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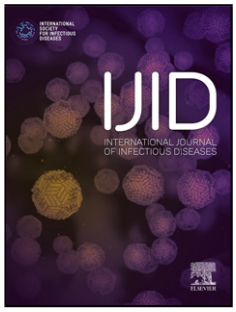

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Polymorphisms in Interferon Pathway Genes and Risk of *Mycobacterium tuberculosis* Infection in Contacts of Tuberculosis Cases in Brazil

Running Head: IFN Pathway SNPs and TB risk.

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Highlights

- High frequency of TST positivity in TB contacts from Brazil was observed
- SNPs in type-I IFN pathway, DNA and RNA sensing genes were screened in TB contacts
- SNPs in PYHIN1-IFI16-AIM2 and in IRF7 were linked to altered susceptibility to TB

ABSTRACT

Background: Host genetic polymorphisms may be important in determining susceptibility to *Mycobacterium tuberculosis* (Mtb) infection, but their role is not fully understood. Detection of microbial DNA and activation of type I interferon (IFN) pathways regulate macrophage responses to Mtb infection.

Methods: We examined whether seven candidate gene SNPs were associated with tuberculin skin test (TST) positivity in close contacts of microbiologically confirmed pulmonary TB patients in Brazil. Independent associations with TST positivity were tested using multivariable logistic regression (using genotypes and clinical variables) and genetic models.

Results: Among 482 contacts of 145 TB index cases, 296 contacts were TST positive. Multivariable regression analysis adjusted for population admixture, age, family relatedness, sex and clinical variables related to increased TB risk demonstrated that SNPs in *PYHIN1-IFI16-AIM2* rs1101998 (adjusted OR [aOR]: 3.72; 95%CI = 1.15–12.0; p=0.028) and in *PYHIN1-IFI16-AIM2* rs1633256 (aOR= 24.84; 95%CI = 2.26–272.95; p=0.009) were associated with TST positivity in a recessive model. Furthermore, an *IRF7* polymorphism (rs11246213) was associated with reduced odds of TST positivity in a dominant model (aOR: 0.50, 95%CI: 0.26-0.93; p=0.029).

Conclusions: Polymorphisms in PYHIN1-*IFI16*-AIM2 rs1633256, rs1101998 and in *IRF7* rs11246213 were associated with altered susceptibility to Mtb infection in this Brazilian cohort.

Keywords: single nucleotide polymorphism, tuberculin skin test, *Mycobacterium tuberculosis*.

Introduction

Tuberculosis (TB) is the leading cause of death from a single infectious agent (WHO, 2018). Approximately one-quarter of the global population is infected with *Mycobacterium tuberculosis* (Mtb) (Houben and Dodd, 2016). Latent tuberculosis infection (LTBI) is defined by immunological sensitization to Mtb antigens in the absence of clinical symptoms of disease and the diagnosis is based on the tuberculin skin test (TST) and/or Interferon-γ (IFN-γ) release assay (IGRA) (Robertson et al., 2012). Nevertheless, these tests do not discriminate between active disease and LTBI and, more importantly, have a low predictive value for progression to active TB (Rangaka et al., 2012). Many risk factors for developing active TB have been described, including HIV co-infection, diabetes, young age and recently-acquired Mtb infection (Reid et al., 2019), but intriguingly some TB patients do not exhibit any known risk factors (Yan et al., 2015). TB occurs as the result of an intricate and dynamic relationship involving host genetics (van Tong et al., 2017) as well as immunological (Mahan et al., 2012, Tameris et al., 2013), and epidemiological (Shin et al., 2016) factors, in addition to characteristics of the Mtb strain itself (Koch and Mizrahi, 2018), that contribute to disease susceptibility (Pai et al., 2016).

Genetic factors are important for TB susceptibility, but the major genes involved remain unknown (van Tong et al., 2017). Candidate gene/pathway studies interrogate selected pathways that are important in the human host response to mycobacterial infection (Kinnear et al., 2017). Type I IFN pathways mediate an important role in TB pathogenesis. Whole blood RNA signatures dominated by Type I IFN-signaling identify individuals who will develop active disease (Berry et al., 2010). In Mtb-infected mice, increased expression of type I IFNs is deleterious for

survival in association with reduced Th1 immunity (Manca et al., 2005). The Type I IFN pathway is activated by DNA (e.g. *IFI16-PYHIN1-AIM2*, cGAS, STING) and RNA sensors (e.g. *IFIT1* and 5), and contains several important signaling molecules and transcription factors (e.g. *IRF* family). For example, the cytosolic DNA sensor cGAS regulates IFN production during Mtb infection of macrophages (Watson et al., 2015). Although these murine and cellular studies suggest an important role for Type I IFNs in TB pathogenesis, the human genetics of this pathway in the context of Mtb infection is poorly understood (Donovan et al., 2017).

In a longitudinal investigation examining TB contacts from Brazil, we recently found that polymorphisms in toll-like receptor 4 (*TLR4*) and tumor necrosis factor (*TNFA*) are associated with increased risk of TST conversion and development of active TB (Cubillos-Angulo et al., 2019). Here we investigated in this same cohort whether genetic variation of Type I IFN pathway genes were associated with susceptibility to Mtb infection by examining single nucleotide polymorphisms (SNPs) involved in DNA and RNA sensing: (rs1101998, rs1633256, rs866484 in *IFI16-PYHIN1-AIM2 region*, rs59633641 and rs10887959 in *IFIT5*), rs304478 and rs304498 in *IFIT1* and the IFN signaling pathway (rs11246213 [*IRF7*]). The objective of this study was to identify potential genetic biomarkers of susceptibility to Mtb infection. We studied close contacts of microbiologically confirmed pulmonary TB patients to estimate factors associated with a positive versus negative TST.

Methods

Study design

The present study was based on analyses performed retrospectively on a cohort of contacts of pulmonary TB patients, recruited between November 1998 through March 2004. The parent study was reported previously (Cubillos-Angulo et al., 2019). The cases and controls were enrolled in the state of Rio de Janeiro, Brazil where the population is mostly white and brown ('*parda,* mixed ethnic ancestries) (IBGE, 2012). Racial/ethnic background was self-reported used the definitions/approaches employed by the Brazilian government for race documentation. TB index cases were diagnosed by acid-fast bacilli (AFB) smear and/or culture, according to Brazilian Ministry of Health Guidelines ((Brasil), 2019). TB index case variables included cough, AFB sputum grade, and chest radiographs. TB contacts were defined as living in the same household or reporting contact with the TB index case for >20 hours weekly for 2 months (Cubillos-Angulo et al., 2019). In the analyses presented here, we used data from a subgroup of 482 individuals, which were selected by such criteria and included contacts with TST-positive or TST-negative results. Patients who developed active TB were excluded from the analysis. Additional details on inclusion and exclusion criteria as well as patient characteristics have been described previously (Cubillos-Angulo et al., 2019).

A standardized questionnaire was administered to obtain demographic and clinical data, including a history of risk factors for TB (e.g., HIV, diabetes, hematologic malignancies, and use of immunosuppressant drugs) and duration of contact with the index case. Consanguinity was considered if a contact was a grandparent, parent or sibling of the index case, whereas spouses or other relationships were not. At study baseline, a medical visit and chest radiograph were performed. BCG scar

was assessed and TST reading was performed 48-72 hours after administration at baseline, using 2 tuberculin units of the purified protein derivative RT 23 (Statens Serum Institute, Copenhagen, Denmark).

TST interpretation and TB diagnosis

A positive TST was defined as an induration larger than ≥5mm induration, according to the Brazilian Ministry of Health ((Brasil), 2019). Contacts with any TST ≥5 mm were not re-tested with TST. The Brazilian National TB Guidelines indicated that treatment of TST-positive individuals was systematically offered but implementation was not mandatory during the study period ((Brasil), 2019). For the index case, active TB was diagnosed when ≥1 specimen yielded a positive microbiologic (AFB smear or culture) result by AFB smear and/or culture in Lowenstein Jensen (LJ) medium (Cubillos-Angulo et al., 2019).

Genotyping

Genomic DNA was extracted from peripheral blood collected from TB contacts at study enrollment. DNA extraction and genotyping were performed using the FlexiGene kit (Qiagen, Germany). Genotypes of 8 gene polymorphisms were chosen for convenience since a RFLP assay was available: rs1101998 (*IFI16-PYHIN1-AIM2*), rs1633256 (*IFI16-PYHIN1-AIM2*), rs866484 (*IFI16-PYHIN1-AIM2*), rs304478 (*IFIT1*), rs304498 (*IFIT1*), rs11246213 (*IRF7*), rs59633641 (*IFIT5*) and rs10887959 (*IFIT5*) were detected using polymerase chain reaction restriction

fragment length polymorphism (RFLP) method (Cubillos-Angulo et al., 2019). The primer sequences are in Supplementary Table 1. The PCR products were digested by the enzymes *EcoRII* for rs1101998 (*IFI16*), *AgsI* for rs1633256 (*IFI16*), *AgsI* for rs866484 (*IFI16*), *AarI* for rs304478 (*IFIT1*), *TfiI* for rs304498 (*IFIT1*), *BsaAI* for rs11246213 (*IRF7*), *ApoI* for rs59633641 (*IFIT5*) and *AgsI* for rs10887959 (*IFIT5*). Hardy-Weinberg equilibrium was tested for each SNP. We did not find significant deviation from Hardy Weinberg equilibrium except in rs304498 (*IFIT1*), and thus this SNP was excluded from further analysis. Linkage disequilibrium coefficients were calculated using Package "LDheatmap" (Ji-Hyung Shin, 2006) in the stats package in R 3.5.2 and using an R^2 and D' cutoff of 0.8. Haplotypes analysis were constructed in the stats package R 3.5.2 using the haplo.stats (version 1.6.0) R package (Jason P. Sinnwell; Daniel J. Schaid, 2018).

Data analysis

Categorical data were presented as proportions and continuous data as medians and interquartile ranges (IQR). For clinical characteristics, a Fisher's exact test was used to perform 2x2 comparisons. Continuous variables were compared using the Mann-Whitney *U* test. For genetic analysis, a Cochrane-Armitage test for trend was used initially to examine the association of genotypes with TST positivity. SNPs were then evaluated with a Fisher's exact test using dominant (00 vs 01/11) and recessive (00/01 vs 11) models. We also estimated significant associations between indicated SNPs and TST positivity using multivariable logistic regression adjusted for race/ethnicity, family relatedness, gender and age in both dominant and recessive models. Finally, we also performed additional investigations with dominant and

recessive models in a multivariable analysis with adjustment for age, gender, race/ethnicity, family relatedness, household contact status and characteristics of TB index case, such as cavities on chest x-ray, ≥2+ AFB sputum smear grade and positive sputum culture for Mtb. We also used the GTEx portal (https://gtexportal.org/home/) to evaluate the expression quantitative trait loci (eQTL) of the SNPs (Consortium, 2013). Furthermore, the likelihood of being a regulatory SNP was examined using the RegulomeDB dataset (http://www.regulomedb.org/snp/chr10/91150921) (Boyle et al., 2012).

Results

Characteristics of the study participants

We used a retrospective cohort study of contacts (N=482) of pulmonary TB index cases (N=145) to examine whether genetic variants of candidate genes were associated with TST positivity. Household contacts were more frequently observed in the group of individuals presenting with a positive TST result than in those with a negative TST (Table 1). Cavitary lesions as well as cough in the index TB cases were more frequent in participants who were TST positive compared to those who had negative results (p=0.04 and p=0.008, respectively). Other characteristics were similar between TST positive and TST negative individuals.

The study population was mostly female (n=321, 67%), with a high frequency of first degree relatives with the index case (n=229, 62%) (Table 1). In addition, the vast majority of participants were household contacts (n=434, 90%). There were low frequencies of HIV infection, illicit drug use, prior TB and use of immunosuppressive

drugs. Approximately 97% (n=141) of the index cases had TB confirmed by culture. TB index cases frequently reported cough for more than 4 weeks (80%) and had high bacterial loads in sputum (60% had AFB grade ≥ +2;). In addition,100 index TB patients had cavitary lesions on chest radiograph.

Association between polymorphisms and TST positivity

Two of seven polymorphisms were associated with TST positivity (rs1633256 and rs59633641 with an unadjusted genotypic trend test, Table 2). *PYHIN1-IFI16-AIM2* SNPs rs1101998 allele C (p=0.01) and rs1633256 allele A (p=<0.01) were more common in TST positive participants and fit a recessive model (Table 2). *IFIT5* rs59633641 allele G (p=0.04) was more common in TST positive individuals (trend test p=0.04, Table 2). *IFIT1* rs304478 and *IFIT5* rs10887959 were also significantly associated with outcomes in recessive and dominant models, respectively.

In a multivariable model that included adjustment for race/ethnicity, family relatedness, gender, and age (Figure 1), we observed in the recessive model that *PYHIN1-IFI16-AIM2* rs1101998 (adjusted OR [aOR] =2.90; 95%CI = 1.24–6.78; p=0.014) and rs1633256 (aOR = 10.1; 95%CI = 2.20–46.28; p=0.003) were associated with an increased risk TST positivity. Moreover, in the dominant model, *IFIT5* rs10887959 (aOR = 0.49; 95%CI = 0.28–0.84; p=0.01) and *IRF7* rs11246213 (aOR = 0.60; 95% CI = 0.36–1.00; p=0.049) were also linked to a lower likelihood of positive TST.

We next used a multivariable regression analysis to adjust for household contact and characteristics of TB index case (cavities on chest x-ray, ≥2 AFB sputum smear and positive Mtb culture) as well as race/ethnicity, family relatedness, gender, and age (Figure 2). We confirmed in the recessive model that *PYHIN1-IFI16-AIM2* rs1101998 (aOR= 3.72; 95%CI = 1.15–12.0; p=0.028) and rs1633256 (aOR= 24.84; 95%CI = 2.26–272.95; p=<0.009) were independently associated with increased odds of a positive TST. In addition, in the dominant model, *IRF7* rs11246213 was also independently associated with a lower likelihood of a positive TST (aOR: 0.50, 95%CI: 0.26-0.93; p=0.029).

We next examined effects of linkage disequilibrium and SNP-SNP interactions in the *PYHIN1-IFI16-AIM2* region on chromosome 1. *PYHIN1-IFI16-AIM2 SNPs* rs8666484, rs1101998 and rs1633256 were all in moderate to high linkage disequilibrium (Supplemental Figure 1). In a haplotype analysis of chromosome 1 adjusted for age, gender, race/ethnicity, family relatedness and household contact, the haplotypes containing allele C from rs1101998 and allele A from rs1633256 did not have a higher risk of TST positivity compared to single SNP analyses (Figure 3 compared to Figure 2).

Using an in silico approach with data from the GTEx portal tool (see Methods for details and also in (Consortium, 2013), we found that six polymorphisms (rs1101998, rs1633256, rs866484, rs304478, rs10887959 and rs11246213) were eQTLs in different tissues (Supplementary Table 2). Interestingly, three different SNPs were reported to be expressed in the spleen and/or lung, which are organs

commonly affected by TB (Figure 4). The findings indicated that the *PYHIN1-IFI16-AIM2* rs1101998 genotype CC was linked to decreased expression of *AIM2* in spleen (Figure 4). The *PYHIN1-IFI16-AIM2* rs1633256 genotype AA was also associated with dampened expression of *AIM2* in spleen tissue (Figure 4). The *IFIT5* rs10887959 genotype CC was associated with lower expression of *IFIT5* in spleen and lung tissues (Figure 4). Finally, using a different online tool, the RegulomeDB dataset, we observed that *PYHIN1-IFI16-AIM2* rs1101998 exhibited high likelihood of being a regulatory SNP for a DNAase I hypersensitivity peak or transcription factor binding. Moreover, *IFIT5* rs10887959 displayed high likelihood of being a regulatory SNP for transcription factor binding and a DNAase I hypersensitivity peak. Together, these data suggest that rs1101998, rs1633256, and rs10887959 are eQTLs.

Discussion

In the present study, we tested associations between SNPs from related genes in different pathways of DNA and RNA sensing and the type I IFN pathway in a large number of TB contacts. The notable finding was that *PYHIN1- IFI16-AIM2* rs1633256 and rs1101998 were associated with an increased risk of TST positivity whereas *IRF7* rs11246213 was associated with a lower probability of TST positivity. To our knowledge, SNPs in these genes have not previously been reported to be associated with the pathogenesis of Mtb infection in contacts.

Our results suggest that the *PYHIN1- IFI16-AIM2* rs1633256 and rs1101998 polymorphisms are associated with increased susceptibility to Mtb infection (i.e., a positive TST). The two polymorphisms are in a 3-gene locus on chromosome

1q23.1; thus, it is not possible to know which specific gene is most likely to exert a functional effect related to these genetic variants. The gene encoding Interferon-γ-inducible protein 16 (*IFI16*) (Trapani et al., 1994) is a multifunctional and ubiquitous host protein (Trapani et al., 1992), and a member of the PyHIN (pyrin and HIN200 domain-containing) protein family that consists of four family members: PYHIN1 (alias *IFIX)*, *IFI16 (*alias PYHIN2*)*, *MNDA (*alias PYHIN3*)* and *AIM2 (*alias PYHIN4*)* (Thompson et al., 2011). During Mtb infection of macrophages, *IFI16* is reported to be localized into the cytosolic compartment (Thompson et al., 2011) and Mtb DNA activates the cytosolic surveillance pathway. Mice genetically lacking IFI204 (a homolog gene of human *IFI16*) show reduced *IFIT1* and *IFN-β* induction against Mtb infection (Manzanillo et al., 2012).Furthermore, mycobacterial infection of AIM2$^{-/-}$ (absent in melanoma 2) mice induces elevated IFN-γ and reduced IFN-γ responses, leading to higher infection burdens and more severe pathology (Yan et al., 2018). In addition, in vitro studies demonstrated that AIM2-deficient macrophages display impaired activation of the inflammasome and defective production of IL-1b and IL-18 upon Mtb infection, making such cells highly susceptible to bacterial proliferation and cell death (Saiga et al., 2012). To the best of our knowledge, there are no previously reported studies on the relationship of PYHIN1 and TB. PYHIN1 detects Herpes Simplex (HSV-1) DNA and contributes to the induction of interferon response in human fibroblasts (Diner et al., 2015). In the present study, the SNPs associated with TST positivity (rs1633256 and rs1101998) are part of a large locus; thus it is possible that at least these two SNPs could be associated with any one of the 3 genes described above (*PYHIN1- IFI16-AIM2*) and influence the detection of

Mtb DNA during infection. Future studies are warranted to directly elucidate the molecular mechanisms underlying these associations.

The human *IRF7* gene is located on chromosome 11p15.5 and is a member of the interferon regulatory factor family of transcription factors, comprised of nine members (IRF1 to 9) (Ning et al., 2011). This family is recognized by the regulation of many facets of innate and adaptive immune responses (Tamura et al., 2008). *IRF7* is the central transcription factor that induces *IFNA/B* gene transcription in response to cytosolic viral DNA and RNA in host cells (McNab et al., 2015). In addition, *IRF7* is produced by murine bone marrow–derived macrophage infected with Mtb (Cheng and Schorey, 2018, Leisching et al., 2017). In a recent meta‐analysis, Mtb infection of THP-1 macrophages induced differential expression of *IRF7* (Zhang et al., 2019). Excessive type I IFN expression has been linked to increased TB-associated immunopathology and susceptibility to severe TB (Mayer-Barber et al., 2011, Mayer-Barber et al., 2014). *IRF7* SNPs have been reported to significant reduce IFNα production by plasmacytoid dendritic cells following stimulation with HIV-1 (Chang et al., 2011). The effect of IRF7 SNPs on reduced IFNα production, if present also in exposure to Mtb, could be a factor explaining the decreased susceptibility to Mtb infection reported here.

We also found that *IFIT5* rs59633641 was less frequently observed in individuals with a positive TST whereas *IFIT5* rs10887959 was more commonly detected in individuals with positive TST. *IFIT5* (IFN-induced protein with tetratricopeptide repeats-5) is a member of an interferon-induced protein with tetratricopeptide

repeats (IFIT) family with five members (*IFIT1*, *IFIT2*, *IFIT3*, *IFIT1B* and *IFIT5*) localized in chromosome 10q23 (Diamond, 2014). The multivariable model with adjustment for race/ethnicity, family relatedness, gender and age demonstrated associations between the *IFIT5* rs10887959 and increased chance of negative TST. It has been recently demonstrated that *IFIT5* physically interacts with MAP3K7/TAK1 and IκB kinase (IKK) to activate the transcription factor NF-κB, which is a key regulator of the expression of genes involved in immune responses, inflammation, cell survival and cancers (Zheng et al., 2015). *IFIT5* is one of the main genes upregulated in active TB patients (Ahmed et al., 2016). The IFN-induced proteins regulate immune response against viruses. For example, it has been recently shown that *IFIT3* has a protective role in response to dengue virus infection of human lung epithelial cells (Hsu et al., 2013).

Our study has several strengths such as systematic TST testing (currently recommended as the diagnostic test for LTBI in most resource-restrained countries) and inclusion criteria that ensures microbiological confirmation of TB index cases. However, it is also important to highlight potential limitations of our investigation, such as the cross-sectional nature of the analyses, which are not able to establish causal relationships. We have not performed functional validation of the findings; however, we showed an analysis of gene expression data in silico. In addition, we considered a common Mtb strain to be responsible for infections within a household, but it is possible that that may not have always been true. In addition, LTBI was only measured by TST with no IGRA assessments. These two tests are not perfectly concordant, so the TST negative group could probably include some individuals with

positive IGRA results. Of note, IGRA was not available in Brazil at the time of the patient enrollment. Food and Drug Administration (FDA) approved IGRA in 2001, and this test was introduced in Brazil in 2014, 10 years after the data collection of the present study was finalized. Regardless, our results clearly indicate associations between polymorphisms in innate immune genes linked to interferon responses and odds of Mtb infection assessed by TST positivity. Further translational studies are required to delineate the molecular events behind these associations.

NOTES

Ethics Statement: The study was approved by the Clementino Fraga Filho University Hospital (HUCFF), Federal University of Rio de Janeiro Ethics Review Board. Written informed consent was obtained from all participants or their legally responsible guardians, and all clinical investigations were conducted according to the principles expressed in the Declaration of Helsinki. The anonymity of study subjects was preserved with a code created with a link to personal identifiers.

Contributions: Study design: BBA, ALK, MMO, JRLS. Data collection: ECS, LEAA, ASdA, MOM, ASRM. Data analysis: MGMM, ECS, JMCA, MBA, KFF, TRS, TRH, MMO, BBA. Writing: JMCA, MBA, TRS, TRH, BBA.

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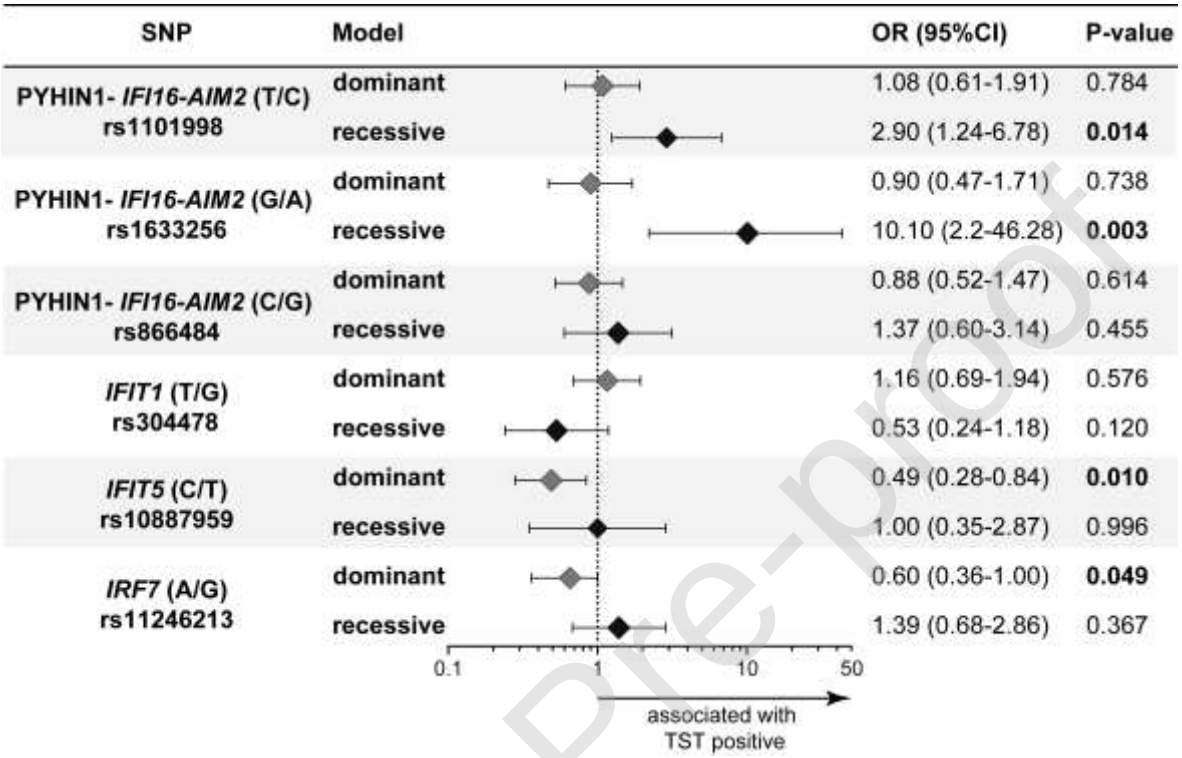
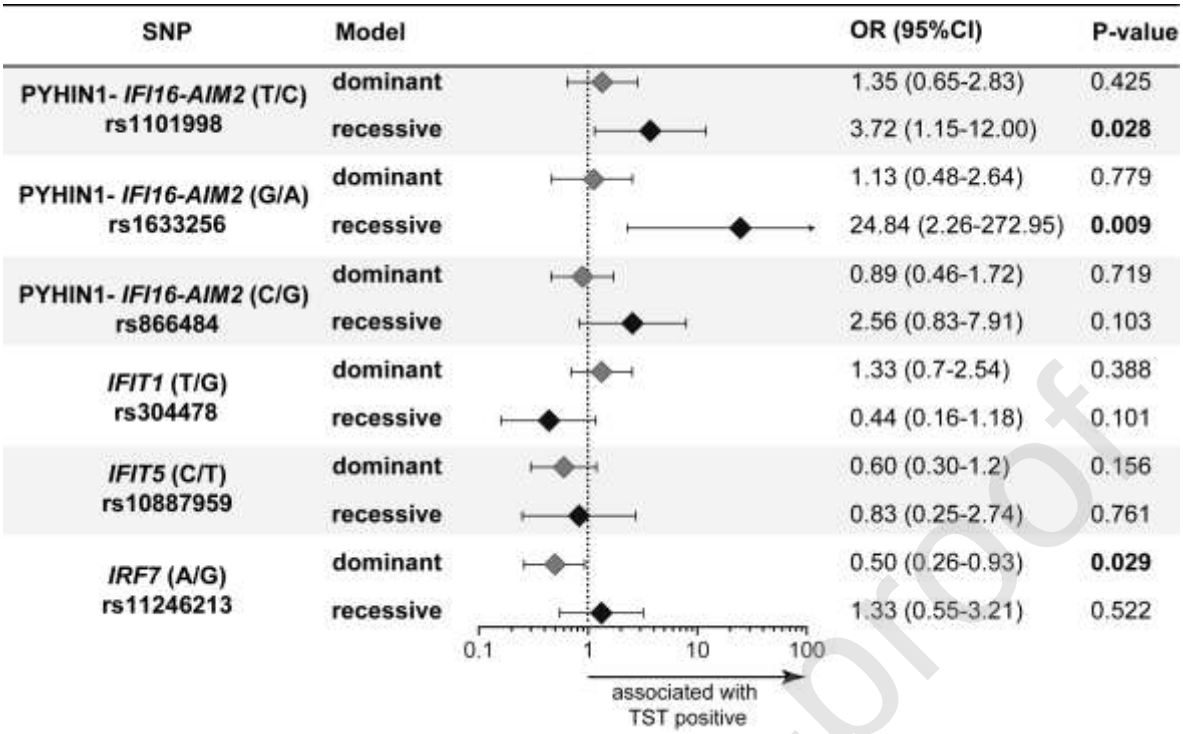
Figures:

Figure 1. Multivariable model of association between genetic variants and TST positivity



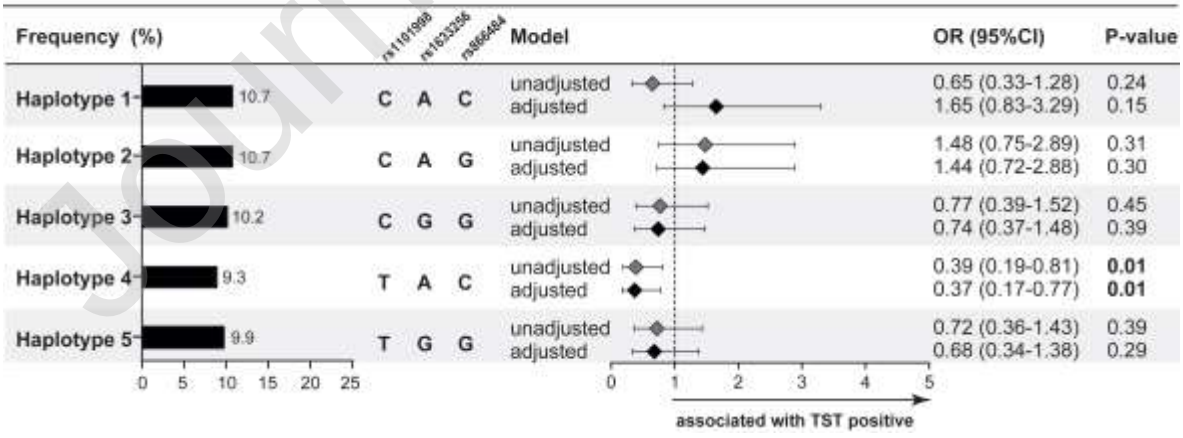
Analysis in all study participants Data represent no. SNP: single-nucleotide polymorphism; OR: odds ratio,95% CI: confidence interval; P-value represents comparison of genotype frequencies in a dominant and recessive model with adjustment for race/ethnicity, family relatedness, gender, and age. OR (Odds ratio) represents association of minor allele with risk of TST positivity.

Figure 2. Multivariable model of association between genetic variants and TST positivity including clinical variables.



Analysis in all study participants Data represent no. SNP: single-nucleotide polymorphism; OR: odds ratio, 95% CI: confidence interval; P-value represents comparison of genotype frequencies in a dominant and recessive model with adjustment for age, gender, race/ethnicity, family relatedness, household contact and characteristics of TB index case: Cavities on chest x-ray, ≥2 AFB sputum smear and positive Mtb culture.

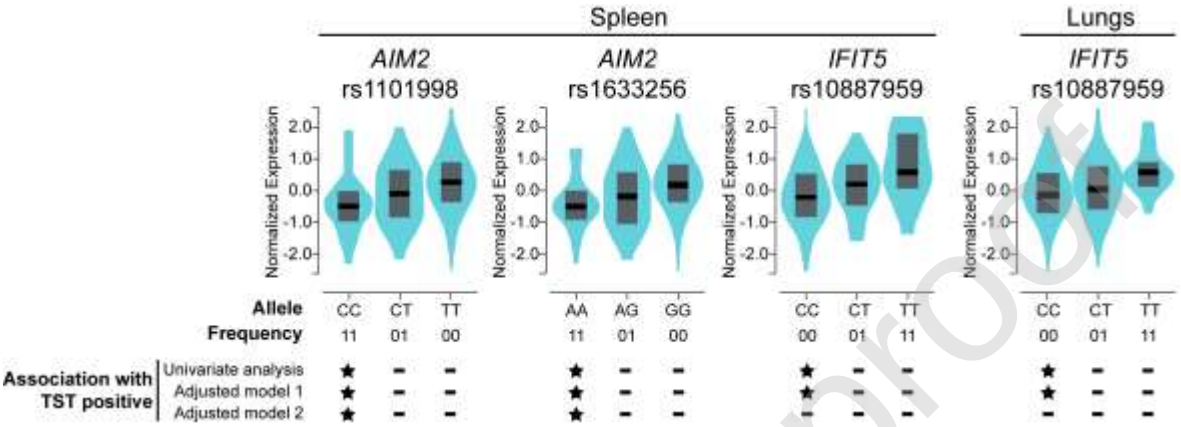
Figure 3. Haplotype analysis chromosome 1.



Haplotype analysis chromosome 1 of SNPs rs1101998, rs1633256, rs866484-*PYHIN1- IFI16-AIM2*. P-value represents comparison of haplotype frequencies with

TST conversion in an unadjusted and adjusted model for age, gender, race/ethnicity, family relatedness and household contact.

Figure 4. *In silico* expression of SNPs rs1101998, rs1633256 and rs10887959 adapted from GTEx eQTL database.



Normalized expression values were obtained from the GTEx eQTL database and violin plots (with median and interquartile range values) were used to represent the trends in data variation between the different SNPs. The full list of the SNPs and tissues evaluated is described in the Supplementary Table 2. The Figures describe the SNPs that had publicly available data on expression in spleen and/or lungs, due to its importance in TB pathogenesis. Thus, data on the SNPs rs1101998, rs1633256 and rs10887959 are shown. Allele frequency was determined as the following: 00, homozygous common allele; 01, heterozygous allele; 11, homozygous rare allele. A summary of the results of the analysis from the present study testing the association between each indicated allele and a positive TST result is shown at the bottom of the graphs. A star denotes statistically significant associations with TST positivity in the following conditions: (i) univariate analysis: a comparison of genotype frequencies without adjustment for any covariates; (ii) Adjusted model 1: analysis in a dominant and recessive model with adjustment for race/ethnicity, family relatedness, sex, and age; and (iii) Adjusted model 2: analysis in a dominant and recessive model with adjustment for age, sex, race/ethnicity, family relatedness, household contact and characteristics of TB index case (cavity on chest x-ray, ≥2 AFB sputum smear and positive Mtb culture). SNP: single-nucleotide polymorphism.

Table 1. Clinical characteristics of the study participants & association with tuberculin skin test (TST) positivity.

Characteristic	n	TST negative	TST positive	P-value
		n=219	n=263	
Age -median (IQR)	482	34 (23-50)	37 (24-49)	0.40
Male sex	482	74 (34)	87 (33)	0.92
First-degree relative of the index case	482	138 (63)	161 (61)	0.71
HIV infection	21	2 (67)	1 (6)	**0.04**
Race (% white)	462	113 (53)	144 (58)	0.40
Illicit drug use[a]	412	3 (2)	3 (1)	1.00
Prior tuberculosis	411	0 (0)	3 (1.4)	0.25
Household contact	480	190 (88)	244 (93)	0.06
Duration of contact (>20 hours)	482	202 (92)	248 (94)	0.46
Comorbid conditions[b]	459	53 (26)	65 (26)	1.00
Immunosuppressant drugs[c]	414	0 (0)	2 (1)	0.50
Cough (> 4 weeks)	481	5 (2)	5 (2)	0.76
Characteristics of TB index case				
Cavities on chest x-ray	473	24 (11)	47 (18)	**0.04**
Cough (> 4 weeks)	481	86 (39)	136 (52)	**0.008**
≥2 AFB sputum smear	443	77 (39)	103 (42)	0.44
Mtb positive culture	339	147 (94)	178 (97)	0.18

"n" is the number of TB contacts for whom such data were available, out of a total of 482 included in the study. Data represents no. (%) or median and interquartile range (IQR) and were compared using the Fisher's exact test (categorical variables) or the Mann-Whitney *U* test (for age). TST: tuberculin skin test; AFB: acid-fast bacilli on sputum smear, CI: confidence interval; OR: odds ratio; [a]illicit drugs: cannabis, cocaine, or crack. [b]co-morbid conditions: diabetes mellitus, heart failure, chronic obstructive pulmonary disease, neoplasia, systemic lupus erythematous and hepatitis. [e]Immunosuppressant drugs: corticosteroids, tumor necrosis factor blockers, calcineurin inhibitors, or interleukin inhibitors.

Table 2. Association between candidate gene polymorphisms and TST.

SNP	Genotype Frequency in TST negative				Genotype Frequency in TST positive				P-value			
	00	01	11	Total	00	01	11	Total	HWE	Genotypic Trend†	Dominant 00 vs 01/11	Recessive 00/01 vs 11
rs1101998 - PYHIN1- IFI16-AIM2 (T/C)	0.43	0.49	0.09	105	0.43	0.35	0.22	102	0.21	0.20	1.00	**0.01**
rs1633256 - *PYHIN1- IFI16-AIM2* (G/A)	0.56	0.41	0.03	80	0.53	0.26	0.22	78	0.02	**0.04**	0.75	**<0.01**
rs866484 - *PYHIN1- IFI16-AIM2* (C/G)	0.55	0.36	0.09	120	0.49	0.39	0.13	127	0.1	0.27	0.37	0.42
rs304478 - *IFIT1* (T/G)	0.37	0.47	0.17	131	0.44	0.48	0.08	135	0.66	0.06	0.26	**0.04**
rs59633641 - *IFIT5** (C/G)	0.97	0.03	0	121	0.9	0.1	0	117	0.59	**0.04**	-	-
rs10887959 - *IFIT5* (C/T)	0.64	0.3	0.06	115	0.46	0.46	0.08	119	1.00	0.06	**0.009**	0.80
rs11246213 - *IRF7* (A/G)	0.48	0.4	0.12	126	0.37	0.46	0.17	133	0.25	0.07	0.08	0.29

Data represent genotype frequency of SNP TST: tuberculin skin test; SNP: single-nucleotide polymorphism; 00, homozygous common allele; 01, heterozygous allele; 11, homozygous rare allele. HWE: Hardy Weinberg equilibrium. Data was analyzed using the Fisher's exact test (2x2 comparisons) or the chi-square trend test (3x2 comparisons). * no uncommon homozygous mutation; in this particular case, the test employed for the genotypic analysis was based on 2x2 comparison. P-value represents comparison of genotype frequencies without adjustment for any covariates. †Cochrane-Armitage trend test.