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(54)【発明の名称】ＤＮＡジャイレース遺伝子中に存在する特徴的な塩基配列を用いた遅発育性マイコバクテリアの同定法及び特異的検出法

(57)【特許請求の範囲】

【請求項１】

配列番号３記載の配列又はそれと相補的な配列で表されるオリゴヌクレオチドを、プライマー又はプローブとして用いることにより、マイコバクテリウム・カンサシイを検出することを特徴とするマイコバクテリウム・カンサシイの検出方法。

【請求項２】

配列番号３記載の配列又はそれと相補的な配列で表されるオリゴヌクレオチドを含むことを特徴とするマイコバクテリウム・カンサシイの検出用キット。

【請求項３】

配列番号５記載の配列又はそれと相補的な配列で表されるオリゴヌクレオチドを、プライマー又はプローブとして用いることにより、マイコバクテリウム・ガストリを検出することを特徴とするマイコバクテリウム・ガストリの検出方法。

【請求項４】

配列番号５記載の配列又はそれと相補的な配列で表されるオリゴヌクレオチドを含むことを特徴とするマイコバクテリウム・ガストリの検出用キット。

【発明の詳細な説明】

【０００１】

【発明の属する技術分野】

本発明は、結核並びに非結核性抗酸症の原因菌として多くの症例数のある遅発育性マイコバクテリアのＤＮＡジャイレースβサブユニットをコードするＤＮＡ（以下、「ｇｙｒＢ

遺伝子」という）の塩基配列を利用した同定・検出法に関するものである。本発明の同定・検出法は、各種産業分野において有用である。

【０００２】

【従来の技術】

ヒトに結核並びに結核類似症を引き起こす抗酸菌種は遅発育性マイコバクテリアの属する種が複数知られている。その中でも臨床例としてはマイコバクテリウム・ツベルクローシス・コンプレックス（Ｍｙｃｏｂａｃｔｅｒｉｕｍ　ｔｕｂｅｒｃｕｌｏｓｉｓ　ｃｏｍｐｌｅｘ）、マイコバクテリウム・アビウム・コンプレックス（Ｍｙｃｏｂａｃｔｅｒｉｕｍ　ａｖｉｕｍ　ｃｏｍｐｌｅｘ）、マイコバクテリウム・カンサシイ（Ｍｙｃｏｂａｃｔｅｒｉｕｍ　ｋａｎｓａｓｉｉ）がその大半を占めている。最近では後天性免疫不全症候群（ＡＩＤＳ）患者等においてはこれらの細菌が全身播種性感染を引き起こし、ＡＩＤＳ患者の予後の重大な問題となっている。

【０００３】

従来これらの菌種の同定・検出は、培養に基づく生理生化学的な方法によって行われていた。例えば、遅発育性マイコバクテリアの中には、１）光を照射した後に暗所で培養した場合にのみ黄色に発色するグループ（光発色菌）、２）光を照射せずに培養しても発色するグループ（暗発色菌）、３）光を照射しても発色しないグループ（非発色菌）の３グループが存在するので、この発色の違いを利用して同定・検出を行うことが行われてきた。また、培養した細菌がカタラーゼ生産を行うかどうか、ウレアーゼ活性、トゥイーン加水分解活性あるいは硝酸塩還元活性を示すかどうか、などにより同定・検出を行う方法も知られていた。

【０００４】

しかし、これらの検査は純粋培養を必要とする上、比較の対象となる表現型は変化しやすく、判定が主観的になりがちであった。その結果、時間がかかる上に、正確な種の判定は極めて困難であった。この様な問題点を解決するために、近年になってポリメラーゼ連鎖反応（以下、「ＰＣＲ」という）法などを用いて遺伝子の特定の塩基配列の有無を判定する同定・検出の方法が考案され利用されるようになった。ＰＣＲ法は、培養を必要とせず迅速かつ客観的な判定を得るという点で、遅発育性のマイコバクテリアの同定・検出に適している。

【０００５】

その際、用いられる遺伝子は多くの場合、ｒＲＮＡ遺伝子である。Ｔ．　Ｒｏｇａｌｌら（１９９０．　Ｊ．　Ｇｅｎ．　Ｍｉｃｒｏｂｉｏｌ．　１３６，　１９１５－１９２０）は、１６Ｓ　ｒＲＮＡ配列を用いたＰＣＲに基づくマイコバクテリア種の同定法を提案した。しかしながら、これらのプライマーは、異なった表現型特性を示すマイコバクテリウム・ガストリ（Ｍｙｃｏｂａｃｔｅｒｉｕｍ　ｇａｓｔｒｉ）とマイコバクテリウム・カンサシイを区別できなかった。一方Ｂ．　Ｂｏｄｄｉｎｇｈａｕｓら（１９９０．　Ｊ．　Ｃｌｉｎ．　Ｍｉｃｒｏｂｉｏｌ．　２８：　１７５１－１７５９）は、ヒト型結核菌グループや鳥型結核菌ーパラ結核菌およびマイコバクテリウム・イントラセルラーレ（Ｍｙｃｏｂａｃｔｅｒｉｕｍ　ｉｎｔｒａｃｅｌｌｕｌａｒｅ）グループに特異的である１６Ｓ　ｒＲＮＡ配列に由来するオリゴヌクレオチドを報告した。このオリゴヌクレオチドを用いても種のレベルでの同定を行う為に必要な解像度は得られなかった。これらのｒＲＮＡ遺伝子配列を利用した同定法は、現在商品化され、日本ロッシュから「アンプリコア・マイコバクテリウム」という商品名の遺伝子診断キットとして販売されている。その他にも、東洋紡社（特開平１０－３２３１８９号公報）やベクトン・ディッキンソン・アンド・カンパニー（特開平１０－０５７０９８号公報）からｒＲＮＡ配列を利用した検出あるいは同定法が開示されている。上に記したような二つの種を判別できない問題を解決するために、１６Ｓ　ｒＲＮＡと２３Ｓ　ｒＲＮＡの間の領域の配列を用いた同定・検出法がＡ．　Ｒｏｔｈらによって提案されている（１９９８．　Ｊ．　Ｃｌｉｎ．　Ｍｉｃｒｏｂｉｏｌ．　３６：　１３９－１４７）。しかし、１６Ｓ　ｒＲＮＡと２３Ｓ　ｒＲＮＡの間の領域は約２００塩基対しかなく、このような短い配列により精度の高い分子系

統学的解析は困難で二菌種のどちらの配列とも一致しない中間的な配列を持つ新規株が現れた場合、どちらにより近縁かといった判断を下すことができない

一方、シュードモナス（Ｐｓｅｕｄｏｍｏｎａｓ）属、アシネトバクター（Ａｃｉｎｅｔｏｂａｃｔｅｒ）属を始め、多くの細菌で、進化速度の速いタンパク質をコードする遺伝子、なかでもｇｙｒＢ遺伝子の１２００塩基対の配列を用いることによって、より詳細で正確な分類・同定ができることが示された（Ｙａｍａｍｏｔｏ， Ｓ． ａｎｄ Ｓ． Ｈａｒａｙａｍａ． １９９５． Ａｐｐｌ． Ｅｎｖｉｒｏｎ． Ｍｉｃｒｏｂｉｏｌ． ６１： １１０４－１１０９． Ｙａｍａｍｏｔｏ， Ｓ． ａｎｄ Ｓ． Ｈａｒａｙａｍａ． １９９６． Ｉｎｔ． Ｊ． Ｓｙｓｔ． Ｂａｃｔｅｒｉｏｌ． ４６： ５０６－５１１． Ｈａｒａｙａｍａ， Ｓ． ａｎｄ Ｓ． Ｙａｍａｍｏｔｏ． １９９６． ｐ２５０－２５８ Ｉｎ Ｍｏｌｅｃｕｌａｒ Ｂｉｏｌｏｇｙ ｏｆ Ｐｓｅｕｄｏｍｏｎａｓ Ｔ． Ｎａｋａｚａｗａ， Ｋ． Ｆｕｋｕｄａ， Ｄ． Ｈａａｓ， Ｓ． Ｓｉｌｖｅｒ （ｅｄｓ） ＡＳＭ ｐｒｅｓｓ， Ｗａｓｈｉｎｇｔｏｎ， Ｄ．Ｃ．， 山本　敏、原山重明、化学と生物　１９９６　第３４巻　第３号　ｐ． １４９－１５１．， 山本　敏、原山重明、農芸化学会誌　１９９７　第７１巻　第９号　ｐ． ８９４－８９７．）。

【０００６】

ｇｙｒＢ遺伝子以外のタンパク質をコードする遺伝子を用いて遅発育性マイコバクテリアの同定を行う試みは行われている。例えば、Ｃ． Ｔ． Ｓｈｉｖａｎｎｖａｒらはスーパーオキシド・ディスムターゼ遺伝子を利用して遅発育性のマイコバクテリアの系統関係と抗原性の関係を論じ（１９９４． Ｊ． Ｃｌｉｎ． Ｍｉｃｒｏｂｉｏｌ． ３２： ２８０１－２８１２）、Ｄ． Ｓ． Ｓｗａｎｓｏｎらは６５ ｋＤ 熱ショックタンパク質遺伝子を用いて鳥型結核菌ーパラ結核菌およびマイコバクテリウム・イントラセルラーレグループの詳細な分類を試みた（１９９７． Ｉｎｔ． Ｊ． Ｓｙｓｔ． Ｂａｃｔｅｒｉｏｌ． ４７： ４１４－４１９）。米国アボット・ラボラトリーズは特表平１０－５００５６７（国際公開番号Ｗ０９５／３１５７１）としてｒＲＮＡ遺伝子以外にもマイコバクテリウム・ツベルクローシスのタンパク質抗原Ｂをコードする遺伝子や、マイコバクテリウム・ツベルクローシスの６５ ｋＤ熱ショックタンパク質、１０ｋＤ熱ショックタンパク質等の遺伝子配列並びに挿入配列ＩＳ９８７やＩＳ６１１０の関連する配列を用いた検出法を開示している。他にもベクトン・ディッキンソン・アンド・カンパニーはマイコバクテリウム・パラツベルクロシスの７０ｋＤ熱ショックタンパク質をコードする遺伝子に由来する検出・同定するプローブを特開平０６－３１９５６０として開示している。しかしながら、これらの遺伝子のうち、分子系統学的に得られるデーターと従来の分類学的な手法による種の同定と比較した場合、矛盾が認められないことが示されているのはｇｙｒＢ遺伝子のみであり（Ｙａｍａｍｏｔｏ ａｎｄ Ｈａｒａｙａｍａ １９９８． Ｉｎｔ． Ｊ． Ｓｙｓｔ． Ｂａｃｔｅｒｉｏｌ． ４８： ８１３－８１９． Ｙａｍａｍｏｔｏ ｅｔ．ａｌ． １９９９． Ｉｎｔ． Ｊ． Ｓｙｓｔ． Ｂａｃｔｅｒｉｏｌ． ４９： ８７－９５． Ｓｕｚｕｋｉ ｅｔ ａｌ． １９９９． Ｉｎｔ． Ｊ． Ｓｙｓｔ． Ｂａｃｔｅｒｉｏｌ． ｉｎ ｐｒｅｓｓ， Ｋａｓａｉ ｅｔ ａｌ． １９９９． Ｉｎｔ． Ｊ． Ｓｙｓｔ． Ｂａｃｔｅｒｉｏｌ． ｉｎ ｐｒｅｓｓ）、新規に分離された株についても正確な分子系統学的な位置を決定でき、更に他の遺伝子では区別できなかった近縁種の区別できることなどから他の遺伝子を用いた方法より有効な方法である。

【０００７】

【発明が解決しようとする課題】

ｇｙｒＢ遺伝子を用いた細菌の同定・検出法については、既に本出願人により出願されている（特開平１１－１６９１７５号公報）。しかし、この公報中では、遅発育性マイコバクテリアの同定・検出を行うに当たってｇｙｒＢ遺伝子中のどの領域を利用すればよいかについては明らかにされていなかった。

【０００８】

遅発育性マイコバクテリアには結核などの重要な疾病の原因細菌が含まれるため、この細菌群を正確に同定・検出するための方法が強く望まれている。一方、遅発育性マイコバクテリアは、生育速度が通常の細菌よりも遅いため、細菌の培養を必須とする生理生化学的方法では同定・検出が難しい。

本発明は、このような技術的背景の下になされたものであり、ｇｙｒＢ遺伝子を利用した遅発育性マイコバクテリアの同定・検出方法を提供することにある。

【０００９】

【課題を解決するための手段】

本発明者らは遅発育性マイコバクテリアの標準株のｇｙｒＢ遺伝子配列を決定した。それらの配列に対して臨床から分離された株の分類学的な位置づけを行った。分類学的位置づけが矛盾のないことを、細菌の種の同定の標準的方法であるＤＮＡ－ＤＮＡ　交雑法によって確認した。

【００１０】

また、遺伝子配列を利用した細菌の検出法として最も一般的に用いられる１６Ｓ　ｒＲＮＡ遺伝子の配列では区別できない非結核性抗酸菌マイコバクテリウム・ガストリとマイコバクテリウム・カンサシイの標準株のＤＮＡからｇｙｒＢ　断片をＰＣＲ法によって増幅し塩基配列を決定した。得られた配列を比較したところ、両株の１６Ｓ　ｒＲＮＡ遺伝子配列は同一であるにも関わらず、両株のｇｙｒＢ遺伝子配列１２５７塩基配列中６６箇所が異なっていることを見い出した（図１）。それらの配列の違いを利用して両菌種それぞれに特異的なＰＣＲ増幅を可能にしたプライマーを設計した。

【００１１】

本発明は、以上の知見により完成されたものである。

即ち、本発明は、遅発育性マイコバクテリアのｇｙｒＢ中の配列番号７～２２に対応する領域を増幅し、その増幅断片の塩基配列を配列番号７～２２記載の塩基配列と比較し、各配列からの遺伝学的距離を求め、その遺伝学的距離により前記遅発育性マイコバクテリアの同定を行うことを特徴とする遅発育性マイコバクテリアの同定方法である。

【００１２】

また、本発明は、配列番号４記載のアミノ酸配列の一部若しくは全部をコードする配列、又はそれと相補的な配列を含み、プライマー又はプローブとして実質的に機能するオリゴヌクレオチドを、プライマー又はプローブとして用いることにより、マイコバクテリウム・カンサシイを検出することを特徴とするマイコバクテリウム・カンサシイの検出方法、及び前記オリゴヌクレオチドを含むマイコバクテリウム・カンサシイの検出用キットである。

【００１３】

更に、本発明は、配列番号６記載のアミノ酸配列の一部若しくは全部をコードする配列、又はそれと相補的な配列を含み、プライマー又はプローブとして実質低に機能するオリゴヌクレオチドを、プライマー又はプローブとして用いることにより、マイコバクテリウム・ガストリを検出することを特徴とするマイコバクテリウム・ガストリの検出方法、及び前記オリゴヌクレオチドを含むマイコバクテリウム・ガストリの検出用キットである。

【００１４】

【発明の実施の形態】

以下、本発明を詳細に説明する。

（１）同定方法

本発明の遅発育性マイコバクテリアの同定方法は、遅発育性マイコバクテリアのｇｙｒＢ中の配列番号７～２２に対応する領域をＰＣＲにより増幅し、その増幅断片の塩基配列を配列番号７～２２記載の塩基配列と比較し、各配列からの遺伝学的距離を求め、その遺伝学的距離により前記遅発育性マイコバクテリアの同定を行うことを特徴とする。

【００１５】

本発明において同定とは、分子系統学的な手法等によって細菌の分類学的な位置を定めることをいう。

ｇｙｒＢ中の配列番号７～２２に対応する領域を増幅するためのプライマーとしては、例えば、配列番号３９及び配列番号４０により表されるプライマーを例示することができるが、これらに限定されるわけではない。

配列番号７～２２記載の塩基配列と、対応するアミノ酸配列及び由来とする微生物の名称との関係は、下表の通りである。

【００１６】

【表１】

塩基配列	アミノ酸配列	由来とする微生物の名称
配列番号７	配列番号２３	マイコバクテリウム・シミエ
配列番号８	配列番号２４	マイコバクテリウム・ボビス
配列番号９	配列番号２５	マイコバクテリウム・スツルガイ
配列番号１０	配列番号２６	マイコバクテリウム・マルモエンセ
配列番号１１	配列番号２７	マイコバクテリウム・イントラセルラーレ
配列番号１２	配列番号２８	マイコバクテリウム・アビウム
配列番号１３	配列番号２９	マイコバクテリウム・ゴルドナエ
配列番号１４	配列番号３０	アミコバクテリウム・アフリカヌム
配列番号１５	配列番号３１	マイコバクテリウム・ツベルクローシス
配列番号１６	配列番号３２	マイコバクテリウム・ガストリ
配列番号１７	配列番号３３	マイコバクテリウム・マリヌム
配列番号１８	配列番号３４	マイコバクテリウム・ミクロティ
配列番号１９	配列番号３５	マイコバクテリウム・アジアティカム
配列番号２０	配列番号３６	マイコバクテリウム・スクロファラセウム
配列番号２１	配列番号３７	マイコバクテリウム・ブランデリ
配列番号２２	配列番号３８	マイコバクテリウム・パラツベルクロシス

【００１７】

遺伝学的距離は、例えば、Ｐｈｙｌｉｐ　プログラムの説明書にあるＦｅｌｓｅｎｓｔｅｉｎ記載の方法に従って求めることができる（Ｆｅｌｓｅｎｓｔｅｉｎ，　Ｊ．　１９９３．　ＰＨＹＬＩＰ（ＰｈｙｌｏｇｅｎｙＩｎｆｅｒｅｎｃｅ　Ｐａｃｋａｇｅ）ｖｅｒｓｉｏｎ　３．５ｃ．　Ｄｉｓｔｒｉｂｕｔｅｄ　ｂｙ　ｔｈｅ　ａｕｔｈｏｒ，　Ｄｅｐａｒｔｍｅｎｔ　ｏｆ　Ｇｅｎｅｔｉｃｓ，　Ｕｎｉｖｅｒｓｉｔｙ　ｏｆ　Ｗａｓｈｉｎｇｔｏｎ，　Ｓｅａｔｔｌｅ，　Ｕ．Ｓ．Ａ．）。

【００１８】

（２）特異的検出

本発明のマイコバクテリウム・カンサシイの検出方法は、配列番号４記載のアミノ酸配列の一部若しくは全部をコードする配列、又はそれと相補的な配列を含み、プライマー又はプローブとして実質的に機能するオリゴヌクレオチドを、プライマー又はプローブとして用いることを特徴とするものである。また、本発明のマイコバクテリウム・カンサシイの検出用キットは、前記オリゴヌクレオチドを含むことを特徴とするものである。

【００１９】

本発明のマイコバクテリウム・ガストリの検出方法は、配列番号６記載のアミノ酸配列の一部若しくは全部をコードする配列、又はそれと相補的な配列を含み、プライマー又はプローブとして実質低に機能するオリゴヌクレオチドを、プライマー又はプローブとして用いることを特徴とするものである。また、本発明のマコバクテリウム・ガストリの検出用キットは、前記オリゴヌクレオチドを含むことを特徴とするものである。

【００２０】

ここで、「プライマー又はプローブとして実質的に機能する」とは、特異的なアニール又はハイブリダイズが可能な程度の長さを有するという意味であり、検出対象とするＤＮＡとアニール又はハイブリダイズする配列を有しているが、その長さが短いため非特異的なアニール又はハイブリダイゼーションを頻繁に起こし、特異的な検出に使用できないよう

なオリゴヌクレオチドを排除する趣旨である。

【００２１】

マイコバクテリウム・カンサシイの検出に利用できるオリゴヌクレオチドとしては、配列番号３により表されるオリゴヌクレオチドを例示でき、マイコバクテリウム・ガストリの検出に利用できるオリゴヌクレオチドとしては、配列番号５により表されるオリゴヌクレオチドを例示できるが、これらに限定されるわけではない。

【００２２】

検出の対象とするＤＮＡの調製、プライマーの作製及びそれを用いたＰＣＲ、プローブの調製及びそれを用いたハイブリダイゼーションは、常法に従って行うことができ、特別な方法を用いる必要はない。

【００２３】

なお、ＰＣＲに使用するプライマーは、両方が特異的にアニールするものである必要は必ずしもなく、一方は非特異的にアニールするものであってもよい。このような非特異的にアニールするプライマーの一例としては、配列番号１記載の塩基配列により表されるプライマーを挙げることができる。

【００２４】

【実施例】

〔実施例１〕

配列番号３９及び配列番号４０記載の塩基配列により表されるオリゴヌクレオチドを利用して、臨床患者より分離された抗酸菌株８菌株（ＫＰＭ　２２０１Ｔ、ＫＰＭ　２２０２、ＫＰＭ　２２０３、ＫＰＭ　２０１３、ＫＰＭ　２０１４、ＫＰＭ　１９８８－５、ＫＰＭ　２２０９、ＫＰＭ　２２１２）のｇｙｒＢ遺伝子配列を決定した。得られたｇｙｒＢ配列と遅発育性マイコバクテリア同定用ｇｙｒＢ配列セット（配列番号７－３８）を利用して分子系統学的解析により系統関係を推定した。分子系統学的解析は、分子系統学的解析用汎用プログラムＣｌｕｓｔａｌ　Ｗ（Ｔｈｏｍｐｓｏｎ，　Ｊ．　Ｄ．，　Ｄ．　Ｇ．　Ｈｉｇｇｉｎｓ，　ａｎｄ　Ｔ．　Ｊ．　Ｇｉｂｓｏｎ．　１９９４．　Ｃｌｕｓｔａｌ　Ｗ：ｉｍｐｒｏｖｉｎｇ　ｔｈｅｓｅｎｓｉｔｉｖｉｔｙ　ｏｆ　ｐｒｏｇｒｅｓｓｉｖｅ　ｍｕｌｔｉｐｌｅ　ｓｅｑｕｅｎｃｅ　ａｌｉｇｎｍｅｎｔ　ｔｈｒｏｕｇｈ　ｓｅｑｕｅｎｃｅｗｅｉｇｈｔｉｎｇ，　ｐｏｓｉｔｉｏｎｓ－ｓｐｅｃｉｆｉｃ　ｇａｐ　ｐｅｎａｌｔｉｅｓ　ａｎｄ　ｗｅｉｇｈｔ　ｍａｔｒｉｘ　ｃｈｏｉｃｅ．　Ｎｕｃｌｅｉｃ　Ａｃｉｄｓ　Ｒｅｓ．　２２：　４６７３－４６８０．）あるいはＰｈｙｌｉｐ（Ｆｅｌｓｅｎｓｔｅｉｎ，　Ｊ．　１９９３．　ＰＨＹＬＩＰ（Ｐｈｙｌｏｇｅｎｙ　Ｉｎｆｅｒｅｎｃｅ　Ｐａｃｋａｇｅ）ｖｅｒｓｉｏｎ　３．５ｃ．　Ｄｉｓｔｒｉｂｕｔｅｄ　ｂｙ　ｔｈｅ　ａｕｔｈｏｒ，　Ｄｅｐａｒｔｍｅｎｔ　ｏｆ　Ｇｅｎｅｔｉｃｓ，　Ｕｎｉｖｅｒｓｉｔｙ　ｏｆ　Ｗａｓｈｉｎｇｔｏｎ，　Ｓｅａｔｔｌｅ，　Ｕ．Ｓ．Ａ．）等を用い、両プログラムの使用説明書に従い、以下のように行った。

配列番号３９及び配列番号４０記載の塩基配列により表されるオリゴヌクレオチドを使用して得られたｇｙｒＢ配列と配列番号７－３８の遅発育性マイコバクテリア同定用ｇｙｒＢ配列セットをＣｌｕｓｔａｌ　Ｗプログラムにより多重整列ファイルを作成する。多重整列させる際に用いるパラメーターの一例は”Ｇａｐ　Ｏｐｅｎ　Ｐｅｎａｌｔｙ：　１５．００；Ｇａｐ　Ｅｘｔｅｎｓｉｏｎ　Ｐｅｎａｌｔｙ　：　６．６６；　ＤＮＡ　ｗｅｉｇｈｔ　ｍａｔｒｉｘ：ＩＵＢ；　ＤＮＡ　ｔｒａｎｓｉｔｉｏｎ　ｗｅｉｇｈｔ：０．５”である。得られた多重整列はアミノ酸配列から得られる多重整列ファイルと比較し、問題のある箇所は訂正する。次に、多重整列ファイルをもとに各配列間の遺伝学的距離を算出する。算出には、Ｐｈｙｌｉｐのｄｎａｄｉｓｔプログラムを使用する。算出はＫｉｍｕｒａ　２－ｐａｒａｍｅｔｅｒ　ｍｏｄｅｌ　に従って行う。得られた遺伝学的距離から近隣結合法により系統樹を作成する。系統樹の分岐の確からしさはｂｏｏｔｓｔｒａｐ確率を計算すること等により検定する。

一方、上記８菌株を１６Ｓ　ｒＲＮＡ遺伝子を利用した手法及び生化学的手法によっても同定した。以上の結果を表２に示す。

【００２５】

【表２】

株名	生化学的試験	16S rRNA 遺伝子	DNA 相同性試験
KPM 2201T	M. gordonae	M. gordonae	M. gordonae
KPM 2202	M. gastori	M. gordonae	M. gordonae
KPM 2203	M. gastori	M. gordonae	M. gordonae
KPM 2013	M. scrofulcerum	M. gordonae	新種
KPM 2014	M. scrofulcerum	M. gordonae	新種
KPM 1988-5	M. scrofulcerum	M. gordonae	新種
KPM 2209	M. scrofulcerum	M. gordonae	新種
KPM 2212	データーなし	M. gordonae	新種

【００２６】

表が示すように、上記８菌株のうち、ＫＰＭ ２２０１Ｔ、ＫＰＭ ２２０２、ＫＰＭ ２２０３の３菌株は、マイコバクテリウム・ゴルドナエに属するものと同定されたが、残りのＫＰＭ ２０１３、ＫＰＭ ２０１４、ＫＰＭ １９８８－５、ＫＰＭ ２２０９、ＫＰＭ ２２１２の５菌株は、マイコバクテリウム・ゴルドナエと近縁ではあるが別種（新種）であることが示唆された（図３）。この結果を、検証するためにＤＮＡ－ＤＮＡ交雑試験（Ｅｚａｋｉ， Ｔ．， Ｈａｓｈｉｍｏｔｏ， Ｙ．， Ｔａｋｅｕｃｈｉ， Ｔ．， Ｙａｍａｍｏｔｏ， Ｈ．， Ｓｈｕ－Ｌｉｎ Ｌｉｕ， Ｍａｔｓｕｉ， Ｋ．， ＆ Ｙａｂｕｕｃｈｉ， Ｅ（１９８８）． Ｊ． Ｃｌｉｎ． Ｍｉｃｒｏｂｉｏｌ． ２６， １７０８－１７１３． Ｅｚａｋｉ， Ｔ．， Ｈａｓｈｉｍｏｔｏ， Ｙ．， Ｔａｋｅｕｃｈｉ ＆ Ｙａｂｕｕｃｈｉ， Ｅ（１９８９）． Ｉｎｔ． Ｊ． Ｓｙｓｔ． Ｂａｃｔｅｒｉｏｌ． ３９， ２２４－２２９）を行ったところ新種であることが支持された。この結果は、遅発育性マイコバクテリア同定用ｇｙｒＢ配列セットが既知の株のみならず新種の株に対しても信頼性の高い結果を与えることを示している。

【００２７】

〔実施例２〕

マイコバクテリウム・カンサシイとマイコバクテリウム・ガストリのｇｙｒＢ遺伝子の塩基配列を比較し（図１）、マイコバクテリウム・カンサシイのｇｙｒＢ遺伝子に特異的にアニールするプライマー（配列番号３）とマイコバクテリウム・ガストリに特異的にアニールするプライマー（配列番号５）を作製した。また、両菌種のｇｙｒＢ遺伝子にアニールするプライマー（配列番号１）も作製した。

【００２８】

これらのプライマーを用いて、臨床患者より単離された株 ＫＰＭ １００４， ＫＰＭ １００７， ＫＰＭ ＫＹ２５６， ＫＰＭ ＫＹ７６１， ＫＰＭ ＫＹ７６８， ＫＰＭ １９８８－１， ＫＰＭ ３５０２， ＫＰＭ ３５０３の菌体破砕液をついてＰＣＲを行った。

ＰＣＲ法による増幅条件は次のとおりである。

【００２９】

９５ ℃ １０分　１サイクル
９５ ℃ １分、６８ ℃ １分３０秒　３０サイクル
７２ ℃ １０分　１サイクル
プライマー濃度　各１ μＭ
ｄＮＴＰ　各 １００ μＭ
Ａｍｐｌｉ Ｔａｑ ＧＯＬＤ^{TM}及び添付のＰＣＲ ｂｕｆｆｅｒ Ｉを使用（米国Ｐｅｒｋｉｎ Ｅｌｍｅｒ社）

【００３０】

増幅されたＤＮＡ 断片を電気泳動法により解析したところ、ＫＰＭ １００４， ＫＰ

M　１００７，　ＫＰＭ　ＫＹ２５６，　ＫＰＭ　ＫＹ７６１，　ＫＰＭ　ＫＹ７６８，　ＫＰＭ　１９８８－１は配列番号１と３に示した組み合わせでのみ増幅断片が観察されたので（表３）、これらの株は　マイコバクテリウム・カンサシイと同定された。また、　ＫＰＭ　３５０２，　ＫＰＭ　３５０３は配列番号１と５に示した組み合わせでのみ増幅断片が観察されたので（表３）、これらの株はマイコバクテリウム・ガストリ　と同定された。判定に用いた電気泳動像は図２に示すとおりである。これらの同定結果はＤＮＡ－ＤＮＡ　ハイブリダイゼーション法による同定結果と一致した。

【００３１】

【表３】

	M. kansasii	M. gastri
配列番号1 配列番号3	増幅可。	増幅不可。
配列番号1 配列番号5	増幅不可。	増幅可。

【００３２】

【発明の効果】

本発明は、これまで同定することが困難であった遅発育性マイコバクテリアの分類同定を正確に行うことを実現するものである。また非結核性抗酸菌のうち１６Ｓ　ｒＲＮＡ　遺伝子配列に基づく同定法では鑑別が困難であった菌種、例えばマイコバクテリウム・カンサシイとマイコバクテリウム・ガストリイの迅速同定が可能となる。

【００３３】

【配列表】

SEQUENCE LISTING

〈110〉 MARINE BIOTECHNOLOGY INSTITUTE CO., LTD

〈120〉 DNA GYIRESU IDENSHICHU NI SONZAISURU TOKUCHYOUTEKINA ENKIHAIRETSU WO MOCHIITA CHIHATSUIKUSEI MAIKOBAKUTERIA NO DOUTEIHOU OYOBI TOKUITEKI KENSHUTSUHOU

〈130〉 P99-0373

〈160〉 40

〈170〉 PatentIn Ver. 2.0

〈210〉 1
〈211〉 20
〈212〉 DNA
〈213〉 Artificial Sequence

〈400〉 1
ggt gtc tcg gtg gtc aac gc

〈210〉 2
〈211〉 6
〈212〉 PRT
〈213〉 Artificial Sequence

〈400〉 2
Gly Val Ser Val Val Asn

〈210〉 3
〈211〉 20
〈212〉 DNA
〈213〉 Artificial Sequence

〈400〉 3
gac ctt gtg cgg ggc ggc gg

〈210〉 4
〈211〉 6
〈212〉 PRT
〈213〉 Artificial Sequence

〈400〉 4
Ala Ala Pro His Lys Val

〈210〉 5
〈211〉 20
〈212〉 DNA
〈213〉 Artificial Sequence

〈400〉 5
cac ctt gtg ggg ggc ggt ga

〈210〉 6
〈211〉 6
〈212〉 PRT
〈213〉 Artificial Sequence

<400> 6
Thr Ala Pro His Lys Val

<210> 7
<211> 1263
<212> DNA
<213> Mycobacterium simiae

<220>
<221> CDS
<222> (1)..(1263)

<400> 7
ggg gag aac agt ggc tac acc gtc agc ggc ggg ttg cac ggg gtc gga 48
Gly Glu Asn Ser Gly Tyr Thr Val Ser Gly Gly Leu His Gly Val Gly
1 5 10 15

gtg tcg gtg gtc aac gcc ctg tcc acc cgc ctg gaa gtc aac gtc aag 96
Val Ser Val Val Asn Ala Leu Ser Thr Arg Leu Glu Val Asn Val Lys
20 25 30

cgt gac ggc tat gag tgg ttc cag tac tac gac cgg gcg gtg ccc ggc 144
Arg Asp Gly Tyr Glu Trp Phe Gln Tyr Tyr Asp Arg Ala Val Pro Gly
35 40 45

acc ctc aag caa ggc gag gcg acc aag aag acc ggc acc acg atc cgg 192
Thr Leu Lys Gln Gly Glu Ala Thr Lys Lys Thr Gly Thr Thr Ile Arg
50 55 60

```
ttc tgg gcc gat cct gag atc ttc gaa acc acc cag tac gac ttc gag    240
Phe Trp Ala Asp Pro Glu Ile Phe Glu Thr Thr Gln Tyr Asp Phe Glu
 65                  70                  75                  80

acg gtg gcg cgc cgg ttg cag gaa atg gcg ttc ctc aac aag ggc ctg    288
Thr Val Ala Arg Arg Leu Gln Glu Met Ala Phe Leu Asn Lys Gly Leu
                 85                  90                  95

acc atc aac ctc acc gac gaa cgt gtc gag cag gac gag gtg gtc gat    336
Thr Ile Asn Leu Thr Asp Glu Arg Val Glu Gln Asp Glu Val Val Asp
            100                 105                 110

gag gtg gtt agc gac acc gcc gag gcg ccg aag tca gcc gag gag cag    384
Glu Val Val Ser Asp Thr Ala Glu Ala Pro Lys Ser Ala Glu Glu Gln
        115                 120                 125

gcg gcc gaa tcg gcc aag ccg cac aag gtc aag cac cgc acg ttc cac    432
Ala Ala Glu Ser Ala Lys Pro His Lys Val Lys His Arg Thr Phe His
    130                 135                 140

tac ccg ggt ggg ttg gtg gat ttc gtc aag cac atc aat cgc acc aaa    480
Tyr Pro Gly Gly Leu Val Asp Phe Val Lys His Ile Asn Arg Thr Lys
145                 150                 155                 160

aac ccg atc cag cag agc gtc atc gac ttc gac ggc aaa gga acc ggg    528
Asn Pro Ile Gln Gln Ser Val Ile Asp Phe Asp Gly Lys Gly Thr Gly
                165                 170                 175
```

```
cac gaa gtc gag atc gcg atg cag tgg aac ggt ggt tat tcg gag tcg    576
His Glu Val Glu Ile Ala Met Gln Trp Asn Gly Gly Tyr Ser Glu Ser
            180                 185                 190

gtg cac acc ttc gcc aac acc atc aac acc cat gag ggc ggc acc cac    624
Val His Thr Phe Ala Asn Thr Ile Asn Thr His Glu Gly Gly Thr His
        195                 200                 205

gag gag ggc ttc cgc agc gcg ctg acc tcg gtg gtg aac aag tac gcc    672
Glu Glu Gly Phe Arg Ser Ala Leu Thr Ser Val Val Asn Lys Tyr Ala
    210                 215                 220

aaa gac aag aag ctg ctc aag gac aag gat ccc aac ctc acc ggc gac    720
Lys Asp Lys Lys Leu Leu Lys Asp Lys Asp Pro Asn Leu Thr Gly Asp
225                 230                 235                 240

gac atc cga gaa ggg ctg gcc gcg gtg atc tcc gtg aag gtc gcc gag    768
Asp Ile Arg Glu Gly Leu Ala Ala Val Ile Ser Val Lys Val Ala Glu
                245                 250                 255

ccg cag ttc gag ggc cag act aag acg aaa ctc ggc aac acc gag gtc    816
Pro Gln Phe Glu Gly Gln Thr Lys Thr Lys Leu Gly Asn Thr Glu Val
            260                 265                 270

aag tcg ttt gtc cag aaa gtc tgt aac gaa caa ctc act cac tgg ttc    864
Lys Ser Phe Val Gln Lys Val Cys Asn Glu Gln Leu Thr His Trp Phe
        275                 280                 285

gag gcg aac ccg tcg gaa gct aaa acc gtt gta aac aag gcg gtt tcg    912
```

```
Glu Ala Asn Pro Ser Glu Ala Lys Thr Val Val Asn Lys Ala Val Ser
    290                 295                 300

tcg gcc cag gcc cgc att gcg gcg cgt aag gcg cgg gag ttg gtg cgg    960
Ser Ala Gln Ala Arg Ile Ala Ala Arg Lys Ala Arg Glu Leu Val Arg
305                 310                 315                 320

cgt aag agt gct acg gat ttg ggt ggg ttg ccg ggc aag ttg gct gat    1008
Arg Lys Ser Ala Thr Asp Leu Gly Gly Leu Pro Gly Lys Leu Ala Asp
                325                 330                 335

tgc cgc tcg acg gat ccg cgg aag tct gag ctg tat gtg gtg gaa ggt    1056
Cys Arg Ser Thr Asp Pro Arg Lys Ser Glu Leu Tyr Val Val Glu Gly
            340                 345                 350

gat tcc gcg ggt ggg tcg gcg aaa agt ggg cgt gat tcg atg ttc cag    1104
Asp Ser Ala Gly Gly Ser Ala Lys Ser Gly Arg Asp Ser Met Phe Gln
        355                 360                 365

gcg atc ttg ccg ctg cgc ggc aag atc atc aac gtc gaa aag gcc cgc    1152
Ala Ile Leu Pro Leu Arg Gly Lys Ile Ile Asn Val Glu Lys Ala Arg
    370                 375                 380

atc gat cgg gtg ctg aaa aac acc gaa gtc cag gcc atc atc acc gcg    1200
Ile Asp Arg Val Leu Lys Asn Thr Glu Val Gln Ala Ile Ile Thr Ala
385                 390                 395                 400

ctg ggc acc ggc atc cac gac gaa ttc gac atc acc aaa ctg cgt tac    1248
Leu Gly Thr Gly Ile His Asp Glu Phe Asp Ile Thr Lys Leu Arg Tyr
```

405 410 415

cac aag atc gtg ttg 1263
His Lys Ile Val Leu
420

〈210〉 8
〈211〉 1257
〈212〉 DNA
〈213〉 Mycobacterium bovis

〈220〉
〈221〉 CDS
〈222〉 (1)..(1257)

〈400〉 8
tcg gac gcg tat gcg ata tct ggt ggt ctg cac ggc gtc ggc gtg tcg 48
Ser Asp Ala Tyr Ala Ile Ser Gly Gly Leu His Gly Val Gly Val Ser
1 5 10 15

gtg gtt aac gcg cta tcc acc cgg ctc gaa gtc gag atc aag cgc gac 96
Val Val Asn Ala Leu Ser Thr Arg Leu Glu Val Glu Ile Lys Arg Asp
20 25 30

ggg tac gag tgg tct cag gtt tat gag aag tcg gaa ccc ctg ggc ctc 144
Gly Tyr Glu Trp Ser Gln Val Tyr Glu Lys Ser Glu Pro Leu Gly Leu
35 40 45

aag caa ggg gcg ccg acc aag aag acg ggg tca acg gta cgg ttc tgg 192

```
Lys Gln Gly Ala Pro Thr Lys Lys Thr Gly Ser Thr Val Arg Phe Trp
     50                  55                  60

gcc gac ccc gct gtt ttc gaa acc acg gaa tac gac ttc gaa acc gtc    240
Ala Asp Pro Ala Val Phe Glu Thr Thr Glu Tyr Asp Phe Glu Thr Val
 65                  70                  75                  80

gcc cgc cgg ctg caa gag atg gcg ttc ctc aac aag ggg ctg acc atc    288
Ala Arg Arg Leu Gln Glu Met Ala Phe Leu Asn Lys Gly Leu Thr Ile
                 85                  90                  95

aac ctg acc gac gag agg gtg acc caa gac gag gtc gtc gac gaa gtg    336
Asn Leu Thr Asp Glu Arg Val Thr Gln Asp Glu Val Val Asp Glu Val
            100                 105                 110

gtc agc gac gtc gcc gag gcg ccg aag tcg gca agt gaa cgc gca gcc    384
Val Ser Asp Val Ala Glu Ala Pro Lys Ser Ala Ser Glu Arg Ala Ala
        115                 120                 125

gaa tcc act gca ccg cac aaa gtt aag agc cgc acc ttt cac tat ccg    432
Glu Ser Thr Ala Pro His Lys Val Lys Ser Arg Thr Phe His Tyr Pro
    130                 135                 140

ggt ggc ctg gtg gac ttc gtg aaa cac atc aac cgc acc aag aac gcg    480
Gly Gly Leu Val Asp Phe Val Lys His Ile Asn Arg Thr Lys Asn Ala
145                 150                 155                 160

att cat agc agc atc gtg gac ttt tcc ggc aag ggc acc ggg cac gag    528
Ile His Ser Ser Ile Val Asp Phe Ser Gly Lys Gly Thr Gly His Glu
```

```
                165                 170                 175

gtg gag atc gcg atg caa tgg aac gcc ggg tat tcg gag tcg gtg cac   576
Val Glu Ile Ala Met Gln Trp Asn Ala Gly Tyr Ser Glu Ser Val His
            180                 185                 190

acc ttc gcc aac acc atc aac acc cac gag ggc ggc acc cac gaa gag   624
Thr Phe Ala Asn Thr Ile Asn Thr His Glu Gly Gly Thr His Glu Glu
        195                 200                 205

ggc ttc cgc agc gcg ctg acg tcg gtg gtg aac aag tac gcc aag gac   672
Gly Phe Arg Ser Ala Leu Thr Ser Val Val Asn Lys Tyr Ala Lys Asp
    210                 215                 220

cgc aag cta ctg aag gac aag gac ccc aac ctc acc ggt gac gat atc   720
Arg Lys Leu Leu Lys Asp Lys Asp Pro Asn Leu Thr Gly Asp Asp Ile
225                 230                 235                 240

cgg gaa ggc ctg gcc gct gtg atc tcg gtg aag gtc agc gaa ccg cag   768
Arg Glu Gly Leu Ala Ala Val Ile Ser Val Lys Val Ser Glu Pro Gln
                245                 250                 255

ttc gag ggc cag acc aag acc aag ttg ggc aac acc gag gtc aaa tcg   816
Phe Glu Gly Gln Thr Lys Thr Lys Leu Gly Asn Thr Glu Val Lys Ser
            260                 265                 270

ttt gtg cag aag gtc tgt aat gaa cag ctg acc cac tgg ttt gaa gcc   864
Phe Val Gln Lys Val Cys Asn Glu Gln Leu Thr His Trp Phe Glu Ala
        275                 280                 285
```

```
aac ccc acc gac tcg aaa gtc gtt gtg aac aag gct gtg tcc tcg gcg    912
Asn Pro Thr Asp Ser Lys Val Val Val Asn Lys Ala Val Ser Ser Ala
    290                 295                 300

caa gcc cgt atc gcg gca cgt aag gca cga gag ttg gtg cgg cgt aag    960
Gln Ala Arg Ile Ala Ala Arg Lys Ala Arg Glu Leu Val Arg Arg Lys
305                 310                 315                 320

agc gcc acc gac atc ggt gga ttg ccc ggc aag ctg gcc gat tgc cgt    1008
Ser Ala Thr Asp Ile Gly Gly Leu Pro Gly Lys Leu Ala Asp Cys Arg
                325                 330                 335

tcc acg gat ccg cgc aag tcc gaa ctg tat gtc gta gaa ggt gac tcg    1056
Ser Thr Asp Pro Arg Lys Ser Glu Leu Tyr Val Val Glu Gly Asp Ser
            340                 345                 350

gcc ggc ggt tct gca aaa agc ggt cgc gat tcg atg ttc cag gcg ata    1104
Ala Gly Gly Ser Ala Lys Ser Gly Arg Asp Ser Met Phe Gln Ala Ile
        355                 360                 365

ctt ccg ctg cgc ggc aag atc atc aat gtg gag aaa gcg cgc atc gac    1152
Leu Pro Leu Arg Gly Lys Ile Ile Asn Val Glu Lys Ala Arg Ile Asp
    370                 375                 380

cgg gtg cta aag aac acc gaa gtt cag gcg atc atc acg gcg ctg ggc    1200
Arg Val Leu Lys Asn Thr Glu Val Gln Ala Ile Ile Thr Ala Leu Gly
385                 390                 395                 400
```

acc ggg atc cac gac gag ttc gat atc ggc aag ctg cgc tac cac aag 1248
Thr Gly Ile His Asp Glu Phe Asp Ile Gly Lys Leu Arg Tyr His Lys
405 410 415

atc gtg ctg 1257
Ile Val Leu

〈210〉 9
〈211〉 1263
〈212〉 DNA
〈213〉 Mycobacterium szulgai

〈220〉
〈221〉 CDS
〈222〉 (1)..(1263)

〈400〉 9
ggc gag aac agt ggc tac aac gtc agt ggt ggt ctg cac ggc gtc ggg 48
Gly Glu Asn Ser Gly Tyr Asn Val Ser Gly Gly Leu His Gly Val Gly
1 5 10 15

gtg tcg gtg gtg aac gcg ctg tcg acc cgg ctc gag gtc gac atc aag 96
Val Ser Val Val Asn Ala Leu Ser Thr Arg Leu Glu Val Asp Ile Lys
20 25 30

cgt gac ggc cac aag tgg tcg cag ttc tac aac aag gcc gtg ccg ggc 144
Arg Asp Gly His Lys Trp Ser Gln Phe Tyr Asn Lys Ala Val Pro Gly
35 40 45

```
acg ctc aaa cag ggt gaa gcc act aag aaa acc gga acg aca att agg   192
Thr Leu Lys Gln Gly Glu Ala Thr Lys Lys Thr Gly Thr Thr Ile Arg
     50                  55                  60

ttc tgg gcc gac ccg gac atc ttc gag acc acc gaa tac gac ttc gag   240
Phe Trp Ala Asp Pro Asp Ile Phe Glu Thr Thr Glu Tyr Asp Phe Glu
 65                  70                  75                  80

acc gtg gca cgc cgg ctg cag gaa atg gca ttc ctg aac aag ggc ttg   288
Thr Val Ala Arg Arg Leu Gln Glu Met Ala Phe Leu Asn Lys Gly Leu
                 85                  90                  95

acc atc aac ctc acc gac gag cga gtt gcc cag gac gag gtt gtc gac   336
Thr Ile Asn Leu Thr Asp Glu Arg Val Ala Gln Asp Glu Val Val Asp
            100                 105                 110

gag gtc gtc agc gac acc gcc gag gca ccc aag tcc gcc gaa gaa aag   384
Glu Val Val Ser Asp Thr Ala Glu Ala Pro Lys Ser Ala Glu Glu Lys
        115                 120                 125

gcg gcc gaa tcc aaa ggg ccg cat aag gtt aag cac cgc act ttc cat   432
Ala Ala Glu Ser Lys Gly Pro His Lys Val Lys His Arg Thr Phe His
    130                 135                 140

tac ccc ggc ggg ctg atc gac ttc gtc aag cac atc aac cgg acc aag   480
Tyr Pro Gly Gly Leu Ile Asp Phe Val Lys His Ile Asn Arg Thr Lys
145                 150                 155                 160

agc ccg atc cag cag agt gtc gtc gcc ttc gac ggc aag ggt gaa ggg   528
```

Ser Pro Ile Gln Gln Ser Val Val Ala Phe Asp Gly Lys Gly Glu Gly
165 170 175

cac gag gtc gag atc gcg atg cag tgg aac ggc ggc tat tcg gag tcg 576
His Glu Val Glu Ile Ala Met Gln Trp Asn Gly Gly Tyr Ser Glu Ser
180 185 190

gtg cac acc ttc gcc aac acc atc aac acc cac gag ggc ggc acc cac 624
Val His Thr Phe Ala Asn Thr Ile Asn Thr His Glu Gly Gly Thr His
195 200 205

gaa gaa ggg ttc cgc agc gca ctg aca tcg gtg gtg aac aag tac gcc 672
Glu Glu Gly Phe Arg Ser Ala Leu Thr Ser Val Val Asn Lys Tyr Ala
210 215 220

aaa gac aag aag ctg ctc aag gag aag gac gcc aac ctc acc ggc gac 720
Lys Asp Lys Lys Leu Leu Lys Glu Lys Asp Ala Asn Leu Thr Gly Asp
225 230 235 240

gac att cgc gag ggc ctg gcc gcg gtc atc tcg gtg aaa gtt gcc gaa 768
Asp Ile Arg Glu Gly Leu Ala Ala Val Ile Ser Val Lys Val Ala Glu
245 250 255

ccg cag ttc gag ggc cag acc aag acc aaa ctg ggt aac acc gag gtc 816
Pro Gln Phe Glu Gly Gln Thr Lys Thr Lys Leu Gly Asn Thr Glu Val
260 265 270

aag tcg ttc gta cag aag gtc tgc aac gaa cag ctg acc cac tgg ttc 864
Lys Ser Phe Val Gln Lys Val Cys Asn Glu Gln Leu Thr His Trp Phe

```
        275                 280                 285

gag gcc aac ccg tcg gaa gcc aaa acc gtc gtg aac aag gcg gtc tcg   912
Glu Ala Asn Pro Ser Glu Ala Lys Thr Val Val Asn Lys Ala Val Ser
    290                 295                 300

tcg gca cag gcg cgt atc gcc gcc cgc aag gca cga gag ttg gtg cgt   960
Ser Ala Gln Ala Arg Ile Ala Ala Arg Lys Ala Arg Glu Leu Val Arg
305                 310                 315                 320

cgc aag agc gct acc gat ctc ggt ggg ctg ccc ggc aag ctg gcc gac   1008
Arg Lys Ser Ala Thr Asp Leu Gly Gly Leu Pro Gly Lys Leu Ala Asp
                325                 330                 335

tgc cgc tcc acc gat ccg cgc aag tcg gaa ttg tat gtg gtg gaa ggg   1056
Cys Arg Ser Thr Asp Pro Arg Lys Ser Glu Leu Tyr Val Val Glu Gly
            340                 345                 350

gac tcg gcc ggc ggc tcc gcc aag agc ggc cgc gac tcg atg ttt cag   1104
Asp Ser Ala Gly Gly Ser Ala Lys Ser Gly Arg Asp Ser Met Phe Gln
        355                 360                 365

gcg ata ctt ccg ttg cgc ggc aag atc atc aac gtc gag aag gcc cgc   1152
Ala Ile Leu Pro Leu Arg Gly Lys Ile Ile Asn Val Glu Lys Ala Arg
    370                 375                 380

atc gac cgg gtg ctg aag aac acc gaa gtc cag gcg atc atc acc gcg   1200
Ile Asp Arg Val Leu Lys Asn Thr Glu Val Gln Ala Ile Ile Thr Ala
385                 390                 395                 400
```

```
ctg ggt acc gga att cac gac gag ttc gac ctc gcc aaa ctg cgc tac   1248
Leu Gly Thr Gly Ile His Asp Glu Phe Asp Leu Ala Lys Leu Arg Tyr
                405                 410                 415

cac aag atc gtg ctg                                               1263
His Lys Ile Val Leu
            420

<210> 10
<211> 1263
<212> DNA
<213> Mycobacterium malmoense

<220>
<221> CDS
<222> (1)..(1263)

<400> 10
ggc gag aac agc gga tac aac gtc agt ggc ggt ttg cac ggt gtc ggc   48
Gly Glu Asn Ser Gly Tyr Asn Val Ser Gly Gly Leu His Gly Val Gly
  1               5                  10                  15

gtg tcg gtg gtc aac gcg ttg tcg acc cgg ctc gag gtg gat gtc gcc   96
Val Ser Val Val Asn Ala Leu Ser Thr Arg Leu Glu Val Asp Val Ala
             20                  25                  30

cgc gac ggc tac atg tgg tca cag ttc tac gat cac gcc gag ccg gga   144
Arg Asp Gly Tyr Met Trp Ser Gln Phe Tyr Asp His Ala Glu Pro Gly
```

```
        35                  40                  45

acc ctc aaa cag ggc gag gcc acc aag acg acg gga acc acc atc agg   192
Thr Leu Lys Gln Gly Glu Ala Thr Lys Thr Thr Gly Thr Thr Ile Arg
    50                  55                  60

ttc tgg gcc gat ccc gac atc ttc gag acc acc gag tac gac ttc gag   240
Phe Trp Ala Asp Pro Asp Ile Phe Glu Thr Thr Glu Tyr Asp Phe Glu
65                  70                  75                  80

acg gtg gcg cgc cga ctg cag gaa atg gcg ttc ctg aac aag ggt ttg   288
Thr Val Ala Arg Arg Leu Gln Glu Met Ala Phe Leu Asn Lys Gly Leu
                85                  90                  95

acg atc aac ctc acc gac gag cgg gtc agt gaa gag gag gtc gtc gac   336
Thr Ile Asn Leu Thr Asp Glu Arg Val Ser Glu Glu Glu Val Val Asp
            100                 105                 110

gat gtc gtc agc gac acc gcc gag gca ccc aag tcc gcc gta gaa aaa   384
Asp Val Val Ser Asp Thr Ala Glu Ala Pro Lys Ser Ala Val Glu Lys
        115                 120                 125

gcg gcc gaa tcg act ggc cca cac aag gtt aag cac cgc acg ttc cac   432
Ala Ala Glu Ser Thr Gly Pro His Lys Val Lys His Arg Thr Phe His
    130                 135                 140

tac ccg ggc ggc ttg gtg gac ttc gtc aag cac atc aat cgg acc aag   480
Tyr Pro Gly Gly Leu Val Asp Phe Val Lys His Ile Asn Arg Thr Lys
145                 150                 155                 160
```

```
aac ccg att cac aac agc atc gtg gat ttc tcc ggc aag gga ccg ggc    528
Asn Pro Ile His Asn Ser Ile Val Asp Phe Ser Gly Lys Gly Pro Gly
                165                 170                 175

cac gag gtc gaa atc gcg atg cag tgg aat gcc ggc tac tcg gag tcg    576
His Glu Val Glu Ile Ala Met Gln Trp Asn Ala Gly Tyr Ser Glu Ser
            180                 185                 190

gtg cac acc ttc gcc aac acc atc aac acc cac gag ggc ggc acc cac    624
Val His Thr Phe Ala Asn Thr Ile Asn Thr His Glu Gly Gly Thr His
        195                 200                 205

gaa gag ggc ttc cgc agc gcg ttg acg tcg gtg gtc aac aaa tac gcc    672
Glu Glu Gly Phe Arg Ser Ala Leu Thr Ser Val Val Asn Lys Tyr Ala
    210                 215                 220

aag gac cgc aaa ctc ctg aag gac aaa gac ccc aac ctc acc ggc gac    720
Lys Asp Arg Lys Leu Leu Lys Asp Lys Asp Pro Asn Leu Thr Gly Asp
225                 230                 235                 240

gac atc cgg gaa ggc ctg gca gcg gtc att tcc gtc aag gtc agc gaa    768
Asp Ile Arg Glu Gly Leu Ala Ala Val Ile Ser Val Lys Val Ser Glu
                245                 250                 255

ccg caa ttc gag ggc cag acc aaa acc aag ctg ggc aac acc gag gtc    816
Pro Gln Phe Glu Gly Gln Thr Lys Thr Lys Leu Gly Asn Thr Glu Val
            260                 265                 270
```

```
aag tcg ttc gtg cag aag gtc tgc aac gaa cag ctc acg cac tgg ttc    864
Lys Ser Phe Val Gln Lys Val Cys Asn Glu Gln Leu Thr His Trp Phe
        275                 280                     285

gaa gcc aac ccg gcg gat gcc aaa act gtt gta aac aag gcg gtt tcg    912
Glu Ala Asn Pro Ala Asp Ala Lys Thr Val Val Asn Lys Ala Val Ser
    290                 295                 300

tcg gcc cag gcc cga atc gca gcg cgc aag gcg cga gaa ctg gtg cgc    960
Ser Ala Gln Ala Arg Ile Ala Ala Arg Lys Ala Arg Glu Leu Val Arg
305                 310                 315                 320

cgc aag agc gcc acc gac ctc ggt ggg ctg ccg ggt aag ctc gca gac    1008
Arg Lys Ser Ala Thr Asp Leu Gly Gly Leu Pro Gly Lys Leu Ala Asp
                325                 330                 335

tgc cgc tcc acc gac ccg cga aag tcg gaa ctg tat gtg gtg gag ggt    1056
Cys Arg Ser Thr Asp Pro Arg Lys Ser Glu Leu Tyr Val Val Glu Gly
            340                 345                 350

gac tcg gcc ggc ggc tcg gcc aag agc ggc cgc gac tcg atg ttc cag    1104
Asp Ser Ala Gly Gly Ser Ala Lys Ser Gly Arg Asp Ser Met Phe Gln
        355                 360                 365

gcg atc ctc ccg ctg cgt ggc aag atc atc aac gtc gag aag gcg cgc    1152
Ala Ile Leu Pro Leu Arg Gly Lys Ile Ile Asn Val Glu Lys Ala Arg
    370                 375                 380

atc gac cgg gtg ctg aag aac acc gaa gtt cag gcg atc atc acc gcg    1200
```

Ile Asp Arg Val Leu Lys Asn Thr Glu Val Gln Ala Ile Ile Thr Ala
385 390 395 400

ctg ggc acg ggg att cac gac gag ttc gac atc acc aag ctc cgg tac 1248
Leu Gly Thr Gly Ile His Asp Glu Phe Asp Ile Thr Lys Leu Arg Tyr
405 410 415

cac aag atc gtg ctg 1263
His Lys Ile Val Leu
420

〈210〉 11
〈211〉 1263
〈212〉 DNA
〈213〉 Mycobacterium intracellulare

〈220〉
〈221〉 CDS
〈222〉 (1)..(1263)

〈400〉 11
ggt gag aac agc ggt tac aac gtc agc ggt ggc ctg cac ggc gtg ggc 48
Gly Glu Asn Ser Gly Tyr Asn Val Ser Gly Gly Leu His Gly Val Gly
1 5 10 15

gtc tcg gtg gtc aac gcg ctg tcg acc cgg ctc gag gtg gac atc gcc 96
Val Ser Val Val Asn Ala Leu Ser Thr Arg Leu Glu Val Asp Ile Ala
20 25 30

```
cgc gat ggc tac gaa tgg tcg cag ttc tac gac cac gcc gta ccc gga   144
Arg Asp Gly Tyr Glu Trp Ser Gln Phe Tyr Asp His Ala Val Pro Gly
         35                  40                  45

acg ctc aaa cag ggt gag gcc acc aag cgg acg ggc acc acg atc agg   192
Thr Leu Lys Gln Gly Glu Ala Thr Lys Arg Thr Gly Thr Thr Ile Arg
     50                  55                  60

ttc tgg gcc gac ccc gac atc ttc gag acc acc gag tac gac ttc gag   240
Phe Trp Ala Asp Pro Asp Ile Phe Glu Thr Thr Glu Tyr Asp Phe Glu
 65                  70                  75                  80

acg gtg gcg cgc cgg ctg cag gaa atg gcg ttc ctc aac aag ggg ttg   288
Thr Val Ala Arg Arg Leu Gln Glu Met Ala Phe Leu Asn Lys Gly Leu
                 85                  90                  95

acc atc aac ctc acc gac gag cgg gtg agc aac gag gag gtc gtc gac   336
Thr Ile Asn Leu Thr Asp Glu Arg Val Ser Asn Glu Glu Val Val Asp
            100                 105                 110

gag gtc gtc agc gat acc gcc gac gca ccc aag tcg gcc cag gaa aag   384
Glu Val Val Ser Asp Thr Ala Asp Ala Pro Lys Ser Ala Gln Glu Lys
        115                 120                 125

gcg gcg gaa tcg act gcg cca cat aag gtt aag cac cgc acc ttc cac   432
Ala Ala Glu Ser Thr Ala Pro His Lys Val Lys His Arg Thr Phe His
    130                 135                 140

tac ccc ggc ggt ctg gtc gac ttc gtc aag cac atc aac cgc acc aag   480
```

```
Tyr Pro Gly Gly Leu Val Asp Phe Val Lys His Ile Asn Arg Thr Lys
145                 150                 155                 160

agc ccg atc cag cag agc atc atc gac ttc gac ggc aaa ggt ccc ggc    528
Ser Pro Ile Gln Gln Ser Ile Ile Asp Phe Asp Gly Lys Gly Pro Gly
                165                 170                 175

cac gag gtc gag atc gcg atg cag tgg aac ggc ggc tac tcg gaa tcc    576
His Glu Val Glu Ile Ala Met Gln Trp Asn Gly Gly Tyr Ser Glu Ser
            180                 185                 190

gtg cac acc ttc gcc aac acc atc aac acc cac gag ggc ggc acc cac    624
Val His Thr Phe Ala Asn Thr Ile Asn Thr His Glu Gly Gly Thr His
        195                 200                 205

gaa gag ggc ttc cgc agc gcg ctg acg tcg gtg gtg aac aag tac gcc    672
Glu Glu Gly Phe Arg Ser Ala Leu Thr Ser Val Val Asn Lys Tyr Ala
    210                 215                 220

aaa gac aag aag ttg ctg aaa gac aag gac ccg aac ctc acc ggc gac    720
Lys Asp Lys Lys Leu Leu Lys Asp Lys Asp Pro Asn Leu Thr Gly Asp
225                 230                 235                 240

gac att cgc gaa ggc ctg gcc gcg gtg atc tcg gtc aag gtc agc gaa    768
Asp Ile Arg Glu Gly Leu Ala Ala Val Ile Ser Val Lys Val Ser Glu
                245                 250                 255

ccg cag ttc gag ggt cag acc aag acc aag ctg ggc aac acc gaa gtg    816
Pro Gln Phe Glu Gly Gln Thr Lys Thr Lys Leu Gly Asn Thr Glu Val
```

```
            260                 265                 270

aag tcg ttc gtg cag aag gtc tgc aac gaa cag ctc acc cac tgg ttc   864
Lys Ser Phe Val Gln Lys Val Cys Asn Glu Gln Leu Thr His Trp Phe
        275                 280                 285

gag gcc aac ccc gcg gac gcc aag gtg gtg gtc aac aag gcg gtg tcg   912
Glu Ala Asn Pro Ala Asp Ala Lys Val Val Val Asn Lys Ala Val Ser
    290                 295                 300

tcg gcg cag gcc cgg atc gcc gcg cgc aag gcg cga gag ttg gtg cgt   960
Ser Ala Gln Ala Arg Ile Ala Ala Arg Lys Ala Arg Glu Leu Val Arg
305                 310                 315                 320

cgc aag agc gcc acc gat ctg ggc ggg ctg ccc ggc aag ctc gcc gac   1008
Arg Lys Ser Ala Thr Asp Leu Gly Gly Leu Pro Gly Lys Leu Ala Asp
                325                 330                 335

tgc cgc tcg acg gat ccg cgc aag tcg gaa ctg tat gtg gtg gag ggt   1056
Cys Arg Ser Thr Asp Pro Arg Lys Ser Glu Leu Tyr Val Val Glu Gly
            340                 345                 350

gat tcg gcc ggc ggc tcg gcg aag agc ggc cgc gac tcg atg ttc cag   1104
Asp Ser Ala Gly Gly Ser Ala Lys Ser Gly Arg Asp Ser Met Phe Gln
        355                 360                 365

gcc atc ctg ccg ctg cgc ggc aag atc atc aac gtc gag aag gcc cgc   1152
Ala Ile Leu Pro Leu Arg Gly Lys Ile Ile Asn Val Glu Lys Ala Arg
    370                 375                 380
```

atc gac cgg gtg ttg aag aac acc gag gtg cag gcc atc atc acc gcc 1200
Ile Asp Arg Val Leu Lys Asn Thr Glu Val Gln Ala Ile Ile Thr Ala
385 390 395 400

ctg ggc acc ggc atc cac gac gag ttc gac atc acc aag ctg cgc tat 1248
Leu Gly Thr Gly Ile His Asp Glu Phe Asp Ile Thr Lys Leu Arg Tyr
405 410 415

cac aag atc gtg ctg 1263
His Lys Ile Val Leu
420

〈210〉 12
〈211〉 1263
〈212〉 DNA
〈213〉 Mycobacterium avium

〈220〉
〈221〉 CDS
〈222〉 (1)..(1263)

〈400〉 12
ggc gag aac agc ggc tac aac gtc agc ggc ggt ctg cac ggc gtc ggc 48
Gly Glu Asn Ser Gly Tyr Asn Val Ser Gly Gly Leu His Gly Val Gly
1 5 10 15

gtc tcg gtg gtc aac gcg ctg tcc act cgg ctc gag gtc aac atc gcc 96
Val Ser Val Val Asn Ala Leu Ser Thr Arg Leu Glu Val Asn Ile Ala

20 25 30

cgc gac ggc tac gag tgg tcg cag tac tac gac cac gcc gtg ccc ggc 144
Arg Asp Gly Tyr Glu Trp Ser Gln Tyr Tyr Asp His Ala Val Pro Gly
35 40 45

acc ctc aag cag ggc gag gcc acc aag cgc acc ggc acc acc atc cgg 192
Thr Leu Lys Gln Gly Glu Ala Thr Lys Arg Thr Gly Thr Thr Ile Arg
50 55 60

ttc tgg gcc gac ccc gac atc ttc gag acc acc gag tac gac ttc gaa 240
Phe Trp Ala Asp Pro Asp Ile Phe Glu Thr Thr Glu Tyr Asp Phe Glu
65 70 75 80

acg gtg gcc cgg cgg ctg cag gaa atg gcg ttc ctc aac aag ggc ctg 288
Thr Val Ala Arg Arg Leu Gln Glu Met Ala Phe Leu Asn Lys Gly Leu
85 90 95

acc atc aac ctc acc gac gag cgg gtg acc aac gaa gag gtc gtc gac 336
Thr Ile Asn Leu Thr Asp Glu Arg Val Thr Asn Glu Glu Val Val Asp
100 105 110

gag gtg gtc agc gac acc gcc gac gca ccc aag tcg gcg cag gag aag 384
Glu Val Val Ser Asp Thr Ala Asp Ala Pro Lys Ser Ala Gln Glu Lys
115 120 125

gcg gcg gaa tcg gct gcg ccg cat aag gtc aag cac cgc acc ttc cac 432
Ala Ala Glu Ser Ala Ala Pro His Lys Val Lys His Arg Thr Phe His
130 135 140

```
tac ccc ggc ggc ctg gtc gac ttc gtc aaa cac atc aat cgc acc aaa   480
Tyr Pro Gly Gly Leu Val Asp Phe Val Lys His Ile Asn Arg Thr Lys
145                 150                 155                 160

aac ccc atc cac cag agc atc atc gat ttc ggt ggg aag ggc ccc ggc   528
Asn Pro Ile His Gln Ser Ile Ile Asp Phe Gly Gly Lys Gly Pro Gly
                165                 170                 175

cac gag gtc gag atc gcg atg cag tgg aac ggc ggc tac tcc gaa tcg   576
His Glu Val Glu Ile Ala Met Gln Trp Asn Gly Gly Tyr Ser Glu Ser
            180                 185                 190

gtg cac acc ttc gcc aac acc atc aac acg cac gag ggc ggc acc cac   624
Val His Thr Phe Ala Asn Thr Ile Asn Thr His Glu Gly Gly Thr His
        195                 200                 205

gag gag ggc ttc cgc agc gcg ctg acc tcc gtg gtc aac aag tac gcc   672
Glu Glu Gly Phe Arg Ser Ala Leu Thr Ser Val Val Asn Lys Tyr Ala
    210                 215                 220

aag gac aag aag ctg ctc aag gac aag gac ccc aac ctg acc ggc gac   720
Lys Asp Lys Lys Leu Leu Lys Asp Lys Asp Pro Asn Leu Thr Gly Asp
225                 230                 235                 240

gac atc cgc gag ggt ttg gcc gcg gtg atc tcg gtc aag gtg agc gaa   768
Asp Ile Arg Glu Gly Leu Ala Ala Val Ile Ser Val Lys Val Ser Glu
                245                 250                 255
```

```
ccg cag ttc gag ggc cag acc aag acc aaa ctg ggc aac acc gag gtg    816
Pro Gln Phe Glu Gly Gln Thr Lys Thr Lys Leu Gly Asn Thr Glu Val
            260                 265                 270

aag tcg ttc gtg cag aag gtg tgc aac gaa cag ctc acc cac tgg ttc    864
Lys Ser Phe Val Gln Lys Val Cys Asn Glu Gln Leu Thr His Trp Phe
        275                 280                 285

gaa gcc aac ccc gca gac gcc aaa gtc att gtc aac aag gcg gtt tca    912
Glu Ala Asn Pro Ala Asp Ala Lys Val Ile Val Asn Lys Ala Val Ser
    290                 295                 300

tca gcg cag gcg cgc atc gcc gcg cgc aag gcg cga gag ttg gtg cgc    960
Ser Ala Gln Ala Arg Ile Ala Ala Arg Lys Ala Arg Glu Leu Val Arg
305                 310                 315                 320

cgc aag agc gca acc gac ctg ggc ggg ctg ccc ggc aag ctc gcc gac    1008
Arg Lys Ser Ala Thr Asp Leu Gly Gly Leu Pro Gly Lys Leu Ala Asp
                325                 330                 335

tgc cgg tcg acc gac ccg cgc aag tcg gaa ttg tat gtg gtc gag ggt    1056
Cys Arg Ser Thr Asp Pro Arg Lys Ser Glu Leu Tyr Val Val Glu Gly
            340                 345                 350

gac tcg gcc ggc ggc tcg gcg aaa agc ggc cgg gac tcg atg ttc cag    1104
Asp Ser Ala Gly Gly Ser Ala Lys Ser Gly Arg Asp Ser Met Phe Gln
        355                 360                 365

gcc atc ctt ccg ctg cgc ggc aag atc atc aac gtc gaa aag gcc cgc    1152
```

```
Ala Ile Leu Pro Leu Arg Gly Lys Ile Ile Asn Val Glu Lys Ala Arg
    370                 375                 380

atc gac cgg gtg ctg aag aac acc gag gtg cag gcg atc atc acc gcg    1200
Ile Asp Arg Val Leu Lys Asn Thr Glu Val Gln Ala Ile Ile Thr Ala
385                 390                 395                 400

ctg ggc acc ggg att cac gac gag ttc gac atc acc aag ctg cgc tac    1248
Leu Gly Thr Gly Ile His Asp Glu Phe Asp Ile Thr Lys Leu Arg Tyr
                405                 410                 415

cac aag atc gtg ttg                                                1263
His Lys Ile Val Leu
            420

<210> 13
<211> 1263
<212> DNA
<213> Mycobacterium gordonae

<220>
<221> CDS
<222> (1)..(1263)

<400> 13
ggc gag aac agc ggc tac acg gtc agc ggt ggg ttg cac ggc gtg ggc    48
Gly Glu Asn Ser Gly Tyr Thr Val Ser Gly Gly Leu His Gly Val Gly
  1               5                  10                  15
```

```
gtg tcg gtg gtt aac gcg ttg tcg acg cgg ttg gaa gtc gac atc aaa    96
Val Ser Val Val Asn Ala Leu Ser Thr Arg Leu Glu Val Asp Ile Lys
             20                  25                  30

cgc gac ggg cac gag tgg tcg cag tat tac aag cgc gcg gtg ccg ggc    144
Arg Asp Gly His Glu Trp Ser Gln Tyr Tyr Lys Arg Ala Val Pro Gly
         35                  40                  45

acc ctc aag cag ggt gag acg acc cgc aag acc ggc acc aca atc cgg    192
Thr Leu Lys Gln Gly Glu Thr Thr Arg Lys Thr Gly Thr Thr Ile Arg
     50                  55                  60

ttc tgg gcg gat ccg gag atc ttc gag acc acc caa tac gac ttc gag    240
Phe Trp Ala Asp Pro Glu Ile Phe Glu Thr Thr Gln Tyr Asp Phe Glu
 65                  70                  75                  80

acg gtg gcg cgc cgg ctg cag gag atg gcg ttc ctg aac aag ggt ctg    288
Thr Val Ala Arg Arg Leu Gln Glu Met Ala Phe Leu Asn Lys Gly Leu
                 85                  90                  95

acg atc aat ctg acc gac gaa cgc gtc gag cag gac gag gtt gtc gac    336
Thr Ile Asn Leu Thr Asp Glu Arg Val Glu Gln Asp Glu Val Val Asp
            100                 105                 110

gag gtc gtc agc gac acc gcc gaa gcg ccc aaa tcc gcc gaa gag aag    384
Glu Val Val Ser Asp Thr Ala Glu Ala Pro Lys Ser Ala Glu Glu Lys
        115                 120                 125

gct gcc gaa tcc aag gcc ccg cac aag gtc aag cag cgc acc ttc cac    432
```

```
Ala Ala Glu Ser Lys Ala Pro His Lys Val Lys Gln Arg Thr Phe His
    130                 135                 140

tat ccc ggt ggt ctg gtc gac ttc gtc aaa cac atc aac cgc acc aaa    480
Tyr Pro Gly Gly Leu Val Asp Phe Val Lys His Ile Asn Arg Thr Lys
145                 150                 155                 160

agc ccg atc cag cag agc gtc atc gac ttc gaa ggc aaa ggc acc ggc    528
Ser Pro Ile Gln Gln Ser Val Ile Asp Phe Glu Gly Lys Gly Thr Gly
                165                 170                 175

cac gag gtc gaa atc gcg atg cag tgg aac ggc ggc tac tcc gaa tcg    576
His Glu Val Glu Ile Ala Met Gln Trp Asn Gly Gly Tyr Ser Glu Ser
            180                 185                 190

gtg cac acc ttc gcc aac acc atc aac acc cac gag ggc ggc acc cac    624
Val His Thr Phe Ala Asn Thr Ile Asn Thr His Glu Gly Gly Thr His
        195                 200                 205

gaa gag ggc ttc cgc agt gcg ctg acc tcg gtg gtc aac aag tac gcc    672
Glu Glu Gly Phe Arg Ser Ala Leu Thr Ser Val Val Asn Lys Tyr Ala
    210                 215                 220

aaa gac aag aag ctg ctc aag gag aag gac ccg aat ctc acc ggt gac    720
Lys Asp Lys Lys Leu Leu Lys Glu Lys Asp Pro Asn Leu Thr Gly Asp
225                 230                 235                 240

gac atc cgg gag ggg ttg gcc gcg gtg atc tcg gtg aag gtc gcc gaa    768
Asp Ile Arg Glu Gly Leu Ala Ala Val Ile Ser Val Lys Val Ala Glu
```

245 250 255

ccg cag ttc gag ggt cag acc aag acc aag ctg ggc aac acc gag gtc 816
Pro Gln Phe Glu Gly Gln Thr Lys Thr Lys Leu Gly Asn Thr Glu Val
260 265 270

aag tcg ttc gtg cag aag gtg tgc aac gaa cag ctc acc cac tgg ttc 864
Lys Ser Phe Val Gln Lys Val Cys Asn Glu Gln Leu Thr His Trp Phe
275 280 285

gag gcc aat ccg tcg gaa gct aaa acc gtt gtg aac aaa gcg gtg tcg 912
Glu Ala Asn Pro Ser Glu Ala Lys Thr Val Val Asn Lys Ala Val Ser
290 295 300

tcc gcc cag gcg cgg atc gcc gcg cgc aaa gcg cga gag ctg gtg cgc 960
Ser Ala Gln Ala Arg Ile Ala Ala Arg Lys Ala Arg Glu Leu Val Arg
305 310 315 320

cgc aag agc gca acc gac ctc ggc ggc ctg ccg ggc aag ctc gcc gac 1008
Arg Lys Ser Ala Thr Asp Leu Gly Gly Leu Pro Gly Lys Leu Ala Asp
325 330 335

tgc cgt tcg acg gat ccc cgc aaa tcc gaa ctg tat gtg gtg gag ggg 1056
Cys Arg Ser Thr Asp Pro Arg Lys Ser Glu Leu Tyr Val Val Glu Gly
340 345 350

gac tcc gcc ggc ggc tcg gcc aag agc ggt cgg gat tcg atg ttc cag 1104
Asp Ser Ala Gly Gly Ser Ala Lys Ser Gly Arg Asp Ser Met Phe Gln
355 360 365

```
gcg att ctt ccg ttg cgc ggc aag atc atc aac gtc gag aag gcc cgc   1152
Ala Ile Leu Pro Leu Arg Gly Lys Ile Ile Asn Val Glu Lys Ala Arg
    370                 375                 380

atc gac cgg gtg ctg aag aac acc gaa gtc cag gcc atc atc acc gcg   1200
Ile Asp Arg Val Leu Lys Asn Thr Glu Val Gln Ala Ile Ile Thr Ala
385                 390                 395                 400

ctg ggc acc ggg atc cac gac gag ttc gac atc acc aaa ctg cgc tac   1248
Leu Gly Thr Gly Ile His Asp Glu Phe Asp Ile Thr Lys Leu Arg Tyr
                405                 410                 415

cac aag atc gta ttg                                               1263
His Lys Ile Val Leu
            420

<210> 14
<211> 1257
<212> DNA
<213> Mycobacterium africanum

<220>
<221> CDS
<222> (1)..(1257)

<400> 14
tcg gac gcg tat gcg ata tct ggt ggt ctg cac ggc gtc ggc gtg tcg   48
Ser Asp Ala Tyr Ala Ile Ser Gly Gly Leu His Gly Val Gly Val Ser
```

```
  1               5                  10                  15

gtg gtt aac gcg cta tcc acc cgg ctc gaa gtc gag atc aag cgc gac   96
Val Val Asn Ala Leu Ser Thr Arg Leu Glu Val Glu Ile Lys Arg Asp
             20                  25                  30

ggg tac gag tgg tct cag gtt tat gag aag tcg gaa ccc ctg ggc ctc   144
Gly Tyr Glu Trp Ser Gln Val Tyr Glu Lys Ser Glu Pro Leu Gly Leu
         35                  40                  45

aag caa ggg gcg ccg acc aag aag acg ggg tca acg gtg cgg ttc tgg   192
Lys Gln Gly Ala Pro Thr Lys Lys Thr Gly Ser Thr Val Arg Phe Trp
     50                  55                  60

gcc gac ccc gct gtt ttc gaa acc acg gaa tac gac ttc gaa acc gtc   240
Ala Asp Pro Ala Val Phe Glu Thr Thr Glu Tyr Asp Phe Glu Thr Val
 65                  70                  75                  80

gcc cgc cgg ctg caa gag atg gcg ttc ctc aac aag ggg ctg acc atc   288
Ala Arg Arg Leu Gln Glu Met Ala Phe Leu Asn Lys Gly Leu Thr Ile
                 85                  90                  95

aac ctg acc gac gag agg gtg acc caa gac gag gtc gtc gac gaa gtg   336
Asn Leu Thr Asp Glu Arg Val Thr Gln Asp Glu Val Val Asp Glu Val
            100                 105                 110

gtc agc gac gtc gcc gag gcg ccg aag tcg gca agt gaa cgc gca gcc   384
Val Ser Asp Val Ala Glu Ala Pro Lys Ser Ala Ser Glu Arg Ala Ala
        115                 120                 125
```

```
gaa tcc act gca ccg cac aaa gtt aag agc cgc acc ttt cac tat ccg    432
Glu Ser Thr Ala Pro His Lys Val Lys Ser Arg Thr Phe His Tyr Pro
    130                 135                 140

ggt ggc ctg gtg gac ttc gtg aaa cac atc aac cgc acc aag aac gcg    480
Gly Gly Leu Val Asp Phe Val Lys His Ile Asn Arg Thr Lys Asn Ala
145                 150                 155                 160

att cat agc agc atc gtg gac ttt tcc ggc aag ggc acc ggg cac gag    528
Ile His Ser Ser Ile Val Asp Phe Ser Gly Lys Gly Thr Gly His Glu
                165                 170                 175

gtg gag atc gcg atg caa tgg aac gcc ggg tat tcg gag tcg gtg cac    576
Val Glu Ile Ala Met Gln Trp Asn Ala Gly Tyr Ser Glu Ser Val His
            180                 185                 190

acc ttc gcc aac acc atc aac acc cac gag ggc ggc acc cac gaa gag    624
Thr Phe Ala Asn Thr Ile Asn Thr His Glu Gly Gly Thr His Glu Glu
        195                 200                 205

ggc ttc cgc agc gcg ctg acg tcg gtg gtg aac aag tac gcc aag gac    672
Gly Phe Arg Ser Ala Leu Thr Ser Val Val Asn Lys Tyr Ala Lys Asp
    210                 215                 220

cgc aag cta ctg aag gac aag gac ccc aac ctc acc ggt gac gat atc    720
Arg Lys Leu Leu Lys Asp Lys Asp Pro Asn Leu Thr Gly Asp Asp Ile
225                 230                 235                 240
```

```
cgg gaa ggc ctg gcc gct gtg atc tcg gtg aag gtc agc gaa ccg cag    768
Arg Glu Gly Leu Ala Ala Val Ile Ser Val Lys Val Ser Glu Pro Gln
                245                 250                 255

ttc gag ggc cag acc aag acc aag ttg ggc aac acc gag gtc aaa tcg    816
Phe Glu Gly Gln Thr Lys Thr Lys Leu Gly Asn Thr Glu Val Lys Ser
            260                 265                 270

ttt gtg cag aag gtc tgt aac gaa cag ctg acc cac tgg ttt gaa gcc    864
Phe Val Gln Lys Val Cys Asn Glu Gln Leu Thr His Trp Phe Glu Ala
        275                 280                 285

aac ccc acc gac tcg aaa gtc gtt gtg aac aag gct gtg tcc tcg gcg    912
Asn Pro Thr Asp Ser Lys Val Val Val Asn Lys Ala Val Ser Ser Ala
    290                 295                 300

caa gcc cgt atc gcg gca cgt aag gca cga gag ttg gtg cgg cgt aag    960
Gln Ala Arg Ile Ala Ala Arg Lys Ala Arg Glu Leu Val Arg Arg Lys
305                 310                 315                 320

agc gcc acc gac atc ggt gga ttg ccc ggc aag ctg gcc gat tgc cgt    1008
Ser Ala Thr Asp Ile Gly Gly Leu Pro Gly Lys Leu Ala Asp Cys Arg
                325                 330                 335

tcc acg gat ccg cgc aag tcc gaa ctg tat gtc gta gaa ggt gac tcg    1056
Ser Thr Asp Pro Arg Lys Ser Glu Leu Tyr Val Val Glu Gly Asp Ser
            340                 345                 350

gcc ggc ggt tct gca aaa agc ggt cgc gat tcg atg ttc cag gcg ata    1104
```

Ala Gly Gly Ser Ala Lys Ser Gly Arg Asp Ser Met Phe Gln Ala Ile
        355   360   365

ctt ccg ctg cgc ggc aag atc atc aat gtg gag aaa gcg cgc atc gac   1152
Leu Pro Leu Arg Gly Lys Ile Ile Asn Val Glu Lys Ala Arg Ile Asp
    370   375   380

cgg gtg cta aag aac acc gaa gtt cag gcg atc atc acg gcg ctg ggc   1200
Arg Val Leu Lys Asn Thr Glu Val Gln Ala Ile Ile Thr Ala Leu Gly
385   390   395   400

acc ggg atc cac gac gag ttc gat atc ggc aag ctg cgc tac cac aag   1248
Thr Gly Ile His Asp Glu Phe Asp Ile Gly Lys Leu Arg Tyr His Lys
                405   410   415

atc gtg ctg   1257
Ile Val Leu

⟨210⟩ 15
⟨211⟩ 1257
⟨212⟩ DNA
⟨213⟩ Mycobacterium tuberculosis

⟨220⟩
⟨221⟩ CDS
⟨222⟩ (1)..(1257)

⟨400⟩ 15
tcg gac gcg tat gcg ata tct ggt ggt ctg cac ggc gtc ggc gtg tcg   48

```
Ser Asp Ala Tyr Ala Ile Ser Gly Gly Leu His Gly Val Gly Val Ser
 1               5                  10                  15

gtg gtt aac gcg cta tcc acc cgg ctc gaa gtc gag atc aag cgc gac      96
Val Val Asn Ala Leu Ser Thr Arg Leu Glu Val Glu Ile Lys Arg Asp
            20                  25                  30

ggg tac gag tgg tct cag gtt tat gag aag tcg gaa ccc ctg ggc ctc     144
Gly Tyr Glu Trp Ser Gln Val Tyr Glu Lys Ser Glu Pro Leu Gly Leu
        35                  40                  45

aag caa ggg gcg ccg acc aag aag acg ggg tca acg gtg cgg ttc tgg     192
Lys Gln Gly Ala Pro Thr Lys Lys Thr Gly Ser Thr Val Arg Phe Trp
    50                  55                  60

gcc gac ccc gct gtt ttc gaa acc acg gaa tac gac ttc gaa acc gtc     240
Ala Asp Pro Ala Val Phe Glu Thr Thr Glu Tyr Asp Phe Glu Thr Val
65                  70                  75                  80

gcc cgc cgg ctg caa gag atg gcg ttc ctc aac aag ggg ctg acc atc     288
Ala Arg Arg Leu Gln Glu Met Ala Phe Leu Asn Lys Gly Leu Thr Ile
                85                  90                  95

aac ctg acc gac gag agg gtg acc caa gac gag gtc gtc gac gaa gtg     336
Asn Leu Thr Asp Glu Arg Val Thr Gln Asp Glu Val Val Asp Glu Val
            100                 105                 110

gtc agc gac gtc gcc gag gcg ccg aag tcg gca agt gaa cgc gca gcc     384
Val Ser Asp Val Ala Glu Ala Pro Lys Ser Ala Ser Glu Arg Ala Ala
```

```
        115                 120                 125

gaa tcc act gca ccg cac aaa gtt aag agc cgc acc ttt cac tat ccg   432
Glu Ser Thr Ala Pro His Lys Val Lys Ser Arg Thr Phe His Tyr Pro
    130                 135                 140

ggt ggc ctg gtg gac ttc gtg aaa cac atc aac cgc acc aag aac gcg   480
Gly Gly Leu Val Asp Phe Val Lys His Ile Asn Arg Thr Lys Asn Ala
145                 150                 155                 160

att cat agc agc atc gtg gac ttt tcc ggc aag ggc acc ggg cac gag   528
Ile His Ser Ser Ile Val Asp Phe Ser Gly Lys Gly Thr Gly His Glu
                165                 170                 175

gtg gag atc gcg atg caa tgg aac gcc ggg tat tcg gag tcg gtg cac   576
Val Glu Ile Ala Met Gln Trp Asn Ala Gly Tyr Ser Glu Ser Val His
            180                 185                 190

acc ttc gcc aac acc atc aac acc cac gag ggc ggc acc cac gaa gag   624
Thr Phe Ala Asn Thr Ile Asn Thr His Glu Gly Gly Thr His Glu Glu
        195                 200                 205

ggc ttc cgc agc gcg ctg acg tcg gtg gtg aac aag tac gcc aag gac   672
Gly Phe Arg Ser Ala Leu Thr Ser Val Val Asn Lys Tyr Ala Lys Asp
    210                 215                 220

cgc aag cta ctg aag gac aag gac ccc aac ctc acc ggt gac gat atc   720
Arg Lys Leu Leu Lys Asp Lys Asp Pro Asn Leu Thr Gly Asp Asp Ile
225                 230                 235                 240
```

```
cgg gaa ggc ctg gcc gct gtg atc tcg gtg aag gtc agc gaa ccg cag    768
Arg Glu Gly Leu Ala Ala Val Ile Ser Val Lys Val Ser Glu Pro Gln
                245                 250                 255

ttc gag ggc cag acc aag acc aag ttg ggc aac acc gag gtc aaa tcg    816
Phe Glu Gly Gln Thr Lys Thr Lys Leu Gly Asn Thr Glu Val Lys Ser
            260                 265                 270

ttt gtg cag aag gtc tgt aac gaa cag ctg acc cac tgg ttt gaa gcc    864
Phe Val Gln Lys Val Cys Asn Glu Gln Leu Thr His Trp Phe Glu Ala
        275                 280                 285

aac ccc acc gac gcg aaa gtc gtt gtg aac aag gct gtg tcc tcg gcg    912
Asn Pro Thr Asp Ala Lys Val Val Val Asn Lys Ala Val Ser Ser Ala
    290                 295                 300

caa gcc cgt atc gcg gca cgt aag gca cga gag ttg gtg cgg cgt aag    960
Gln Ala Arg Ile Ala Ala Arg Lys Ala Arg Glu Leu Val Arg Arg Lys
305                 310                 315                 320

agc gcc acc gac atc ggt gga ttg ccc ggc aag ctg gcc gat tgc cgt    1008
Ser Ala Thr Asp Ile Gly Gly Leu Pro Gly Lys Leu Ala Asp Cys Arg
                325                 330                 335

tcc acg gat ccg cgc aag tcc gaa ctg tat gtc gta gaa ggt gac tcg    1056
Ser Thr Asp Pro Arg Lys Ser Glu Leu Tyr Val Val Glu Gly Asp Ser
            340                 345                 350
```

```
gcc ggc ggt tct gca aaa agc ggt cgc gat tcg atg ttc cag gcg ata   1104
Ala Gly Gly Ser Ala Lys Ser Gly Arg Asp Ser Met Phe Gln Ala Ile
        355                 360                 365

ctt ccg ctg cgc ggc aag atc atc aat gtg gag aaa gcg cgc atc gac   1152
Leu Pro Leu Arg Gly Lys Ile Ile Asn Val Glu Lys Ala Arg Ile Asp
    370                 375                 380

cgg gtg cta aag aac acc gaa gtt cag gcg atc atc acg gcg ctg ggc   1200
Arg Val Leu Lys Asn Thr Glu Val Gln Ala Ile Ile Thr Ala Leu Gly
385                 390                 395                 400

acc ggg atc cac gac gag ttc gat atc ggc aag ctg cgc tac cac aag   1248
Thr Gly Ile His Asp Glu Phe Asp Ile Gly Lys Leu Arg Tyr His Lys
                405                 410                 415

atc gtg ctg                                                       1257
Ile Val Leu
```

〈210〉 16
〈211〉 1257
〈212〉 DNA
〈213〉 Mycobacterium gastri

〈220〉
〈221〉 CDS
〈222〉 (1)..(1257)

〈400〉 16

```
tcc gac gcc tat gcg ata tcg ggt gga ctg cac ggt gtg ggt gtc tcg      48
Ser Asp Ala Tyr Ala Ile Ser Gly Gly Leu His Gly Val Gly Val Ser
 1               5                   10                  15

gtg gtc aac gcg ctg tcc atc cgg ctg gag gtg gag atc aag cgc gac      96
Val Val Asn Ala Leu Ser Ile Arg Leu Glu Val Glu Ile Lys Arg Asp
             20                  25                  30

ggc cat gag tgg tcg caa gtt tat gag aag tcc gag ccg atg gga ctc      144
Gly His Glu Trp Ser Gln Val Tyr Glu Lys Ser Glu Pro Met Gly Leu
         35                  40                  45

aag caa ggc gcg ccg acg aag aag acc ggc acg acg gtg cgg ttc tgg      192
Lys Gln Gly Ala Pro Thr Lys Lys Thr Gly Thr Thr Val Arg Phe Trp
     50                  55                  60

gcc gac ccc aac gtt ttt gaa acc acc gag tac gac ttc gaa acc gtc      240
Ala Asp Pro Asn Val Phe Glu Thr Thr Glu Tyr Asp Phe Glu Thr Val
 65                  70                  75                  80

gcg cga cgg ttg cag gag atg gcg ttt ctc aac aag ggg ctc acc atc      288
Ala Arg Arg Leu Gln Glu Met Ala Phe Leu Asn Lys Gly Leu Thr Ile
                 85                  90                  95

aac ctg acc gat cag cgg gta acc cag gac gaa gtg gtc gac gag gtg      336
Asn Leu Thr Asp Gln Arg Val Thr Gln Asp Glu Val Val Asp Glu Val
            100                 105                 110

gtc agc gac gtc gcc gag gcc ccg aag tcg gcc agt gag aag gcg gcc      384
```

```
Val Ser Asp Val Ala Glu Ala Pro Lys Ser Ala Ser Glu Lys Ala Ala
        115                 120                 125

gaa ttc acc gcc ccc cac aag gtg aag aag cgt acc ttt cac tat ccc    432
Glu Phe Thr Ala Pro His Lys Val Lys Lys Arg Thr Phe His Tyr Pro
    130                 135                 140

ggt ggc ttg gtt gac ttc gtc aag cac atc aac cgc acc aag aac gcc    480
Gly Gly Leu Val Asp Phe Val Lys His Ile Asn Arg Thr Lys Asn Ala
145                 150                 155                 160

atc cac agc agc atc gtc gac ttc tcc gga aag ggg acc ggc cac gaa    528
Ile His Ser Ser Ile Val Asp Phe Ser Gly Lys Gly Thr Gly His Glu
                165                 170                 175

gtg gag atc gcg atg cag tgg aat gcc ggc tat tcg gag tcg gtg cac    576
Val Glu Ile Ala Met Gln Trp Asn Ala Gly Tyr Ser Glu Ser Val His
            180                 185                 190

acc ttc gcc aac acc atc aac acc cat gag ggc ggg acc cat gaa gaa    624
Thr Phe Ala Asn Thr Ile Asn Thr His Glu Gly Gly Thr His Glu Glu
        195                 200                 205

ggg ttc cgc agc gcg ctc acg tcc gtg gtg aac aag tac gcc aag gac    672
Gly Phe Arg Ser Ala Leu Thr Ser Val Val Asn Lys Tyr Ala Lys Asp
    210                 215                 220

cgc aaa ctg ctc aaa gac aag gac ccc aac ctc acc ggc gac gac atc    720
Arg Lys Leu Leu Lys Asp Lys Asp Pro Asn Leu Thr Gly Asp Asp Ile
```

225 230 235 240

cgg gaa ggg ttg gcc gcg gtg att tcg gtc aaa gtc agc gaa ccg cag 768
Arg Glu Gly Leu Ala Ala Val Ile Ser Val Lys Val Ser Glu Pro Gln
245 250 255

ttc gag ggc cag acc aag acg aaa cta ggc aac acc gag gtg aag tcg 816
Phe Glu Gly Gln Thr Lys Thr Lys Leu Gly Asn Thr Glu Val Lys Ser
260 265 270

ttc gtg cag aag gtg tgc aat gaa cag ctc acc cat tgg ttc gag gcc 864
Phe Val Gln Lys Val Cys Asn Glu Gln Leu Thr His Trp Phe Glu Ala
275 280 285

aac ccc gct gat gct aaa acc gtt gtc aac aag gca gtt tca tcg gcg 912
Asn Pro Ala Asp Ala Lys Thr Val Val Asn Lys Ala Val Ser Ser Ala
290 295 300

cag gcc agg att gcg gcc cgc aag gcg cgc gag ttg gtg cgc cgc aag 960
Gln Ala Arg Ile Ala Ala Arg Lys Ala Arg Glu Leu Val Arg Arg Lys
305 310 315 320

agc gca acc gat ctg ggc gga cta ccg ggc aag ttg gcc gac tgc cgc 1008
Ser Ala Thr Asp Leu Gly Gly Leu Pro Gly Lys Leu Ala Asp Cys Arg
325 330 335

tcg acc gac ccc cgt aag tcc gaa tta tat gtg gtg gag ggt gat tca 1056
Ser Thr Asp Pro Arg Lys Ser Glu Leu Tyr Val Val Glu Gly Asp Ser
340 345 350

```
gcc ggc ggc tcg gcg aag agc ggc cgc gac tcg atg ttt caa gcg atc    1104
Ala Gly Gly Ser Ala Lys Ser Gly Arg Asp Ser Met Phe Gln Ala Ile
        355                 360                 365

ttg ccg ttg cgc ggc aag atc atc aac gtc gag aag gcc cgc atc gac    1152
Leu Pro Leu Arg Gly Lys Ile Ile Asn Val Glu Lys Ala Arg Ile Asp
    370                 375                 380

cgg gtg ctg aag aac acc gaa gtc cag gcg atc atc acc gcg ttg ggc    1200
Arg Val Leu Lys Asn Thr Glu Val Gln Ala Ile Ile Thr Ala Leu Gly
385                 390                 395                 400

acc ggt att cac gac gaa ttc gac atc gcg aga ctg cgt tac cac aag    1248
Thr Gly Ile His Asp Glu Phe Asp Ile Ala Arg Leu Arg Tyr His Lys
                405                 410                 415

atc gtg ctg                                                        1257
Ile Val Leu
```

〈210〉 17
〈211〉 1263
〈212〉 DNA
〈213〉 Mycobacterium marinum

〈220〉
〈221〉 CDS
〈222〉 (1)..(1263)

〈400〉 17

```
ggc gag aac agt ggt tac aac gtc agt ggt ggt ctg cac ggc gtg ggt     48
Gly Glu Asn Ser Gly Tyr Asn Val Ser Gly Gly Leu His Gly Val Gly
 1               5                  10                  15

gtg tcg gtg gtc aac gcg ctg tcc acc cga ctg gaa gtc gac atc aag     96
Val Ser Val Val Asn Ala Leu Ser Thr Arg Leu Glu Val Asp Ile Lys
            20                  25                  30

cgc gac gga tac gag tgg tcg cag ttc tac gac cgc gcc cag ccg ggc    144
Arg Asp Gly Tyr Glu Trp Ser Gln Phe Tyr Asp Arg Ala Gln Pro Gly
        35                  40                  45

acc ctc aaa cag ggc gag gca acc aag aag acc gga acc acc atc cgg    192
Thr Leu Lys Gln Gly Glu Ala Thr Lys Lys Thr Gly Thr Thr Ile Arg
    50                  55                  60

ttc tgg gcc gac tcg gac atc ttt gag acc acc gaa tac gac ttc gag    240
Phe Trp Ala Asp Ser Asp Ile Phe Glu Thr Thr Glu Tyr Asp Phe Glu
65                  70                  75                  80

acg gtg gcg cgg cgc ctg cag gag atg gcg ttc ctc aac aag ggc ctg    288
Thr Val Ala Arg Arg Leu Gln Glu Met Ala Phe Leu Asn Lys Gly Leu
                85                  90                  95

acc atc aac ctc acc gac gag cgg gtc acc ccg gac gag gtc gtc gac    336
Thr Ile Asn Leu Thr Asp Glu Arg Val Thr Pro Asp Glu Val Val Asp
            100                 105                 110
```

```
gac gtc gtc agt gat acc gcc gaa gca cca aag tcc gcc cag gag aag   384
Asp Val Val Ser Asp Thr Ala Glu Ala Pro Lys Ser Ala Gln Glu Lys
        115                 120                 125

gcc gcc gaa tcg acc gcg ccg cac aag gtc aag agc cgc acc ttc cac   432
Ala Ala Glu Ser Thr Ala Pro His Lys Val Lys Ser Arg Thr Phe His
    130                 135                 140

tat ccc ggc ggt ttg gtc gat ttc gtc aag cac atc aac cgc acc aag   480
Tyr Pro Gly Gly Leu Val Asp Phe Val Lys His Ile Asn Arg Thr Lys
145                 150                 155                 160

agt ccg att cag cag agc atc gtc gac ttc gag ggc aag ggc tcc ggc   528
Ser Pro Ile Gln Gln Ser Ile Val Asp Phe Glu Gly Lys Gly Ser Gly
                165                 170                 175

cac gaa gtc gaa atc gcg atg cag tgg aac ggc ggc tac tcg gag tcg   576
His Glu Val Glu Ile Ala Met Gln Trp Asn Gly Gly Tyr Ser Glu Ser
            180                 185                 190

gtg cac acc ttc gcc aac acc atc aac acc cat gag ggt gga acg cac   624
Val His Thr Phe Ala Asn Thr Ile Asn Thr His Glu Gly Gly Thr His
        195                 200                 205

gaa gag ggc ttc cgc agt gcg ttg acc tcg gtg gtg aac aag tac gcc   672
Glu Glu Gly Phe Arg Ser Ala Leu Thr Ser Val Val Asn Lys Tyr Ala
    210                 215                 220

aaa gac aag aag ctg ctc aag gac aag gac ccc aac ctc acc ggt gac   720
```

```
Lys Asp Lys Lys Leu Leu Lys Asp Lys Asp Pro Asn Leu Thr Gly Asp
225                 230                 235                 240

gac atc cgc gag ggg ttg gcc gcg gtc atc tcg gtg cgg gtg gca gag    768
Asp Ile Arg Glu Gly Leu Ala Ala Val Ile Ser Val Arg Val Ala Glu
                245                 250                 255

ccg cag ttc gag ggt cag acg aag acc aag ctg ggc aac acc gag gtc    816
Pro Gln Phe Glu Gly Gln Thr Lys Thr Lys Leu Gly Asn Thr Glu Val
            260                 265                 270

aag tcg ttt gtc cag aag gtt tgt aac gag cag ctc acc cac tgg ttc    864
Lys Ser Phe Val Gln Lys Val Cys Asn Glu Gln Leu Thr His Trp Phe
        275                 280                 285

gag gcc aat cct tcg gaa gcc aaa acc att gtg aac aag gcg gta tcc    912
Glu Ala Asn Pro Ser Glu Ala Lys Thr Ile Val Asn Lys Ala Val Ser
    290                 295                 300

tcg gcg cag gca cgt ctc gcc gcg cgc aag gcg cga gag ttg gtg cgt    960
Ser Ala Gln Ala Arg Leu Ala Ala Arg Lys Ala Arg Glu Leu Val Arg
305                 310                 315                 320

cgc aag agc gca acc gat ctc ggt ggg ctg ccc ggc aag ttg gcc gac    1008
Arg Lys Ser Ala Thr Asp Leu Gly Gly Leu Pro Gly Lys Leu Ala Asp
                325                 330                 335

tgc cgc tcg aca gat ccg cgt aag tcg gaa ctg tat gtg gtg gag ggt    1056
Cys Arg Ser Thr Asp Pro Arg Lys Ser Glu Leu Tyr Val Val Glu Gly
```

```
            340                 345                 350

gac tcg gcc ggc ggc tcg gca aag agt ggc cgc gat tcg atg ttc cag    1104
Asp Ser Ala Gly Gly Ser Ala Lys Ser Gly Arg Asp Ser Met Phe Gln
        355                 360                 365

gcg atc ctg ccg ctg cgc ggc aag atc atc aat gtc gaa aag gca cgc    1152
Ala Ile Leu Pro Leu Arg Gly Lys Ile Ile Asn Val Glu Lys Ala Arg
    370                 375                 380

atc gac cga gtc ctg aaa aac act gaa gtc cag gcg atc atc acc gcg    1200
Ile Asp Arg Val Leu Lys Asn Thr Glu Val Gln Ala Ile Ile Thr Ala
385                 390                 395                 400

ttg ggt acc ggt att cac gac gaa ttc gac ctc tcg aag ctg cgc tat    1248
Leu Gly Thr Gly Ile His Asp Glu Phe Asp Leu Ser Lys Leu Arg Tyr
                405                 410                 415

cac aag atc gtc ttg                                                1263
His Lys Ile Val Leu
            420

<210> 18
<211> 1257
<212> DNA
<213> Mycobacterium microti

<220>
<221> CDS
```

〈222〉 (1)..(1257)

〈400〉 18

```
tcg gac gcg tat gcg ata tct ggt ggt ctg cac ggc gtc ggc gtg tcg       48
Ser Asp Ala Tyr Ala Ile Ser Gly Gly Leu His Gly Val Gly Val Ser
  1               5                  10                  15

gtg gtt aac gcg cta tcc acc cgg ctc gaa gtc gag atc aag cgc gac       96
Val Val Asn Ala Leu Ser Thr Arg Leu Glu Val Glu Ile Lys Arg Asp
             20                  25                  30

ggg tat gag tgg tct cag gtt tat gag aag tcg gaa ccc ctg ggc ctc      144
Gly Tyr Glu Trp Ser Gln Val Tyr Glu Lys Ser Glu Pro Leu Gly Leu
         35                  40                  45

aag caa ggg gcg ccg acc aag aag acg ggg tca acg gtg cgg ttc tgg      192
Lys Gln Gly Ala Pro Thr Lys Lys Thr Gly Ser Thr Val Arg Phe Trp
     50                  55                  60

gcc gac ccc gct gtt ttc gaa acc acg gaa tac gac ttc gaa acc gtc      240
Ala Asp Pro Ala Val Phe Glu Thr Thr Glu Tyr Asp Phe Glu Thr Val
 65                  70                  75                  80

gcc cgc cgg ctg caa gag atg gcg ttc ctc aac aag ggg ctg acc atc      288
Ala Arg Arg Leu Gln Glu Met Ala Phe Leu Asn Lys Gly Leu Thr Ile
                 85                  90                  95

aac ctg acc gac gag agg gtg acc caa gac gag gtc gtc gac gaa gtg      336
Asn Leu Thr Asp Glu Arg Val Thr Gln Asp Glu Val Val Asp Glu Val
```

```
            100                 105                 110

gtc agc gac gtc gcc gag gcg ccg aag tcg gca agt gaa cgc gca gcc    384
Val Ser Asp Val Ala Glu Ala Pro Lys Ser Ala Ser Glu Arg Ala Ala
        115                 120                 125

gaa tcc act gca ccg cac aaa gtt aag agc cgc acc ttt cac tat ccg    432
Glu Ser Thr Ala Pro His Lys Val Lys Ser Arg Thr Phe His Tyr Pro
    130                 135                 140

ggt ggc ctg gtg gac ttc gtg aaa cac atc aac cgc acc aag aac gcg    480
Gly Gly Leu Val Asp Phe Val Lys His Ile Asn Arg Thr Lys Asn Ala
145                 150                 155                 160

att cat agc agc atc gtg gac ttt tcc ggc aag ggc acc ggg cac gag    528
Ile His Ser Ser Ile Val Asp Phe Ser Gly Lys Gly Thr Gly His Glu
                165                 170                 175

gtg gag atc gcg atg caa tgg aac gcc ggg tat tcg gag tcg gtg cac    576
Val Glu Ile Ala Met Gln Trp Asn Ala Gly Tyr Ser Glu Ser Val His
            180                 185                 190

acc ttc gcc aac acc atc aac acc cac gag ggc ggc acc cac gaa gag    624
Thr Phe Ala Asn Thr Ile Asn Thr His Glu Gly Gly Thr His Glu Glu
        195                 200                 205

ggc ttc cgc agc gcg ctg acg tcg gtg gtg aac aag tac gcc aag gac    672
Gly Phe Arg Ser Ala Leu Thr Ser Val Val Asn Lys Tyr Ala Lys Asp
    210                 215                 220
```

```
cgc aag cta ctg aag gac aag gac ccc aac ctc acc ggt gac gat atc    720
Arg Lys Leu Leu Lys Asp Lys Asp Pro Asn Leu Thr Gly Asp Asp Ile
225                 230                 235                 240

cgg gaa ggc ctg gcc gct gtg atc tcg gtg aag gtc agc gaa ccg cag    768
Arg Glu Gly Leu Ala Ala Val Ile Ser Val Lys Val Ser Glu Pro Gln
                245                 250                 255

ttc gag ggc cag acc aag acc aag ttg ggc aac acc gag gtc aaa tcg    816
Phe Glu Gly Gln Thr Lys Thr Lys Leu Gly Asn Thr Glu Val Lys Ser
            260                 265                 270

ttt gtg cag aag gtc tgt aac gaa cag ctg acc cac tgg ttt gaa gcc    864
Phe Val Gln Lys Val Cys Asn Glu Gln Leu Thr His Trp Phe Glu Ala
        275                 280                 285

aac ccc acc gac tcg aaa gtc gtt gtg aac aag gct gtg tcc tcg gcg    912
Asn Pro Thr Asp Ser Lys Val Val Val Asn Lys Ala Val Ser Ser Ala
    290                 295                 300

caa gcc cgt atc gcg gca cgt aag gca cga gag ttg gtg cgg cgt aag    960
Gln Ala Arg Ile Ala Ala Arg Lys Ala Arg Glu Leu Val Arg Arg Lys
305                 310                 315                 320

agc gcc acc gac atc ggt gga ttg ccc ggc aag ctg gcc gat tgc cgt    1008
Ser Ala Thr Asp Ile Gly Gly Leu Pro Gly Lys Leu Ala Asp Cys Arg
                325                 330                 335
```

```
tcc acg gat ccg cgc aag tcc gaa ctg tat gtc gta gaa ggt gac tcg   1056
Ser Thr Asp Pro Arg Lys Ser Glu Leu Tyr Val Val Glu Gly Asp Ser
            340                 345                 350

gcc ggc ggt tct gca aaa agc ggt cgc gat tcg atg ttc cag gcg ata   1104
Ala Gly Gly Ser Ala Lys Ser Gly Arg Asp Ser Met Phe Gln Ala Ile
        355                 360                 365

ctt ccg ctg cgc ggc aag atc atc aat gtg gag aaa gcg cgc atc gac   1152
Leu Pro Leu Arg Gly Lys Ile Ile Asn Val Glu Lys Ala Arg Ile Asp
    370                 375                 380

cgg gtg cta aag aac acc gaa gtt cag gcg atc atc acg gcg ctg ggc   1200
Arg Val Leu Lys Asn Thr Glu Val Gln Ala Ile Ile Thr Ala Leu Gly
385                 390                 395                 400

acc ggg atc cac gac gag ttc gat atc ggc aag ctg cgc tac cac aag   1248
Thr Gly Ile His Asp Glu Phe Asp Ile Gly Lys Leu Arg Tyr His Lys
                405                 410                 415

atc gtg ctg                                                       1257
Ile Val Leu

〈210〉 19
〈211〉 1263
〈212〉 DNA
〈213〉 Mycobacterium asiaticum

〈220〉
```

〈221〉 CDS
〈222〉 (1)..(1263)

〈400〉 19

```
ggt gag aac agc ggc tac acc gtc agc ggt ggg ctg cac ggt gtc ggt    48
Gly Glu Asn Ser Gly Tyr Thr Val Ser Gly Gly Leu His Gly Val Gly
  1               5                  10                  15

gtg tca gtg gtc aac gcg ttg tcg acc cga ctc gag gtc gac atc aag    96
Val Ser Val Val Asn Ala Leu Ser Thr Arg Leu Glu Val Asp Ile Lys
             20                  25                  30

cgc gac ggg cac gag tgg tcc cag tat tac gag cgc gcc gtt cct ggc   144
Arg Asp Gly His Glu Trp Ser Gln Tyr Tyr Glu Arg Ala Val Pro Gly
         35                  40                  45

acg ctc aag cag ggc gag gcg acc aag aag acc ggc acc acc atc cgg   192
Thr Leu Lys Gln Gly Glu Ala Thr Lys Lys Thr Gly Thr Thr Ile Arg
     50                  55                  60

ttc tgg gcg gac ccg gac atc ttc gag acc acc cag tac gac ttc gag   240
Phe Trp Ala Asp Pro Asp Ile Phe Glu Thr Thr Gln Tyr Asp Phe Glu
 65                  70                  75                  80

acg gtg gcg cgc cgg ctc caa gag atg gcg ttc ctg aac aag ggc ttg   288
Thr Val Ala Arg Arg Leu Gln Glu Met Ala Phe Leu Asn Lys Gly Leu
                 85                  90                  95

acc atc aac ttg acc gac gag cgg gtg gac cag gac gag gtc gtc gat   336
```

```
Thr Ile Asn Leu Thr Asp Glu Arg Val Asp Gln Asp Glu Val Val Asp
            100                 105                 110

gaa gtc gtc agc gac acc gcc gat gcg ccc aag tcc gcc gaa gag aag    384
Glu Val Val Ser Asp Thr Ala Asp Ala Pro Lys Ser Ala Glu Glu Lys
        115                 120                 125

gcg gcc gaa tcc aaa gcg ccg cac aag gtt aag cac cgc acc ttc cac    432
Ala Ala Glu Ser Lys Ala Pro His Lys Val Lys His Arg Thr Phe His
    130                 135                 140

tac ccc ggc ggc ttg gtc gac ttc gtc aag cac atc aac cgg acc aag    480
Tyr Pro Gly Gly Leu Val Asp Phe Val Lys His Ile Asn Arg Thr Lys
145                 150                 155                 160

agc ccg atc caa cag agc gtc atc gac ttc gag ggc aaa ggc acc ggc    528
Ser Pro Ile Gln Gln Ser Val Ile Asp Phe Glu Gly Lys Gly Thr Gly
                165                 170                 175

cac gag gtc gag atc gcg atg cag tgg aac ggt ggc tac tcg gag tcg    576
His Glu Val Glu Ile Ala Met Gln Trp Asn Gly Gly Tyr Ser Glu Ser
            180                 185                 190

gtg cac acc ttc gcc aac acg atc aac acc cac gag ggc ggt acg cac    624
Val His Thr Phe Ala Asn Thr Ile Asn Thr His Glu Gly Gly Thr His
        195                 200                 205

gaa gaa ggg ttc cgc agt gcg ctg acg tcg gtg gtg aac aaa tac gcc    672
Glu Glu Gly Phe Arg Ser Ala Leu Thr Ser Val Val Asn Lys Tyr Ala
```

```
    210                 215                 220

aaa gac aag aag ctg ctg aaa gac aag gac ccg aac ctc acc ggt gac    720
Lys Asp Lys Lys Leu Leu Lys Asp Lys Asp Pro Asn Leu Thr Gly Asp
225                 230                 235                 240

gac atc cgc gag gga ctg gcc gcg gtg atc tcg gtc aag gtc gcc gaa    768
Asp Ile Arg Glu Gly Leu Ala Ala Val Ile Ser Val Lys Val Ala Glu
                245                 250                 255

ccc cag ttc gag ggc cag aca aag acc aag ctg ggc aac acc gag gtc    816
Pro Gln Phe Glu Gly Gln Thr Lys Thr Lys Leu Gly Asn Thr Glu Val
            260                 265                 270

aag tcg ttc gtg cag aag gtg tgc aac gaa cag ctc acc cac tgg ttc    864
Lys Ser Phe Val Gln Lys Val Cys Asn Glu Gln Leu Thr His Trp Phe
        275                 280                 285

gag gcc aat ccg tcg gaa gcc aaa acc gtt gtc aac aag gcg gtt tcg    912
Glu Ala Asn Pro Ser Glu Ala Lys Thr Val Val Asn Lys Ala Val Ser
    290                 295                 300

tcc gca cag gcc cgg atc gcg gcg cgg aag gcc cga gag ttg gtg cgg    960
Ser Ala Gln Ala Arg Ile Ala Ala Arg Lys Ala Arg Glu Leu Val Arg
305                 310                 315                 320

cgc aag agc gcg acc gat ttg ggc ggg ctg ccc ggc aag ctg gcc gac    1008
Arg Lys Ser Ala Thr Asp Leu Gly Gly Leu Pro Gly Lys Leu Ala Asp
                325                 330                 335
```

```
tgc cgt tcc acc gac ccg cgc aag tcc gaa ctg tat gtg gtg gag ggt   1056
Cys Arg Ser Thr Asp Pro Arg Lys Ser Glu Leu Tyr Val Val Glu Gly
            340                 345                 350

gac tcg gca ggt ggc tcg gcc aag agc ggc cgt gac tcg atg ttc cag   1104
Asp Ser Ala Gly Gly Ser Ala Lys Ser Gly Arg Asp Ser Met Phe Gln
        355                 360                 365

gcc atc ctg ccg ctg cgc ggc aag atc atc aac gtc gag aag gcc cgc   1152
Ala Ile Leu Pro Leu Arg Gly Lys Ile Ile Asn Val Glu Lys Ala Arg
    370                 375                 380

atc gac cgg gtc ctg aag aac acc gaa gtc cag gcg atc atc acc gcg   1200
Ile Asp Arg Val Leu Lys Asn Thr Glu Val Gln Ala Ile Ile Thr Ala
385                 390                 395                 400

ctg ggt acc ggt att cac gac gag ttc gac att tct aaa ctg cgt tac   1248
Leu Gly Thr Gly Ile His Asp Glu Phe Asp Ile Ser Lys Leu Arg Tyr
                405                 410                 415

cac aag atc gtg ttg                                               1263
His Lys Ile Val Leu
            420
```

〈210〉 20
〈211〉 1263
〈212〉 DNA
〈213〉 Mycobacterium scrofulceum

```
<220>
<221> CDS
<222> (1)..(1263)

<400> 20
ggc gag aac agc ggc tac acc gtc agc ggt ggg ttg cac gga gtg ggc    48
Gly Glu Asn Ser Gly Tyr Thr Val Ser Gly Gly Leu His Gly Val Gly
 1               5                   10                  15

gtg tcg gtg gtc aac gcg ctg tcc acc cgc ctg gag gtc acc atc aag    96
Val Ser Val Val Asn Ala Leu Ser Thr Arg Leu Glu Val Thr Ile Lys
             20                  25                  30

cgc gac ggg cac gag tgg ttt cag tac tac gac cgc gcc gtg ccc gga    144
Arg Asp Gly His Glu Trp Phe Gln Tyr Tyr Asp Arg Ala Val Pro Gly
         35                  40                  45

acc ctc aag cag ggc gag gcc acc aag aag acc gga acc acg atc agg    192
Thr Leu Lys Gln Gly Glu Ala Thr Lys Lys Thr Gly Thr Thr Ile Arg
     50                  55                  60

ttc tgg gcg gac ccc gaa atc ttc gaa acc aca cag tac gac ttc gag    240
Phe Trp Ala Asp Pro Glu Ile Phe Glu Thr Thr Gln Tyr Asp Phe Glu
 65                  70                  75                  80

acc gtg gcg cgg cgg ctg cag gag atg gcc ttc ctc aac aag ggc ctc    288
Thr Val Ala Arg Arg Leu Gln Glu Met Ala Phe Leu Asn Lys Gly Leu
                 85                  90                  95
```

```
acc atc aac ctc acc gac gaa cga gtg gag cag gac gag gtc gtc gac    336
Thr Ile Asn Leu Thr Asp Glu Arg Val Glu Gln Asp Glu Val Val Asp
            100                 105                 110

gag gtc gtc agc gac acc gcc gag gca ccg aag tcc gcc gaa gag aag    384
Glu Val Val Ser Asp Thr Ala Glu Ala Pro Lys Ser Ala Glu Glu Lys
        115                 120                 125

gcc gcg gaa tcg act gcg cca cac aag gtc aag cac cgc acc ttc cac    432
Ala Ala Glu Ser Thr Ala Pro His Lys Val Lys His Arg Thr Phe His
    130                 135                 140

tac ccc ggc ggt ctg gtc gac ttc gtc aag cac atc aac cgc acc aag    480
Tyr Pro Gly Gly Leu Val Asp Phe Val Lys His Ile Asn Arg Thr Lys
145                 150                 155                 160

agc ccg atc cag cag agc gtc atc gat ttc gac ggc aag ggc acc ggc    528
Ser Pro Ile Gln Gln Ser Val Ile Asp Phe Asp Gly Lys Gly Thr Gly
                165                 170                 175

cac gag gtc gag atc gcc atg cag tgg aac ggc ggc tac tcg gag tcc    576
His Glu Val Glu Ile Ala Met Gln Trp Asn Gly Gly Tyr Ser Glu Ser
            180                 185                 190

gtc cac acc ttc gcc aac acc atc aac acg cac gag ggc ggc acc cac    624
Val His Thr Phe Ala Asn Thr Ile Asn Thr His Glu Gly Gly Thr His
        195                 200                 205
```

```
gag gag ggc ttc cgc agc gcg ctg acg tcg gtg gtg aac aag tac gcc    672
Glu Glu Gly Phe Arg Ser Ala Leu Thr Ser Val Val Asn Lys Tyr Ala
    210                 215                 220

aaa gac aag aaa ctg ctg aag gac aaa gat ccc aac ctc acc ggt gac    720
Lys Asp Lys Lys Leu Leu Lys Asp Lys Asp Pro Asn Leu Thr Gly Asp
225                 230                 235                 240

gac atc cgt gag ggc ttg gcc gcg gtc atc tcg gtg aag gtc gcc gag    768
Asp Ile Arg Glu Gly Leu Ala Ala Val Ile Ser Val Lys Val Ala Glu
                245                 250                 255

cca cag ttc gaa ggc cag acc aag aca aag ctg ggc aac acc gag gtg    816
Pro Gln Phe Glu Gly Gln Thr Lys Thr Lys Leu Gly Asn Thr Glu Val
            260                 265                 270

aag tcg ttc gtg cag aag gtg tgc aac gag cag ctc acc cac tgg ttc    864
Lys Ser Phe Val Gln Lys Val Cys Asn Glu Gln Leu Thr His Trp Phe
        275                 280                 285

gag gcc aac cca tcc gag gcg aaa acg gtg gtg aac aaa gcg gtg tcg    912
Glu Ala Asn Pro Ser Glu Ala Lys Thr Val Val Asn Lys Ala Val Ser
    290                 295                 300

tcg gct cag gcg cgc att gcc gcc cgc aag gcg cgt gaa ctg gtg cgc    960
Ser Ala Gln Ala Arg Ile Ala Ala Arg Lys Ala Arg Glu Leu Val Arg
305                 310                 315                 320

cgc aag agc gcc acc gac ctc ggc ggt ctg ccc ggg aag ctg gcc gac    1008
```

```
Arg Lys Ser Ala Thr Asp Leu Gly Gly Leu Pro Gly Lys Leu Ala Asp
                325                 330                 335

tgc cgc tcc acc gac ccg cgg aaa tcg gaa ctg tat gtg gtg gag ggc   1056
Cys Arg Ser Thr Asp Pro Arg Lys Ser Glu Leu Tyr Val Val Glu Gly
            340                 345                 350

gat tcg gcc ggc ggc tcg gcc aag agc ggg cgc gac tcg atg ttc cag   1104
Asp Ser Ala Gly Gly Ser Ala Lys Ser Gly Arg Asp Ser Met Phe Gln
        355                 360                 365

gcg atc ctg ccg ctg cgc ggc aag atc atc aat gtc gag aag gcc cgc   1152
Ala Ile Leu Pro Leu Arg Gly Lys Ile Ile Asn Val Glu Lys Ala Arg
    370                 375                 380

atc gac cgg gtg ctg aag aac acc gaa gtt cag gcg atc atc acc gcg   1200
Ile Asp Arg Val Leu Lys Asn Thr Glu Val Gln Ala Ile Ile Thr Ala
385                 390                 395                 400

ctg ggt acc ggg att cac gac gag ttc gac atc acc aag ctg cgc tat   1248
Leu Gly Thr Gly Ile His Asp Glu Phe Asp Ile Thr Lys Leu Arg Tyr
                405                 410                 415

cac aag atc gtg ctg                                               1263
His Lys Ile Val Leu
            420

<210> 21
<211> 1260
```

〈212〉 DNA
〈213〉 Mycobacterium branderi

〈220〉
〈221〉 CDS
〈222〉 (1)..(1260)

〈400〉 21
ggc gat gac agc gcc tac gcg gtc tcg ggt ggt ctg cac ggc gtg ggc 48
Gly Asp Asp Ser Ala Tyr Ala Val Ser Gly Gly Leu His Gly Val Gly
1 5 10 15

gtg tcg gtg gtc aac gca ttg tcg act cga ctc gag gtg gag atc gcg 96
Val Ser Val Val Asn Ala Leu Ser Thr Arg Leu Glu Val Glu Ile Ala
20 25 30

acc gac ggg tac gag tgg ttt cag cat tac gac cgc tct gtc ccc ggc 144
Thr Asp Gly Tyr Glu Trp Phe Gln His Tyr Asp Arg Ser Val Pro Gly
35 40 45

acg ctc aag caa ggc gag aaa acc aaa aag acc ggc acc acg gtc cgc 192
Thr Leu Lys Gln Gly Glu Lys Thr Lys Lys Thr Gly Thr Thr Val Arg
50 55 60

ttc tgg gcc gac ccg gac atc ttc gag acg acg gat tac gac ttc gag 240
Phe Trp Ala Asp Pro Asp Ile Phe Glu Thr Thr Asp Tyr Asp Phe Glu
65 70 75 80

acg gtc gca cgc cgg ctg cag gaa atg gcg ttc ctc aac aaa ggg ctg 288

```
Thr Val Ala Arg Arg Leu Gln Glu Met Ala Phe Leu Asn Lys Gly Leu
                85                  90                  95

acc atc aac ctg acc gac gag cgg gtg cga aac gaa gaa gtc gtc gac     336
Thr Ile Asn Leu Thr Asp Glu Arg Val Arg Asn Glu Glu Val Val Asp
            100                 105                 110

gag gtc gtc agc gac acc gcc gac gcg ccg aag tcg gcg cgc gaa gag     384
Glu Val Val Ser Asp Thr Ala Asp Ala Pro Lys Ser Ala Arg Glu Glu
        115                 120                 125

gcc gaa gaa cgg acc acg cag aaa gtc aag cac cgc acg ttc cat tac     432
Ala Glu Glu Arg Thr Thr Gln Lys Val Lys His Arg Thr Phe His Tyr
    130                 135                 140

ccc ggc ggc ttg gtc gat ttc gtc aaa cac atc aac cgc aca aag aac     480
Pro Gly Gly Leu Val Asp Phe Val Lys His Ile Asn Arg Thr Lys Asn
145                 150                 155                 160

ccc atc cat tcg agc atc gtc gac ttc tcc ggc aag ggt ccc ggc cac     528
Pro Ile His Ser Ser Ile Val Asp Phe Ser Gly Lys Gly Pro Gly His
                165                 170                 175

gag gtc gag atc gca atg cag tgg aac gcc ggc tat tcg gag tcg gtg     576
Glu Val Glu Ile Ala Met Gln Trp Asn Ala Gly Tyr Ser Glu Ser Val
            180                 185                 190

cac acc ttc gcc aac acc atc aac acc cac gag ggc ggc acc cac gaa     624
His Thr Phe Ala Asn Thr Ile Asn Thr His Glu Gly Gly Thr His Glu
```

```
        195                 200                 205

gaa ggg ttc cgc gcg gca ctg acg tcc gtg gtg aac aag tac gcc aag   672
Glu Gly Phe Arg Ala Ala Leu Thr Ser Val Val Asn Lys Tyr Ala Lys
    210                 215                 220

gac cga aaa ctg ctg aag gac aag gac ccc aac ctc acc ggc gac gac   720
Asp Arg Lys Leu Leu Lys Asp Lys Asp Pro Asn Leu Thr Gly Asp Asp
225                 230                 235                 240

att cgt gag ggc ctg gcg gcg gtc atc tcg gtc aag gtc agc gag ccg   768
Ile Arg Glu Gly Leu Ala Ala Val Ile Ser Val Lys Val Ser Glu Pro
                245                 250                 255

cag ttc gag ggc cag acc aaa acc aaa ctc ggc aac acc gaa gtc aag   816
Gln Phe Glu Gly Gln Thr Lys Thr Lys Leu Gly Asn Thr Glu Val Lys
            260                 265                 270

tcg ttt gtg cag aag gtc tgc aac gaa cag ctc acc cac tgg ttc gag   864
Ser Phe Val Gln Lys Val Cys Asn Glu Gln Leu Thr His Trp Phe Glu
        275                 280                 285

gcc aat ccc agc gac gcc aag acc gtc gtc aac aaa gcg gtg tcg tcg   912
Ala Asn Pro Ser Asp Ala Lys Thr Val Val Asn Lys Ala Val Ser Ser
    290                 295                 300

gcg cag gcc cgc att gcc gcc cgc aaa gcg cga gaa ttg gtg cgc cgc   960
Ala Gln Ala Arg Ile Ala Ala Arg Lys Ala Arg Glu Leu Val Arg Arg
305                 310                 315                 320
```

```
aag agc gca acc gat ctt ggc ggg ctg ccg ggc aag ctg gct gac tgc   1008
Lys Ser Ala Thr Asp Leu Gly Gly Leu Pro Gly Lys Leu Ala Asp Cys
                325                 330                 335

cgc tcg acc gat cca cgc aag tcc gaa ttg tat gtg gtg gag ggt gat   1056
Arg Ser Thr Asp Pro Arg Lys Ser Glu Leu Tyr Val Val Glu Gly Asp
            340                 345                 350

tcg gcc ggc ggc tcg gcc aag agc ggc cgc gac tcg atg ttt cag gcg   1104
Ser Ala Gly Gly Ser Ala Lys Ser Gly Arg Asp Ser Met Phe Gln Ala
        355                 360                 365

atc ctg ccg ttg cgg ggc aag atc atc aac gtg gag aag gcc cgc atc   1152
Ile Leu Pro Leu Arg Gly Lys Ile Ile Asn Val Glu Lys Ala Arg Ile
    370                 375                 380

gac cgg gtg ctg aag aac act gag gtg cag gcg atc atc acc gcg ctg   1200
Asp Arg Val Leu Lys Asn Thr Glu Val Gln Ala Ile Ile Thr Ala Leu
385                 390                 395                 400

ggc acc ggg att cac gac gag ttc gac atc tcc aag ctg cgc tac cac   1248
Gly Thr Gly Ile His Asp Glu Phe Asp Ile Ser Lys Leu Arg Tyr His
                405                 410                 415

aag atc gtg ctg                                                   1260
Lys Ile Val Leu
            420
```

〈210〉 22
〈211〉 1263
〈212〉 DNA
〈213〉 Mycobacterium paratuberculosis

〈220〉
〈221〉 CDS
〈222〉 (1)..(1263)

〈400〉 22

```
ggc gag aac agc ggc tac aac gtc agc ggc ggt ctg cac ggc gtc ggc    48
Gly Glu Asn Ser Gly Tyr Asn Val Ser Gly Gly Leu His Gly Val Gly
  1               5                  10                  15

gtc tcg gtg gtc aac gcg ctg tcc act cgg ctc gag gtc aac atc gcc    96
Val Ser Val Val Asn Ala Leu Ser Thr Arg Leu Glu Val Asn Ile Ala
             20                  25                  30

cgc gac ggc tac gag tgg tcg cag tac tac gac cac gcc gtg ccc ggc   144
Arg Asp Gly Tyr Glu Trp Ser Gln Tyr Tyr Asp His Ala Val Pro Gly
         35                  40                  45

acc ctc aag cag ggc gag gcc acc aag cgc acc ggc acc acc atc cgg   192
Thr Leu Lys Gln Gly Glu Ala Thr Lys Arg Thr Gly Thr Thr Ile Arg
     50                  55                  60

ttc tgg gcc gac ccc gac atc ttc gag acc acc gag tac gac ttc gaa   240
Phe Trp Ala Asp Pro Asp Ile Phe Glu Thr Thr Glu Tyr Asp Phe Glu
 65                  70                  75                  80
```

```
acg gtg gcc cgg cgg ctg cag gaa atg gcg ttc ctc aac aag ggc ctg    288
Thr Val Ala Arg Arg Leu Gln Glu Met Ala Phe Leu Asn Lys Gly Leu
                 85                  90                  95

acc atc aac ctc acc gac gag cgg gtg acc aac gaa gag gtc gtc gac    336
Thr Ile Asn Leu Thr Asp Glu Arg Val Thr Asn Glu Glu Val Val Asp
            100                 105                 110

gag gtg gtc agc gac acc gcc gac gca ccc aag tcg gcg cag gag aag    384
Glu Val Val Ser Asp Thr Ala Asp Ala Pro Lys Ser Ala Gln Glu Lys
        115                 120                 125

gcg gcg gaa tcg gct gcg ccg cat aag gtc aag cac cgc acc ttc cac    432
Ala Ala Glu Ser Ala Ala Pro His Lys Val Lys His Arg Thr Phe His
    130                 135                 140

tac ccc ggc ggc ctg gtc gac ttc gtc aaa cac atc aat cgc acc aaa    480
Tyr Pro Gly Gly Leu Val Asp Phe Val Lys His Ile Asn Arg Thr Lys
145                 150                 155                 160

aac ccc atc cac cag agc atc atc gat ttc ggt ggg aag ggc ccc ggc    528
Asn Pro Ile His Gln Ser Ile Ile Asp Phe Gly Gly Lys Gly Pro Gly
                165                 170                 175

cac gag gtc gag atc gcg atg cag tgg aac ggc ggc tac tcc gaa tcg    576
His Glu Val Glu Ile Ala Met Gln Trp Asn Gly Gly Tyr Ser Glu Ser
            180                 185                 190
```

gtg cac acc ttc gcc aac acc atc aac acg cac gag ggc ggc acc cac 624
Val His Thr Phe Ala Asn Thr Ile Asn Thr His Glu Gly Gly Thr His
195 200 205

gag gag ggc ttc cgc agc gcg ctg acc tcc gtg gtc aac aag tac gcc 672
Glu Glu Gly Phe Arg Ser Ala Leu Thr Ser Val Val Asn Lys Tyr Ala
210 215 220

aag gac aag aag ctg ctc aag gac aag gac ccc aac ctg acc ggt gac 720
Lys Asp Lys Lys Leu Leu Lys Asp Lys Asp Pro Asn Leu Thr Gly Asp
225 230 235 240

gac atc cgc gag ggt ttg gcc gcg gtg atc tcg gtc aag gtg agc gaa 768
Asp Ile Arg Glu Gly Leu Ala Ala Val Ile Ser Val Lys Val Ser Glu
245 250 255

ccg cag ttc gag ggc cag acc aag acc aaa ctg ggc aac acc gag gtg 816
Pro Gln Phe Glu Gly Gln Thr Lys Thr Lys Leu Gly Asn Thr Glu Val
260 265 270

aag tcg ttc gtg cag aag gtg tgc aac gaa cag ctc acc cac tgg ttc 864
Lys Ser Phe Val Gln Lys Val Cys Asn Glu Gln Leu Thr His Trp Phe
275 280 285

gaa gcc aac ccc gca gac gcc aaa gtc att gtc aac aag gcg gtt tca 912
Glu Ala Asn Pro Ala Asp Ala Lys Val Ile Val Asn Lys Ala Val Ser
290 295 300

tca gcg cag gcg cgc atc gcc gcg cgc aag gcg cga gag ttg gtg cgc 960

```
Ser Ala Gln Ala Arg Ile Ala Ala Arg Lys Ala Arg Glu Leu Val Arg
305                 310                 315                 320

cgc aag agc gca acc gac ctg ggc ggg ctg ccc ggc aag ctc gcc gac    1008
Arg Lys Ser Ala Thr Asp Leu Gly Gly Leu Pro Gly Lys Leu Ala Asp
                325                 330                 335

tgc cgg tcg acc gac ccg cgc aag tcg gaa ttg tat gtg gtc gag ggt    1056
Cys Arg Ser Thr Asp Pro Arg Lys Ser Glu Leu Tyr Val Val Glu Gly
            340                 345                 350

gac tcg gcc ggc ggc tcg gcg aaa agc ggc cgg gac tcg atg ttc cag    1104
Asp Ser Ala Gly Gly Ser Ala Lys Ser Gly Arg Asp Ser Met Phe Gln
        355                 360                 365

gcc atc ctt ccg ctg cgc ggc aag atc atc aac gtc gaa aag gcc cgc    1152
Ala Ile Leu Pro Leu Arg Gly Lys Ile Ile Asn Val Glu Lys Ala Arg
    370                 375                 380

atc gac cgg gtg ctg aag aac acc gag gtg cag gcg atc atc acc gcg    1200
Ile Asp Arg Val Leu Lys Asn Thr Glu Val Gln Ala Ile Ile Thr Ala
385                 390                 395                 400

ctg ggc acc ggg att cac gac gag ttc gac atc acc aag ctg cgc tac    1248
Leu Gly Thr Gly Ile His Asp Glu Phe Asp Ile Thr Lys Leu Arg Tyr
                405                 410                 415

cac aag atc gtg ttg                                                1263
His Lys Ile Val Leu
```

420

〈210〉 23
〈211〉 421
〈212〉 PRT
〈213〉 Mycobacterium simiae

〈400〉 23
Gly Glu Asn Ser Gly Tyr Thr Val Ser Gly Gly Leu His Gly Val Gly
1 5 10 15

Val Ser Val Val Asn Ala Leu Ser Thr Arg Leu Glu Val Asn Val Lys
20 25 30

Arg Asp Gly Tyr Glu Trp Phe Gln Tyr Tyr Asp Arg Ala Val Pro Gly
35 40 45

Thr Leu Lys Gln Gly Glu Ala Thr Lys Lys Thr Gly Thr Thr Ile Arg
50 55 60

Phe Trp Ala Asp Pro Glu Ile Phe Glu Thr Thr Gln Tyr Asp Phe Glu
65 70 75 80

Thr Val Ala Arg Arg Leu Gln Glu Met Ala Phe Leu Asn Lys Gly Leu
85 90 95

Thr Ile Asn Leu Thr Asp Glu Arg Val Glu Gln Asp Glu Val Val Asp
100 105 110

```
Glu Val Val Ser Asp Thr Ala Glu Ala Pro Lys Ser Ala Glu Glu Gln
        115                 120                 125

Ala Ala Glu Ser Ala Lys Pro His Lys Val Lys His Arg Thr Phe His
    130                 135                 140

Tyr Pro Gly Gly Leu Val Asp Phe Val Lys His Ile Asn Arg Thr Lys
145                 150                 155                 160

Asn Pro Ile Gln Gln Ser Val Ile Asp Phe Asp Gly Lys Gly Thr Gly
                165                 170                 175

His Glu Val Glu Ile Ala Met Gln Trp Asn Gly Gly Tyr Ser Glu Ser
            180                 185                 190

Val His Thr Phe Ala Asn Thr Ile Asn Thr His Glu Gly Gly Thr His
        195                 200                 205

Glu Glu Gly Phe Arg Ser Ala Leu Thr Ser Val Val Asn Lys Tyr Ala
    210                 215                 220

Lys Asp Lys Lys Leu Leu Lys Asp Lys Asp Pro Asn Leu Thr Gly Asp
225                 230                 235                 240

Asp Ile Arg Glu Gly Leu Ala Ala Val Ile Ser Val Lys Val Ala Glu
                245                 250                 255

Pro Gln Phe Glu Gly Gln Thr Lys Thr Lys Leu Gly Asn Thr Glu Val
            260                 265                 270
```

Lys Ser Phe Val Gln Lys Val Cys Asn Glu Gln Leu Thr His Trp Phe
        275   280   285

Glu Ala Asn Pro Ser Glu Ala Lys Thr Val Val Asn Lys Ala Val Ser
    290   295   300

Ser Ala Gln Ala Arg Ile Ala Ala Arg Lys Ala Arg Glu Leu Val Arg
305   310   315   320

Arg Lys Ser Ala Thr Asp Leu Gly Gly Leu Pro Gly Lys Leu Ala Asp
                325   330   335

Cys Arg Ser Thr Asp Pro Arg Lys Ser Glu Leu Tyr Val Val Glu Gly
            340   345   350

Asp Ser Ala Gly Gly Ser Ala Lys Ser Gly Arg Asp Ser Met Phe Gln
        355   360   365

Ala Ile Leu Pro Leu Arg Gly Lys Ile Ile Asn Val Glu Lys Ala Arg
    370   375   380

Ile Asp Arg Val Leu Lys Asn Thr Glu Val Gln Ala Ile Ile Thr Ala
385   390   395   400

Leu Gly Thr Gly Ile His Asp Glu Phe Asp Ile Thr Lys Leu Arg Tyr
                405   410   415

His Lys Ile Val Leu

420

〈210〉 24
〈211〉 419
〈212〉 PRT
〈213〉 Mycobacterium bovis

〈400〉 24
Ser Asp Ala Tyr Ala Ile Ser Gly Gly Leu His Gly Val Gly Val Ser
1 5 10 15

Val Val Asn Ala Leu Ser Thr Arg Leu Glu Val Glu Ile Lys Arg Asp
20 25 30

Gly Tyr Glu Trp Ser Gln Val Tyr Glu Lys Ser Glu Pro Leu Gly Leu
35 40 45

Lys Gln Gly Ala Pro Thr Lys Lys Thr Gly Ser Thr Val Arg Phe Trp
50 55 60

Ala Asp Pro Ala Val Phe Glu Thr Thr Glu Tyr Asp Phe Glu Thr Val
65 70 75 80

Ala Arg Arg Leu Gln Glu Met Ala Phe Leu Asn Lys Gly Leu Thr Ile
85 90 95

Asn Leu Thr Asp Glu Arg Val Thr Gln Asp Glu Val Val Asp Glu Val
100 105 110

Val Ser Asp Val Ala Glu Ala Pro Lys Ser Ala Ser Glu Arg Ala Ala
115 120 125

Glu Ser Thr Ala Pro His Lys Val Lys Ser Arg Thr Phe His Tyr Pro
130 135 140

Gly Gly Leu Val Asp Phe Val Lys His Ile Asn Arg Thr Lys Asn Ala
145 150 155 160

Ile His Ser Ser Ile Val Asp Phe Ser Gly Lys Gly Thr Gly His Glu
165 170 175

Val Glu Ile Ala Met Gln Trp Asn Ala Gly Tyr Ser Glu Ser Val His
180 185 190

Thr Phe Ala Asn Thr Ile Asn Thr His Glu Gly Gly Thr His Glu Glu
195 200 205

Gly Phe Arg Ser Ala Leu Thr Ser Val Val Asn Lys Tyr Ala Lys Asp
210 215 220

Arg Lys Leu Leu Lys Asp Lys Asp Pro Asn Leu Thr Gly Asp Asp Ile
225 230 235 240

Arg Glu Gly Leu Ala Ala Val Ile Ser Val Lys Val Ser Glu Pro Gln
245 250 255

Phe Glu Gly Gln Thr Lys Thr Lys Leu Gly Asn Thr Glu Val Lys Ser
260 265 270

```
Phe Val Gln Lys Val Cys Asn Glu Gln Leu Thr His Trp Phe Glu Ala
        275                 280                 285

Asn Pro Thr Asp Ser Lys Val Val Val Asn Lys Ala Val Ser Ser Ala
    290                 295                 300

Gln Ala Arg Ile Ala Ala Arg Lys Ala Arg Glu Leu Val Arg Arg Lys
305                 310                 315                 320

Ser Ala Thr Asp Ile Gly Gly Leu Pro Gly Lys Leu Ala Asp Cys Arg
                325                 330                 335

Ser Thr Asp Pro Arg Lys Ser Glu Leu Tyr Val Val Glu Gly Asp Ser
            340                 345                 350

Ala Gly Gly Ser Ala Lys Ser Gly Arg Asp Ser Met Phe Gln Ala Ile
        355                 360                 365

Leu Pro Leu Arg Gly Lys Ile Ile Asn Val Glu Lys Ala Arg Ile Asp
    370                 375                 380

Arg Val Leu Lys Asn Thr Glu Val Gln Ala Ile Ile Thr Ala Leu Gly
385                 390                 395                 400

Thr Gly Ile His Asp Glu Phe Asp Ile Gly Lys Leu Arg Tyr His Lys
                405                 410                 415

Ile Val Leu
```

〈210〉 25
〈211〉 421
〈212〉 PRT
〈213〉 Mycobacterium szulgai

〈400〉 25
Gly Glu Asn Ser Gly Tyr Asn Val Ser Gly Gly Leu His Gly Val Gly
1 5 10 15

Val Ser Val Val Asn Ala Leu Ser Thr Arg Leu Glu Val Asp Ile Lys
20 25 30

Arg Asp Gly His Lys Trp Ser Gln Phe Tyr Asn Lys Ala Val Pro Gly
35 40 45

Thr Leu Lys Gln Gly Glu Ala Thr Lys Lys Thr Gly Thr Thr Ile Arg
50 55 60

Phe Trp Ala Asp Pro Asp Ile Phe Glu Thr Thr Glu Tyr Asp Phe Glu
65 70 75 80

Thr Val Ala Arg Arg Leu Gln Glu Met Ala Phe Leu Asn Lys Gly Leu
85 90 95

Thr Ile Asn Leu Thr Asp Glu Arg Val Ala Gln Asp Glu Val Val Asp
100 105 110

```
Glu Val Val Ser Asp Thr Ala Glu Ala Pro Lys Ser Ala Glu Glu Lys
        115                 120                 125

Ala Ala Glu Ser Lys Gly Pro His Lys Val Lys His Arg Thr Phe His
    130                 135                 140

Tyr Pro Gly Gly Leu Ile Asp Phe Val Lys His Ile Asn Arg Thr Lys
145                 150                 155                 160

Ser Pro Ile Gln Gln Ser Val Val Ala Phe Asp Gly Lys Gly Glu Gly
                165                 170                 175

His Glu Val Glu Ile Ala Met Gln Trp Asn Gly Gly Tyr Ser Glu Ser
            180                 185                 190

Val His Thr Phe Ala Asn Thr Ile Asn Thr His Glu Gly Gly Thr His
        195                 200                 205

Glu Glu Gly Phe Arg Ser Ala Leu Thr Ser Val Val Asn Lys Tyr Ala
    210                 215                 220

Lys Asp Lys Lys Leu Leu Lys Glu Lys Asp Ala Asn Leu Thr Gly Asp
225                 230                 235                 240

Asp Ile Arg Glu Gly Leu Ala Ala Val Ile Ser Val Lys Val Ala Glu
                245                 250                 255

Pro Gln Phe Glu Gly Gln Thr Lys Thr Lys Leu Gly Asn Thr Glu Val
            260                 265                 270
```

```
Lys Ser Phe Val Gln Lys Val Cys Asn Glu Gln Leu Thr His Trp Phe
        275                 280                 285

Glu Ala Asn Pro Ser Glu Ala Lys Thr Val Val Asn Lys Ala Val Ser
    290                 295                 300

Ser Ala Gln Ala Arg Ile Ala Ala Arg Lys Ala Arg Glu Leu Val Arg
305                 310                 315                 320

Arg Lys Ser Ala Thr Asp Leu Gly Gly Leu Pro Gly Lys Leu Ala Asp
                325                 330                 335

Cys Arg Ser Thr Asp Pro Arg Lys Ser Glu Leu Tyr Val Val Glu Gly
            340                 345                 350

Asp Ser Ala Gly Gly Ser Ala Lys Ser Gly Arg Asp Ser Met Phe Gln
        355                 360                 365

Ala Ile Leu Pro Leu Arg Gly Lys Ile Ile Asn Val Glu Lys Ala Arg
    370                 375                 380

Ile Asp Arg Val Leu Lys Asn Thr Glu Val Gln Ala Ile Ile Thr Ala
385                 390                 395                 400

Leu Gly Thr Gly Ile His Asp Glu Phe Asp Leu Ala Lys Leu Arg Tyr
                405                 410                 415

His Lys Ile Val Leu
```

420

⟨210⟩ 26
⟨211⟩ 421
⟨212⟩ PRT
⟨213⟩ Mycobacterium malmoense

⟨400⟩ 26
Gly Glu Asn Ser Gly Tyr Asn Val Ser Gly Gly Leu His Gly Val Gly
1 5 10 15

Val Ser Val Val Asn Ala Leu Ser Thr Arg Leu Glu Val Asp Val Ala
20 25 30

Arg Asp Gly Tyr Met Trp Ser Gln Phe Tyr Asp His Ala Glu Pro Gly
35 40 45

Thr Leu Lys Gln Gly Glu Ala Thr Lys Thr Thr Gly Thr Thr Ile Arg
50 55 60

Phe Trp Ala Asp Pro Asp Ile Phe Glu Thr Thr Glu Tyr Asp Phe Glu
65 70 75 80

Thr Val Ala Arg Arg Leu Gln Glu Met Ala Phe Leu Asn Lys Gly Leu
85 90 95

Thr Ile Asn Leu Thr Asp Glu Arg Val Ser Glu Glu Glu Val Val Asp
100 105 110

```
Asp Val Val Ser Asp Thr Ala Glu Ala Pro Lys Ser Ala Val Glu Lys
        115                 120                 125

Ala Ala Glu Ser Thr Gly Pro His Lys Val Lys His Arg Thr Phe His
    130                 135                 140

Tyr Pro Gly Gly Leu Val Asp Phe Val Lys His Ile Asn Arg Thr Lys
145                 150                 155                 160

Asn Pro Ile His Asn Ser Ile Val Asp Phe Ser Gly Lys Gly Pro Gly
                165                 170                 175

His Glu Val Glu Ile Ala Met Gln Trp Asn Ala Gly Tyr Ser Glu Ser
            180                 185                 190

Val His Thr Phe Ala Asn Thr Ile Asn Thr His Glu Gly Gly Thr His
        195                 200                 205

Glu Glu Gly Phe Arg Ser Ala Leu Thr Ser Val Val Asn Lys Tyr Ala
    210                 215                 220

Lys Asp Arg Lys Leu Leu Lys Asp Lys Asp Pro Asn Leu Thr Gly Asp
225                 230                 235                 240

Asp Ile Arg Glu Gly Leu Ala Ala Val Ile Ser Val Lys Val Ser Glu
                245                 250                 255

Pro Gln Phe Glu Gly Gln Thr Lys Thr Lys Leu Gly Asn Thr Glu Val
            260                 265                 270
```

Lys Ser Phe Val Gln Lys Val Cys Asn Glu Gln Leu Thr His Trp Phe
275 280 285

Glu Ala Asn Pro Ala Asp Ala Lys Thr Val Val Asn Lys Ala Val Ser
290 295 300

Ser Ala Gln Ala Arg Ile Ala Ala Arg Lys Ala Arg Glu Leu Val Arg
305 310 315 320

Arg Lys Ser Ala Thr Asp Leu Gly Gly Leu Pro Gly Lys Leu Ala Asp
325 330 335

Cys Arg Ser Thr Asp Pro Arg Lys Ser Glu Leu Tyr Val Val Glu Gly
340 345 350

Asp Ser Ala Gly Gly Ser Ala Lys Ser Gly Arg Asp Ser Met Phe Gln
355 360 365

Ala Ile Leu Pro Leu Arg Gly Lys Ile Ile Asn Val Glu Lys Ala Arg
370 375 380

Ile Asp Arg Val Leu Lys Asn Thr Glu Val Gln Ala Ile Ile Thr Ala
385 390 395 400

Leu Gly Thr Gly Ile His Asp Glu Phe Asp Ile Thr Lys Leu Arg Tyr
405 410 415

His Lys Ile Val Leu

420

〈210〉 27

〈211〉 421

〈212〉 PRT

〈213〉 Mycobacterium intracellulare

〈400〉 27

Gly Glu Asn Ser Gly Tyr Asn Val Ser Gly Gly Leu His Gly Val Gly

1 5 10 15

Val Ser Val Val Asn Ala Leu Ser Thr Arg Leu Glu Val Asp Ile Ala

20 25 30

Arg Asp Gly Tyr Glu Trp Ser Gln Phe Tyr Asp His Ala Val Pro Gly

35 40 45

Thr Leu Lys Gln Gly Glu Ala Thr Lys Arg Thr Gly Thr Thr Ile Arg

50 55 60

Phe Trp Ala Asp Pro Asp Ile Phe Glu Thr Thr Glu Tyr Asp Phe Glu

65 70 75 80

Thr Val Ala Arg Arg Leu Gln Glu Met Ala Phe Leu Asn Lys Gly Leu

85 90 95

Thr Ile Asn Leu Thr Asp Glu Arg Val Ser Asn Glu Glu Val Val Asp

100 105 110

Glu Val Val Ser Asp Thr Ala Asp Ala Pro Lys Ser Ala Gln Glu Lys
115 120 125

Ala Ala Glu Ser Thr Ala Pro His Lys Val Lys His Arg Thr Phe His
130 135 140

Tyr Pro Gly Gly Leu Val Asp Phe Val Lys His Ile Asn Arg Thr Lys
145 150 155 160

Ser Pro Ile Gln Gln Ser Ile Ile Asp Phe Asp Gly Lys Gly Pro Gly
165 170 175

His Glu Val Glu Ile Ala Met Gln Trp Asn Gly Gly Tyr Ser Glu Ser
180 185 190

Val His Thr Phe Ala Asn Thr Ile Asn Thr His Glu Gly Gly Thr His
195 200 205

Glu Glu Gly Phe Arg Ser Ala Leu Thr Ser Val Val Asn Lys Tyr Ala
210 215 220

Lys Asp Lys Lys Leu Leu Lys Asp Lys Asp Pro Asn Leu Thr Gly Asp
225 230 235 240

Asp Ile Arg Glu Gly Leu Ala Ala Val Ile Ser Val Lys Val Ser Glu
245 250 255

Pro Gln Phe Glu Gly Gln Thr Lys Thr Lys Leu Gly Asn Thr Glu Val
260 265 270

```
Lys Ser Phe Val Gln Lys Val Cys Asn Glu Gln Leu Thr His Trp Phe
        275                 280                 285

Glu Ala Asn Pro Ala Asp Ala Lys Val Val Val Asn Lys Ala Val Ser
    290                 295                 300

Ser Ala Gln Ala Arg Ile Ala Ala Arg Lys Ala Arg Glu Leu Val Arg
305                 310                 315                 320

Arg Lys Ser Ala Thr Asp Leu Gly Gly Leu Pro Gly Lys Leu Ala Asp
                325                 330                 335

Cys Arg Ser Thr Asp Pro Arg Lys Ser Glu Leu Tyr Val Val Glu Gly
            340                 345                 350

Asp Ser Ala Gly Gly Ser Ala Lys Ser Gly Arg Asp Ser Met Phe Gln
        355                 360                 365

Ala Ile Leu Pro Leu Arg Gly Lys Ile Ile Asn Val Glu Lys Ala Arg
    370                 375                 380

Ile Asp Arg Val Leu Lys Asn Thr Glu Val Gln Ala Ile Ile Thr Ala
385                 390                 395                 400

Leu Gly Thr Gly Ile His Asp Glu Phe Asp Ile Thr Lys Leu Arg Tyr
                405                 410                 415

His Lys Ile Val Leu
```

420

〈210〉 28
〈211〉 421
〈212〉 PRT
〈213〉 Mycobacterium avium

〈400〉 28
Gly Glu Asn Ser Gly Tyr Asn Val Ser Gly Gly Leu His Gly Val Gly
1 5 10 15

Val Ser Val Val Asn Ala Leu Ser Thr Arg Leu Glu Val Asn Ile Ala
20 25 30

Arg Asp Gly Tyr Glu Trp Ser Gln Tyr Tyr Asp His Ala Val Pro Gly
35 40 45

Thr Leu Lys Gln Gly Glu Ala Thr Lys Arg Thr Gly Thr Thr Ile Arg
50 55 60

Phe Trp Ala Asp Pro Asp Ile Phe Glu Thr Thr Glu Tyr Asp Phe Glu
65 70 75 80

Thr Val Ala Arg Arg Leu Gln Glu Met Ala Phe Leu Asn Lys Gly Leu
85 90 95

Thr Ile Asn Leu Thr Asp Glu Arg Val Thr Asn Glu Glu Val Val Asp
100 105 110

```
Glu Val Val Ser Asp Thr Ala Asp Ala Pro Lys Ser Ala Gln Glu Lys
        115                 120                 125

Ala Ala Glu Ser Ala Ala Pro His Lys Val Lys His Arg Thr Phe His
    130                 135                 140

Tyr Pro Gly Gly Leu Val Asp Phe Val Lys His Ile Asn Arg Thr Lys
145                 150                 155                 160

Asn Pro Ile His Gln Ser Ile Ile Asp Phe Gly Gly Lys Gly Pro Gly
                165                 170                 175

His Glu Val Glu Ile Ala Met Gln Trp Asn Gly Gly Tyr Ser Glu Ser
            180                 185                 190

Val His Thr Phe Ala Asn Thr Ile Asn Thr His Glu Gly Gly Thr His
        195                 200                 205

Glu Glu Gly Phe Arg Ser Ala Leu Thr Ser Val Val Asn Lys Tyr Ala
    210                 215                 220

Lys Asp Lys Lys Leu Leu Lys Asp Lys Asp Pro Asn Leu Thr Gly Asp
225                 230                 235                 240

Asp Ile Arg Glu Gly Leu Ala Ala Val Ile Ser Val Lys Val Ser Glu
                245                 250                 255

Pro Gln Phe Glu Gly Gln Thr Lys Thr Lys Leu Gly Asn Thr Glu Val
            260                 265                 270
```

Lys Ser Phe Val Gln Lys Val Cys Asn Glu Gln Leu Thr His Trp Phe
275 280 285

Glu Ala Asn Pro Ala Asp Ala Lys Val Ile Val Asn Lys Ala Val Ser
290 295 300

Ser Ala Gln Ala Arg Ile Ala Ala Arg Lys Ala Arg Glu Leu Val Arg
305 310 315 320

Arg Lys Ser Ala Thr Asp Leu Gly Gly Leu Pro Gly Lys Leu Ala Asp
325 330 335

Cys Arg Ser Thr Asp Pro Arg Lys Ser Glu Leu Tyr Val Val Glu Gly
340 345 350

Asp Ser Ala Gly Gly Ser Ala Lys Ser Gly Arg Asp Ser Met Phe Gln
355 360 365

Ala Ile Leu Pro Leu Arg Gly Lys Ile Ile Asn Val Glu Lys Ala Arg
370 375 380

Ile Asp Arg Val Leu Lys Asn Thr Glu Val Gln Ala Ile Ile Thr Ala
385 390 395 400

Leu Gly Thr Gly Ile His Asp Glu Phe Asp Ile Thr Lys Leu Arg Tyr
405 410 415

His Lys Ile Val Leu

420

〈210〉 29
〈211〉 421
〈212〉 PRT
〈213〉 Mycobacterium gordonae

〈400〉 29
Gly Glu Asn Ser Gly Tyr Thr Val Ser Gly Gly Leu His Gly Val Gly
1 5 10 15

Val Ser Val Val Asn Ala Leu Ser Thr Arg Leu Glu Val Asp Ile Lys
20 25 30

Arg Asp Gly His Glu Trp Ser Gln Tyr Tyr Lys Arg Ala Val Pro Gly
35 40 45

Thr Leu Lys Gln Gly Glu Thr Thr Arg Lys Thr Gly Thr Thr Ile Arg
50 55 60

Phe Trp Ala Asp Pro Glu Ile Phe Glu Thr Thr Gln Tyr Asp Phe Glu
65 70 75 80

Thr Val Ala Arg Arg Leu Gln Glu Met Ala Phe Leu Asn Lys Gly Leu
85 90 95

Thr Ile Asn Leu Thr Asp Glu Arg Val Glu Gln Asp Glu Val Val Asp
100 105 110

Glu Val Val Ser Asp Thr Ala Glu Ala Pro Lys Ser Ala Glu Glu Lys
        115   120   125

Ala Ala Glu Ser Lys Ala Pro His Lys Val Lys Gln Arg Thr Phe His
    130   135   140

Tyr Pro Gly Gly Leu Val Asp Phe Val Lys His Ile Asn Arg Thr Lys
145   150   155   160

Ser Pro Ile Gln Gln Ser Val Ile Asp Phe Glu Gly Lys Gly Thr Gly
                165   170   175

His Glu Val Glu Ile Ala Met Gln Trp Asn Gly Gly Tyr Ser Glu Ser
            180   185   190

Val His Thr Phe Ala Asn Thr Ile Asn Thr His Glu Gly Gly Thr His
        195   200   205

Glu Glu Gly Phe Arg Ser Ala Leu Thr Ser Val Val Asn Lys Tyr Ala
    210   215   220

Lys Asp Lys Lys Leu Leu Lys Glu Lys Asp Pro Asn Leu Thr Gly Asp
225   230   235   240

Asp Ile Arg Glu Gly Leu Ala Ala Val Ile Ser Val Lys Val Ala Glu
                245   250   255

Pro Gln Phe Glu Gly Gln Thr Lys Thr Lys Leu Gly Asn Thr Glu Val
            260   265   270

Lys Ser Phe Val Gln Lys Val Cys Asn Glu Gln Leu Thr His Trp Phe
275 280 285

Glu Ala Asn Pro Ser Glu Ala Lys Thr Val Val Asn Lys Ala Val Ser
290 295 300

Ser Ala Gln Ala Arg Ile Ala Ala Arg Lys Ala Arg Glu Leu Val Arg
305 310 315 320

Arg Lys Ser Ala Thr Asp Leu Gly Gly Leu Pro Gly Lys Leu Ala Asp
325 330 335

Cys Arg Ser Thr Asp Pro Arg Lys Ser Glu Leu Tyr Val Val Glu Gly
340 345 350

Asp Ser Ala Gly Gly Ser Ala Lys Ser Gly Arg Asp Ser Met Phe Gln
355 360 365

Ala Ile Leu Pro Leu Arg Gly Lys Ile Ile Asn Val Glu Lys Ala Arg
370 375 380

Ile Asp Arg Val Leu Lys Asn Thr Glu Val Gln Ala Ile Ile Thr Ala
385 390 395 400

Leu Gly Thr Gly Ile His Asp Glu Phe Asp Ile Thr Lys Leu Arg Tyr
405 410 415

His Lys Ile Val Leu

420

<210> 30
<211> 419
<212> PRT
<213> Mycobacterium africanum

<400> 30
Ser Asp Ala Tyr Ala Ile Ser Gly Gly Leu His Gly Val Gly Val Ser
1 5 10 15

Val Val Asn Ala Leu Ser Thr Arg Leu Glu Val Glu Ile Lys Arg Asp
20 25 30

Gly Tyr Glu Trp Ser Gln Val Tyr Glu Lys Ser Glu Pro Leu Gly Leu
35 40 45

Lys Gln Gly Ala Pro Thr Lys Lys Thr Gly Ser Thr Val Arg Phe Trp
50 55 60

Ala Asp Pro Ala Val Phe Glu Thr Thr Glu Tyr Asp Phe Glu Thr Val
65 70 75 80

Ala Arg Arg Leu Gln Glu Met Ala Phe Leu Asn Lys Gly Leu Thr Ile
85 90 95

Asn Leu Thr Asp Glu Arg Val Thr Gln Asp Glu Val Val Asp Glu Val
100 105 110

```
Val Ser Asp Val Ala Glu Ala Pro Lys Ser Ala Ser Glu Arg Ala Ala
        115                 120                 125

Glu Ser Thr Ala Pro His Lys Val Lys Ser Arg Thr Phe His Tyr Pro
    130                 135                 140

Gly Gly Leu Val Asp Phe Val Lys His Ile Asn Arg Thr Lys Asn Ala
145                 150                 155                 160

Ile His Ser Ser Ile Val Asp Phe Ser Gly Lys Gly Thr Gly His Glu
                165                 170                 175

Val Glu Ile Ala Met Gln Trp Asn Ala Gly Tyr Ser Glu Ser Val His
            180                 185                 190

Thr Phe Ala Asn Thr Ile Asn Thr His Glu Gly Gly Thr His Glu Glu
        195                 200                 205

Gly Phe Arg Ser Ala Leu Thr Ser Val Val Asn Lys Tyr Ala Lys Asp
    210                 215                 220

Arg Lys Leu Leu Lys Asp Lys Asp Pro Asn Leu Thr Gly Asp Asp Ile
225                 230                 235                 240

Arg Glu Gly Leu Ala Ala Val Ile Ser Val Lys Val Ser Glu Pro Gln
                245                 250                 255

Phe Glu Gly Gln Thr Lys Thr Lys Leu Gly Asn Thr Glu Val Lys Ser
            260                 265                 270
```

```
Phe Val Gln Lys Val Cys Asn Glu Gln Leu Thr His Trp Phe Glu Ala
        275                 280                 285

Asn Pro Thr Asp Ser Lys Val Val Val Asn Lys Ala Val Ser Ser Ala
    290                 295                 300

Gln Ala Arg Ile Ala Ala Arg Lys Ala Arg Glu Leu Val Arg Arg Lys
305                 310                 315                 320

Ser Ala Thr Asp Ile Gly Gly Leu Pro Gly Lys Leu Ala Asp Cys Arg
                325                 330                 335

Ser Thr Asp Pro Arg Lys Ser Glu Leu Tyr Val Val Glu Gly Asp Ser
            340                 345                 350

Ala Gly Gly Ser Ala Lys Ser Gly Arg Asp Ser Met Phe Gln Ala Ile
        355                 360                 365

Leu Pro Leu Arg Gly Lys Ile Ile Asn Val Glu Lys Ala Arg Ile Asp
    370                 375                 380

Arg Val Leu Lys Asn Thr Glu Val Gln Ala Ile Ile Thr Ala Leu Gly
385                 390                 395                 400

Thr Gly Ile His Asp Glu Phe Asp Ile Gly Lys Leu Arg Tyr His Lys
                405                 410                 415

Ile Val Leu
```

〈210〉 31
〈211〉 419
〈212〉 PRT
〈213〉 Mycobacterium tuberculosis

〈400〉 31
Ser Asp Ala Tyr Ala Ile Ser Gly Gly Leu His Gly Val Gly Val Ser
1 5 10 15

Val Val Asn Ala Leu Ser Thr Arg Leu Glu Val Glu Ile Lys Arg Asp
20 25 30

Gly Tyr Glu Trp Ser Gln Val Tyr Glu Lys Ser Glu Pro Leu Gly Leu
35 40 45

Lys Gln Gly Ala Pro Thr Lys Lys Thr Gly Ser Thr Val Arg Phe Trp
50 55 60

Ala Asp Pro Ala Val Phe Glu Thr Thr Glu Tyr Asp Phe Glu Thr Val
65 70 75 80

Ala Arg Arg Leu Gln Glu Met Ala Phe Leu Asn Lys Gly Leu Thr Ile
85 90 95

Asn Leu Thr Asp Glu Arg Val Thr Gln Asp Glu Val Val Asp Glu Val
100 105 110

```
Val Ser Asp Val Ala Glu Ala Pro Lys Ser Ala Ser Glu Arg Ala Ala
        115                 120                 125

Glu Ser Thr Ala Pro His Lys Val Lys Ser Arg Thr Phe His Tyr Pro
    130                 135                 140

Gly Gly Leu Val Asp Phe Val Lys His Ile Asn Arg Thr Lys Asn Ala
145                 150                 155                 160

Ile His Ser Ser Ile Val Asp Phe Ser Gly Lys Gly Thr Gly His Glu
                165                 170                 175

Val Glu Ile Ala Met Gln Trp Asn Ala Gly Tyr Ser Glu Ser Val His
            180                 185                 190

Thr Phe Ala Asn Thr Ile Asn Thr His Glu Gly Gly Thr His Glu Glu
        195                 200                 205

Gly Phe Arg Ser Ala Leu Thr Ser Val Val Asn Lys Tyr Ala Lys Asp
    210                 215                 220

Arg Lys Leu Leu Lys Asp Lys Asp Pro Asn Leu Thr Gly Asp Asp Ile
225                 230                 235                 240

Arg Glu Gly Leu Ala Ala Val Ile Ser Val Lys Val Ser Glu Pro Gln
                245                 250                 255

Phe Glu Gly Gln Thr Lys Thr Lys Leu Gly Asn Thr Glu Val Lys Ser
            260                 265                 270
```

```
Phe Val Gln Lys Val Cys Asn Glu Gln Leu Thr His Trp Phe Glu Ala
        275                 280                 285

Asn Pro Thr Asp Ala Lys Val Val Val Asn Lys Ala Val Ser Ser Ala
    290                 295                 300

Gln Ala Arg Ile Ala Ala Arg Lys Ala Arg Glu Leu Val Arg Arg Lys
305                 310                 315                 320

Ser Ala Thr Asp Ile Gly Gly Leu Pro Gly Lys Leu Ala Asp Cys Arg
                325                 330                 335

Ser Thr Asp Pro Arg Lys Ser Glu Leu Tyr Val Val Glu Gly Asp Ser
            340                 345                 350

Ala Gly Gly Ser Ala Lys Ser Gly Arg Asp Ser Met Phe Gln Ala Ile
        355                 360                 365

Leu Pro Leu Arg Gly Lys Ile Ile Asn Val Glu Lys Ala Arg Ile Asp
    370                 375                 380

Arg Val Leu Lys Asn Thr Glu Val Gln Ala Ile Ile Thr Ala Leu Gly
385                 390                 395                 400

Thr Gly Ile His Asp Glu Phe Asp Ile Gly Lys Leu Arg Tyr His Lys
                405                 410                 415

Ile Val Leu
```

〈210〉 32
〈211〉 419
〈212〉 PRT
〈213〉 Mycobacterium gastri

〈400〉 32

```
Ser Asp Ala Tyr Ala Ile Ser Gly Gly Leu His Gly Val Gly Val Ser
 1               5                  10                  15

Val Val Asn Ala Leu Ser Ile Arg Leu Glu Val Glu Ile Lys Arg Asp
            20                  25                  30

Gly His Glu Trp Ser Gln Val Tyr Glu Lys Ser Glu Pro Met Gly Leu
        35                  40                  45

Lys Gln Gly Ala Pro Thr Lys Lys Thr Gly Thr Thr Val Arg Phe Trp
    50                  55                  60

Ala Asp Pro Asn Val Phe Glu Thr Thr Glu Tyr Asp Phe Glu Thr Val
65                  70                  75                  80

Ala Arg Arg Leu Gln Glu Met Ala Phe Leu Asn Lys Gly Leu Thr Ile
                85                  90                  95

Asn Leu Thr Asp Gln Arg Val Thr Gln Asp Glu Val Val Asp Glu Val
            100                 105                 110
```

Val Ser Asp Val Ala Glu Ala Pro Lys Ser Ala Ser Glu Lys Ala Ala
115 120 125

Glu Phe Thr Ala Pro His Lys Val Lys Lys Arg Thr Phe His Tyr Pro
130 135 140

Gly Gly Leu Val Asp Phe Val Lys His Ile Asn Arg Thr Lys Asn Ala
145 150 155 160

Ile His Ser Ser Ile Val Asp Phe Ser Gly Lys Gly Thr Gly His Glu
165 170 175

Val Glu Ile Ala Met Gln Trp Asn Ala Gly Tyr Ser Glu Ser Val His
180 185 190

Thr Phe Ala Asn Thr Ile Asn Thr His Glu Gly Gly Thr His Glu Glu
195 200 205

Gly Phe Arg Ser Ala Leu Thr Ser Val Val Asn Lys Tyr Ala Lys Asp
210 215 220

Arg Lys Leu Leu Lys Asp Lys Asp Pro Asn Leu Thr Gly Asp Asp Ile
225 230 235 240

Arg Glu Gly Leu Ala Ala Val Ile Ser Val Lys Val Ser Glu Pro Gln
245 250 255

Phe Glu Gly Gln Thr Lys Thr Lys Leu Gly Asn Thr Glu Val Lys Ser
260 265 270

Phe Val Gln Lys Val Cys Asn Glu Gln Leu Thr His Trp Phe Glu Ala
275 280 285

Asn Pro Ala Asp Ala Lys Thr Val Val Asn Lys Ala Val Ser Ser Ala
290 295 300

Gln Ala Arg Ile Ala Ala Arg Lys Ala Arg Glu Leu Val Arg Arg Lys
305 310 315 320

Ser Ala Thr Asp Leu Gly Gly Leu Pro Gly Lys Leu Ala Asp Cys Arg
325 330 335

Ser Thr Asp Pro Arg Lys Ser Glu Leu Tyr Val Val Glu Gly Asp Ser
340 345 350

Ala Gly Gly Ser Ala Lys Ser Gly Arg Asp Ser Met Phe Gln Ala Ile
355 360 365

Leu Pro Leu Arg Gly Lys Ile Ile Asn Val Glu Lys Ala Arg Ile Asp
370 375 380

Arg Val Leu Lys Asn Thr Glu Val Gln Ala Ile Ile Thr Ala Leu Gly
385 390 395 400

Thr Gly Ile His Asp Glu Phe Asp Ile Ala Arg Leu Arg Tyr His Lys
405 410 415

Ile Val Leu

〈210〉 33
〈211〉 421
〈212〉 PRT
〈213〉 Mycobacterium marinum

〈400〉 33
```
Gly Glu Asn Ser Gly Tyr Asn Val Ser Gly Gly Leu His Gly Val Gly
 1               5                  10                  15

Val Ser Val Val Asn Ala Leu Ser Thr Arg Leu Glu Val Asp Ile Lys
            20                  25                  30

Arg Asp Gly Tyr Glu Trp Ser Gln Phe Tyr Asp Arg Ala Gln Pro Gly
        35                  40                  45

Thr Leu Lys Gln Gly Glu Ala Thr Lys Lys Thr Gly Thr Thr Ile Arg
    50                  55                  60

Phe Trp Ala Asp Ser Asp Ile Phe Glu Thr Thr Glu Tyr Asp Phe Glu
65                  70                  75                  80

Thr Val Ala Arg Arg Leu Gln Glu Met Ala Phe Leu Asn Lys Gly Leu
                85                  90                  95

Thr Ile Asn Leu Thr Asp Glu Arg Val Thr Pro Asp Glu Val Val Asp
            100                 105                 110
```

Asp Val Val Ser Asp Thr Ala Glu Ala Pro Lys Ser Ala Gln Glu Lys
        115   120   125

Ala Ala Glu Ser Thr Ala Pro His Lys Val Lys Ser Arg Thr Phe His
    130   135   140

Tyr Pro Gly Gly Leu Val Asp Phe Val Lys His Ile Asn Arg Thr Lys
145   150   155   160

Ser Pro Ile Gln Gln Ser Ile Val Asp Phe Glu Gly Lys Gly Ser Gly
                165   170   175

His Glu Val Glu Ile Ala Met Gln Trp Asn Gly Gly Tyr Ser Glu Ser
            180   185   190

Val His Thr Phe Ala Asn Thr Ile Asn Thr His Glu Gly Gly Thr His
        195   200   205

Glu Glu Gly Phe Arg Ser Ala Leu Thr Ser Val Val Asn Lys Tyr Ala
    210   215   220

Lys Asp Lys Lys Leu Leu Lys Asp Lys Asp Pro Asn Leu Thr Gly Asp
225   230   235   240

Asp Ile Arg Glu Gly Leu Ala Ala Val Ile Ser Val Arg Val Ala Glu
                245   250   255

Pro Gln Phe Glu Gly Gln Thr Lys Thr Lys Leu Gly Asn Thr Glu Val
            260   265   270

Lys Ser Phe Val Gln Lys Val Cys Asn Glu Gln Leu Thr His Trp Phe
275 280 285

Glu Ala Asn Pro Ser Glu Ala Lys Thr Ile Val Asn Lys Ala Val Ser
290 295 300

Ser Ala Gln Ala Arg Leu Ala Ala Arg Lys Ala Arg Glu Leu Val Arg
305 310 315 320

Arg Lys Ser Ala Thr Asp Leu Gly Gly Leu Pro Gly Lys Leu Ala Asp
325 330 335

Cys Arg Ser Thr Asp Pro Arg Lys Ser Glu Leu Tyr Val Val Glu Gly
340 345 350

Asp Ser Ala Gly Gly Ser Ala Lys Ser Gly Arg Asp Ser Met Phe Gln
355 360 365

Ala Ile Leu Pro Leu Arg Gly Lys Ile Ile Asn Val Glu Lys Ala Arg
370 375 380

Ile Asp Arg Val Leu Lys Asn Thr Glu Val Gln Ala Ile Ile Thr Ala
385 390 395 400

Leu Gly Thr Gly Ile His Asp Glu Phe Asp Leu Ser Lys Leu Arg Tyr
405 410 415

His Lys Ile Val Leu

420

〈210〉 34
〈211〉 419
〈212〉 PRT
〈213〉 Mycobacterium microti

〈400〉 34
Ser Asp Ala Tyr Ala Ile Ser Gly Gly Leu His Gly Val Gly Val Ser
1 5 10 15

Val Val Asn Ala Leu Ser Thr Arg Leu Glu Val Glu Ile Lys Arg Asp
20 25 30

Gly Tyr Glu Trp Ser Gln Val Tyr Glu Lys Ser Glu Pro Leu Gly Leu
35 40 45

Lys Gln Gly Ala Pro Thr Lys Lys Thr Gly Ser Thr Val Arg Phe Trp
50 55 60

Ala Asp Pro Ala Val Phe Glu Thr Thr Glu Tyr Asp Phe Glu Thr Val
65 70 75 80

Ala Arg Arg Leu Gln Glu Met Ala Phe Leu Asn Lys Gly Leu Thr Ile
85 90 95

Asn Leu Thr Asp Glu Arg Val Thr Gln Asp Glu Val Val Asp Glu Val
100 105 110

Val Ser Asp Val Ala Glu Ala Pro Lys Ser Ala Ser Glu Arg Ala Ala
115 120 125

Glu Ser Thr Ala Pro His Lys Val Lys Ser Arg Thr Phe His Tyr Pro
130 135 140

Gly Gly Leu Val Asp Phe Val Lys His Ile Asn Arg Thr Lys Asn Ala
145 150 155 160

Ile His Ser Ser Ile Val Asp Phe Ser Gly Lys Gly Thr Gly His Glu
165 170 175

Val Glu Ile Ala Met Gln Trp Asn Ala Gly Tyr Ser Glu Ser Val His
180 185 190

Thr Phe Ala Asn Thr Ile Asn Thr His Glu Gly Gly Thr His Glu Glu
195 200 205

Gly Phe Arg Ser Ala Leu Thr Ser Val Val Asn Lys Tyr Ala Lys Asp
210 215 220

Arg Lys Leu Leu Lys Asp Lys Asp Pro Asn Leu Thr Gly Asp Asp Ile
225 230 235 240

Arg Glu Gly Leu Ala Ala Val Ile Ser Val Lys Val Ser Glu Pro Gln
245 250 255

Phe Glu Gly Gln Thr Lys Thr Lys Leu Gly Asn Thr Glu Val Lys Ser
260 265 270

```
Phe Val Gln Lys Val Cys Asn Glu Gln Leu Thr His Trp Phe Glu Ala
        275                 280                 285

Asn Pro Thr Asp Ser Lys Val Val Val Asn Lys Ala Val Ser Ser Ala
    290                 295                 300

Gln Ala Arg Ile Ala Ala Arg Lys Ala Arg Glu Leu Val Arg Arg Lys
305                 310                 315                 320

Ser Ala Thr Asp Ile Gly Gly Leu Pro Gly Lys Leu Ala Asp Cys Arg
                325                 330                 335

Ser Thr Asp Pro Arg Lys Ser Glu Leu Tyr Val Val Glu Gly Asp Ser
            340                 345                 350

Ala Gly Gly Ser Ala Lys Ser Gly Arg Asp Ser Met Phe Gln Ala Ile
        355                 360                 365

Leu Pro Leu Arg Gly Lys Ile Ile Asn Val Glu Lys Ala Arg Ile Asp
    370                 375                 380

Arg Val Leu Lys Asn Thr Glu Val Gln Ala Ile Ile Thr Ala Leu Gly
385                 390                 395                 400

Thr Gly Ile His Asp Glu Phe Asp Ile Gly Lys Leu Arg Tyr His Lys
                405                 410                 415

Ile Val Leu
```

〈210〉 35
〈211〉 421
〈212〉 PRT
〈213〉 Mycobacterium asiaticum

〈400〉 35
Gly Glu Asn Ser Gly Tyr Thr Val Ser Gly Gly Leu His Gly Val Gly
1 5 10 15

Val Ser Val Val Asn Ala Leu Ser Thr Arg Leu Glu Val Asp Ile Lys
20 25 30

Arg Asp Gly His Glu Trp Ser Gln Tyr Tyr Glu Arg Ala Val Pro Gly
35 40 45

Thr Leu Lys Gln Gly Glu Ala Thr Lys Lys Thr Gly Thr Thr Ile Arg
50 55 60

Phe Trp Ala Asp Pro Asp Ile Phe Glu Thr Thr Gln Tyr Asp Phe Glu
65 70 75 80

Thr Val Ala Arg Arg Leu Gln Glu Met Ala Phe Leu Asn Lys Gly Leu
85 90 95

Thr Ile Asn Leu Thr Asp Glu Arg Val Asp Gln Asp Glu Val Val Asp
100 105 110

```
Glu Val Val Ser Asp Thr Ala Asp Ala Pro Lys Ser Ala Glu Glu Lys
        115                 120                 125

Ala Ala Glu Ser Lys Ala Pro His Lys Val Lys His Arg Thr Phe His
    130                 135                 140

Tyr Pro Gly Gly Leu Val Asp Phe Val Lys His Ile Asn Arg Thr Lys
145                 150                 155                 160

Ser Pro Ile Gln Gln Ser Val Ile Asp Phe Glu Gly Lys Gly Thr Gly
                165                 170                 175

His Glu Val Glu Ile Ala Met Gln Trp Asn Gly Gly Tyr Ser Glu Ser
            180                 185                 190

Val His Thr Phe Ala Asn Thr Ile Asn Thr His Glu Gly Gly Thr His
        195                 200                 205

Glu Glu Gly Phe Arg Ser Ala Leu Thr Ser Val Val Asn Lys Tyr Ala
    210                 215                 220

Lys Asp Lys Lys Leu Leu Lys Asp Lys Asp Pro Asn Leu Thr Gly Asp
225                 230                 235                 240

Asp Ile Arg Glu Gly Leu Ala Ala Val Ile Ser Val Lys Val Ala Glu
                245                 250                 255

Pro Gln Phe Glu Gly Gln Thr Lys Thr Lys Leu Gly Asn Thr Glu Val
            260                 265                 270
```

```
Lys Ser Phe Val Gln Lys Val Cys Asn Glu Gln Leu Thr His Trp Phe
        275                 280                 285

Glu Ala Asn Pro Ser Glu Ala Lys Thr Val Val Asn Lys Ala Val Ser
    290                 295                 300

Ser Ala Gln Ala Arg Ile Ala Ala Arg Lys Ala Arg Glu Leu Val Arg
305                 310                 315                 320

Arg Lys Ser Ala Thr Asp Leu Gly Gly Leu Pro Gly Lys Leu Ala Asp
                325                 330                 335

Cys Arg Ser Thr Asp Pro Arg Lys Ser Glu Leu Tyr Val Val Glu Gly
            340                 345                 350

Asp Ser Ala Gly Gly Ser Ala Lys Ser Gly Arg Asp Ser Met Phe Gln
        355                 360                 365

Ala Ile Leu Pro Leu Arg Gly Lys Ile Ile Asn Val Glu Lys Ala Arg
    370                 375                 380

Ile Asp Arg Val Leu Lys Asn Thr Glu Val Gln Ala Ile Ile Thr Ala
385                 390                 395                 400

Leu Gly Thr Gly Ile His Asp Glu Phe Asp Ile Ser Lys Leu Arg Tyr
                405                 410                 415

His Lys Ile Val Leu
```

420

〈210〉 36
〈211〉 421
〈212〉 PRT
〈213〉 Mycobacterium scrofulceum

〈400〉 36
Gly Glu Asn Ser Gly Tyr Thr Val Ser Gly Gly Leu His Gly Val Gly
1 5 10 15

Val Ser Val Val Asn Ala Leu Ser Thr Arg Leu Glu Val Thr Ile Lys
20 25 30

Arg Asp Gly His Glu Trp Phe Gln Tyr Tyr Asp Arg Ala Val Pro Gly
35 40 45

Thr Leu Lys Gln Gly Glu Ala Thr Lys Lys Thr Gly Thr Thr Ile Arg
50 55 60

Phe Trp Ala Asp Pro Glu Ile Phe Glu Thr Thr Gln Tyr Asp Phe Glu
65 70 75 80

Thr Val Ala Arg Arg Leu Gln Glu Met Ala Phe Leu Asn Lys Gly Leu
85 90 95

Thr Ile Asn Leu Thr Asp Glu Arg Val Glu Gln Asp Glu Val Val Asp
100 105 110

Glu Val Val Ser Asp Thr Ala Glu Ala Pro Lys Ser Ala Glu Glu Lys
115 120 125

Ala Ala Glu Ser Thr Ala Pro His Lys Val Lys His Arg Thr Phe His
130 135 140

Tyr Pro Gly Gly Leu Val Asp Phe Val Lys His Ile Asn Arg Thr Lys
145 150 155 160

Ser Pro Ile Gln Gln Ser Val Ile Asp Phe Asp Gly Lys Gly Thr Gly
165 170 175

His Glu Val Glu Ile Ala Met Gln Trp Asn Gly Gly Tyr Ser Glu Ser
180 185 190

Val His Thr Phe Ala Asn Thr Ile Asn Thr His Glu Gly Gly Thr His
195 200 205

Glu Glu Gly Phe Arg Ser Ala Leu Thr Ser Val Val Asn Lys Tyr Ala
210 215 220

Lys Asp Lys Lys Leu Leu Lys Asp Lys Asp Pro Asn Leu Thr Gly Asp
225 230 235 240

Asp Ile Arg Glu Gly Leu Ala Ala Val Ile Ser Val Lys Val Ala Glu
245 250 255

Pro Gln Phe Glu Gly Gln Thr Lys Thr Lys Leu Gly Asn Thr Glu Val
260 265 270

```
Lys Ser Phe Val Gln Lys Val Cys Asn Glu Gln Leu Thr His Trp Phe
        275                 280                 285

Glu Ala Asn Pro Ser Glu Ala Lys Thr Val Val Asn Lys Ala Val Ser
    290                 295                 300

Ser Ala Gln Ala Arg Ile Ala Ala Arg Lys Ala Arg Glu Leu Val Arg
305                 310                 315                 320

Arg Lys Ser Ala Thr Asp Leu Gly Gly Leu Pro Gly Lys Leu Ala Asp
                325                 330                 335

Cys Arg Ser Thr Asp Pro Arg Lys Ser Glu Leu Tyr Val Val Glu Gly
            340                 345                 350

Asp Ser Ala Gly Gly Ser Ala Lys Ser Gly Arg Asp Ser Met Phe Gln
        355                 360                 365

Ala Ile Leu Pro Leu Arg Gly Lys Ile Ile Asn Val Glu Lys Ala Arg
    370                 375                 380

Ile Asp Arg Val Leu Lys Asn Thr Glu Val Gln Ala Ile Ile Thr Ala
385                 390                 395                 400

Leu Gly Thr Gly Ile His Asp Glu Phe Asp Ile Thr Lys Leu Arg Tyr
                405                 410                 415

His Lys Ile Val Leu
```

```
            420

<210> 37
<211> 420
<212> PRT
<213> Mycobacterium branderi

<400> 37
Gly Asp Asp Ser Ala Tyr Ala Val Ser Gly Gly Leu His Gly Val Gly
 1               5                  10                  15

Val Ser Val Val Asn Ala Leu Ser Thr Arg Leu Glu Val Glu Ile Ala
            20                  25                  30

Thr Asp Gly Tyr Glu Trp Phe Gln His Tyr Asp Arg Ser Val Pro Gly
        35                  40                  45

Thr Leu Lys Gln Gly Glu Lys Thr Lys Lys Thr Gly Thr Thr Val Arg
    50                  55                  60

Phe Trp Ala Asp Pro Asp Ile Phe Glu Thr Thr Asp Tyr Asp Phe Glu
65                  70                  75                  80

Thr Val Ala Arg Arg Leu Gln Glu Met Ala Phe Leu Asn Lys Gly Leu
                85                  90                  95

Thr Ile Asn Leu Thr Asp Glu Arg Val Arg Asn Glu Glu Val Val Asp
            100                 105                 110
```

Glu Val Val Ser Asp Thr Ala Asp Ala Pro Lys Ser Ala Arg Glu Glu
115 120 125

Ala Glu Glu Arg Thr Thr Gln Lys Val Lys His Arg Thr Phe His Tyr
130 135 140

Pro Gly Gly Leu Val Asp Phe Val Lys His Ile Asn Arg Thr Lys Asn
145 150 155 160

Pro Ile His Ser Ser Ile Val Asp Phe Ser Gly Lys Gly Pro Gly His
165 170 175

Glu Val Glu Ile Ala Met Gln Trp Asn Ala Gly Tyr Ser Glu Ser Val
180 185 190

His Thr Phe Ala Asn Thr Ile Asn Thr His Glu Gly Gly Thr His Glu
195 200 205

Glu Gly Phe Arg Ala Ala Leu Thr Ser Val Val Asn Lys Tyr Ala Lys
210 215 220

Asp Arg Lys Leu Leu Lys Asp Lys Asp Pro Asn Leu Thr Gly Asp Asp
225 230 235 240

Ile Arg Glu Gly Leu Ala Ala Val Ile Ser Val Lys Val Ser Glu Pro
245 250 255

Gln Phe Glu Gly Gln Thr Lys Thr Lys Leu Gly Asn Thr Glu Val Lys
260 265 270

```
Ser Phe Val Gln Lys Val Cys Asn Glu Gln Leu Thr His Trp Phe Glu
        275                 280                 285

Ala Asn Pro Ser Asp Ala Lys Thr Val Val Asn Lys Ala Val Ser Ser
    290                 295                 300

Ala Gln Ala Arg Ile Ala Ala Arg Lys Ala Arg Glu Leu Val Arg Arg
305                 310                 315                 320

Lys Ser Ala Thr Asp Leu Gly Gly Leu Pro Gly Lys Leu Ala Asp Cys
                325                 330                 335

Arg Ser Thr Asp Pro Arg Lys Ser Glu Leu Tyr Val Val Glu Gly Asp
            340                 345                 350

Ser Ala Gly Gly Ser Ala Lys Ser Gly Arg Asp Ser Met Phe Gln Ala
        355                 360                 365

Ile Leu Pro Leu Arg Gly Lys Ile Ile Asn Val Glu Lys Ala Arg Ile
    370                 375                 380

Asp Arg Val Leu Lys Asn Thr Glu Val Gln Ala Ile Ile Thr Ala Leu
385                 390                 395                 400

Gly Thr Gly Ile His Asp Glu Phe Asp Ile Ser Lys Leu Arg Tyr His
                405                 410                 415

Lys Ile Val Leu
```

420

⟨210⟩ 38
⟨211⟩ 421
⟨212⟩ PRT
⟨213⟩ Mycobacterium paratuberculosis

⟨400⟩ 38

```
Gly Glu Asn Ser Gly Tyr Asn Val Ser Gly Gly Leu His Gly Val Gly
 1               5                  10                  15

Val Ser Val Val Asn Ala Leu Ser Thr Arg Leu Glu Val Asn Ile Ala
            20                  25                  30

Arg Asp Gly Tyr Glu Trp Ser Gln Tyr Tyr Asp His Ala Val Pro Gly
        35                  40                  45

Thr Leu Lys Gln Gly Glu Ala Thr Lys Arg Thr Gly Thr Thr Ile Arg
    50                  55                  60

Phe Trp Ala Asp Pro Asp Ile Phe Glu Thr Thr Glu Tyr Asp Phe Glu
65                  70                  75                  80

Thr Val Ala Arg Arg Leu Gln Glu Met Ala Phe Leu Asn Lys Gly Leu
                85                  90                  95

Thr Ile Asn Leu Thr Asp Glu Arg Val Thr Asn Glu Glu Val Val Asp
            100                 105                 110
```

```
Glu Val Val Ser Asp Thr Ala Asp Ala Pro Lys Ser Ala Gln Glu Lys
        115                 120                 125

Ala Ala Glu Ser Ala Ala Pro His Lys Val Lys His Arg Thr Phe His
    130                 135                 140

Tyr Pro Gly Gly Leu Val Asp Phe Val Lys His Ile Asn Arg Thr Lys
145                 150                 155                 160

Asn Pro Ile His Gln Ser Ile Ile Asp Phe Gly Gly Lys Gly Pro Gly
                165                 170                 175

His Glu Val Glu Ile Ala Met Gln Trp Asn Gly Gly Tyr Ser Glu Ser
            180                 185                 190

Val His Thr Phe Ala Asn Thr Ile Asn Thr His Glu Gly Gly Thr His
        195                 200                 205

Glu Glu Gly Phe Arg Ser Ala Leu Thr Ser Val Val Asn Lys Tyr Ala
    210                 215                 220

Lys Asp Lys Lys Leu Leu Lys Asp Lys Asp Pro Asn Leu Thr Gly Asp
225                 230                 235                 240

Asp Ile Arg Glu Gly Leu Ala Ala Val Ile Ser Val Lys Val Ser Glu
                245                 250                 255

Pro Gln Phe Glu Gly Gln Thr Lys Thr Lys Leu Gly Asn Thr Glu Val
            260                 265                 270
```

Lys Ser Phe Val Gln Lys Val Cys Asn Glu Gln Leu Thr His Trp Phe
275 280 285

Glu Ala Asn Pro Ala Asp Ala Lys Val Ile Val Asn Lys Ala Val Ser
290 295 300

Ser Ala Gln Ala Arg Ile Ala Ala Arg Lys Ala Arg Glu Leu Val Arg
305 310 315 320

Arg Lys Ser Ala Thr Asp Leu Gly Gly Leu Pro Gly Lys Leu Ala Asp
325 330 335

Cys Arg Ser Thr Asp Pro Arg Lys Ser Glu Leu Tyr Val Val Glu Gly
340 345 350

Asp Ser Ala Gly Gly Ser Ala Lys Ser Gly Arg Asp Ser Met Phe Gln
355 360 365

Ala Ile Leu Pro Leu Arg Gly Lys Ile Ile Asn Val Glu Lys Ala Arg
370 375 380

Ile Asp Arg Val Leu Lys Asn Thr Glu Val Gln Ala Ile Ile Thr Ala
385 390 395 400

Leu Gly Thr Gly Ile His Asp Glu Phe Asp Ile Thr Lys Leu Arg Tyr
405 410 415

His Lys Ile Val Leu

420

〈210〉 39
〈211〉 38
〈212〉 DNA
〈213〉 Artificial Sequence

〈400〉 39
tgtaaaacga cggccagtca ygcnggnggn aarttyga

〈210〉 40
〈211〉 36
〈212〉 DNA
〈213〉 Artificial Sequence

〈400〉 40
ctgcgttcgt atatgagcnc crtcnacrtc ngcrtc

【図面の簡単な説明】
【図１】マイコバクテリウム・カンサシイとマイコバクテリウム・ガストリのｇｙｒＢ遺伝子の塩基配列を示す図。
【図２】配列番号１、３、５により表されるプライマーを用いたＰＣＲの結果を示す図。
【図３】分子系統解析により作製された遅発育性マイコバクテリアの系統樹を示す図。

【図１】

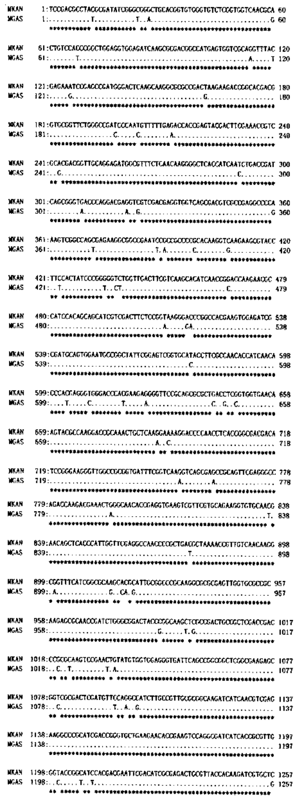

図1：Mycobacterium kansasii(上段)と Mycobacterium gastri(下段)の gyrB 配列の比較。
同一の塩基配列の部分は＊印で示し、Mycobacterium kansasii の配列のみを示した。

【図２】

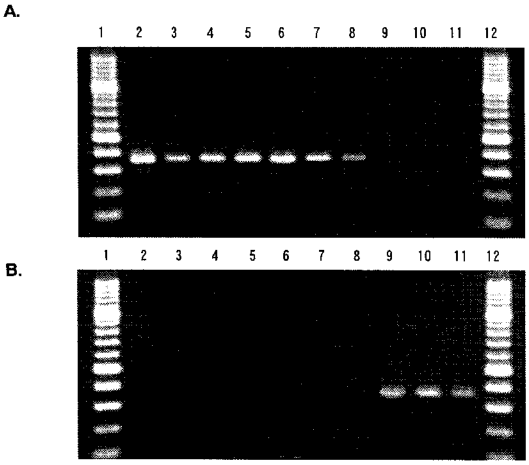

図2：配列番号1、3、5を用いた同定結果を示す図
パネルAが*Mycobacterium kansasii* 特異的プライマー（配列番号1、3）、パネルBが、*Mycobacterium gastri* 特異的プライマー（配列番号1、5）にて増幅した結果を示している。それぞれ同じレーン番号は同一の株からの増幅結果を示している。レーン1、12は分子量マーカーである。レーン2：KPM 1001T株, 3: KPM 1004株, 4: KPM 1007株, 5: KPM KY256株, 6: KPM KY761株, 7: KPM KY798株, 8: KPM 1988-1株, 9: KPM 3504T株, 10: KPM 3502株, 11: KPM 3503株。

【図３】

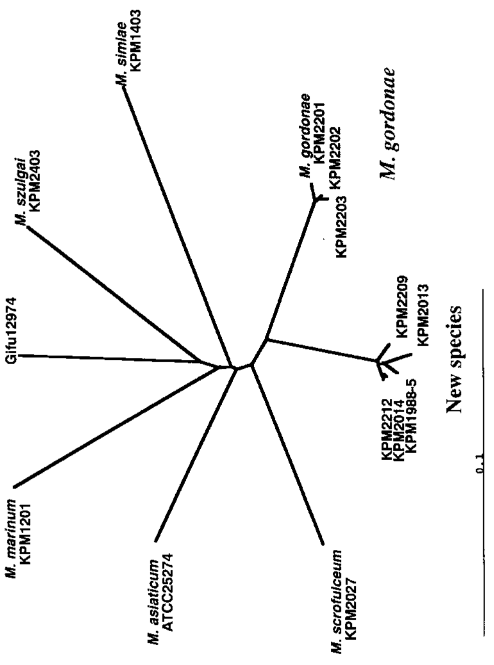

図3：gyrB配列の解析から新しい種の遅育性マイコバクテリアの存在が示された例
分子系統解析を行い、得られたgyrB配列と既に調べられているgyrB配列を比較することにより、KPM 2212, 2014, 1988-5, 2209, 2013の一群の株が新規の種であることが示された。

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