High-Content Screening Technology Combined with a Human Granuloma Model as a New Approach To Evaluate the Activities of Drugs against Mycobacterium tuberculosis

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Tuberculosis remains a major health problem due to the emergence of drug-resistant strains of Mycobacterium tuberculosis.

Some models have provided valuable information about drug resistance and efficacy; however, the translation of these results into effective human treatments has mostly proven unsuccessful. In this study, we adapted high-content screening (HCS) technology to investigate the activities of antitubercular compounds in the context of an in vitro granuloma model. We observed significant shifts in the MIC50s between the activities of the compounds under extracellular and granuloma conditions.

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The plates were sealed with optical adhesive film (Excel Scientific), and the images were recorded using CellInsight Thermo Array-Scan HCS equipment (Thermo Fisher Scientific) with a 10× objective. A 386-nm laser with an exposure time of 4 ms was used to analyze Hoechst staining, and a 485-nm laser with an exposure time of 597.286 ms was used to analyze GFP fluorescence. Each image was processed using Cellomics ArrayScan compartmental analysis (version 3). For the acquisition of the entire 384-well microtiter plate, 16 fields within each well were recorded. All fields contained two images, cell nuclei (blue channel) and bacteria (green channel). The granuloma structures were selected according to nuclei staining, due to the complexity of the size and form of the cells. Tests were carried out to evaluate the different settings used to identify granulomas, and the blue channel was finally chosen for identifying the granulomas (Fig. 1B). Using this approach, the granulomas could easily be distinguished from the PBMC and single cells, and cell aggregates could be eliminated. Spot detection was used to detect bacteria, because this approach can detect a single bacterium and thus give the exact number of bacteria (Fig. 1C). This method was validated in experiments involving suspensions of bacteria of known concentrations. Some variables generated from the granuloma protocol are the number of granulomas, area, size, intensity, spot, and number of granulomas/spot.

A dose-response assay to determine the MICs was performed by testing four drugs: isoniazid (INH), moxifloxacin (MOX), linezolid (LZD), and pyrazinamide (PZA). We used INH as a reference control because it is a potent mycobactericidal drug and a vital component of current combination regimens. LZD was chosen as an example of a compound that has recently shown great promise in the clinical setting, despite poor performance in murine animal models of TB (16). PZA has poor in vitro anti-TB activity when used alone but can boost other anti-TB drugs when used in combination, both in animal models and in the clinic setting. MOX is a promising potential candidate for future drug regimens, given its advanced clinical development status. We did not observe any toxic effects to cells with the concentrations of drugs tested. Stock solutions were prepared in high-grade dimethyl sulfoxide (DMSO) (Sigma) at a concentration of 200 mM and diluted for the assay with RPMIc to an appropriate concentration. The granulomas were exposed to compounds for 5 days under the same conditions as those previously described in order to evaluate their effect on MTB-GFP-colonized granulomas. After exposure, intragranuloma bacterial quantification was done as previously described. All experimental settings were kept constant to ensure that the same parameters were used in all analyses. However, all settings were recalibrated with respect to the granuloma control image for each sample. The ArrayScan Cellomics software provides many experimental variables; however, we focused on the number of granulomas, the total spot count (number of bacteria), and the number of spots per granuloma (M. tuberculosis cells per granuloma). The control granulomas and drug-treated granulomas were compared to evaluate whether the drug brought about a reduction in the number of bacteria in the granuloma (MTB/granuloma). The number of spots and the number of gran-

**FIG 1** Typical granuloma images recorded by the automated CellInsight Thermo ArrayScan. Shown are the same image at 10× objective in one field (A), in the blue channel, with selected granulomas in blue and isolated cells or aggregated cells in orange (B), in the green channel, with bacteria as green spots (C), and as a composite image of the two channels (D).
ulomas were used as internal controls. The effect of the drug was calculated as the percentage of inhibition of infection (PII), as follows: $\text{PII} = \frac{1 - \frac{\text{sampleMTB/granuloma/DMSOMTB/granuloma}}{\text{DMSOMTB/granuloma} \times 9M}}{0.05} \times 100$. The experiment was repeated six times for each concentration for each donor. The intragranuloma MIC50 was defined as the concentration of drug required to achieve a 50% inhibition of bacillus growth after 5 days of drug exposure. The MIC50 was determined from the dose-response curves. The data analysis was carried out with the GraphPad Prism version 5.02 software.

In the assay, DMSO did not show any toxic effect for cells at its highest concentration (0.05% [vol/vol]). The number of granulomas was used in our assay as an internal control for compound toxicity. We verified the lack of toxicity of DMSO at a concentration of 0.05% in granulomas by comparing the number of granulomas obtained in the presence of DMSO and that obtained with control samples (without the addition of any compound); no differences were found in the number of granulomas. Reference compounds, such as INH, containing the same DMSO concentration were evaluated in parallel. We found that the number of MTB-GFP inside the granulomas was unchanged after 5 days of incubation of infected cells with any compound (as a control) or with DMSO. The reduction in the number of MTB-GFP inside the granulomas treated with INH was thus due only to the effect of the drug and not to any toxic effect of the DMSO contained in the drug sample added to the cells (data not shown).

The GFP-based readout reflects the number of viable bacteria in the sample after antibiotic treatment. We used INH as a reference drug against MTB-GFP as previously described for a single-cell assay (12, 13). Dose-response curves were calculated with concentrations ranging from $1 \times 10^{-9}$ M to $1 \times 10^{-4}$ M, which were the same as those used for a previously reported single-cell assay (12). We calculated the PII of various concentrations of INH plotted as an INH dose-response curve (Fig. 2). Each point represents the PBMC isolated from at least nine healthy donors, and the standard deviation is shown. At a concentration of $10^{-9}$ M, the PII was 18% and was directly proportional to the INH concentration until reaching a plateau of 60% at $10^{-7}$ M. Thus, the MIC50 under these experimental conditions was around 0.59 $\times 10^{-6}$ or 0.59 $\mu$M (i.e., 0.081 $\mu$g/ml) (Fig. 2A). This value is similar to that calculated for INH in the single-cell assay, with an MIC50 of 0.57 $\mu$M (i.e., 0.078 $\mu$g/ml) (Fig. 2B). In addition, the single-cell assay results have been demonstrated to show a good correlation between the fluorescence counts and CFU counts obtained for reference compounds (12, 13). However, HCS screening would never replace the CFU determination method, which is currently the only technique that enables the exact determination of intracellular bacterial load, even though it gives a faster determination of the ability of a given drug to kill bacteria and enables a faster determination of the MIC of a drug.

The antitubercular activities of various compounds against MTB-GFP were determined by calculating the PII for each experimental concentration (ranging from 1 nM to 1 mM) to assess the sensitivities of the bacteria inside artificial granulomas. At low compound concentrations, the mean of the PII was low as a result of MTB-GFP replication (high number of bacilli in granulomas). At higher concentrations, the mean of the PII increased, due to the diminished number of bacilli in the granulomas. An inhibition of infection of 100% was not reached with any drug (Fig. 3). We calculated the MIC50s of drugs from dose-response curves and compared them to those of extracellular and intracellular (in isolated macrophage cultures) bacterial growth assays, performed in parallel. The extracellular and intracellular MIC50 values were obtained as previously described by Remuñán et al. (17) and Christophe et al. (13), respectively. Under normal assay conditions (medium pH ~7), the MIC50s of INH, MOX, LZD, and PZA against intracellular (artificial granuloma) MTB-GFP were 0.081, 4.12, 1.65, and >5 $\mu$g/ml, respectively (Fig. 3). The MIC50s of INH, MOX, LZD, and PZA against extracellular MTB-GFP were 0.05, 0.33, 0.098, and >5 $\mu$g/ml, respectively. The MIC50s of INH, MOX, LZD, and PZA to intracellular bacteria (in macrophages) were 0.052, 0.27, 0.159, and >5 $\mu$g/ml, respectively. A modest but still measurable activity of PZA under the artificial granuloma conditions was observed. Previous reports found that PZA is devoid of any significant anti-TB activity under extracellular growth conditions at concentrations up to 2 mg/ml (18), although some activity is observed when bacteria are grown at pH 5.5, with an MIC50 between 62.5 and 125 $\mu$g/ml (19). Reports of the activity of PZA in infected macrophages are conflicting; some studies found that PZA was completely inactive (20, 21), whereas another report found that PZA had a modest effect at around 20 $\mu$g/ml (22). For MOX and LZD, our results showed a shift (10- to 15-fold) in the MIC50s between the activities of the compounds under extracellular and artificial granuloma conditions. The MTB-GFP resistance in an artificial granuloma model can be explained by the poor permeability associated with the complex cellular composition of the granuloma, which may prevent the compound from
reaching the mycobacteria (8, 9). In addition, it has been well-known for decades that inside the granuloma, the bacteria change their physiological characteristics (11) and especially their external envelope; therefore, their susceptibility to a given drug may be completely different from that under extracellular conditions or even within single cells. Indeed, without the lymphocyte environment present around infected macrophages within the granulomas, the macrophage intracellular environment is different in single-cell assays, and a different environment with the bacterial physiology may obviously trigger different types of physiological adaptation by the bacteria and thus a different susceptibility to the same drug. Indeed, in this setting, systemic exposure to high concentrations of anti-TB agents is generally required for prolonged periods to generate significant reductions in the CFU burdens of infected patients during the prolonged phase of anti-TB treatment (23, 24).

The main advantage of this technology is that the MIC can quickly be determined for compounds effective against intracellular bacilli, and these values show a good correlation with the CFU counts obtained for reference compounds (12). We adapted HCS to screen reference compounds that target mycobacteria inside artificial granulomas. We used FBS in our assay to avoid interference with human immune factors, except for those produced by PBMC. Additionally, we removed the extracellular nonphagocytosed bacilli by selecting only mature granulomas of index 2 to 4, as described previously (25). This ensured that only internalized bacteria were counted, such that the assay specifically measured the effects of compounds on mycobacteria inside the granuloma. The significant shifts in the MICs observed between the activities of the compounds under extracellular and artificial granuloma conditions highlight the important differences between traditional methods to assess MICs and the artificial in vitro granuloma system. The assessment of MICs in granulomas is consistent with the clinical reality that high concentrations of antibiotic administered over long periods of time are required to generate significant reductions in the CFU burdens of infected patients.

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