Distribution of 19 major virulence genes in *Legionella pneumophila* serogroup 1 isolates from patients and water in Queensland, Australia

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The distribution of 19 major virulence genes and the presence of plasmids were surveyed in 141 *Legionella pneumophila* serogroup (SG) 1 isolates from patients and water in Queensland, Australia. The results showed that 16 of the virulence genes examined were present in all isolates, suggesting that they are life-essential genes for isolates in the environment and host cells. The 65 kb pathogenicity island identified originally in strain Philadelphia-1T was detected more frequently in isolates from water (44.2%) than in those from patients (2.7%), indicating that the 65 kb DNA fragment may aid the survival of *L. pneumophila* in the sampled environment. However, the low frequency of the 65 kb fragment in isolates from patients suggests that the pathogenicity island may not be necessary for *L. pneumophila* to cause disease. Plasmids were not detected in the *L. pneumophila* SG1 isolates from patients or water studied. There was an association of both *lvh* and *rtxA* with the virulent and predominant genotype detected by amplified fragment length polymorphism, termed AF1, whereas the avirulent common isolate from water termed AF16 did not have *lvh* or *rtxA* genes, with the exception of one isolate with *rtxA*. It was found that a PCR detection test strategy with *lvh* and *rtxA* as pathogenesis markers would be useful for determining the infection potential of an isolate.

**INTRODUCTION**

Legionellae, the aetiologic agents of legionellosis, are ubiquitous worldwide in rivers and lakes (Fliermans et al., 1981), as well as in man-made water systems such as cooling towers and spas (Fields et al., 2002). The vast majority of cases of legionellosis are caused by *Legionella pneumophila*, mostly serogroup (SG) 1 strains (Yu et al., 2002). To understand the pathogenicity of *L. pneumophila*, a number of virulence genes of *L. pneumophila* have been well-characterized and extensively reviewed (Cianciotto, 2001; Dowling et al., 1992). The virulence factors characterized include genes required for the whole infection process, such as bacterial cell attachment to host cells, survival and intracellular replication and cell-to-cell spread. The products of genes involved in the initial attachment to host cells and early stages of intracellular infection include type IV pili, the 60 kDa heat-shock protein Hsp60, the poreformation protein RtxA, the macrophage infectivity potentiator Mip and the macrophage-specific infectivity protein MilA (Cianciotto & Fields, 1992; Cirillo et al., 2001; Garduño et al., 1998; Harb & Abu Kwaik, 2000). The genes required for bacterial survival and intracellular replication are a group of genes called icm (intracellular multiplication) (Segal et al., 1998) or dot (defect in organelle trafficking) (Vogel et al., 1998). They form a type IV secretion system to deliver effectors to host cells to control organelle trafficking (Segal & Shuman, 1998). A number of effectors have been characterized, including RalF (Nagai et al., 2002), LIdA (Conover et al., 2003) and LepA/B (Chen et al., 2004) and other recently identified effectors (Shohdy et al., 2005).

In addition, the type II protein secretion system is required to deliver effectors to host cells to control organelle trafficking (Segal & Shuman, 1998). A number of effectors have been characterized, including RalF (Nagai et al., 2002), LIdA (Conover et al., 2003) and LepA/B (Chen et al., 2004) and other recently identified effectors (Shohdy et al., 2005).

Abbreviations: AFLP, amplified fragment length polymorphism; SG, serogroup.

Sequences of primers used are available as supplementary material in JMM Online.
Iron acquisition genes *feoB*, *iraA* and *ccmC* can be determinants of intracellular growth and virulence (Robey & Cianciotto, 2002; Viswanathan et al., 2000, 2002). Moreover, some regulators such as RpoS, a stationary-phase sigma factor, and LetA, a GacA homologue response regulator, are required for efficient infection and intracellular multiplication of *L. pneumophila* (Bachman & Swanson, 2004; Gal-Mor & Segal, 2003). Other virulence factors include a 65 kb DNA fragment encoding some known virulence factors as a pathogenicity island (Brassinga et al., 2003) and various plasmids (Brown et al., 1982).

The genomes sequenced show that *L. pneumophila* has high genome plasticity. The difference between strain-specific genes in isolates within the same serogroup varied from 10 to 14% (Cazalet et al., 2004). In a previous study, a predominant genotype termed AF1, detected by amplified fragment length polymorphism (AFLP), was identified in isolates from both patients (40.5%) and water (49.0%) (Huang et al., 2004). All AF1-type isolates have been found to have the virulence genes *lvh*, a new type IV secretion gene locus where the products of *lvh* genes interact with components of the *icm/dot* system (Segal et al., 1999), and *rtxA*, encoding the *dot/icm*-regulated, pore-forming toxin for bacterial entry into cells (Zink et al., 2002). The second most-frequent type (36.5%), termed AF16, identified in isolates from water, has not been detected in isolates from patients. *lvh* and *rtxA* genes are not present in AF16 isolates, with the exception of one isolate with *rtxA*. The interaction of the products of both *lvh* and *rtxA* with the major *dot/icm* virulence factors and the strong association of both *lvh* and *rtxA* with the virulent AF1 strain suggest that *lvh* and *rtxA* could be used as indicators (markers) of infection potential for *L. pneumophila* SG1 isolates (Huang et al., 2004).

Although the relationship between *icm/dot* type IV protein secretion genes and other virulence factors associated with the pathogenicity of *L. pneumophila* has been widely studied (Bandopadhayay et al., 2004; Segal et al., 1999), the distribution of virulence genes in clinical or environmental isolate collections has not been examined. Therefore, the aims of this study were to determine whether there was a different distribution pattern between the clinical and environmental isolates of the well-studied virulence genes that play important roles in various steps of the whole infection process, and to examine whether these genes, together with *lvh* and *rtxA*, could be used as indicators of infection potential for *L. pneumophila* SG1 isolates.

**METHODS**

**Collection of *L. pneumophila* SG1 isolates.** The *L. pneumophila* SG1 isolates used were the same as those typed using AFLP in our previous study (Huang et al., 2004). Legionellosis is a notifiable disease in Australia. A total of 141 *L. pneumophila* SG1 isolates were used in this study. They included 37 isolates from patients with clinical symptoms of Legionnaires’ disease who had been referred to our laboratory during 1990–2003, and 96 isolates from water that were detected between July and December 2003 and eight isolates that were referred to our laboratory between 1994 and 2003. Water samples were taken from free-flowing water in cooling water towers, according to the current sampling method for Australian/New Zealand Standards (Standards Australia, 2000). All isolates were epidemiologically unrelated, except for one water isolate from 1994 that was epidemiologically related to a case. These isolates from patients and water were from Brisbane and neighbouring regions in Queensland.

**PCR primer design and reaction conditions.** The virulence genes were chosen on the basis of two factors: (1) genes involved in different infection steps and (2) genes cited in published *Legionella* genome papers (Cazalet et al., 2004; Chien et al., 2004). In total, 19 gene targets were examined, including *lvh*, *rtxA*, 65 kb fragment, loci 1 and 2 of the type IV secretion system, loci 1 and 2 of the type II secretion system and *pilB*, *pilD*, *ralF*, *lidA*, *lepA*, *rpoS*, *letA*, *feoB*, *iraA*, *ccmC*, *hsps60* and *milA* (see Table 1). The *lvh* and *rtxA* regions were detected using the same primers as in previous studies (Samrakandi et al., 2002). The 65 kb pathogenicity island encodes a total of 64 genes; two genes, *magA* and *traD*, were chosen for detection of the 65 kb fragment. The primer pairs *MagF/MagR* (referred to as F MagA5134/R MagA5603 in the original paper) and F9/R9 were used to amplify *magA* and *traD*, respectively, as described by Brassinga et al. (2003). The other primer pairs used were designed using the three *L. pneumophila* SG1 genome sequences published (Cazalet et al., 2004; Chien et al., 2004). The type II protein secretion system has two loci; primer pairs designed for *ispD* and *ispE* were used for the first locus (ispDE) and primer pairs for *ispG* and *ispI* for the second locus (*ispGHIJK*). The two loci of the *icm/dot* type IV secretion system in the genome were tested. The genes in locus 1 include *icmTSQQOLMKEGCDJBF*; primers were designed to detect *icmB*, *icmK* and *icmT*. The genes in locus 2 include *dotABC-icmVWX*; primers were designed to detect *dotA*, *dotC* and *icmX*. Primers for detection of type IV pili of *L. pneumophila* were designed for *pilD* and *pilB* (Sequences of the primers used are available in Supplementary Table S1 in JMM Online.) PCR reaction conditions were the same as those described by Samrakandi et al. (2002). The amplified PCR products were sequenced to verify their authenticity.

**Plasmid isolation.** Plasmids have been identified in *L. pneumophila* isolates (Bezanson et al., 1992). They encode specific virulence factors that may contribute to the pathogenicity of this organism (Brown et al., 1982). The extraction method used was described by Brown et al. (1982) and the plasmid-positive strain *Legionella bozemanae* 336/H7 was included as a control (Institute of Medical and Veterinary Science, Australia).

**RESULTS AND DISCUSSION**

Virulence gene PCR products were separated in agarose gels (Fig. 1). The results in Table 1 show that the following genes were detected in all *L. pneumophila* SG1 Queensland isolates examined: *icm/dot* type IV and type II protein secretion systems, type IV pili genes (*pilD* and *pilB*), virulence effector genes (*ralF*, *lidA* and *lepA*), virulence regulator genes (*rpoS* and *letA*), iron acquisition genes (*feoB*, *iraA* and *ccmC*) and surface protein genes (*hsps60* and *milA*). The data suggest that these genes, although they have been identified as essential virulence genes, are also crucial for survival, because mutations of these genes result in significant reduction of growth or no growth in vitro or in host cells (Conover et al., 2003; Gal-Mor & Segal, 2003; Rossier et al., 2004; Viswanathan et al., 2000). They do not appear to be useful as indicators of the infection potential
Table 1. Detection of virulence genes in *L. pneumophila* SG1 isolates from patients and water

Data for *lvh* and *rtxA* are taken from Huang et al. (2004), with the permission of the American Society for Microbiology. Primer sequences are available in Supplementary Table S1 in JMM Online.

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<th><em>rtxA</em></th>
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<th>Type IV Locus 2</th>
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![Fig. 1. PCR products of virulence genes in strains ATCC 33152T (Philadelphia-1) and 03M1684 (an isolate from water). Lane M, GeneRuler DNA ladder mix (Fermentas). (a) PCR of strain ATCC 33152T. Lanes 1–12 show amplified bands using primers for the following genes: 1, icmX; 2, 65 kb DNA fragment of MagF/MagR; 3, 65 kb DNA fragment of F9/R9; 4, dotA and icmT; 5, lidA and hsp60; 6, lepA1 and leTA; 7, rpoS, ralF and lepA2; 8, icmK, icmB and dotC; 9, lspD, pilB and lspJ; 10, lspE, pilD and lspG; 11, feoB, iraA and ccmC; and 12, milA. Amplified PCR bands of the virulence genes are stated from high molecular mass to low molecular mass in a multiplex-PCR lane. In addition, two primer sets (lepA1 and lepA2) were used to detect the lepA gene because of its large size. (b) PCR of strain 03M1684 using the same primer pairs as in (a). No products were detected in lanes 2 and 3 (65 kb DNA fragment of MagF/MagR and F9/R9), suggesting that the 65 kb DNA fragment was not present in this isolate. of an isolate, as they were present in all isolates of *L. pneumophila* studied.

However, the survey of the 65 kb DNA fragment in these isolates demonstrated a difference in detection rates (Table 1). Only one AF1-type isolate from all the isolates from patients tested was found to have the 65 kb DNA fragment (2–7%, 1/37). In contrast, the 65 kb DNA fragment was frequently present in the isolates from water, with a detection rate of 44–2% (46/104). In particular, the 65 kb fragment was more frequently present in the predominant AF1-type from water, with a detection rate of 80–4% (41/51). Interestingly, the 65 kb DNA fragment was not present in isolates of the second most-frequent AF16-type from water (0/38). Although Southern blotting would be the method of choice to verify the 65 kb PCR-negative isolates, these detection results were obtained by using two pairs of primers to detect *magA* and *traD* genes, respectively, within the 65 kb DNA fragment to minimize possible mutation in one of the primer annealing regions. Therefore, the probability of false-negative detection of the 65 kb DNA fragment was significantly reduced. The results suggest that the 65 kb DNA fragment-bearing predominant AF1 strain is better adapted for survival in the sampled environment. The low frequency of the 65 kb fragment in the isolates from patients suggests that the pathogenicity island may not be necessary for *L. pneumophila* to cause disease (see Table 1). This contradicts the presumption that the pathogenicity island in the 65 kb DNA fragment would enhance the ability to cause disease in humans, as suggested by Brassinga et al. (2003).

Plasmids were not detected in the *L. pneumophila* SG1 isolates from water or patients analysed in this study (Table 1). Plasmid extraction was carried out using the method of
Brown et al. (1982) and was retested using another plasmid miniprep method (Sambrook et al., 1989). A positive plasmid band was produced consistently on gels with the positive-control strain L. bozemanae 336/H7 using the two extraction methods. The isolates of L. pneumophila SG1 used in this study were primary isolates and were stored at \(-70\) °C. It is notable that plasmids are frequently present in isolates of L. pneumophila from water from other countries, with detection rates ranging from 20 to 60% (Bezanson et al., 1992; Brown et al., 1982; Maher et al., 1983). This suggests that L. pneumophila isolates from Australia might be different from those from other countries in this regard.

In the AF1-type isolates, lvh and rtxA, respectively, were positive in 14 and 15 out of 15 isolates from patients and in 51 and 51 out of 51 isolates from water (Table 1). In the second most-common AF16-type isolates from water, a genotype that was not detected in patients, neither lvh nor rtxA was present in the 38 isolates, except for one isolate with rtxA. Therefore, lvh and rtxA may not be required for survival in water. Statistical analyses (Fisher’s exact test) indicated that, in L. pneumophila SG1 isolates from water, there was a significant association of lvh and rtxA with AF1-type isolates \((n=51, P<0.0001)\) and a significant association of the absence of lvh and rtxA with AF16-type isolates \((n=38, P<0.0001)\). Because either lvh or rtxA or both were present in all L. pneumophila SG1 isolates from patients tested, no significant association of lvh or rtxA with AF1-type isolates was found \((n=15, P>0.07)\), suggesting that lvh and rtxA could be used as indicators to assess the infection potential of an isolate. lvh genes encode a new type IV protein secretion system and do not resemble the homologous icm/dot type IV protein secretion genes that are required for intracellular growth of L. pneumophila in human macrophages and protozoan hosts (Segal et al., 1999). However, they enhance intracellular growth and can replace the functions of some icm/dot genes in plasmid RSF1010 conjugation, suggesting that the components of the lvh type IV protein secretion system can interact with components of the icm/dot system (Segal et al., 1999). In addition, lvh has a substantial effect on the efficiency of infection of host cells in a temperature-dependent manner. lvh is crucial for intracellular survival and replication when the bacteria are grown at 30 °C and less so when they are grown at 37 °C (Ridenour et al., 2003). The rtxA gene product has eight RTX amino-acid repeats that have been identified in a number of RTX toxins of pathogens, such as the cytotoxin of Bordetella pertussis, the leukotoxin of Actinobacillus actinomycetemcomitans and the haemolysin of Escherichia coli (Cirillo et al., 2000, 2001). Interestingly, the function of the pore-forming toxin gene rtxA is regulated by the dot/icm complex (Zink et al., 2002). A rtxA mutant of L. pneumophila has been shown to have a reduced ability to attach to monocytes and epithelial cells, and reduced cytotoxicity and intracellular replication (Cirillo et al., 2000, 2001). An isolate with the rtxA gene would have enhanced abilities for attachment, cytotoxicity and intracellular growth. Consequently, isolates bearing either lvh or rtxA, or both, appear to be more virulent. Therefore, they could be considered as indicators of the infection potential of an isolate.

In summary, there was an association of both lvh and rtxA with the virulent and predominant AFLP genotype termed AF1. Functionally, there is an interaction of the products of lvh and rtxA with the products of the major virulence icm/dot system (Ridenour et al., 2003; Zink et al., 2002), conferring greater virulence on isolates bearing either lvh or rtxA, or both. We found that a test strategy for lvh and rtxA as pathogenesis markers using an easy PCR would be useful for determining the infection potential of an isolate.

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**REFERENCES**


Distribution of virulence genes in *L. pneumophila*


