Development of a diagnostic PCR assay that targets a heat-shock protein gene (groES) for detection of Pseudomonas spp. in cystic fibrosis patients

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Laboratory detection of Pseudomonas spp., in particular Pseudomonas aeruginosa, remains an important assay in the management of patients with cystic fibrosis (CF). As the groES and groEL genes of P. aeruginosa have now been cloned and their nucleotide sequences determined, the aim of this study was to develop a novel PCR assay for the detection of Pseudomonas spp. from patients with CF by employing conserved primer regions of the groE heat-shock protein domain gene. A PCR assay was designed that targeted a 536 bp region of the groE gene to detect Pseudomonas spp. PCR amplification of genomic DNA from extracted organisms generated an amplicon of the expected size (approx. 536 bp) for all P. aeruginosa (n = 60), Pseudomonas putida, Pseudomonas fluorescens and Pseudomonas stutzeri isolates examined, but did not produce a positive amplicon for several other genera and species that are commonly isolated from the sputum of CF patients. RFLP analysis of the amplicons of all P. aeruginosa isolates demonstrated a single RFLP type that consisted of three bands at approximately 80, 190 and 250 bp; direct sequencing of the amplicons demonstrated the presence of a single sequence type, indicating the highly conserved nature of this region. In addition, the assay successfully produced a positive signal from primary non-selective plates of three known P. aeruginosa culture-positive CF patients, but was unable to generate a signal in a further six CF patients who had no history of infection with P. aeruginosa or other Pseudomonas spp. This assay is recommended to detect the presence of Pseudomonas spp., including P. aeruginosa, from primary culture plates that originate from laboratory analysis of CF patients’ sputum, particularly at review, in those patients with no previous history of Pseudomonas infection or those who appear to be transiently colonized by this organism. Employment of such molecular methodologies, in conjunction with routine clinical sputum cultures, may provide improved information on the microbial status of CF patients, which will aid clinicians in both optimum patient management in terms of antibiotic regimes and CF centre infection-control practices.

INTRODUCTION

Cystic fibrosis (CF) is the most common genetic disease of Caucasians, with an incidence of 1 in 2500 live births and a carriage rate of 1 in 20 individuals. CF patients continue to suffer from recurrent and chronic respiratory tract infections and most of the morbidity and mortality of this disease is due to such infections, which occur throughout their life (Høiby, 1991). These infections are usually dominated by Gram-negative organisms, especially the pseudomonnads (particularly Pseudomonas aeruginosa). However, various other
species of the genus *Pseudomonas* have been identified as clinically significant in such patients (Klinger & Thomassen, 1985; Garske et al., 2002).

The heat-shock response is an important homeostatic mechanism that enables cells to survive a variety of environmental stresses. A set of heat-shock proteins, also known as chaperonins, are induced when cells are exposed to higher temperatures. This phenomenon has been observed in all organisms, from bacteria and fungi to plants and animals. The chaperonins form a well-characterized subgroup of molecular chaperones; this subgroup includes the GroEL subcomplex, which comprises two proteins: chaperonin 60 and chaperonin 10. The GroEL protein is Escherichia coli chaperonin 60 and GroES is the *E. coli* chaperonin 10 protein; these are the most extensively studied chaperonins. GroEL is critical for the correct folding of a number of cellular proteins under both normal and stress conditions. Indeed, in *E. coli*, deletion of the groE operon is lethal and the GroEL and GroES proteins are required for survival. The chaperonin 60 family have a double-ring structure that comprises 14 subunits; a central cavity is formed, in which the unfolded substrate protein binds by hydrophobic interactions. The GroES subunit protein also binds to the apical domain of GroEL. The process of protein folding requires ATP, which binds to GroEL; when ATP binding occurs, GroES forms a lid on top of the GroEL barrel, causing enlargement of the central cavity and protein folding.

Heat-shock proteins appear to be constituents of the cellular machinery of protein folding, degradation and repair (Felltham & Gierasch, 2000). These bacterial molecular chaperones play an important role in normal growth by mediating the folding and/or assembly of different polypeptides, as well as the transport of some secretory proteins across membranes. For successful reactivation and assembly of some proteins, GroEL requires the presence of another heat-shock protein, GroES. The general properties of the heat-shock response of *P. aeruginosa* have been characterized; synthesis of at least 17 proteins, including DnaK and GroEL, is transiently induced by an increase in cell temperature.

As the GroES and GroEL genes of *P. aeruginosa* have now been cloned and their nucleotide sequences determined (Fujita et al., 1998), the aim of this study was to develop a novel PCR assay for detection of *Pseudomonas* spp. from the sputum of patients with CF by employing conserved primer regions of the groE heat-shock protein domain gene.

**METHODS**

**Patient population.** *P. aeruginosa* isolates (*n* = 60) were obtained from 35 adult patients with a confirmed and well-documented history of CF who attended the Northern Ireland Regional Adult CF Centre, Belfast City Hospital, from January 1996 to June 1998. The age range of the patients was 17–30 years, with one patient aged 70 years. The male:female ratio was 24:11. All *Pseudomonas* isolates were obtained from fresh sputum specimens cultured on Columbia Blood Agar (Oxoid) that contained 5 % (v/v) defibrinated horse blood. The identity of all isolates was confirmed by using an API 20NE biochemical testing kit (bioMérieux).

**Design of oligonucleotide primers.** DNA sequence data of the heat-shock protein genes (groES and groEL) were obtained from GenBank; conserved and variable regions were subsequently identified by aligning published sequences of *P. aeruginosa* (accession numbers U17072, U17078, U64101, U64104, U64103, S77424 and M63957), *Pseudomonas putida* (X76833), *Pseudomonas stutzeri* (Y18328), *Burkholderia viannii* (AF104901), *Burkholderia cepacia* (AE104907), *Stenotrophomonas maltophilia* (U68787), *Salmonella typhimurium* (U10039), *Salmonella typhimurium* (AB033231), *Erwinia carotovora* (AB008152) and *E. coli* (M11294, X07850) by the CLUSTAL alignment method in the DNAstar sequence alignment software package. A novel primer pair was designed, forward [groESf: 5’TATGACCTGTGGCTCTTCAT-3’] and reverse [groESr: 5’TCTTTCAGCTCGAT-3’] (15 mer) [reverse [groESr: 5’TCTTTCAGCTCGAT-3’] (15 mer)], which targeted conserved regions of the heat-shock protein gene for *Pseudomonas* spp. The binding sites of the groES and groESr primers in *P. aeruginosa* (GenBank no. M63957) relate to positions 42–63 and 577–563, respectively, yielding a fragment of 536 bp.

**DNA extraction.** All DNA isolation procedures were carried out in a Class II Biological Safety Cabinet (Astec Microflow) in a room physically separated from that used to set up nucleic acid amplification reaction mixes and also from the ‘post-PCR’ room, in accordance with the Good Molecular Diagnostic Procedures guidelines of Millar et al. (2002), in order to minimize contamination and hence the possibility of false-positive results. Bacterial genomic DNA was extracted from *P. aeruginosa* reference strain ATCC 27853, as well as from 60 well-characterized wild-type *P. aeruginosa* isolates from the sputum of adult CF patients, by employment of the Roche High Pure PCR Template Preparation kit in accordance with the manufacturer’s instructions. Genomic DNA was also extracted from well-characterized isolates of *P. putida*, *P. fluorescens* and *P. stutzeri*, as well as from the following 21 non-*Pseudomonas* organisms: *Asaia* sp., *Alcaligenes xylosoxidans* NIPH 96/01, *Bacillus licheniformis*, *Burkholderia cepacia* genomovar *Illa* NIPH CF97/08, *Burkholderia cepacia* genomovar *Illa* NIPH CF96/27, *Burkholderia cepacia* genomovar *Illa* NIPH CF96/02, *Burkholderia multivorans*, *Campylobacter jejuni*, *Chromobacterium violaceum* NIPH 96/5, *Curtobacterium sp.*, *Haemophilus influenzae*, *Inquilinus limosus*, *Lactobacillus gasseri*, *Mycobacterium malmoense*, *Pandorea apiana* NIPH 02/02, *Raltionia paucula*, *Serratia marcescens* NIPH CF97/27, *Sphingomonas paucimobilis* NIPH 97/03 and *Thermoactinomyces*sp. Extracted DNA was stored at ~80 °C prior to PCR amplification. For each batch of extractions, a negative extraction control was performed that contained all reagents minus any organism, as well as an extraction positive control with *P. aeruginosa*.

**PCR amplification.** Amplification reactions were set up in accordance with Good Molecular Diagnostic Procedures, as detailed in the guideline lines of Millar et al. (2002). All reaction mixes were set up in a PCR hood in a room separate from that used to extract DNA and the amplification and ‘post-PCR’ room, in order to minimize contamination. Initially, PCR amplification conditions were optimized by varying the following conditions separately: magnesium chloride concentration, annealing temperature, primer concentration and DNA template concentration. Following optimization, reaction mixes (100 µl) were set up as follows: 10 mM Tris/HCl, pH 8.3; 50 mM KCl; 2.5 mM MgCl2; 200 µM (each) dATP, dCTP, dGTP and dTTP; 1× Taq DNA polymerase (Amplitaq; PerkinElmer); 0.1 µM (each) primer (groESf and groESr); and 4 µl DNA template. Reaction mixtures, following a ‘hot start’, were subjected to the following empirically optimized thermal cycling parameters in a PerkinElmer 2400 thermocycler: 96 °C for 5 min, followed by 40 cycles of 96 °C for 1 min, 50 °C for 1 min and 72 °C for 1 min, followed by a final extension at 72 °C for 10 min. Positive (*P. aeruginosa* ATCC 27853, S. typhimurium AB008152, B. licheniformis CM23697, E. coli M11294) and negative controls were included in each amplification reaction to monitor contamination and verify the specificity of the amplification product.
DNA and multiple negative (water) amplification controls were included in every set of PCRs. In addition to all (n = 60) P. aeruginosa isolates from CF patients, genomic DNA from P. stutzeri, P. fluorescens, P. putida and the non-Pseudomonas organisms described above was amplified by using these conditions.

Detection of amplicons. Following amplification, aliquots (10 μl) were removed from each reaction mixture and examined by electrophoresis (80 V, 45 min) in gels composed of 2 % (w/v) agarose (Gibco) in TAE buffer (40 mM Tris, 20 mM acetic acid, 1 mM EDTA, pH 8-9), stained with ethidium bromide (0.05 μg ml⁻¹). Gels were visualized under UV illumination by using a gel image analysis system (UV illuminator) and all images were archived as digital graphic files.

Restriction-site map. A restriction-site map was constructed of the theoretical PCR product by using MapDraw Software (DNASTAR) and compared with those stored in GenBank by using BLAST alignment software.

RESULTS AND DISCUSSION

In silico analysis of the primer pair groES and groES demonstrated that, of currently available sequence data, only Pseudomonas spp. had 100 % similarity to these primers. PCR amplification of genomic DNA from extracted organisms generated an amplicon of the expected size (approx. 536 bp) for all P. aeruginosa (n = 60), P. putida, P. fluorescens and P. stutzeri isolates examined, but was not able to produce this amplicon for any of the 21 non-Pseudomonas isolates that were challenged (Fig. 1). RFLP analysis of the amplicons of all P. aeruginosa isolates demonstrated a single RFLP type that consisted of three bands at approximately 80, 190 and 250 bp (data not shown). Sequence analysis of all P. aeruginosa amplicons demonstrated the presence of a single sequence type and direct sequence analysis showed a highly conserved amplified region. This sequence, which encodes a partial region of the heat-shock protein GroES, has subsequently been deposited in GenBank under accession no. AY150814. This sequence demonstrated 98·2 % similarity to that of P. aeruginosa (GenBank accession no. S77424), followed by 76·7 % similarity to P. stutzeri (Y13828), 72·7 % similarity to P. putida (X78435) and 62·5 % similarity to Enterobacter cloacae (M88012).

Screening of total-cell harvests from sputum of nine adult CF patients on non-selective plates generated a positive PCR result for the three patients (A–C) with a history of P. aeruginosa.
P. aeruginosa infection, but was unable to generate a product for those patients (D–I) who had no previous history of P. aeruginosa or other Pseudomonas sp. infection.

Sequence-based typing and identification systems most often employ well-characterized 'housekeeping' genes for analysis. These genes are under no strong selective pressure and therefore acquire mutations in their DNA at a slow and constant rate, which can be measured by sequence analysis. The genes chosen should be found in all bacterial species. Genes involved in the heat-shock response seem to be ideally suited to this purpose (Zeilstra-Ryalls et al., 1991).

P. aeruginosa is the single most important bacterial pathogen in patients with CF (Speert, 2002), as demonstrated with high prevalence data in most national CF registries. Chronic Pseudomonas colonization of the major airways, which leads to debilitating exacerbation of pulmonary infection, is the major cause of morbidity and mortality in patients with CF. Although P. aeruginosa is the most important species that causes pulmonary infection, several other species in this genus have also been reported (Klinger & Thomassen, 1985). Historical review at our CF centre of laboratory reports of 120 adult CF patients since approximately 1997 has demonstrated a small but important presence of three other Pseudomonas species, namely P. putida, P. fluorescens and P. stutzeri, which were considered to be clinically significant in eight patients (8/120; 6.7 %) (Table 2). Consequently, it is important not only to reliably detect P. aeruginosa but also other species within this genus, albeit at a lower incidence.

It is important that primary diagnostic bacteriology laboratories have the ability to detect Pseudomonas spp. as early as...
possible so that aggressive antibiotic regimes may be commenced and the patient is managed optimally, in an attempt to avoid early biofilm formation and chronic colonization by Pseudomonas spp. More recently, West et al. (2002) showed by using a combination of serum IgG, IgA and IgM anti- P. aeruginosa antibodies, in conjunction with these authors’ Wisconsin Cystic Fibrosis Radiograph score, that P. aeruginosa infection occurred approximately 6–12 months before the organism was recovered from respiratory secretions. In addition, this study demonstrated that mixing of a young child with chronically colonized older children was associated with a significantly increased risk of P. aeruginosa acquisition.

Given that not all laboratories employ selective media for the detection of Pseudomonas spp, from sputum or other respiratory secretions, small numbers of Pseudomonas colonies (n = 1–2) may be missed when present in the early stages of infection after colonization of the patient’s airways, particularly where such single colonies are mixed with other phenotypically similar genera on the primary culture plate. Pragmatic, practical and cost implications render it impossible to qualitatively identify total bacterial microflora present on non-selective primary plates from sputum. Therefore, any rapid screening method that uses these plates should be encouraged to detect low copy numbers of cells in the early stages of infection. The main value of this diagnostic assay is for the rapid screening of patients with no or an intermittent history of Pseudomonas colonization. The above PCR assay offers the opportunity to screen for Pseudomonas spp, by modifying the above methodology to include an additional stage, whereby total colonies from primary non-selective plates from sputum are harvested in Tris/HCl (pH 8.0) and examined as described.

Given that the groES locus is highly conserved in multiple bacterial genera, the current database of available groES sequences is not as comprehensive as those for other highly conserved gene loci, such as the 16S rRNA gene, and hence may not contain sequence data for several commonly isolated, as well as newly emerging, CF organisms. Therefore, the proposed use of these primers in diagnostic screening assays, where Pseudomonas spp, are detected in a molecular manner, should be confirmed phenotypically and antibiotic susceptibility patterns should be obtained.

Overall, we recommend employment of this assay to detect the presence of Pseudomonas spp, including P. aeruginosa, from primary culture plates that originate from laboratory analysis of CF patients’ sputum, particularly at review, in those patients with no previous history of Pseudomonas infection or in those patients who appear to be transiently colonized by this organism. Employment of molecular methodologies, in conjunction with routine clinical sputum cultures, may provide improved information on the microbiological status of CF patients, which will aid clinicians in both optimum management of patients and CF centre infection-control practices.

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