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## Multiplex PCR assay for genotyping of *Mycobacterium tuberculosis* in Lima, Peru



### PCR Múltiple para el Genotipaje de *Mycobacterium tuberculosis* en Lima, Perú

Dear Editor,

In South American countries it is necessary to have molecular methods as epidemiological tools as well as low costs and good level of discrimination capacity for polymorphisms that may enable molecular laboratories to perform the tasks for other regional laboratories having minimum standards. The methodology proposed in this article addresses this need.

We used the Proportion Method<sup>2</sup> for susceptibility testing of *Mycobacterium tuberculosis* isolates against isoniazid (INH), rifampicin (RMP), ethambutol (EMB), para-aminosalicylic acid (PAS), thioacetazone (T), kanamycin (KM) and streptomycin (SM). Cultures were grown on Lowenstein Jensen medium at 37 °C for 21 days, and slides were processed with the Ziehl–Neelsen stain. DNA from samples was extracted by using the phenol chloroform method<sup>6</sup>. In a simple PCR for *M. tuberculosis* strain differentiation, primer Mtb2 (5'-CGGCGGCAACGGCGGCA) was used with primers IS1 (5'-CGGACTCACCGGGCGGTTCA) and IS2 (5'-CGGACATGCCGGGCGGTTCA) that anneal at the inverted repeats flanking IS6110<sup>7</sup>. PCR was done in a mixture containing 25 pmol of each primer, 1 U of Platinum Taq DNA polymerase (Invitrogen), 0.2 mM of each deoxyribonucleotide triphosphate, 10 mM Tris–HCl (pH 8.4), 1.65 mM MgCl<sub>2</sub>, 50 mM KCl, and 0.1% Triton X-100 and overlaid with mineral oil. Cycling conditions were as follows: denaturation at 94 °C for 5 min, followed by amplification for 35 cycles of 94 °C for 1 min, 62 °C for 1 min, and 72 °C for 1 min, followed by a final extension at 72 °C for 10 min. A total of 20 µl of amplified DNA was subjected to electrophoresis in a 2% agarose gel, detected by ethidium bromide staining, and visualized under UV light. For the genetic polymorphism study, we used the Bionumerics program version 5.0 (Applied-Maths).

The drug resistance study showed that out of 49 strains belonging to TB patients in the Guillermo Almenara Irigoyen National Hospital, 18 strains (36.74%) were drug-sensitive,

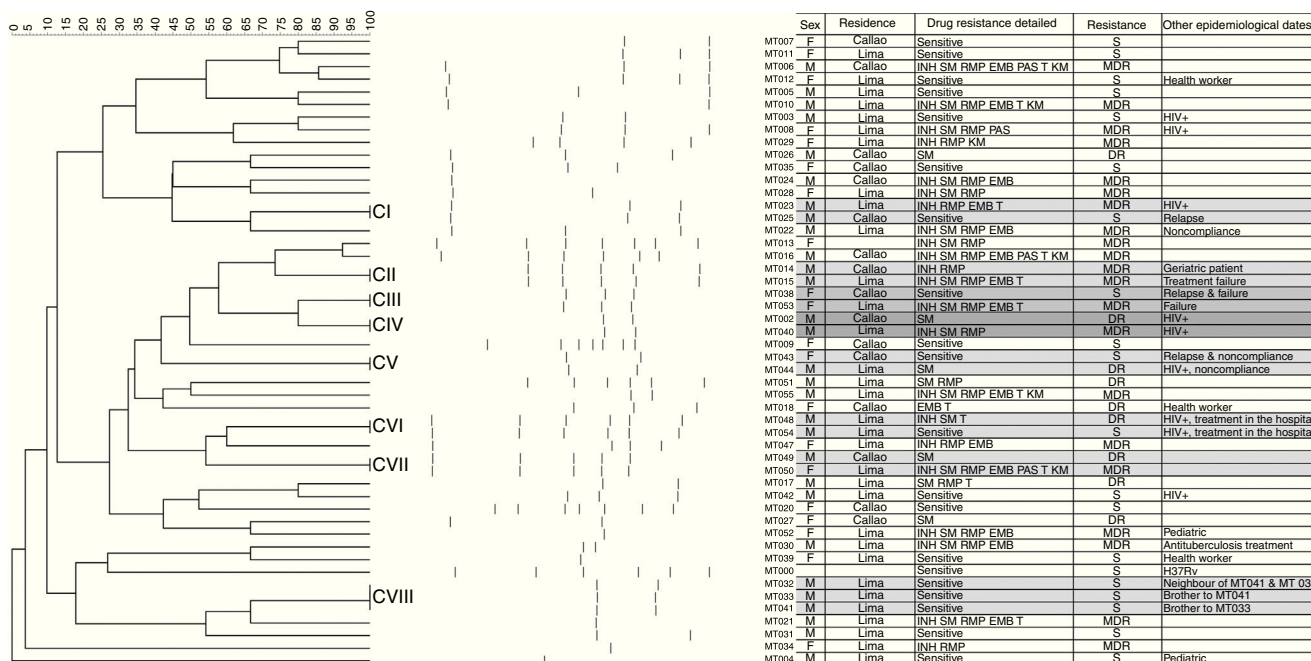
10 (20.4%) were drug-resistant TB (DR) and 21 (42.8%) were multidrug-resistant TB (MDR), 3 of which were TB/HIV cases. Forty-two (42) different banding patterns were observed, which were classified into 10 clusters (Fig. 1). We suspect that cases MT009 and MT029 belong to heteroresistant strains, i.e. mixed wild-type and mutant strains because the banding pattern seems to overlap<sup>5</sup>.

The transmission study showed Cluster II. Two male patients with MDR-TB, one of whom (MT014) had undergone previous MDR-TB treatment, were both hospitalized; Cluster IV. Two male patients with TB/HIV co-infection, both residing in the same district; Cluster VI. Two male patients with TB/HIV co-infection, both living in the same district and receiving their treatment in the same hospital, one of them (MT048) with DR TB and the other (MT054) with a sensitive case; Cluster VIII. Three male patients aged 44, 34 and 28 years, respectively, two of whom were brothers (MT033 and MT041) and the other a neighbor (MT032), all of them sensitive cases. The other clusters did not have an epidemiological link. A statistical risk study was performed<sup>4,13</sup> and the result was that the patients with HIV infections had the highest contagion risk in our population ( $p=0.174$ ; OR = 3.150; CI = 0.568–17.477). The repetition rate was good (Cronbach's alpha = 0.82). This genotyping method could be an alternative for other PCR-based typing procedures, such as spoligotyping and MIRU-VNTR typing as cited in other studies<sup>7</sup> and could help in the study of transmission relationship with heteroresistance, HIV-TB patients and outbreaks. Our TB survey system has many complications<sup>3,9,11</sup> and the lack of surveillance in DOTS<sup>3</sup> results in patients having a great diversity of genotypes and drug-resistant profiles<sup>1,5</sup>, as well as heteroresistance of wild type to resistant, resistant to resistant, and wild type to MDR strains<sup>1,4,8,10,12,13</sup>. Our country needs a strategy based on epidemiology with molecular tools that will assist us in the analysis of the genetic diversity existing in Peru.

### Ethical disclosures

**Protection of human and animal subjects.** The authors declare that no experiments were performed on humans or animals for this study.

**Confidentiality of data.** The authors declare that they have followed the protocols of their work center on the publication of patient data.



**Figure 1** The dendrogram of fragment to Multiplex PCR of 50 strains of *M. tuberculosis* was constructed using the similarity coefficient of Dice and UPGMA, using a tolerance of 1.2% and optimization of 0.17%. The clusters CI, CII, CIII, CIV, CV, CVI, CVII y CVIII are indicate in the dendrogram. The banding patterns obtained by PCR-based methodology are in the right of the dendrogram. The attached table contains demographic and drug resistant date of the cases.

**Right to privacy and informed consent.** The authors declare that no patient data appear in this article.

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