Deciphering the Transcriptional Regulation of Cholesterol Catabolic Pathway in Mycobacteria

IDENTIFICATION OF THE INDUCER OF KstR REPRESSOR

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Background: KstR represses expression of numerous genes responsible for cholesterol catabolism in Mycobacterium. Results: 3-Oxo-4-cholestenoic acid is identified as the inducer molecule of M. smegmatis KstR repressor.

Conclusion: Oxidation of C3 and C26 of cholesterol is required to activate the system.

Significance: The finding of the KstR inducer molecule represents new insights in developing new targets to fight against M. tuberculosis.

Cholesterol degradation plays a prominent role in Mycobacterium tuberculosis infection; therefore, to develop new tools to combat this disease, we need to decipher the components comprising and regulating the corresponding pathway. A TetR-like repressor (KstR) regulates the upper part of this complex catabolic pathway, but the induction mechanism remains unknown. Using a biophysical approach, we have discovered that the inducer molecule of KstR in M. smegmatis is not cholesterol but 3-oxo-4-cholestenoic acid, one of the first metabolic intermediates. Binding this compound induces dramatic conformational changes in KstR that promote the KstR-DNA interaction to be released from the operator, retaining its dimeric state. Our findings suggest a regulatory model common to all cholesterol degrading bacteria in which the first steps of the pathway are critical to its mineralization and explain the high redundancy of the enzymes involved in these initial steps.

Mycobacterium smegmatis is a model organism, widely used to study the biology of Mycobacterium tuberculosis. Recent research has used this model to investigate different aspects of cholesterol catabolism (1–3), exploited as a carbon and energy source by the pathogen and necessary for persistence in animal infection models (4). Although a compendium of biochemical and structural studies describe mycobacterial cholesterol catabolism, the degradation pathway and its transcriptional regulation are not yet fully established (5–7). The two first steps in cholesterol catabolism are the oxidation of C3 by cholesterol oxidases or 3β-hydroxysteroid dehydrogenase/isomerases (8–14) and the oxidation of C26 by P450 cytochromes (CYP125 and CYP142) (15–18), which are carried out sequentially and/or simultaneously. These biochemical reactions render the molecules cholest-4-en-3-ona (cholestenone) (after cholesterol C3 oxidation), 3β-hydroxy-5-cholestenic acid (3OHChA) (after cholesterol C26 oxidation), and 3-oxo-4-cholestenoic acid (3OChA) (after C3 and C26 oxidations) (Fig. 1). Remarkably, the enzymes performing these biochemical reactions are highly redundant in M. smegmatis (11, 18, 19).

This study aims to shed light on the regulation of the cholesterol degradation pathway in mycobacteria, which is apparently controlled by only two TetR-type transcriptional repressors: KstR and KstR2 (2, 3, 20). KstR is encoded by gene Rv3574 in M. tuberculosis and gene MSMEG_6042 in M. smegmatis and controls the expression of 83 cholesterol catabolic genes (kstR regulon) responsible for activating the upper and central pathway (2, 19). KstR2 is encoded by gene Rv3557c in M. tuberculosis and gene MSMEG_6009 in M. smegmatis and controls the expression of 15 cholesterol catabolic genes (kstR2 regulon) responsible for the lower pathway (3). Both regulators belong to the TetR family of transcriptional repressors, which is well represented and widely distributed among bacteria and easily recognized by their characteristic HTH DNA-binding motif (21).

Several genes in the kstR regulon are essential for virulence, demonstrating the importance of cholesterol catabolism in the pathogenesis of M. tuberculosis (7, 22–26). KstR binds to the target promoters as a dimer through a conserved motif (TNNAACNGTNTNNA) (2, 20). Despite the critical role played by kstR regulon, the mechanisms involved in this regulation are still poorly understood, and the inducer molecules of KstR are still unidentified (20). The repression of most described TetR-like regulators is released in the presence of an inducer molecule, causing a conformational change in the protein promoting gene transcription (21). Thus, KstR and KstR2 might be induced by cholesterol or cholesstenone because these compounds induce the expression of the kstR and kstR2 regulons in vivo (2, 3, 19, 20). In this respect, we used EMSA analyses to demonstrate the ability of KstR to bind the MSMEG_5228...
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**FIGURE 1. Initial steps of aerobic cholesterol degradation in bacteria.** Sterol degradation proceeds via steroid ring oxidation and side chain degradation (upper route). The exact order of side chain degradation and ring oxidation in vivo is unknown. The depicted metabolites are: (1) cholest-5-en-3β-ol (cholesterol), (1') cholest-4-en-3-one, (2) 26OHCh, (2') 26OHCh-3O, (3) 3OChA, (3') 3OHChA, (4) 3OHChA, (4') cholest-4-en-3-one, (5) AD, and (6) ADD. CYP125 and CYP142, steroid 26-monoxigenases; 3-β-HSD, 3-β-hydroxysteroid dehydrogenase; KstD, 3-ketosteroid Δ1-dehydrogenase; FadD, steroid CoA ligase.

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**EXPERIMENTAL PROCEDURES**

**Chemicals**—Cholesterol, cholest-4-en-3-one, 4-androstene-3,17-dione (AD), 1,4-androstadiene-3,17-dione (ADD), palmitic acid, palmitoyl alcohol, oleic acid, oleyl alcohol, 1-octanol, octanoic acid, decane, tyloxapol, Tween 80, Triton X-100, and streptomycin sulfate were purchased from Sigma-Aldrich. Cholesterol, cholest-4-en-3-one, 4-androstene-3,17-dione (AD), 1,4-androstadiene-3,17-dione (ADD), palmitic acid, palmitoyl alcohol, oleic acid, oleyl alcohol, 1-octanol, octanoic acid, decane, tyloxapol, Tween 80, Triton X-100, and streptomycin sulfate were purchased from Sigma-Aldrich.

Cholesterol-5-ene-3β,26-diol (26-hydroxycholesterol (26OHCh)), 3OHChA, and 3OChA were obtained from Avanti Polar Lipids.

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The promoter region. However, the analyses to evaluate the KstR interactions with its putative inducers, i.e. cholesterol or cholest-4-en-3-one, did not render positive results, and therefore, we could not conclude that these substances directly induce kstR regulon (20). The crystal structure of KstR from *M. tuberculosis* has recently been revealed (Protein Data Bank code 3MNL) but was solved in the absence of inducers.

The literature provides examples of regulators induced by steroids. CmeR from *Campylobacter jejuni* and BreR from *Vibrio cholerae* belong to the TetR family of regulators, and both repress the expression of genes that encode multidrug efflux system components in the absence of bile acids (27, 28). Researchers have described the crystal structure of CmeR in a complex with the bile acids cholate and taurocholate (29). Furthermore, the specific interaction between the negative regulator RepA and testosterone has been also demonstrated in *Comamonas testosteroni* (30).

To provide further insights into the KstR-mediated repression mechanism in mycobacteria, we used circular dichroism to measure the physical interactions of KstR with several intermediates of the pathway that could act as putative inducers. The compounds that modified the secondary structure of KstR were further tested as inducers in transcription assays in vitro. Our results showed that the concerted action of the two primary independent oxidative steps in cholesterol catabolism at C3 and C26 are necessary to produce the metabolite inducing kstR regulon expression.
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TABLE 1
Bacterial strains, plasmids, and primers used in this study

<table>
<thead>
<tr>
<th>Strain, plasmids, and primers</th>
<th>Genotype, description, or sequence</th>
<th>Source or reference</th>
</tr>
</thead>
<tbody>
<tr>
<td>Mycobacterium smegmatis</td>
<td>ept-1, mc26 mutant efficient for electroporation mc2155 strain containing a 666-bp pair deletion in the MSMEG_6042 gene</td>
<td>Ref. 54</td>
</tr>
<tr>
<td></td>
<td>rpoCT, rpsL, endA1, nupG, mc2155, kstR/lacZ (pSEVAP5228 and pMV261)</td>
<td>Ref. 2</td>
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<tr>
<td>Escherichia coli</td>
<td>DH10B, F−, mcrA, Δ (mrr hsdRMS-mcrBC), Φ80lacZΔM15, ΔlacX74, deoR, recA1, araD139, Δ (ara-levu7697, galI, galK, l−, rpsL, endA1, supE44)</td>
<td>Invitrogen</td>
</tr>
<tr>
<td></td>
<td>BL21(DE3), F−, ompT, hsdSB (rB−mB−), gal, dcm, ΔADE3 (harboring gene 1 of the RNA polymerase from the phage T7 under the PlacIJS promoter)</td>
<td>Ref. 31</td>
</tr>
<tr>
<td>Plasmids</td>
<td>pET6042, pET29a (+) cloning and expression vector (KanR, oriColE1, T7 promoter) containing MSMEG_6042 gene</td>
<td>Ref. 20</td>
</tr>
<tr>
<td></td>
<td>pU9JPQ3, pU9J vector containing the chimeric promoter P5228 cloned into EcoRI and BamHI restriction sites</td>
<td>This study</td>
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<tr>
<td></td>
<td>pUI5228, pU9J vector containing the P5228 promoter cloned into EcoRI and BamHI restriction sites</td>
<td>Ref. 20</td>
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<tr>
<td></td>
<td>pUC9 derivative, vector for in vitro transcription, Ap−</td>
<td>Ref. 36</td>
</tr>
<tr>
<td></td>
<td>pCD01 vector containing the chimeric promoter P5228 cloned into EcoRI and PstI restriction sites</td>
<td>This study</td>
</tr>
<tr>
<td></td>
<td>pSEVA651, Promoterless cloning vector, GmR, RFS1010</td>
<td>Ref. 33</td>
</tr>
<tr>
<td></td>
<td>pSEVAPQ3, pSEVA651 vector containing the P5228::lacZ translational fusion</td>
<td>This study</td>
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<tr>
<td></td>
<td>pMV261, Shuttle expression vector for expressing genes under the control of phsp60 promoter, K−R</td>
<td>Ref. 34</td>
</tr>
<tr>
<td></td>
<td>pMV6042, pMV261 containing MSMEG_6042 gene cloned into PstI and Sall restriction sites</td>
<td>This study</td>
</tr>
<tr>
<td>Primers</td>
<td>pU9JPQ3-F, pU9JPQ-R, GAATTCCTGACATCGAATCGCCACCATAG</td>
<td>This study</td>
</tr>
<tr>
<td></td>
<td>pMV6042-F, pMV6042-R, CTGCGAGCTTTCTGCTAGCCACGCGTTGG</td>
<td>This study</td>
</tr>
<tr>
<td></td>
<td>pET29bhisR-F, pET29bhisR-R, GCCACGACCTGGCTTGGTGCA</td>
<td>This study</td>
</tr>
<tr>
<td></td>
<td>pCD01-F, pCD01-R, GTCTTCTGCTGCGTTTTC</td>
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<tr>
<td></td>
<td>pMV6042-F, pMV6042-R, GCCACGACCTGGCGTTTTC</td>
<td>This study</td>
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<tr>
<td></td>
<td>pU9JPQ3-F, pU9JPQ3-R, GAATTCCTGACATCGAATCGCCACCATAG</td>
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<td>pMV6042-F, pMV6042-R, GCCACGACCTGGCGTTTTC</td>
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<td>pCD01-F, pCD01-R, GTCTTCTGCTGCGTTTTC</td>
<td>This study</td>
</tr>
<tr>
<td></td>
<td>pMV6042-F, pMV6042-R, GCCACGACCTGGCGTTTTC</td>
<td>This study</td>
</tr>
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</table>

Ndel and Sfil were included four nucleotides downstream of the Shine-Dalgarno sequence. An EcoRI restriction site was also added five nucleotides upstream of the −35 box. The EcoRI-SfoI-digested fragment carrying the chimeric promoter P5228 was cloned into the promoter-probe pU9J plasmid (Table 1). The resulting plasmid pU9JPQ3 was used as a PCR template to amplify the synthetic promoter region using the primers pU9JPQ-F and pU9JPQ-R (Table 1) carrying the EcoRI and PstI restriction sites, respectively (indicated in bold). The PCR product was digested with EcoRI and PstI and subsequently cloned into the plasmid pCD01, which contains the pUC19 polylinker flanked by the divergent terminators rpoCT and rrrBT1T2, respectively (Table 1). The resulting plasmid pCDPQ3 was used as a template to amplify the PQ3 probe used in the EMSAs and for the transcription assays.

P5228::lacZ and P5228::lacZ Translational Fusion Construction—To perform the in vivo experiments, plasmids pUI5228 (20) and pU9JPQ3 (Table 1) harboring the P5228::lacZ and P5228::lacZ translational fusions, respectively, were digested with NotI and ligated to a NotI-digested plasmid pSEVA651 (33) (Table 1) generating plasmids pSEVAP5228 and pSEVAPQ3, respectively. The resulting plasmids were extracted from E. coli DH10B and electroporated into competent M. smegmatis ΔkstR (2) cells generating the strains M. smegmatis mc2155 ΔkstR (pSEVAP5228) and M. smegmatis mc2155 ΔkstR (pSEVAPQ3), respectively. Then both strains were complemented with gene kstR. To do so, gene MSMEG_6042 was amplified using as a template the pET6042 plasmid and the oligonucleotides pMV6042-F and pET29bhisR (Table 1) carrying the PstI and Sall restriction sites, respectively (indicated in bold). The PCR product was digested with PstI and Sall and subsequently cloned into pMV261 (34) (Table 1). The resulting plasmid pMV6042 was extracted from E. coli DH10B and electroporated into competent cells of M. smegmatis ΔkstR (pSEVAP5228) and M. smegmatis ΔkstR (pSEVAPQ3), respectively. As a control, the empty vector PMV261 was electroporated into both strains ΔkstR (pSEVAP5228) and ΔkstR (pSEVAPQ3) giving rise to strains ΔkstR (pSEVAP5228 and pMV261) and ΔkstR (pSEVAPQ3 and pMV261).

KstR Overexpression and Purification—The recombinant strain E. coli BL21 (DE3) carrying plasmid pET6042 (Table 1),
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Analytical Ultracentrifugation—Sedimentation velocity experiments were carried out using an Optima XL-I analytical ultracentrifuge (Beckman-Coulter) equipped with UV-visible absorbance optics at 20 °C in an AnTi50 rotor and 12-mm double sector centerpieces. Experiments were performed using 1 mg mL⁻¹ of KstR in 20 mM potassium phosphate buffer at pH 7.5 containing 150 mM KCl in the absence and in the presence of 250 μM of palmitic acid, 3OHChA, or 3OChA. The sedimentation coefficient distributions were calculated by least squares boundary modeling of sedimentation velocity data using the c(s) method, as implemented in the SEDFIT software (36, 37). Partial specific volume, , for KstR samples without ligands was calculated at 0.7303 mg/mL based on the amino acid sequence and at 0.7305 mg/mL for the KstR-250 μM ligands as a sum of weight fractions of for protein (0.7334) and for ligand (0.9880) in solution (38). The value of for the ligands 3OHChA and 3OChA was assumed to be the same as cholesterol because of the high similarity of the molecules.

Dynamic Light Scattering—Dynamic light scattering experiments were performed with a DynaPro instrument (Protein Solutions Inc.). Measurements were taken at 25 °C. A solution of protein with a concentration of 0.25 mg mL⁻¹ in 20 mM potassium phosphate buffer at pH 7.5 containing 150 mM KCl in the absence and in the presence of 250 μM of 3OHChA or 3OChA was used. The software provided by the manufacturer was used to calculate the diffusion coefficient of the protein.

Electromobility Shift Assays—Probe 5228FP was prepared as previously described (20). Probe PQ3, containing the chimeric F₃₃₉₉₉₉ promoter, was prepared in the same way but using pJD01-F and pJD01-R (Table 1) as labeled and unlabeled oligonucleotides, respectively, and 10 ng of the plasmid pJCDPQ3 as a template. Varying amounts of purified KstR were incubated with 0.5 nm of labeled probes in binding buffer (20 mM Tris-HCl at pH 8, 150 mM KCl, 10 mM MgCl₂, 10% glycerol, 2 mM β-mercaptoethanol, and 50 μg mL⁻¹ BSA) in a final volume of 9 μL. For specific and nonspecific competition reaction mixtures, 40-, 400-, or 4000-fold excess of unlabeled probe and 0.5, 1, and 2 μg of unspecific DNA (salmon sperm) were added, respectively. To test the binding of KstR to DNA in the presence of the different inducers, the compounds were dissolved in methanol and were incubated with KstR for 10 min at room temperature before adding the DNA probe. The EMSA reaction mixtures were incubated for 20 min at room temperature and fractionated by electrophoresis on a 5% polyacrylamide gels buffered with 0.5× TBE (45 mM Tris borate, 1 mM EDTA). The gels were dried onto Whatman 3MM paper and exposed to Hyperfilm MP (Amersham Biosciences) using amplifying screens (Cronex DuPont Lightning Plus). Bands corresponding to free DNA probes and KstR-DNA complex were quantified using the program Multi Gauge V 3.0 (FUJIFILM). The apparent dissociation constants (Kₛ) for the binding of 5228FP DNA probe to KstR were estimated using data from EMSA titration experiments, where the amount of DNA was maintained constant, and the amount of protein was varied. The intensity of the bands served to estimate the percentage of 5228FP DNA probe shifted by the binding to KstR, and these data were plotted against the concentration of protein to calculate the apparent
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dissociation constant. $K_d$ for the displacement of KstR from the 5228FP and PQ3 DNA probes was estimated using the intensity percentage of the nonshifted band in the presence of different concentrations of the putative inducers.

Run-off Transcription Assays—Multiple-round transcription by E. coli RNA polymerase (RNAP) was carried out under standard conditions (39), using buffer T (50 mM Tris- HCl at pH 7.5, 10 mM MgCl$_2$, and 100 mM KCl) containing 1 mM DTT and 500 $\mu$g ml$^{-1}$ BSA. The final volume of the reaction mixture was 20 $\mu$l, containing 1 mM supercoiled DNA plasmid pCDPQ3 (or pCD01 for control reactions) (Table 1), 0.5 $\mu$m KstR, 40 mM $\sigma^{70}$-containing RNAP (USB), 1 mM ATP, 1 mM GTP, 1 mM CTP, 0.1 mM UTP (Roche), and 2.5 $\mu$Ci of [$\alpha\text{-}^{32}\text{P}$]UTP (3000 Ci/mmol) (PerkinElmer Life Sciences). First, a reaction mixture containing KstR (8 $\mu$l) and DNA plasmid (5 $\mu$l) was incubated at 37 $^\circ$C for 5 min. To test the effect of the inducers in the transcription reaction, they were dissolved in methanol and incubated with KstR for 10 min at room temperature before adding DNA. Elongation was started by the addition of 7 $\mu$l of prewarmed mixture containing cold nucleotides, [$\alpha\text{-}^{32}\text{P}$]UTP and RNAP in buffer T. The reactions were allowed to proceed for 5 min at 37 $^\circ$C and were stopped by adding 10 $\mu$l of loading buffer (20 mM EDTA, pH 8, in 96% v/v formamide containing bromphenol blue and xylene cyanol blue). After heating samples to 70 $^\circ$C, they were subjected to electrophoresis on denaturing 7M urea-containing polyacrylamide gels, buffer with 0.5 $\times$ TBE at 300 V. Drying, exposition, and quantification were as described for EMSA experiments.

RNA Extraction—RNA for real time quantitative PCR was extracted from 15 ml of cultured M. smegmatis mc$^{\text{155}}$ growing in 1.8 mM cholesterol, 18 mM glycerol, or 3 mM palmitic acid as described previously (11). RNA was treated with the DNase I and removal treatment kit (Ambion) according to the manufacturer’s instructions. RNA quantity was measured using a NanoPhotometer® Pearl (Implen).

Real Time Quantitative PCR—Reverse transcription was performed using the transcriptor first strand cDNA synthesis kit (Roche). Reactions were done in a volume of 20 $\mu$l containing 1 $\mu$g of purified RNA, 60 $\mu$m of random hexamer primer, 1 mM of dNTPs, and 10 units of reverse transcriptase. The template-primer mixture was first denatured by heating for 10 min at 65 $^\circ$C and immediately cooling on ice. The remaining components were added and then incubated 10 min at 25 $^\circ$C followed by 30 min at 55 $^\circ$C. Finally, the reverse transcriptase was inactivated by heating 5 min at 85 $^\circ$C. Real time quantitative polymerase chain reactions for the analysis of expression of single genes were performed using a LightCycler® 480 instrument (Roche). Reactions contained 5 $\mu$l of a 1:5 cDNA dilution, 0.25 $\mu$m of each primer (Table 1) and 10 $\mu$l of LightCycler® 480 SYBR Green I Master (Roche) in a total volume of 20 $\mu$l. The reactions were denatured at 95 $^\circ$C for 5 min before cycling for 50 cycles of 95 $^\circ$C for 10 s, 62 $^\circ$C for 10 s, and 72 $^\circ$C for 10 s. Each gene was measured in triplicate in three independent experiments. The relative amount of mRNA for each gene was determined using the mRNA levels of sigA (MSMEG_2758) as internal control (40).

RESULTS

KstR-Effector Interaction Analyzed by Thermal Denaturation—We assumed that the previous EMSA analyses to determine KstR interaction with its postulated inducers, i.e. cholesterol or cholestenone, did not render positive results because of the low solubility of these compounds and the presence of detergents interfering with the interactions (20). This assumption prompted us to study the KstR-effector interactions by CD to monitor the conformational changes produced by these interactions and effects on the thermal stability of the regulator in less complex conditions (i.e. in the absence of DNA) (35). In the absence of ligands, KstR showed a denaturation profile consistent with two states: folded and unfolded (Fig. 2A, black squares), and a $T_{m}$ of 62.4 ± 0.1 $^\circ$C (Table 2). The addition of 0.5 mM of cholesterol or cholestenone did not induce any significant changes in the thermal denaturation profile (Table 2), suggesting that these compounds do not interact with KstR, as previously reported (20).

In microarray assays, Schnappinger et al. (23) showed that palmitic acid induced the expression of several genes in the kstR regulon in M. tuberculosis, suggesting that perhaps this compound could be an effector of KstR. Surprisingly, when we tested the effect of palmitic acid on the thermal stability of KstR, we observed that higher concentrations of this compound resulted in lower KstR thermal stability, reaching a maximum of 41 $^\circ$C at saturating concentrations (i.e. 250 $\mu$m) (Fig. 2A and Table 2). This reduced thermal stability clearly indicates drastic conformational changes, which occur upon binding of palmitic acid to KstR. This effect could only be reproduced with long chain fatty acids, like oleic acid (Table 2). The corresponding long chain alcohols, palmityl and oleyl alcohols, did not significantly affect the stability of KstR even at 500 $\mu$m. Neither did medium chain fatty acid nor its corresponding alcohols (octanoic acid and octanol) or alkanes (decane) (Table 2). These results indicated that only compounds with a long hydrophobic carbon chain and carboxylic moiety were able to induce the conformational changes that reduced the thermal stability of KstR.

To check whether the changes observed in the presence of palmitic acid might be due to detergent effects, we analyzed the influence of two typical detergents: cholic and deoxycholic acids (Fig. 2D). However, these molecules did not alter KstR stability, and therefore, the effect of palmitic acid cannot be ascribed to detergent effects.

We realized that two hydrophobic acid substances, 3OHChA and 3OChA (Fig. 1) that are produced in the initial steps of the cholesterol catabolic pathway (see Introduction) have structural similarities with palmitic acid, i.e. they have a carboxylic acid group at C26 and an aliphatic side chain at C17. When we tested both molecules by CD, they also induced a huge reduction in the $T_{m}$ of KstR (43 and 34 $^\circ$C, respectively, at a concentration of 250 $\mu$m) (Table 2). 3OHChA induced the same denaturation profile in KstR as palmitic acid, showing both states: folded and unfolded (Fig. 2B). However, the denaturation profile induced by 3OChA was very different, showing two denaturation states at lower concentrations (i.e. ≤50 $\mu$m) and a bimodal profile at higher concentrations (i.e. ≥100 $\mu$m).
The bimodal profile is consistent with the presence of at least three states (folded, intermediate, and unfolded). This bimodal behavior suggested that the conformational changes induced by the interaction of the ligand with the protein could affect both repressor domains (i.e. DNA- and effector-binding domains) differently and consequently relax the interactions between them and permit observation of two separate transitions, corresponding to two structurally independent domains. The clear effect of 3OHChA and 3OChA on the thermal stability of KstR suggested that they, or other related substances, could be inducers of the kstR regulon, rather than cholesterol or cholestene, as postulated previously. Therefore, we also checked whether KstR thermal stability was affected by other intermediate compounds of the catabolic pathway, such as 26OHCh, AD, and ADD (Fig. 1). Interestingly, 26OHCh is the first catabolic intermediate resulting from oxidation of the aliphatic side chain by the P450 cytochromes CYP125 and CYP142, whereas AD and ADD are central metabolites lacking the aliphatic side chain. None of these compounds showed any significant effect on the thermal stability of the regulator (Table 2). These results reinforced our hypothesis that the aliphatic side chain and the carboxylic group in the molecule are necessary to support the interaction of the effector with KstR.

To further analyze the effect of inducers in the KstR structure, we determined the far-UV CD spectra of KstR in both the absence and presence of palmitic acid, 3OHChA, and 3OChA (Fig. 3) and estimated its secondary structure content (Table 3).
As expected, the spectrum of the free KstR (Fig. 3, black line) corresponds to a protein with a high α-helical content (63%), in reasonable agreement with the α-helical content of the crystallographic structure of *M. tuberculosis* KstR (84%, Protein Data Bank code 3MNL). The addition of palmitic acid (Fig. 3, red line), 3OHChA (Fig. 3, green line), and 3OChA (Fig. 3, blue line) at saturating concentrations (250 μM) showed a significant decrease in α-helical content of the protein by 50, 39, and 44%, respectively (Table 3). This reduction in α-helical content is consistent with the lower thermal stability of KstR observed on adding these compounds.

**KstR Is Homodimeric in Solution**—Many TetR-family regulators show a homodimeric arrangement (21). Given the major changes in secondary structure content of KstR induced upon binding of the putative effectors, we performed analytical ultracentrifugation and dynamic light scattering experiments to check whether, upon binding, these compounds were able to modify the homodimeric arrangement of free KstR observed in solution. The sedimentation velocity profiles (Fig. 4) and the calculated molecular mass obtained using the Svedberg equation with the values of the sedimentation and the diffusion coefficients (data not shown) showed that most of the KstR protein was present as a dimer in the solution, independent of the presence or absence of effectors. Curiously, a small fraction of KstR was present as a tetramer (≈14%), but the physiological relevance of this finding is uncertain given the high concentration of the purified protein in the assay.

**3-β-Oxo-cholestenoic Acid Released KstR-DNA Interaction**—To determine whether the putative inducers of KstR promoting thermal instability were able to release the KstR binding from its...
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In Vitro Activation of a Chimeric KstR-regulated Promoter by 3OChA—In vitro transcription experiments were performed to study the functionality of KstR as a transcriptional repressor and to analyze the induction effect of 3OChA, 3OHChA, and palmitic acid on the KstR-regulated promoters under conditions that could better mimic their physiological performances. It is noteworthy that previous experiments showed that the M. smegmatis P\textsubscript{5228} promoter is hardly recognized in vitro by the E. coli RNAP (data not shown), and therefore, we designed a chimeric synthetic promoter P\textsubscript{PQ3} containing the –35 and –10 boxes of the lacUV5 promoter from E. coli and the consensus KstR operator sequence from M. smegmatis. Because the operator region of the P\textsubscript{5228} promoter from M. smegmatis is located between the –10 and –35 boxes (20), we located the KstR operator recognition sequence in the same position of the chimeric P\textsubscript{PQ3} promoter (Fig. 6A).

To demonstrate that the P\textsubscript{PQ3} promoter is functional in M. smegmatis, the P\textsubscript{PQ3}:\textit{lacZ} translational fusion present in plasmid pUJ9PQ3 was cloned into the pSEVA651 vector (Table 1), which replicates in M. smegmatis, resulting in plasmid pSEVAPQ3. As expected, the deregulated \textit{M. smegmatis \Delta kstR} (pSEVAPQ3) transformants turned blue in X-Gal-containing medium, because of the expression of \textit{lacZ} (Fig. 7). Moreover, when this recombinant strain was transformed with plasmid pMV6042, which expresses \textit{kstR}, the resulting \textit{M. smegmatis \Delta kstR} (pSEVAPQ3 and pMV6042) cells turned white in X-Gal-containing medium, suggesting that KstR is able to repress the expression of P\textsubscript{PQ3}:\textit{lacZ}. Similar results were obtained using the \textit{lacZ} fusion with the native promoter P\textsubscript{5228} (Fig. 7).

To determine \textit{in vitro} viability of the synthetic promoter, first we checked whether KstR was able to recognize the P\textsubscript{PQ3} promoter by EMSA assays, using the labeled PQ3 DNA probe containing this promoter. Fig. 6B shows that, as expected, KstR is able to bind to the PQ3 DNA probe in a protein concentration-dependent manner. Furthermore, the interaction is specific because an excess of unlabeled PQ3 DNA probe abolished its retardation, whereas the unrelated DNA from salmon sperm did not. Fig. 6C shows that, as described above for 5228FP DNA probe, KstR was also released from the PQ3 DNA probe in the presence of a low concentration of 3OChA. Remarkably, the effect of palmitic acid was greater for the PQ3 DNA probe than for the 5228FP DNA probe. Nonetheless, higher concentrations of palmitic acid than 3OChA are required to fully release KstR (Fig. 6C). The apparent $K_d$ values estimated for 3OChA and palmitic acid were 7.3 ± 2.4 and 226 ± 26 μM, respectively, using the PQ3 DNA probe (0.5 nM) and KstR (500 nM) (Fig. 6E). The finding that 3OChA and palmitic acid released the KstR-PQ3 interaction more efficiently than the KstR-P5228 could simply be a consequence of a less effective interaction between KstR and the artificial P\textsubscript{PQ3} promoter. As described above for the 5228FP DNA probe, 3OHChA was unable to release KstR from the PQ3 DNA probe, suggesting that this compound is not an effector (Fig. 6D).

![Figure 5. Inhibition of KstR-P5228 interaction by 3OChA.](http://www.jbc.org/)

A. analysis by EMSA of KstR binding to the P\textsubscript{5228} promoter. The 5228FP DNA probe concentration was 0.5 nM. Purified KstR were used at 0 nM (lane 1), 100 nM (lane 2), 500 nM (lane 3), and 1 μM (lane 4). For lanes 5–10, the KstR concentration was 500 nM. Lanes 5–7 contained unlabeled 5228FP DNA probe (40-, 400-, and 4000-fold, respectively). Lanes 8–10 contained unrelated DNA from salmon sperm (0.5, 1.0, and 2.0 μg, respectively). B. analysis by EMSA of the KstR-5228FP DNA probe complex in the presence of 3OChA, palmitic acid, and 3OHChA. KstR concentration was 500 nM, except in lanes 1 and 16 (0 nM). 3OChA (lanes 4–9), palmitic acid (lanes 10–15), and 3OHChA (lanes 19–24) were added at 1, 3, 6, 12, 25, and 50 μM. KstR plus 5% of methanol (lane 3 and 18) was included as control. C. analysis by EMSA of the KstR-5228FP complex in the presence of related compounds at 250 μM: cholestenone (lane 4), cholesterol (lane 5), 3OChA (lane 6), 3OHChA (lane 7), ADD (lane 8), palmitic acid (lane 9), palmitoyl alcohol (lane 10), oleic acid (lane 11), oleyl alcohol (lane 12), α-octanoyl (lane 13), and octanoic acid (lane 14). Controls without inducers (lane 2) and with 5% of methanol were included. KstR concentration was 500 nM except in lane 1 (0 nM). D. determination of the apparent $K_d$ for KstR binding to the 5228FP probe in the presence of 3OChA. The apparent $K_d$ is the 3OChA concentration at which 50% of the total DNA probe was bound to KstR. This value was determined from the experiment in B.

target DNA, we performed EMSA assays using the labeled 5228FP DNA probe containing the P\textsubscript{5228} promoter (20). This interaction is specific because an excess of unlabeled 5228FP DNA probe abolishes its retardation, whereas unspecific DNA from salmon sperm did not (Fig. 5A). The apparent dissociation constant ($K_d$) of KstR for the 5228FP DNA probe (0.5 nM) deduced from EMSA experiments was 0.21 ± 0.07 μM (data not shown).

To check whether palmitic acid, 3OHChA, or 3OChA was able to release the KstR (500 nM) binding from its operator region, we used the 5228FP DNA probe (0.5 nM) in the EMSA assays. Fig. 5B shows that no significant decrease in affinity of KstR to the probe was observed in the presence of palmitic acid or 3OHChA, whereas KstR was clearly released from DNA in the presence of 3OChA at very low concentrations, i.e. from 3 to 50 μM with an estimated apparent $K_d$ of 8.5 ± 2.2 μM (Fig. 5D). These results suggest that only 3OChA is able to induce the precise conformational change required to release the KstR-DNA interaction. However, when lower concentrations of KstR (250 nM) were used in the EMSA assays, interestingly, a release of the DNA probe was observed in the presence of high palmitic acid concentrations (1 mM), but not in the presence of 3OHChA (data not shown). The other compounds tested as putative effectors in CD experiments (Table 2) were also checked by gel retardation, but none of them released KstR from the 5228FP DNA probe (Fig. 5C).
These results indicated the possible analysis of the effect of KstR and the putative inducer molecules on transcription initiation in the chimeric *E. coli*-M. smegmatis *P*<sub>Q3</sub> promoter by multiple-round in vitro transcription using *E. coli* RNA polymerase. For these experiments, the *P*<sub>Q3</sub> promoter was cloned into pCD01 plasmid to yield pCDPQ3 (Table 1). As expected, when this plasmid was used as a template, a 152-nucleotide transcript was observed because of the *P*<sub>Q3</sub> promoter activity (Fig. 8, *A*, lanes 2 and 3, and *B*, lane 2), whereas the empty control plasmid pCD01 only rendered the RNA1 control transcript (108 nucleotides) (Fig. 8, *A*, lane 1, and *B*, lane 1).

KstR addition to the reaction mixture repressed *P*<sub>Q3</sub> activity (Fig. 8A, lanes 4 and 5, and *B*, lanes 3 and 4), demonstrating that KstR can repress the chimeric *P*<sub>Q3</sub> promoter in vitro. Increasing concentrations of 3OChA (1–50 μM) (Fig. 8A, lanes 6–11) restored the transcription level of the *P*<sub>Q3</sub> promoter. However, the addition of palmitic acid, even at high concentrations (250 μM) did not cause such derepression (Fig. 8, *B*, lane 9, and *C*).

The same negative result was observed in the presence of cholesterol, cholestenone, and 3OHChA (Fig. 8, *B*, lanes 5–7, and *C*). These results demonstrate that 3OChA was the only compound able to activate the KstR mediated repression at the *P*<sub>Q3</sub> promoter (Fig. 8B, lane 8).

To further discard the palmitic acid as effector of the KstR protein, we analyzed the expression of several genes included in the KstR regulon that are up-regulated in the presence of cholesterol by quantitative real-time PCR experiments. As is shown in Fig. 9, we selected some genes involved in the cholesterol side chain degradation, *cyt125A3* (*MSMEG_5995*) and *fadA5* (*MSMEG_5996*), and also genes implicated in the first steps of the sterol ring catabolism, *kstD* (*MSMEG_5941*) and *kshA* (*MSMEG_5925*). All the genes tested were induced in the presence of cholesterol but not in the presence of palmitic acid. These results confirm the in vitro transcription results in which the palmitic acid is not able to activate repression mediated by KstR.

**DISCUSSION**

Bacterial catabolism of cholesterol, and other related steroid compounds, has acquired greater relevance in recent years, not only because of their importance as environmental pollutants...
but because of the fundamental role cholesterol plays in *M. tuberculosis* infections (22, 23, 26, 43, 44). Expression of the genes constituting the cholesterol catabolic pathway is controlled by two proteins: KstR and KstR2 (2, 3, 19). Previous studies have failed to identify the inducer of the pathway, but it was putatively ascribed to cholesterol or cholestenone (2, 3, 19).

To date, all *in vitro* experiments attempting to show that these substances could interact with KstR to trigger the pathway have failed (20). Moreover, attempts to demonstrate the implication of these compounds in the induction of KstR, by constructing *M. smegmatis* mutants blocked in the first steps of the pathway, were unsuccessful because of the high redundancy of the enzymes involved in these processes (11, 18).

Here, the thermal denaturation analyses with palmitic acid constitute the first experimental evidence that KstR can selectively interact with large hydrophobic carboxylic acids. This led to the exploration of other carboxylic compounds as putative effectors, such as 3OHChA and 3OChA, which are the first intermediates of the cholesterol catabolic pathway. CD showed that the binding of these molecules caused a conformational change in KstR, drastically reducing its thermal stability. Such structural destabilization can most likely be ascribed to a decrease in the α-helix content, as confirmed by comparing the far-UV CD spectra of KstR with and without these compounds (Fig. 3).

Conformational changes in the secondary structure caused by the binding of an effector have been described for other regulators, either repressors or activators. Interestingly, in most cases the effectors increased the stability of the protein (45–47), in contrast with the huge decrease in KstR stability. In this respect, most ligands stabilize proteins upon binding, thereby increasing their melting temperature; however, some ligands destabilize proteins by binding primarily to the unfolded state of the protein and destabilizing it (i.e. reducing protein melting temperature) (48). Ligands that stabilize proteins may be called N-binders (N-ligands, upshifters), and...
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FIGURE 9. Effect of cholesterol and palmitic acid on the expression levels of kshA (MSMEG_5925), ksdD (MSMEG_5941), cyp125A3 (MSMEG_5995), and fada5 (MSMEG_5996) in M. smegmatis. The data represent the fold change relative to expression in glycerol. The error bars represent standard deviation calculated from the results of three independent experiments.

ligands that destabilize proteins may be called U-binders (U-ligands, downshifters) (48). Mathematical models that quantitatively describe protein destabilization by ligands consider ligand binding not only to the native state but also to the unfolded state of the protein. Consequently, the KstR ligands (i.e. palmitic, 3OHChA, and 3OChA acids) can be classified as U-binders and appear to stabilize the unfolded state.

The interaction between KstR and 3OChA appears to differ from that observed with palmitic acid or 3OHChA, as reflected by the atypical bimodal denaturation curve observed by CD. This result suggests that 3OChA induces a more complex effect on the KstR structure than the other compounds. Such a specific effect might be critical to release the regulator from the effector molecule of the KstR repressor, allowing the expression of genes in the cholesterol catabolic pathway in mycobacteria. This is of great relevance because these compounds are not commercially available, we could not test them as putative inducers. Moreover, a recent study suggests that side chain and ring degradation of cholesterol could occur simultaneously in M. tuberculosis (53); therefore, other ring- and side chain-degraded intermediates of the pathway might be alternative inducers.

Although other alternative inducers may exist, our results demonstrate, for the first time, that 3OChA (an intermediate of the cholesterol side chain degradation) acts as an inducer molecule of the KstR repressor, allowing the expression of genes in the kstR regulon. We do not fully understand why some regulatory systems select an intermediate metabolite as inducer rather than the initial substrate of the pathway. We could speculate that mycobacterial cells have selected 3OChA as inducer of the kstR regulon, instead of cholesterol, because 3OChA is more soluble than cholesterol. Solubility should facilitate its cytoplasmic diffusion, reaching the multiple KstR-regulated promoters distributed in different clusters all around the chromosome. It is worth mentioning that the bacterial regulators CmeR and BreR recognize soluble bile acids as effectors (27, 28).

In summary, our findings provide new insights into the transcriptional regulation mechanisms involved in the cholesterol catabolic pathway in mycobacteria. This is of great relevance given the critical role of cholesterol degradation in the survival of M. tuberculosis. The data presented here may represent the first step to developing new drugs aimed at disrupting the regulation of cholesterol catabolism and help to fight the infection caused by this pathogen.
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Identification of the Inducer of KstR Repressor

Deciphering the Transcriptional Regulation of Cholesterol Catabolic Pathway in Mycobacteria: IDENTIFICATION OF THE INDUCER OF KstR REPRESSOR

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