

Mycobacterium tuberculosis produces pili during human infection

Christopher J. Alteri*[†], Juan Xicohténcatl-Cortes*, Sonja Hess[‡], Guillermo Caballero-Olin[§], Jorge A. Girón*, and Richard L. Friedman*

*Department of Immunobiology, University of Arizona, 1501 North Campbell Avenue, LSN 649, Tucson, AZ 85724; [†]Proteomics and Mass Spectrometry Facility, National Institute of Diabetes and Digestive and Kidney Diseases, National Institutes of Health, Bethesda, MD 20892; and [§]Instituto Mexicano del Seguro Social, Monterrey, Nuevo León, 64010, Mexico

Edited by Barry R. Bloom, Harvard School of Public Health, Boston, MA, and approved January 17, 2007 (received for review March 21, 2006)

Mycobacterium tuberculosis is responsible for nearly 3 million human deaths worldwide every year. Understanding the mechanisms and bacterial factors responsible for the ability of *M. tuberculosis* to cause disease in humans is critical for the development of improved treatment strategies. Many bacterial pathogens use pili as adherence factors to colonize the host. We discovered that *M. tuberculosis* produces fine (2- to 3-nm-wide), aggregative, flexible pili that are recognized by IgG antibodies contained in sera obtained from patients with active tuberculosis, indicating that the bacilli produce pili or pili-associated antigen during human infection. Purified *M. tuberculosis* pili (MTP) are composed of low-molecular-weight protein subunits encoded by the predicted *M. tuberculosis* H37Rv ORF, designated Rv3312A. MTP bind to the extracellular matrix protein laminin *in vitro*, suggesting that MTP possess adhesive properties. Isogenic *mtp* mutants lost the ability to produce Mtp *in vitro* and demonstrated decreased laminin-binding capabilities. MTP shares morphological, biochemical, and functional properties attributed to bacterial pili, especially with curli amyloid fibers. Thus, we propose that MTP are previously unidentified host-colonization factors of *M. tuberculosis*.

adherence | antigen | laminin | amyloid

Tuberculosis remains the most devastating bacterial cause of human mortality (1). Despite improved diagnosis, surveillance, and treatment regimens, the incidence of TB increases annually (2). The ability to combat this deadly pathogen hinges on the dissection and understanding of the mechanisms of pathogenesis for *Mycobacterium tuberculosis*. Central to the ability of the microbe to cause disease is the capability to survive and replicate within macrophages by avoiding lysosomal fusion with the mycobacteria-containing phagosome (3). *M. tuberculosis* interacts with and invades various human and animal epithelial cells in culture and appears to possess multiple mechanisms of entry into macrophages (4–6). Despite these long-standing and recent observations, very little is known regarding host-microbe interactions and events between *M. tuberculosis* and host cells before survival and replication within the macrophage. Furthermore, the specific bacterial adhesins involved in the complex interplay between *M. tuberculosis* and the human host are largely unknown. Nevertheless, a few potential adherence factors are considered, including a heparin-binding hemagglutinin (HBHA), a fibronectin-binding protein family or antigen 85 complex, and the subfamily of polymorphic acidic, glycine-rich proteins, called PE_PGRS. HBHA is a surface-exposed protein that is involved in binding of the bacillus to epithelial cells but not to phagocytes (7–9), and the experimental data available suggest that HBHA is important in extrapulmonary spread after the initial long-term colonization of the host. Fibronectin-binding proteins, first identified as the 30-kDa or α -antigen (10, 11), are mycolyltransferase enzymes (12) that can bind to the extracellular matrix (ECM) protein fibronectin *in vitro* (11). This property may represent a mechanism of tissue colonization. The surface-exposed PE_PGRS proteins are found in *M. tuberculosis*

and *Mycobacterium bovis* (13–16). *M. bovis* bacillus Calmette-Guérin with a mutation in the PE_PGRS gene Rv1818 was found to be less aggregative in liquid culture and showed reduced ability to infect J774 macrophages (14). The *M. tuberculosis* PE_PGRS protein encoded by the ORF Rv1759c also shows fibronectin-binding properties (17).

Many bacteria pathogenic to plants and animals produce polymeric adhesive organelles termed pili, or fimbriae, to facilitate the initial attachment and subsequent successful colonization of eukaryotic cells (18). Pili are polymeric, hydrophobic, proteinaceous structures generally composed of a major repeating subunit called pilin and, in some cases, a minor tip-associated adhesin subunit. Pili are involved in many virulence-associated functions, such as agglutination of human and animal erythrocytes, bacterial aggregation, biofilm formation, adherence, and colonization of mucosal surfaces (18, 19). Because of their key role in bacterial pathogenesis, pili are viewed as virulence factors and, therefore, as important targets for vaccine development (18). It is widely held that mycobacteria do not produce pili. Here, we provide compelling ultrastructural, biochemical, and genetic data that show that *M. tuberculosis* produces pili, whose pilin subunit is encoded by the Rv3312A gene. Sera from convalescent TB patients contain antibodies that specifically react to the previously unidentified fibrous organelle. Furthermore, the role of MTP as adhesive structures is supported by our findings that purified MTP bind to the extracellular matrix protein laminin and that *mtp* mutants are unable to bind to laminin. In all, our data suggest that MTP could be used by the mycobacteria as a mechanism to colonize the human host.

Results

***M. tuberculosis* Cells Produce Pili.** Pili are present on many bacteria that cause disease in the human respiratory tract including the Gram-positive pathogens Group B *Streptococcus* and *Corynebacterium diphtheriae* (20, 21); this latter being a close relative of *Mycobacterium* in terms of phylogeny and complex cell-wall architecture (22). Previous ultrastructural analyses have suggested that pathogenic mycobacteria produce fibers reminiscent

Author contributions: J.A.G. and R.L.F. contributed equally to this work; C.J.A., J.A.G., and R.L.F. designed research; C.J.A., J.X.-C., and S.H. performed research; S.H. and G.C.-O. contributed new reagents/analytic tools; C.J.A., S.H., J.A.G., and R.L.F. analyzed data; and C.J.A., J.A.G., and R.L.F. wrote the paper.

The authors declare no conflict of interest.

This article is a PNAS direct submission.

Freely available online through the PNAS open access option.

Abbreviations: ECM, extracellular matrix; IF, immunofluorescence; MTP, *M. tuberculosis* pili; TEM, transmission electron microscopy.

[†]To whom correspondence should be sent at the present address: University of Michigan Medical School, Department of Microbiology and Immunology, 5641 Medical Science II, 1150 West Medical Center Drive, Ann Arbor, MI 48109. E-mail: alteri@umich.edu.

This article contains supporting information online at www.pnas.org/cgi/content/full/0602304104/DC1.

© 2007 by The National Academy of Sciences of the USA

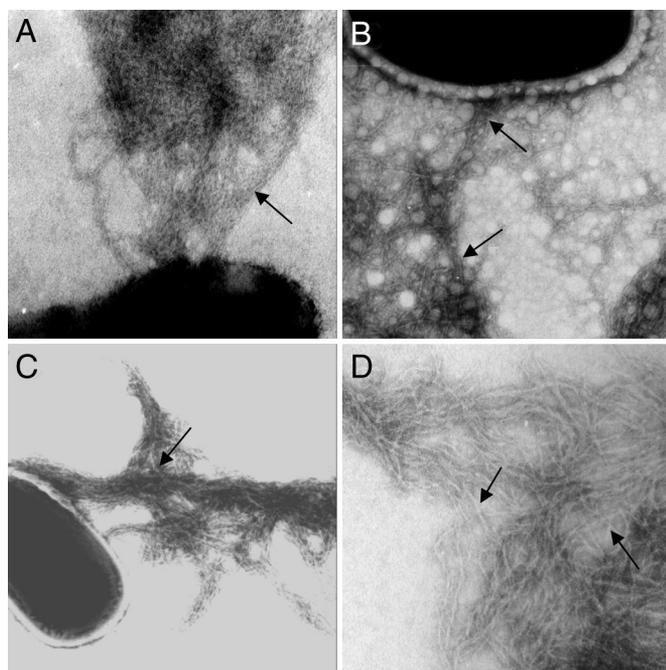


Fig. 1. Demonstration of pili production by *M. tuberculosis* strains. Transmission electron micrographs of negatively stained *M. tuberculosis* strains H37Rv (A), avirulent H37Ra (B), clinical isolate CDC1551 (C), and purified MTP (D). Black arrows point to MTP pili fibers. (Magnification: $\times 45,000$.)

of pili (23, 24). We investigated the production of pili in *M. tuberculosis* cells propagated under various standard culture conditions by negative staining and transmission electron microscopy (TEM). We found that *M. tuberculosis* H37Rv, when grown for 2–3 weeks on Middlebrook 7H10 or 7H11 solid mycobacteriological medium, produced a dense fibrillar meshwork composed of thin (2- to 3-nm-wide), coiled-coil, aggregated fibers, resembling pili that extended many microns away from the bacterial surface (Fig. 1A). These organelles were named *Mycobacterium tuberculosis* pili or MTP. At least 10% of individual mycobacteria ($n = 100$) examined under these culture conditions produced these MTP structures. Similar structures were seen in avirulent strain H37Ra (Fig. 1B) and the clinical isolate CDC1551 (Fig. 1C), suggesting that MTP production is a common property among *M. tuberculosis* strains. The morphology of MTP is strikingly similar to that of the well characterized pili called curli produced by *Escherichia coli* and *Salmonella enterica* (25, 26).

***M. tuberculosis* ORF Rv3312A Encodes the MTP Structural Subunit.** MTP was isolated from *M. tuberculosis* by using mechanical shearing and differential centrifugation techniques commonly used to prepare pili from other microorganisms (27). Because of the lipid-rich nature of the *M. tuberculosis* cell wall, an additional extraction step involving chloroform and methanol was performed to remove unwanted lipids from the pili preparation. Copious amount of intact pili were observable by TEM in the chloroform/methanol-insoluble MTP fraction (Fig. 1D). However, after analysis by SDS/PAGE and Coomassie brilliant blue and silver staining procedures, no obvious MTP monomer in the range typical for pilins, 10–25 kDa, was obtained [see supporting information (SI) Fig. 5]. Thus, it appears that MTP are not readily dissociated into subunits by standard reducing and denaturing conditions, a characteristic consistent with the biochemical properties known for curli and type I pili (26, 28).

Because of the difficulty in dissociating MTP into monomeric

subunits, we sought to identify the nature of the pilin subunit by direct analysis using liquid chromatography-tandem mass spectrometry of acid hydrolysates from purified MTP (SI Fig. 6). Three independently prepared pili-enriched fractions produced a mass spectrum (SI Fig. 6A) associated with a peptide fragment having a monoisotopic mass (M_r) of 1,086.55 Da and a sequence of PGAAPPPPAAGGGA (SI Fig. 6B). The MTP-associated sequence corresponded to the carboxyl terminus of a predicted protein of 10.5 kDa encoded by *M. tuberculosis* H37Rv ORF Rv3312A (herein called *mtp*) (SI Fig. 6C) (13). The MTP-associated protein is predicted to have a transmembrane domain located between residues 10 and 30 (SI Fig. 7). These are traits consistent with a pilin protein (29). Affinity-purified antibodies produced against a peptide containing amino acids 60–79 (SI Fig. 6C) of the identified *mtp*-encoded protein, specifically detected a 5-kDa product in Western blots of purified MTP (SI Fig. 8). Preimmune serum did not react with protein (SI Fig. 8A, lane 2). This result is in agreement with the MS/MS analysis of MTP and suggests the presence of a cleaved signal sequence or other proteolytic modification of the prepilin, Mtp. These observations regarding the molecular mass of the mature *mtp*-encoded protein are also consistent with the internal amino terminus sequence noted in the reannotation of this particular *M. tuberculosis* ORF (30). ImmunoGold electron microscopy experiments provided further evidence that the *mtp* gene product is the MTP structural subunit, because Mtp peptide-specific antibodies bound to purified fibers (SI Fig. 8B). Nearly all of the gold particles are seen decorating individual filaments. In contrast, no labeling was obtained with preimmune serum (data not shown). To further confirm these findings, *M. tuberculosis* H37Rv *mtp* was amplified from chromosomal DNA, cloned, and expressed as a recombinant His₆-tagged protein in *E. coli* BL21. The recombinant His-Mtp migrated with an apparent molecular mass of 14.5 kDa (SI Fig. 8C, lane 2) and reacted specifically with anti-Mtp peptide-specific antibodies (anti-Mtp) by Western blotting (SI Fig. 8C, lane 3). The fact that recombinant Mtp ran as a full-length product suggests that *E. coli* lacks the mechanism for the putative cleavage of the Mtp prepilin because the mature molecule from purified MTP migrates at 5 kDa. Taken together, these data show that MTP are composed of the *mtp* (Rv3312A) gene product in *M. tuberculosis*.

Rv3312A Is Required for Production of MTP Fibers in *M. tuberculosis*.

To provide genetic evidence of the role of *mtp* in production of the fibers, *mtp* of H37Rv and the homologous ORF MT3413 of CDC1551 were targeted for mutation by means of specialized transduction (31). The mutations were confirmed by PCR using internal gene-specific primers and flanking primers (SI Fig. 9), and the effect of the deletion on the ability of the mutants to produce pili was determined by TEM and Western blotting. Neither H37Rv Δ *mtp* nor CDC1551 Δ *mtp* were able to produce MTP (Fig. 2A and B), and no synthesis of the subunit occurred in the mutants (Fig. 2C). Lastly, surface production of Mtp in the wild-type strains and lack thereof in the derivative *mtp* mutants was confirmed by flow cytometry using anti-Mtp antibody (Fig. 2D). Eighteen percent of H37Rv and 20% of CDC1551 cells analyzed ($n = 50,000$), expressed MTP on their surface, whereas the *mtp* mutants lacked detectable MTP (Fig. 2E).

***M. tuberculosis* Pili Bind to Laminin.** Pili mediate specific recognition of host-cell receptors facilitating close contact and tissue colonization (18, 32). Previous studies have shown that *M. tuberculosis* preferentially attaches to and invades damaged areas of the human respiratory mucosa in an organ culture system (33). In these instances of tissue damage, ECM proteins may be more highly exposed than in healthy tissue. Purified MTP was tested for its ability to interact with ECM proteins by using an ELISA-based assay. We found that MTP has a strong dose-

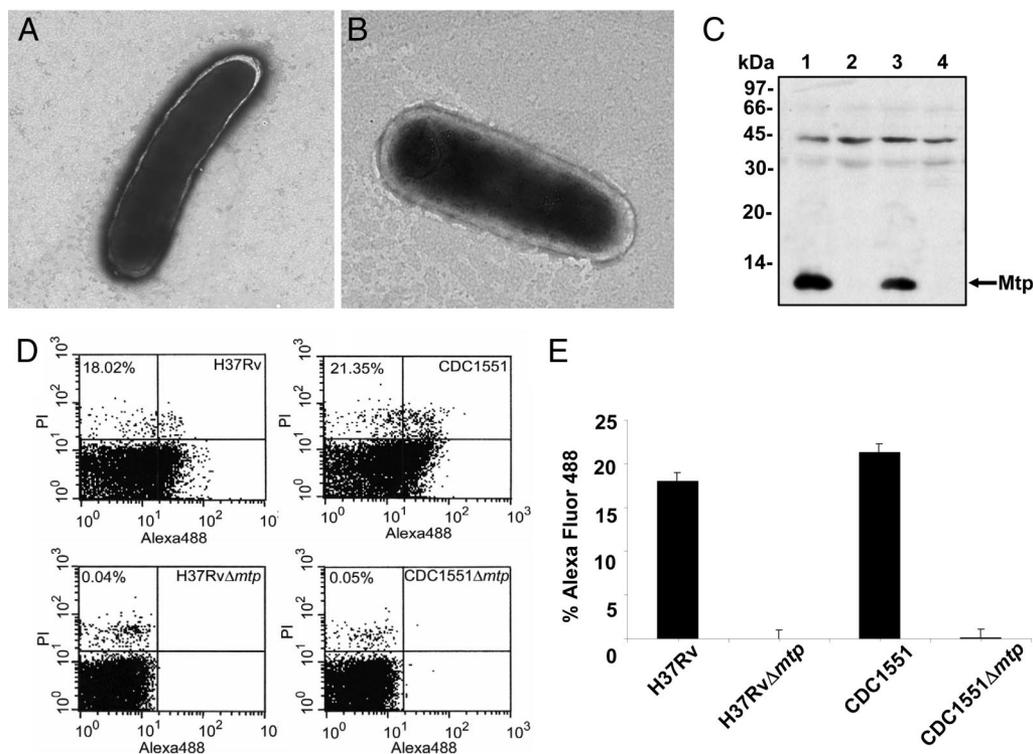


Fig. 2. Isogenic *M. tuberculosis* *mtp* mutants lack production of pili fibers. (A and B) Electron micrographs of H37RvΔ *mtp* (A) and CDC1551Δ *mtp* (B) showing no filamentous structures. (Magnification: $\times 25,000$.) (C) Anti-Mtp Western blot of whole bacteria extracts showing production of the pilus protein in H37Rv (lane 1) and CDC1551 (lane 3) and absence of the pilin in both H37RvΔ *mtp* (lane 2) and CDC1551Δ *mtp* (lane 4). (D) Surface detection of MTP in wild-type parental and derivative *mtp* deletion strains by flow cytometry ($n = 50,000$) using anti-Mtp antisera. MTP-antibody complexes were detected by using Alexa Fluor conjugate. (E) Plot of the flow cytometry values obtained in D.

dependent affinity for laminin (Fig. 3A) but lacked significant binding affinity for fibronectin or type IV collagen. To determine whether the laminin-binding property observed for the native MTP fibers was attributable to the *mtp* gene product, the ability of *M. tuberculosis* H37RvΔ *mtp* and CDC1551Δ *mtp* to bind laminin were compared with the wild-type parental strains by using flow cytometry. It was found that both *mtp* mutants demonstrated a 40-fold reduction in laminin-binding capacity versus the wild-type strains (Fig. 3B and C). These data suggest that MTP mediates adhesion of *M. tuberculosis* to the extracellular matrix, an event that would facilitate direct interaction between the bacilli and the host epithelium during TB infection in the lung or other tissues.

Sera from TB Patients Contain MTP-Reactive IgG Antibodies. During TB infection, *M. tuberculosis*-specific molecules are recognized as antigens by the host immune system and induce the production of antibodies. The presence of these antibodies represents a powerful indication that the antigen is produced during natural infection. If *M. tuberculosis* produces MTP during infection of the human host, it would be possible to detect anti-Mtp antibodies in sera collected from TB patients. Thus, MTP was used in immunofluorescence (IF) microscopy experiments using sera from TB patients ($n = 36$) in various stages of treatment to detect antibody-MTP complexes. Sera from healthy donors ($n = 5$) were used as negative controls. Among the 36 individual TB patient sera tested, 60% produced a positive reaction defined by the presence of a characteristic fibrous meshwork of intense fluorescence (Fig. 4A). In contrast, none of the control sera gave a positive reaction with MTP because no fluorescent fibers were observed (Fig. 4B). No reactivity was obtained between purified MTP and goat anti-human IgG Alexa Fluor conjugate (in the

absence of human sera), confirming the specificity of the IF reaction (data not shown).

ELISA was used to determine the titer of anti-MTP IgG in the panel of TB patient sera. It was observed that 60% had anti-MTP IgG titers $>3,200$, whereas healthy control sera did not react significantly with MTP (Fig. 4C). As predicted, nearly all of the human sera that displayed positive reactivity to MTP by IF had ELISA anti-MTP IgG titers of 3,200 or greater (Fig. 4C). The finding that MTP-specific antibodies were found in human sera obtained from TB patients provides compelling evidence that MTP are immunogenic and are produced by *M. tuberculosis* during infection of the human host. Showing that MTP are antigenic is supported by the reannotation of Rv3312A as a secreted antigen (30).

Discussion

Pili-mediated attachment to phagocytic cells is important for host-defense mechanisms either through direct pilus-macrophage interaction or by the presence of anti-pilin opsonizing antibody (19). It is well documented that *M. tuberculosis* adheres to and invades macrophages and epithelial cells; however, the bacterial factors involved in the colonization of the host are largely unknown. Here, we provide compelling ultrastructural, biochemical, and genetic data that support the notion that *M. tuberculosis* produces pili, herein called MTP, and this observation has important implications regarding our understanding of both pathogenesis and basic physiology of the tubercle bacillus.

Although much study has been devoted to the identification of cell surface components involved in virulence of and protective immunity against *M. tuberculosis*, the majority of studies have been conducted on the complex lipids associated with the cell

and adjusted for consistent contrast by using Photoshop 7.0 (Adobe Systems, Mountain View, CA).

ELISA. Flat-bottom ELISA plates (Greiner, Monroe, NC) were coated overnight at 4°C with 1.5 µg per well of MTP in 150 mM carbonate buffer, pH 9.5. After washing and blocking, the wells were incubated with serial dilutions of human sera, followed by incubation with the secondary antibody (DAKO, Glostrup, Denmark). The reaction was developed with TMB single solution substrate (Zymed) and stopped with 1 M HCl before reading absorbance at 450 nm by using a microtiter plate reader (Bio-Rad, Hercules, CA). Background absorbance from empty control wells was subtracted from test samples.

Flow Cytometry. Flow cytometry was used to detect the production of Mtp and to measure binding of the mycobacteria to ECMs. *M. tuberculosis* cells were harvested from 7H11 plates into sterile PBS, vortexed, and allowed to settle. To avoid clumping bacteria, the upper portion of the suspension was removed and diluted to an optical density of 1.1, and 45-µl aliquots were incubated with 25 µl of anti-Mtp peptide antibodies by using dilutions of 1:1,000 for 1 h on ice. After three gentle washes with PBS, the bacteria were resuspended in 25 µl of a dilution of goat anti-rabbit IgG (H+L) Alexa Fluor conjugate (Invitrogen, Carlsbad, CA). After 1-h incubation at 4°C, the bacteria were gently washed three times with PBS and resuspended in 800-µl final volume of PBS. For the analysis, the bacteria were labeled with 5 µl of a propidium iodide solution (Sigma, St. Louis, MO). Propidium iodide was visualized through a 42-nm band pass centered at 585. These experiments were repeated in triplicate. The FITC fluorescence emission was collected through a 30-nm band-pass filter centered at 530 in

which 50,000 events were measured. The samples were analyzed at the ARL Biotechnology/ACCC Cytometry Core Facility at the University of Arizona, by using a FACScan (Becton Dickinson, Franklin Lakes, NJ). For measuring the binding of bacteria to ECMs, mycobacteria were incubated for 1 h at 4°C with 0.125 µg of laminin, fibronectin, or type IV collagen. After incubation, the cells were washed with PBS and incubated with anti-ECM antibodies. Before analysis, the ECM-antibody complexes were detected by using anti-rabbit or anti-mouse Alexa Fluor conjugate (Invitrogen).

ECM Binding Assay. A sandwich ELISA was used to detect and quantitate the binding affinity of MTP for ECM proteins by using 1.5 µg of purified MTP immobilized onto ELISA plates as described above. Serial dilutions of fibronectin, laminin, or type IV collagen were added for 1 h, followed by incubation with rabbit anti-fibronectin, rabbit anti-laminin, or mouse anti-type IV collagen (Sigma). The sandwiched complex was detected by using anti-rabbit or anti-mouse IgG peroxidase conjugate (Sigma), developed and read as described above.

Construction of mtp Mutants by Specialized Transduction. Propagation and titering of mycobacteriophages, construction of allelic exchange substrates, and specialized transduction of *M. tuberculosis* were performed essentially as described (31). Additional details are provided as *SI Materials and Methods*.

We thank Esteban A. Roberts and James W. Moulder for critical review of the manuscript and Frederick J. Cassels, Lee W. Riley, and Bentley A. Fane for helpful discussions. This work was supported by National Institutes of Health Grant AI45537-01 (to R.L.F.) and a University of Arizona Small Grant (to R.L.F. and J.A.G.).

1. Dye C, Scheele S, Dolin P, Pathania V, Raviglione MC (1999) *J Am Med Assoc* 282:677–686.
2. Frieden TR, Sterling TR, Munsiff SS, Watt CJ, Dye C (2003) *Lancet* 362:887–899.
3. Armstrong JA (1971) *J Exp Med* 134:713–740.
4. Shepard CC (1955) *Proc Soc Exp Biol Med* 90:392–396.
5. Schlesinger LS, Bellinger-Kawahara CG, Payne NR, Horwitz MA (1990) *J Immunol* 144:2771–2780.
6. Bermudez LE, Goodman J (1996) *Infect Immun* 64:1400–1406.
7. Pethe K, Alonso S, Biet F, Delogu G, Brennan MJ, Loch C, Menozzi FD (2001) *Nature* 412:190–194.
8. Menozzi FD, Rouse JH, Alavi M, Laude-Sharp M, Muller J, Bischoff R, Brennan MJ, Loch C (1996) *J Exp Med* 184:993–1001.
9. Menozzi FD, Bischoff R, Fort E, Brennan MJ, Loch C (1998) *Proc Natl Acad Sci USA* 95:12625–12630.
10. Abou-Zeid C, Ratliff TL, Wiker HG, Harboe M, Bennedsen J, Rook GA (1988) *Infect Immun* 56:3046–3051.
11. Ratliff TL, McGarr JA, Abou-Zeid C, Rook GA, Stanford JL, Aslanzadeh J, Brown EJ (1988) *J Gen Microbiol* 134:1307–1313.
12. Belisle JT, Vissa VD, Sievert T, Takayama K, Brennan PJ, Besra GS (1997) *Science* 276:1420–1422.
13. Cole ST, Brosch R, Parkhill J, Garnier T, Churcher C, Harris D, Gordon SV, Eiglmeier K, Gas S, Barry CE, III, et al. (1998) *Nature* 393:537–544.
14. Brennan MJ, Delogu G, Chen Y, Bardarov S, Kriakov J, Alavi M, Jacobs WR, Jr (2001) *Infect Immun* 69:7326–7333.
15. Banu S, Honore N, Saint-Joanis B, Philpott D, Prevost MC, Cole ST (2002) *Mol Microbiol* 44:9–19.
16. Delogu G, Puseddu C, Bua A, Fadda G, Brennan MJ, Zanetti S (2004) *Mol Microbiol* 52:725–733.
17. Espitia C, Laclette JP, Mondragon-Palomino M, Amador A, Campuzano J, Martens A, Singh M, Cicero R, Zhang Y, Moreno C (1999) *Microbiology* 145(Pt 12):3487–3495.
18. Finlay BB, Falkow S (1997) *Microbiol Mol Biol Rev* 61:136–169.
19. Strom MS, Lory S (1993) *Annu Rev Microbiol* 47:565–596.
20. Ton-That H, Schneewind O (2003) *Mol Microbiol* 50:1429–1438.
21. Lauer P, Rinaudo CD, Soriani M, Margarit I, Maione D, Rosini R, Taddei AR, Mora M, Rappuoli R, Grandi G, Telford JL (2005) *Science* 309:105.
22. De Sousa-D'Auria C, Kacem R, Puech V, Tropis M, Leblon G, Houssin C, Daffe M (2003) *FEMS Microbiol Lett* 224:35–44.
23. Barksdale L, Kim KS (1977) *Bacteriol Rev* 41:217–372.
24. Xalabarder C (1957) *Mikroskopie* 11:406–410.
25. Olsen A, Jonsson A, Normark S (1989) *Nature* 338:652–655.
26. Collinson SK, Emody L, Muller KH, Trust TJ, Kay WW (1991) *J Bacteriol* 173:4773–4781.
27. Giron JA, Ho AS, Schoolnik GK (1991) *Science* 254:710–713.
28. McMichael JC, Ou JT (1979) *J Bacteriol* 138:969–975.
29. Krogh A, Larsson B, von Heijne G, Sonnhammer EL (2001) *J Mol Biol* 305:567–580.
30. Camus JC, Pryor MJ, Medigue C, Cole ST (2002) *Microbiology* 148:2967–2973.
31. Bardarov S, Bardarov S, Jr, Pavelka MS, Jr, Sambandamurthy V, Larsen M, Tufariello J, Chan J, Hatfull G, Jacobs WR, Jr (2002) *Microbiology* 148:3007–3017.
32. Klemm P, Schembri MA (2000) *Int J Med Microbiol* 290:27–35.
33. Middleton AM, Chadwick MV, Nicholson AG, Dewar A, Groger RK, Brown EJ, Ratliff TL, Wilson R (2002) *Tuberculosis (Edinburgh)* 82:69–78.
34. Andersen RJ (1939) *Fortschr Chem Org Naturst* 3:145–202.
35. Andersen RJ (1943) *Yale J Biol Med* 15:311–345.
36. Draper P (1998) *Front Biosci* 3:D1253–D1261.
37. Barrow WW, Ullom BP, Brennan PJ (1980) *J Bacteriol* 144:814–822.
38. Draper P, Rees RJ (1970) *Nature* 228:860–861.
39. Kim KS, Salton MR, Barksdale L (1976) *J Bacteriol* 125:739–743.
40. Ton-That H, Marraffini LA, Schneewind O (2004) *Mol Microbiol* 53:251–261.
41. Paterson GK, Mitchell TJ (2004) *Trends Microbiol* 12:89–95.
42. Chapman MR, Robinson LS, Pinkner JS, Roth R, Heuser J, Hammar M, Normark S, Hultgren SJ (2002) *Science* 295:851–855.
43. Olsen A, Herwald H, Wikstrom M, Persson K, Mattsson E, Bjorck L (2002) *J Biol Chem* 277:34568–34572.
44. Kinkhikar AG, Vargas D, Li H, Mahaffey SB, Hinds L, Belisle JT, Laal S (2006) *Mol Microbiol* 60:999–1013.
45. Samanich K, Belisle JT, Laal S (2001) *Infect Immun* 69:4600–4609.
46. Walters SB, Dubnau E, Kolesnikova I, Laval F, Daffe M, Smith I (2006) *Mol Microbiol* 60:312–330.
47. Perez E, Samper S, Bordas Y, Guilhot C, Gicquel B, Martin C (2001) *Mol Microbiol* 41:179–187.
48. Giron JA, Torres AG, Freer E, Kaper JB (2002) *Mol Microbiol* 44:361–379.
49. Laemmli UK (1970) *Nature* 227:680–685.