Transposon mutagenesis of Mycobacterium marinum identifies a locus linking pigmentation and intracellular survival

Lian-Yong Gao  
*University of California - San Francisco*

Richard Groger  
*Washington University School of Medicine in St. Louis*

Jeffery S. Cox  
*University of California - San Francisco*

Stephen M. Beverley  
*Washington University School of Medicine in St. Louis*

Elise H. Lawson  
*University of California - San Francisco*

*See next page for additional authors*

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Transposon Mutagenesis of *Mycobacterium marinum* Identifies a Locus Linking Pigmentation and Intracellular Survival

Lian-Yong Gao,1 Richard Groger,2 Jeffery S. Cox,1,3 Stephen M. Beverley,4 Elise H. Lawson,1 and Eric J. Brown1**

Program in Host-Pathogen Interactions1 and Department of Microbiology and Immunology,3 University of California, San Francisco, San Francisco, California 94143, and Departments of Medicine1 and Molecular Microbiology,3 Washington University School of Medicine, St. Louis, Missouri 63110

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Pathogenic mycobacteria survive and replicate within host macrophages, but the molecular mechanisms involved in this necessary step in the pathogenesis of infection are not completely understood. *Mycobacterium marinum* has recently been used as a model for aspects of the pathogenesis of tuberculosis because of its close genetic relationship to *Mycobacterium tuberculosis* and because of similarities in the pathology and course of infection caused by this organism in its natural hosts, fish and frogs, with tuberculosis in humans. In order to advance the utility of the *M. marinum* model, we have developed efficient transposon mutagenesis of the organism by using a *Drosophila melanogaster* mariner-based transposon. To determine the efficiency of transposition, we have analyzed pigmentation mutants from the transposon mutant library. In addition to insertions in four known genes in the pathway of pigment biosynthesis, two insertions in novel genes were identified in our mutant library. One of these is in a putative inhibitor of the carotenoid biosynthesis pathway. The second unexpected insertion is in an intergenic region between two genes homologous to Rv2603c and Rv2604c of *M. tuberculosis*. In addition to a pigmentation defect, this mutant showed increased susceptibility to singlet oxygen and grew poorly in murine macrophages. Complementation with *M. tuberculosis* genomic DNA encompassing Rv2603c to Rv2606c corrected the pigmentation and growth defects of the mutant. These data demonstrate the utility of mariner-based transposon mutagenesis of *M. marinum* and that *M. marinum* can be used to study the function of *M. tuberculosis* genes involved in intracellular survival and replication.

The global burden of *Mycobacterium tuberculosis* infection is overwhelming, with approximately one-third of the world’s population infected and 2 million deaths each year (9). As an intracellular obligate human pathogen, *M. tuberculosis* has evolved a complex parasitic lifestyle and sophisticated mechanisms to combat host defense machinery. It modulates a number of host cell processes, including inhibition of acidification of the bacterium-containing phagosome and its maturation to a phagolysosome (7, 34), inhibition of host cell apoptosis to benefit intracellular bacterial growth and to evade detection and destruction by the host immune system (12, 17), and inhibition of the macrophage response to gamma interferon, thus altering antigen presentation (20, 24, 42). All of these mechanisms are thought to lead ultimately to enhanced survival of *M. tuberculosis* within macrophages. Despite this understanding of the exploitation of host cell processes by mycobacteria, the bacterial components responsible for mediating these processes are largely unknown. In addition to these basic issues in host-microbe interaction, efforts to understand the molecular bases for mycobacterial subversion of host defense has value for the development of new antibiotics that target these bacterial mediators. One direct and effective approach to this goal is to generate, isolate, and characterize defined mutations that affect steps in the pathogenesis of infection.

Transposon mutagenesis is a powerful technique for the identification of bacterial virulence factors which uses a traceable mobile element to randomly disrupt genes in the chromosome. Several transposable elements have been identified and isolated from *Mycobacterium* species, such as IS1096 (from *Mycobacterium smegmatis*) and IS6110 (from *M. tuberculosis*), and used to generate transposon mutants in mycobacteria (15, 21). However, these transposons do not function in all mycobacteria (22, 41) and seem to require recognition of relatively large sequences for insertion (21). Therefore, the development of a transposon that functions in a broad host range, recognizes a short sequence for insertion, and segregates from transposase upon chromosomal insertion should provide an extremely useful and potentially more-general tool for genetic studies of mycobacteria as well as other microorganisms. Such potentially valuable transposon systems have been identified, initially in insects, and include members of the *mariner/Tc1* transposon superfamily (16, 27). *Mos1* (from *Drosophila melanogaster* [32]) and *Himar1* (from horn fly *Haematobia irritans* [19]) are among the best-studied *mariner* transposons that target insertion at a TA dinucleotide recognition site (27). *Mariner* transposons are able to insert into diverse genomes of distantly related organisms, including both eukaryotes and prokaryotes (3, 11, 14, 19, 33, 36).

*Mycobacterium marinum*, a fish, amphibian, and opportunistic human pathogen, has recently been developed as a model system for studying *M. tuberculosis* pathogenesis (6, 28, 29, 31, 40). *M. marinum* is phylogenetically closest to members of the *M. tuberculosis* complex (43), and the infection it causes in its natural hosts manifests pathological hallmarks of tuberculosis, including granulomas (6, 31, 40). These observations suggest...
that many of the basic mechanisms of disease initiation are conserved between \textit{M. marinum} and \textit{M. tuberculosis}. \textit{M. marinum} grows significantly faster than \textit{M. tuberculosis} and other slow-growing mycobacteria, with a generation time of 4 h compared to 20 h for \textit{M. tuberculosis} (28). Therefore, \textit{M. marinum} offers an attractive and potentially valuable model for studying the molecular biology of mycobacterial pathogenesis. In the present work, we demonstrate that a \textit{mariner}-based transposon system can be used for facile generation of random mutations in \textit{M. marinum} (\textit{M. marinum mariner}-based mutagenesis [\textit{M}]) and that these mutants can be used to identify and study genes involved in intracellular survival.

**MATERIALS AND METHODS**

**Bacterial strains and media.** \textit{M. marinum} strain M (the kind gift of Lalita Ramakrishnan, University of Washington, Seattle) was cultured either on Middlebrook 7H9 (Difco) supplemented with 0.2% glycerol, 0.05% Tween 80, and 10% albumin-dextrose-catalase enrichment (7H9 broth) or on Middlebrook 7H10 agar (Difco), supplemented with 0.5% glycerol and 10% oleic acid-albumin-dextrose-catalase enrichment. The initial inoculum was cultured at 32°C in 7H9 broth to mid-log phase with slow shaking (100 rpm), and the culture was concentrated in 7H9 broth containing 30% glycerol, aliquoted, and frozen at −80°C (passage 1). Subsequent cultures were carried out by thawing frozen aliquots of passage 1 on ice and growing them in 50 ml of 7H9 broth for 4 days to reach an optical density at 600 nm (OD600) of 1.5 (passage 2). For infection or transformation experiments, passage 2 cultures were diluted 50 times and cultured for an additional 48 h to reach an OD600 of 1.8 to 1.9 (post-log phase) (passage 3). When required, the Middlebrook media were supplemented with the antibiotic kanamycin (KAN) or Zeocin (ZEO) (Invitrogen) at a concentration of 100 μg/ml, and 10% sucrose (Suc) (negative selection) at 30°C (passage 2). As a negative control to estimate the efficiency of transformation, the transformants obtained after 7 days of incubation were pooled [strain \textit{M}].

**Transformation of \textit{M. marinum} with \textit{mariner}-based transposon mutagenesis vectors and selection for transposition mutations.** A passage 3 culture of the wild-type \textit{M. marinum} strain M was washed three times in a wash buffer containing 10% glycerol and 0.05% Tween 80 and resuspended in an appropriate volume of wash buffer to an OD600 of ~1.5 (competent bacteria) prior to electroporation. In preliminary experiments, we examined growth stage, bacterial clumping, electroporation conditions, and temperature as variables that could affect the efficiency of transformation. In addition, we tested one-step selection against sequential positive and negative selections for transposition of the mini-transposon into the bacterial chromosome. Finally, we compared the four \textit{mariner} mutagenesis vectors described above for transformation and transposition efficiencies. Our final \textit{M} protocol for efficient transformation and transposition is illustrated in Fig. 1B. \textit{M. marinum} bacteria grown to an OD600 of ~1.9 were repeatedly passed through a 26-gauge needle and then centrifuged at 500 × g to remove clumps. All procedures were carried out at room temperature. Competent bacteria (200 μl) were mixed with ~2 μg of plasmid pM272B, incubated for 10 min to facilitate DNA adsorption, transferred into a 0.2-cm-gap electroporation cuvette, and subjected to a pulse of 2.5 kV, 25 μF, and 1,000 Ω (Gene Pulser II; Bio-Rad). Electroporated bacteria were incubated in 10 ml of 7H9 broth at 30°C for 6 h or overnight before being plated onto 7H10 agar containing KAN (positive selection) at ~104 CFU/ml and 3% sucrose (Suc) (negative selection) at ~105 bacteria/plate.
insertion mutants were obtained after 7 to 10 days of incubation at 32°C. The transposition efficiency was approximately 3 × 10^6 Kan' and Suc' bacteria/10^9 Kan' bacteria. To ensure that each colony arose from a single mutant, bacteria were resuspended, passed through a 26-gauge needle, centrifuged, and re-plated. The colonies were cultured in 1 ml of 7H9 broth containing 1% glycerol and frozen at −80°C (passage 1).

Detection of mariner-based transposon insertions by PCR. Transposon insertion mutants selected on 7H10 agar containing Kan and Suc were initially characterized by PCR to amplify elements that define transposon insertion into the chromosome, including Kan’, sucR, and mts-ori. The primers used for detecting Kan' were KN-15 (5’ GAGGCACTTCCATGATTGG) and KN-23 (5’ TCAAGTGCCACAATTATCAG). The primers used for detecting sacB were SACB-15 (5’ ACCACCATACATACTGCCC) and SACB-23 (5’ ATCGTGTAGAAGAATGCGGT). The primers used for detecting essential open reading frames (ORFs) 1 and 2 of mts-ori were MORI-15 (5’ ACGAGACCAGAAGATGTTCCG) and MORI-23 (5’ GATCTATGCAGGTTGCCAGCC). Transposon insertion mutant bacteria were resuspended in H2O, and ~10^6 bacteria were added to each PCR as a source of template DNA. The PCR products were examined by agarose gel electrophoresis.

Southern blot analysis. Passage 3 cultures (OD_600 of ~1.0, 50 ml) of strains of M. marinum were used for isolation of genomic DNA by the cetyltrimethylammonium bromide-NaCl method with minor modifications. After delipidation with 1 ml of chloroform-methanol (2:1) for 5 min, the bacteria were resuspended in 10 mM Tris–1 mM EDTA (pH 8.0), digested with lysozyme (10 mg/ml) at 37°C for 5 h, and further digested with protease K (200 μg/ml) in 1% sodium dodecyl sulfate at 55°C for an additional 3 h. Fully digested bacteria were extracted once with cetyltrimethylammonium bromide-NaCl and then twice with phenol-chloroform-isooctyl alcohol (25:24:1) before precipitation of genomic DNA with isopropanol. Approximately 1 μg of Tris-HCl-dissolved genomic DNA was digested with PstI or BamHI and subjected to Southern blotting by following standard procedures (32). The probe was labeled and hybridized was detected by using an enhanced chemiluminescence random prime labeling and detection system (Amersham Pharmacia, Piscataway, N.J.) according to the manufacturer’s instructions.

Recovery of mariner transposon insertion sites from mutants and sequencing of the insertion junction. Genomic DNA (~200 ng) of transposition insertion mutants was digested with PstI or BamHI, and the restriction fragments were self-ligated. The genomic sequence surrounding the transposon was amplified by performing inverse PCR with the outward primers 821A (5’ CGCATCTTCCCGAACAGCCAGCCCTCGGCGA) and 822A (5’ TAATTCGCGCTTCGACGCAAAGCGTTCGCCCG). Inverse PCR products were confirmed for the appropriate sizes by agarose gel electrophoresis or verified by Southern blotting and then sequenced with either primer 821A or primer 822A.

Isolation of pigmentation mutants of M. marinum and localization of the transposon insertions. A pool of ~15,000 transposition insertion mutants was screened for the isolation of pigmentation mutants. After growth of the mutant colonies to a visible size in the dark, the agar plates were exposed to light on the bench top. Wild-type M. marinum turned gold upon exposure to light in approximately 48 h. Pigmentation variants were identified by Southern blotting and then sequencing of the insertion junction.

Molecular characterization of transposon insertion into the chromosome of M. marinum. M. marinum strain M was transformed with the mariner-based transposon mutagenesis vector pLYG204.Zeo. A mycobacterial expression vector pLYG204.Zeo was constructed based on the genomic sequences surrounding the transposon insertion in MmR03. The Zeor gene was PCR amplified from genomic DNA of the Erdman strain and ultimately cloned into pLYG204.Zeo to create pLYG602. The electroporation of pLYG602 into MmW04 and the selection of transformants were performed as described above.

Detection of J774 macrophages by M. marinum. The mouse macrophage-like cell line J774 (ATCC TIB67) was maintained at 37°C in 5% CO2 in Dulbecco’s modified Eagle medium (DMEM) supplemented with 10% fetal bovine serum (FBS; HyClone). Immediately prior to infection, J774 monolayers were washed once with FBS-free DMEM. Single disaggregated bacilli of passage 3 cultures of wild-type, mutant, or complemented M. marinum (OD_600 ~1.9) were added to J774 monolayers at a multiplicity of infection of 3 and incubated for 2 h at 32°C and 5% CO2. At the end of the 2-h incubation period, infected monolayers were washed twice with DMEM and further incubated in DMEM containing 2% FBS and 200 μg of amikacin/ml for 2 h to kill extracellular bacteria. At the end of the antibiotic treatment, monolayers were washed twice with DMEM and incubated in DMEM containing 1% FBS at 32°C and 5% CO2. This was designated time zero. The incubation medium was changed at 48 h. At 96 h after infection, bacteria were enumerated by growing complemented and hypotonic-based cell monolayers for quantitation of CFU. M. marinum grows poorly in tissue culture medium containing small amounts of FBS (data not shown), and at 96 h following infection, the cells infected with wild-type M. marinum showed some cytotoxicity. Therefore, the bacteria in the supernatant (always <10% of the total) represent bacteria that have escaped from macrophages, probably after 96 h.

RESULTS

Molecular characterization of transposon insertion into the chromosome of M. marinum. M. marinum strain M was transformed with the mariner-based transposon mutagenesis vector pM272B (Fig. 1A), and the transposition mutants were selected by using the M^+ protocol described in Materials and Methods and illustrated in Fig. 1B. Since the vector contains a sacB gene for counterselection, the Kan r and Sucr bacteria potentially had a chromosomal insertion(s) by mariner, with loss of the delivery vector. To test this, we examined the presence of the Kan gene, sacB, and mts-ori by PCR in 15 randomly picked Kan' and Suc' colonies (data not shown). All contained the Kan' gene but had lost mts-ori and sacB, suggesting the integration of the transposon to the chromosome. Southern blots of PstI-digested or BamHI-digested genomic DNA probed with the transposon sequences yielded a single hybridization fragment for each of the colonies, suggesting a single transposition event for each colony, and each hybridization fragment had a unique size, indicating that the transposon had inserted at different sites of the chromosome (data not shown). There was no hybridization with sequences from the plasmid backbone (data not shown), indicating loss of the delivery vector sequence. In subsequent Southern blot analyses of over 50 colonies, only 2 have shown evidence of more than one insertion, suggesting that the vast majority of colonies arose from single transposition events. Additional proof for transposon insertion into the chromosome was obtained by

mmW01 and mmR02, and the transformants were selected on 7H10 plates containing ZEO. The empty vector pLYG204.Zeo was used as a negative control for complementation.

To restore the mutants of mmW04, M. tuberculosis genomic fragment encompassing Rv2603c to Rv2606c (corresponding to bases 2930803 to 2934068 of the published H37Rv sequence [8]) was PCR amplified from genomic DNA of the Erdman strain and ultimately cloned into pLYG204.Zeo to create pLYG602. The electroporation of pLYG602 into mmW04 and the selection of transformants were performed as described above.
hybridization of undigested genomic DNA from the Kan' and Suc' bacteria with the Kan' gene probe: hybridization was detected only at the size range for genomic DNA (data not shown). Definitive proof for transposon insertion into the chromosome was obtained by sequencing across the transposon insertion junctions outwards from mariner. All sequences (now from 40 independent colonies) have a TA dinucleotide at the transposon-chromosome junction, followed by diverse GC-rich genomic sequences. Taken together, these results prove that M4 leads to integration of the mariner transposon into the chromosome of M. marinum at random sites, usually as a single copy per genome, and that the delivery vector is completely lost upon transposition.

**Identification and characterization of transposon insertion within genes of the carotenoid biosynthesis pathway.** Using the M4 protocol, we obtained a M. marinum mutant library consisting of ~15,000 individual transposon insertion mutants from a single electroporation. To evaluate the randomness of mariner transposition, we screened for pigmentation mutants. Assuming that M. marinum has about the same number of genes as M. tuberculosis (~4,000), if transposition is random, the Poisson statistic predicts that the likelihood of failure to find in this library at least one insertion in any gene involved in pigmentation is approximately 2%. Normally, M. marinum is gold when exposed to light because of the production of carotenoid pigments (30, 45). As diagrammed in Fig. 3A, MmW01 and MmW02 had an insertion in the crtB gene and MmW03 had an insertion in the crtI gene. MmR01, MmR02, and MmR04 had independent insertions in two previously identified (30) but uncharacterized ORFs (ORF-3 and ORF-4) of this M. marinum locus. We found that ORF-3 and ORF-4 have significant homology to crtYc and crtYd, respectively, of Mycobacterium aurum and Brevibacterium linens (18, 30, 45). Both the sequence and genomic organization of crtI, crtB, crtYc, and crtYd are highly conserved among M. marinum, M. aurum, and B. linens (18, 30, 45). As diagrammed in Fig. 3A, our transposon mutant library contained at least one mutation in each of these ORFs identified in the M. marinum carotenoid biosynthesis gene locus. Although only one locus was analyzed, this frequency is consistent with the generation of random mutations throughout the M. marinum genome by mariner.

CrtB (phytoene synthase) and CrtI (phytoene desaturase) are thought to catalyze two consecutive biochemical reactions leading to the synthesis of lycopene, which has a red pigment (Fig. 3A) (45). Mutations in either of these genes in MmW01/MmW02 and MmW03 produced no colored pigments (intermediates before lycopene in the pathway are not bright colored) (Fig. 2). MmR01, MmR02, and MmR04 had mutations in the crtY locus, which controls the conversion of lycopene (red) to beta carotene (gold) (18, 45). As predicted, these mutants accumulated lycopene and were therefore red (Fig. 2).

In addition to these five insertions within the locus known to be involved in carotene biosynthesis, we identified two mutants, MmR03 and MmW04, that had insertions within novel genes. The sequence at the transposon insertion junction of MmR03 was used in a BLAST search of the M. marinum database at the Sanger Center (http://www.sanger.ac.uk/Projects/M_marinum/). The insertion junction sequence was

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**FIG. 2.** Pigmentation of M. marinum mutants in the presence or absence of light. M. marinum colonies were grown in the dark (left) and then exposed to light for 48 h (right). Wild-type (WT) M. marinum is pigmented only after light exposure. R01, MmR01; R02, MmR02; R03, MmR03; R04, MmR04; W01, MmW01; W03, MmW03; W04, MmW04.
identical in reverse orientation to bases 77208 to 77843 of the assembled contig sequence mar502f07.plk. This sequence is within a hypothetical ORF that contains a domain homologous to the helix-turn-helix MarR family of transcription repressors (1). Thus, the gene interrupted by the transposon in MmR03 (crtR) is likely a repressor of the crt locus, consistent with production of red pigment in the mutant in the absence of light induction. We examined the chromosomal location of the MmR03 transposon insertion relative to the known carotenoid biosynthesis genes by a PCR protocol that amplified sequences between the transposon inserts. As shown in Fig. 3B, the MmR03 insertion is approximately 2.8 kb downstream from that of MmR02.

The second unanticipated transposon insertion (in MmW04) was in an intergenic sequence immediately downstream of a coding sequence homologous to Rv2604c of M. tuberculosis (8) (Fig. 3A). In the M. tuberculosis genome, Rv2604c and the two upstream genes, Rv2605c and Rv2606c, are likely in a single operon (Fig. 3A). Rv2603c is 130 bp downstream of Rv2604c and thus might also be part of the putative operon. Both Rv2603c and Rv2604c are highly conserved but without known function. Rv2605c is homologous to acyl coenzyme A thioesterase II genes in bacteria, and Rv2606c is homologous to a family of genes conserved among prokaryotes and eukaryotes that confer resistance to singlet oxygen generated by light induction of photosensitizers such as methylene blue. Consistent with the possibility that these genes have a similar function in mycobacteria, MmW04 showed a fivefold increase in sensitivity to singlet oxygen produced by light induction of methylene blue (Fig. 4A). The increased sensitivity did not result from the loss of pigment because the other white mutants were equivalent to the wild type in this assay. Unlike the other pigment mutants, MmW04 also showed reduced intracellular growth in J774 cells, with an eightfold-lower CFU count than the wild type at 4 days after infection (Fig. 4B). Thus, in addition to the lack of pigmentation, this mutant showed a general decrease in the ability to survive environmental stress. The transposon insertion in MmW04 is not sufficiently close to the known carotenoid biosynthesis genes to be linked by PCR or to be on the same BamHI fragment (~10 kb) as the pigmentation locus, as assessed by Southern blot analysis (data not shown).

**Complementation of the pigmentation mutants.** To prove that the mutant phenotypes were specifically caused by the transposon insertions, we carried out complementation studies by expressing the corresponding wild-type coding sequence within an appropriate mutant. We first developed a mycobacterial expression vector, pLYG204.Zeo, which carries a Zeo' gene immediately downstream from a mycobacterial groEL promoter and multiple cloning sites for the insertion of a gene of interest. The M. marinum crtB gene coding sequence (30) was cloned into the multiple cloning site of pLYG204.Zeo and transformed into MmW01, and the Zeo' colonies were examined for complementation of pigmentation. As shown in Fig. 5A, the mutant MmW01 was fully complemented by episomal expression of crtB to produce wild-type pigment. Complementation of MmW01 by crtB was specific, since the empty vector did not complement (data not shown), and the expression of crtB did not complement the MmR02 mutant (Fig. 5A).

The homology of the insertion site in MmW04 with an M. tuberculosis locus provided an opportunity to assess the ability

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**FIG. 3.** *M. marinum* carotenoid biosynthesis and regulatory genes, their genomic organization, and location of transposon insertions. (A) The known carotenoid biosynthesis locus in *M. marinum* is shown as a gene cluster from *crtI* to ORF-4. Below these genes the biosynthetic pathway is depicted; GGPP represents the initial substrate, geranylgeranylpyrophosphate. The novel *crtR* and *crtP* genes encode a putative repressor and a positive regulator, respectively, for the carotenoid biosynthesis locus. *crtP* indicates the locus containing the Rv2606c to Rv2603c homologues. The star symbols represent putative light-inducible promoters. Triangles indicate sites of transposon insertion, and arrows represent the orientation of a positive regulator, respectively, for the carotenoid biosynthesis locus.
of M. tuberculosis genes to function in M. marinum. Because of the possibilities that (i) several of the genes in the region from Rv2603c to 2606c are likely in an operon, (ii) the direction of transcription of the transposon insertion is opposite to the direction of transcription of these genes (Fig. 3A), leading to the possibility of antisense transcripts arising from the transposon, and (iii) the insertion was in a regulatory region for one or more of these genes, we attempted to complement the MmW04 phenotypes by using an M. tuberculosis genomic fragment encompassing Rv2603c to Rv2606c. A ~3.3-kb genomic fragment containing these genes was PCR amplified from the M. tuberculosis Erdman strain and cloned into pLYG204. The expression plasmid was transformed into MmW04, and the phenotypes of the transformants were determined. The defects of the MmW04 mutant in pigmentation, resistance to singlet oxygen, and intracellular growth were completely restored to wild-type levels by expression of this M. tuberculosis genomic fragment encompassing Rv2603c to Rv2606c. An ~3.3-kb genomic
DISCUSSION

We have developed a method for M4 that is efficient and simple. The mariner transposon inserts at a TA recognition site in M. marinum, without any other apparent consensus sequence requirement, as is the case in other organisms. This property allowed for the construction of a transposon mutant library containing remarkably random insertions. There are ~70,000 possible mariner insertion sites in a typical mycobacterial chromosome. Since there are ~4,000 genes, this suggests that there are many potential sites of transposition in each gene. Indeed, in our library of ~15,000 individual mutants, we found mutations in multiple expected genes of M. marinum in the carotenoid biosynthesis pathway, suggesting that with M4 it will be possible to generate mutations within most genes compatible with survival in vitro. The ~15,000 mutants that we screened were generated from a single electroporation, and a mutant library with a larger size can be easily obtained by plating out more Kan^R bacteria on Kan- and Suc-containing plates, which could potentially saturate all possible TA sites. High-efficiency transposition by a slightly different mariner transposon has been reported for E. coli and several mycobacterial species (33). Together, these studies demonstrate the utility of the mariner transposon in random bacterial mutagenesis.

Our first mutant screen has enhanced the understanding of the regulation of carotenoid biosynthesis in M. marinum. We found one mutant (MmR03) that produces a red pigment in the dark, unlike wild-type M. marinum, which is white in the absence of light. Since the MmR03 mutant accumulated lycopene in the dark and produced beta-carotene upon exposure to light, the normal gene product (CrtR) likely has an inhibitory activity on crtI and crtB that is released upon light induction. Consistent with this, the ORF interrupted by the transposon in MmR03 shows homology to the MarR family of transcription repressors, which bind DNA through a helix-turn-helix motif. Release of repression by MarR is thought to occur by direct binding of inducers to the repressor, leading to loss of DNA binding. Based on this, we hypothesize that CrtR is a constitutive inhibitor of crtI and crtB that is released when M. marinum is exposed to light. It will be interesting to determine the nature of the light-activated inducer of the crtI/crtB pathway in M. marinum. Expression of ctry also apparently requires induction by light, since the MmR03 mutant accumulates red, but not gold, pigment in the dark, yet it does develop a gold color when exposed to light. It is possible that there is a common inducer for both steps in carotenoid production.

Our screen also identified one nonpigmented mutant (MmW04) that had a transposon insertion outside the known carotenoid biosynthesis locus within a region that exhibits significant sequence homology to M. tuberculosis genes. Since the mutation also caused decreased resistance of M. marinum to singlet oxygen and compromised intracellular growth, the normal gene product (CrtP) is likely involved in the positive regulation of a general stress response in mycobacteria. M. tuberculosis does not produce colored pigments, yet its homologous locus complemented the defects of MmW04 in pigmentation, resistance to singlet oxygen, and intracellular growth. Thus, the role of the locus in regulating stress response is conserved among Mycobacterium species. In fact, genes homologous to those in this locus, such as SOR1 (singlet oxygen resistance) (10), SNZ1 (stationary-phase gene) (4), pyroA (pyridoxine biosynthesis) (25), and HEVER (Hevea ethylene responsive) (37), are conserved in distantly related organisms. All of these genes have been implicated in responses to a variety of stresses. As intracellular pathogens, mycobacteria must have mechanisms for protection from the stresses of the intraphagosomal environment; it is likely that the ctp locus (Rv2606c to Rv2603c) has a role in this response in M. tuberculosis, as its homologue does in M. marinum. In M. marinum, this locus has an additional role in regulating carotenoid biosynthesis. Since no other nonpigmented mutants have defects in intracellular survival or resistance to singlet oxygen, carotenoids apparently are not directly involved in protection against either of these stresses. This implies that the ctp locus activates stress responses in addition to pigmentation that more directly affect bacterial survival in the intracellular environment. We are currently investigating which gene(s) of the ctp locus is responsible for mediating the stress response in M. marinum.

The potential for using M. marinum as a model to study molecular mechanisms of M. tuberculosis pathogenesis has been explored systematically by Chan et al. (5) and Ramakrishnan et al. (29) as well as others (40). We have extended the potential utility of this model by showing that for genes with M. tuberculosis homologues, the M. tuberculosis genes can be used to complement the mutant M. marinum phenotypes. While this has been done to some extent in M. smegmatis, this organism does not persist in macrophages or other host cells and therefore cannot be used to study genes involved in intracellular growth and/or persistence. In contrast, M. marinum is able to replicate within macrophages, making it possible to screen for mutants defective in intracellular survival or growth by using the random transposon mutagenesis technique we describe here. Indeed, we have screened ~1,000 mutants from this library for the ability to survive in macrophages and have identified 23 different genes, in addition to the MmW04 gene, that are involved in intracellular survival. Significantly, each of these genes has an M. tuberculosis homologue, and in all 10 mutants in which we have tried, we have successfully corrected the intracellular survival defect of the mutant with the M. tuberculosis homologue. Thus, M. marinum is a model organism well suited not only for discovery of mycobacterial genes involved in intracellular survival but also for functional analysis of M. tuberculosis genes required for this aspect of pathogenesis.

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