BLAST searches using the H37Rv gene sequence as the type standard. Gene sequences obtained from the Broad institute [57] were not used if they contained the following messages suggesting possible low sequence quality: “At least one base has a quality score <10”, “EST-based feature contains predicted/unverified ORF” or “Frame Shift: Sequence Error”. Sequence alignments were done using CLUSTALW [79].

Confirmation of whole genome sequence accuracy. Genomic DNA from 3 of the whole genome sequenced isolates (F11, CPHL A, K05, T17 and T92) was used to check the accuracy of 40 variations that were found in various pe and ppe genes (Table S4). Primers were designed to amplify a region surrounding the variation point and PCRs and sequencing of the amplicons were performed as described below. Recently, a number of nucleotides in the H37Rv sequence, including some within pe and ppe genes, were found to be incorrect [78]. These SNPs were corrected before analysis.

dN/dS values. Due to the general low level of SNPs present when analysing individual genes, a concatenated alignment for each gene category (ppe, pe and pe_pgrs) was generated combining all individual genes. Prior to concatenation the consensus sequence of each gene was aligned with the equivalent sequence containing all SNP’s identified using CLUSTALW [79]. Other variations (eg frameshifts or in-frame indels) that had been
identified were ignored. The resultant alignment files for each gene were concatenated using DnaSP [80] and pairwise dN/dS values were determined by subjecting the alignment to the DnaSP program package.

DNA sequencing of clinical isolates

Bacterial culture conditions, molecular typing and strain selection. Sputum samples were obtained from primary health care clinics in metropolitan Cape Town, South Africa. This region has a very high tuberculosis incidence and has been used extensively in an ongoing, prospective epidemiological study [81]. According to the National Tuberculosis Control Program in line with the Directly Observed Therapy Short-course strategy, diagnosis of tuberculosis is made by sputum smear microscopy in new cases, and by smear microscopy and culture in retreatment cases. We recovered these sputum specimens for our study area of interest from the National Health Laboratory Service (NHLS) after routine processing. M. tuberculosis strains present in sputum culture were genotyped using IS6110 RFLP [82] and spoligotyping [83,84]. DNA fingerprints were analysed with GelCompare software using the unweighted-pair group method, average linkages and Dice coefficients [85]. Isolates with an IS6110 similarity index of ≥65% were grouped into strain lineages [86]. Forty isolates of divergent lineages were selected for analysis. Table 2 shows phylogenetic details of these clinical isolates.

Selection of pe/ppe genes for whole gene sequence analysis. A phylogenetic analysis of both the pe and ppe gene families has previously been reported [8]. This has demonstrated that each gene family can be divided into several subfamilies (Fig. 1). In order to maximise the scope of our analysis we selected genes representative of several different subfamilies in each case. Where possible, genes for which some aspect of their biology (such as antigenicity) had been previously reported were chosen. A total of 14 pe/ppe genes were selected. These included the ancestral member of each family as well as 5 pe_ppe genes. Details of the selected genes are listed in Table 3.

PCR and sequencing. Primer sequences for the 14 selected genes are listed in Table S6. PCRs were done in a reaction mixture containing 0.1 µg template DNA, 3 µl GC-rich solution, 1.5 µl 10x buffer containing MgCl₂, 2.4 µl 10 mM dNTPs, 0.6 µl each primer (5 pmol/µl) and 0.12 µl FastStart Taq (Roche, Germany) made up to 15 µl with H₂O. Amplification comprised an initial 6 min template denaturation followed by 35 cycles using the appropriate annealing temperature (listed in Table S6) and an extension time of 30 s to 1 min 30 s depending on the length of the amplicon. PCR product was checked by electrophoresis through an agarose gel and an aliquot was treated with ExoSAP-IT (USB). Sequencing was performed using an ABI 3100 automated DNA sequencer. Sequence editing and manipulation was done using the BioEdit Sequence Alignment Editor [87].

Supporting Information

Table S1

Table S2 2 homologous genes (PPE38 & PPE71) in most isolates. Hotspot for IS6110 integration and homologous recombination [26].

Table S3

Table S4

Table S5

Table S6

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Author Contributions

Conceived and designed the experiments: CREM NGvP RMW SG PDvH. Performed the experiments: CREM RC BM. Analyzed the data: CREM NGvP AS BM. Contributed reagents/materials/analysis tools: NGvP PDvH. Wrote the paper: CREM NGvP.


