Molecular characterization of the major outer-membrane protein OprF from plant root-colonizing Pseudomonas fluorescens

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INTRODUCTION

Plant root colonization by bacteria is a complex process in which constituents from roots, bacteria and soil interact. This phenomenon is considered crucial for enabling so-called plant growth-promoting rhizobacteria, of which certain fluorescent Pseudomonas species are the most prominent representatives, to exert their beneficial effect on the host plant (Lugtenberg et al., 1991; O'Sullivan & O'Gara, 1992).

From the cell envelope of the wheat-rhizosphere-colonizing strain P. fluorescens OE 28.3, we purified a protein displaying in vitro adhesion to plant roots (De Mot & Vanderleyden, 1991). Subsequent cloning of the structural gene revealed a strong homology with the constitutive major outer-membrane protein (OprF) from the opportunistic human pathogen P. aeruginosa (Duchêne et al., 1988) and the plant pathogen P. syringae (Ullstrom et al., 1991). However, the P. fluorescens OprF differed substantially in the central domain where a conspicuous proline-rich repeat replaced the cysteine-rich part that is highly conserved in P. aeruginosa and P. syringae (De Mot et al., 1992). A structural role has been assigned to the P. aeruginosa OprF, similar to the enterobacterial OmpA protein (Gotoh et al., 1989a, b; Woodruff & Hancock, 1989). In addition, pore-forming activity has been reported for both proteins (Nikaido et al., 1991; Bellido et al., 1992; Sugawara & Nikaido, 1992), though lower than

The GenBank accession numbers for the sequences of the oprF genes from P. fluorescens strains NRRL B-15132, PGSB 7941, PGSB 8059, PGSB 8472, OE 46.1, and from P. tolaasii CH 36 reported in this paper are L21197, L21198, L21199, L21200, L21202 and L21201, respectively.

Keywords: Pseudomonas fluorescens, major outer-membrane protein, OprF
Table 1. Pseudomonas strains used in this study

<table>
<thead>
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<th>Strain*</th>
<th>Relevant characteristic</th>
<th>Source or reference†</th>
</tr>
</thead>
<tbody>
<tr>
<td>P. aeruginosa PA01</td>
<td>Pathogen of Enterococcus faecalis (The Netherlands)</td>
<td>D. Haas, ETH</td>
</tr>
<tr>
<td>P. aureofaciens LMG 1245T</td>
<td>Isolate from rice rhizosphere (Sri Lanka)</td>
<td>Vlassak et al. (1992)</td>
</tr>
<tr>
<td>P. cepacia [II] RW5P1</td>
<td>Pathogen of chicory (Germany)</td>
<td>LMG</td>
</tr>
<tr>
<td>P. echinorhizus LMG 2162T</td>
<td>Plate contaminant</td>
<td>LMG</td>
</tr>
<tr>
<td>P. chlororaphis LMG 5004T</td>
<td>Fresh water stream (USA)</td>
<td>LMG</td>
</tr>
<tr>
<td>P. fluorescens</td>
<td>Isolate from wheat rhizosphere (Belgium)</td>
<td>LMG</td>
</tr>
<tr>
<td>OE 28.3</td>
<td>Isolate from wheat rhizosphere (Belgium)</td>
<td>LMG</td>
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<td>OE 46.1</td>
<td>Isolate from maize rhizosphere (Belgium)</td>
<td>H. Joos, PGS</td>
</tr>
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<td>PGSB 7941</td>
<td>Isolate from maize rhizosphere (France)</td>
<td>Weller &amp; Cook (1983)</td>
</tr>
<tr>
<td>PGSB 8059</td>
<td>Isolate from maize rhizosphere (France)</td>
<td>Weller &amp; Cook (1983)</td>
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</tr>
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<td>P. mendocina LMG 1223T</td>
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<td>LMG</td>
</tr>
<tr>
<td>P. putida RW1P1</td>
<td>Isolate from rice rhizosphere (New Zealand)</td>
<td>Vlassak et al. (1992)</td>
</tr>
<tr>
<td>P. syringae pv. syringae</td>
<td>Isolate from rice rhizosphere (Sri Lanka)</td>
<td>Vlassak et al. (1992)</td>
</tr>
<tr>
<td>P. syringae pv. glycinea</td>
<td>Pathogen of Syringa vulgaris (UK)</td>
<td>LMG</td>
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<tr>
<td>P. tolaasi CH 36</td>
<td>Pathogen of Agaricus bisporus (Belgium)</td>
<td>LMG</td>
</tr>
<tr>
<td>P. syringae pv. glycinea</td>
<td>Pathogen of Glycine max (New Zealand)</td>
<td>LMG</td>
</tr>
<tr>
<td>P. viridiflava LMG 2352†</td>
<td>Isolate from Phasolus sp. (Switzerland)</td>
<td>H. Joos, PGS</td>
</tr>
<tr>
<td>X. maltophilia [V] PGSB 1894</td>
<td>Soil isolate (USA)</td>
<td>H. Joos, PGS</td>
</tr>
</tbody>
</table>

* The strains all belong to the Pseudomonas rRNA group I, unless indicated otherwise (roman numerals in square brackets after species name). Type strains or pathovar reference strains are labelled † or ‡, respectively.

† Abbreviations used: ETH, Eidgenössische Technische Hochschule, Zürich, Switzerland; LMG, Culture Collection of Laboratory of Microbiology, University of Gent, Gent, Belgium; PGS, Plant Genetic Systems, Gent, Belgium.

with most porins. Although OmpA and OprF proteins are homologous in their C-terminal regions, different membrane topologies have been proposed (Vogel & Jähnig, 1986; Finnen et al., 1992; Wong et al., 1993).

In this paper, the topology of the OprF from P. fluorescens OE 28.3 was investigated using protease treatment of membrane-embedded OprF. In addition, the extent of inter-strain variation in the primary sequence of OprF from several rhizosphere isolates of P. fluorescens was analysed.

METHODS

Bacterial strains and culture conditions. The bacterial strains used in this work are listed in Table 1. The Pseudomonas strains were grown in 3% trypticase soy broth (TSB) at 30 °C.

Immunological techniques. Purified OprF protein (10 μg) mixed with Freund’s complete adjuvant was used to immunize BALB/c mice subcutaneously. After 2 and 6 weeks, another 10 μg of antigen in Freund’s incomplete adjuvant and in physiological salt solution, respectively, were injected intra-peritoneally. Two days after the last injection, an intraperitoneal booster dose (10 μg) was administered. Two days later, spleen lymphocytes were isolated and fused with mouse myeloma cells P3X63-Ag8-6.5.3. Hybridomas were selected in hypoxanthine–aminopterine–thymidine-containing medium and the supernatants were screened for specific antibody production by ELISA in microtitre plates coated with purified OprF protein, using rabbit anti-mouse IgG-peroxidase (Bio-Rad) for detection. Positive hybridomas were cloned by limiting dilution. Ascitic fluid from pristane-primed mice injected with the respective hybridomas was used for purification of IgG by affinity chromatography on protein A-Sepharose (Pharmacia Biotech). Four monoclonal antibodies thus obtained (MA-28B9, MA-29A6, MA-40D1 and MA-8F5) were used in this study. Immunodetection after Western blotting was carried out with goat anti-mouse IgG-conjugated alkaline phosphatase (Harlowe & Lane, 1988). For whole-cell ELISA, the method of Charbit et al. (1991) was adopted. Microtitre plate wells were coated with a suspension of about 5 × 10⁷ cells and incubated with primary antibody at 10 μg ml⁻¹, FITC-labelled rabbit anti-mouse IgG (SeroTec) was used to monitor whole cell binding of antibodies by flow cytometry as described by Srikumar et al. (1992). In these experiments, a mutant lacking OprF constructed
by reverse genetics (R. De Mot, unpublished data) was used as a negative control. **Sequencing of PCR-amplified oprF genes.** Two sets of PCR primers, based on the sequence of P. fluorescens OE 28.3 oprF, were designed to amplify two overlapping fragments of the oprF genes from total DNA of selected fluorescent Pseudomonas strains. For the N-terminal regions, OLIPCR1: 5' AAGAA-TTCGATGGGATATTACGGATGAAGCT 3'; and OLIPCR3: 5' AAGGTCTGTTCCGAAATCCGATCTTNA-CRTC 3' (where R = A, G; Y = C, T; and N = A, G, C, T) were used. The forward primer (OLIPCR1) covers a perfectly conserved sequence around the ATG start (in bold) of the oprF genes from P. aeruginosa, P. fluorescens and P. syringae. The reverse primer (OLIPCR3) reflects the OprF consensus sequence DVKDFDK, taking the codon usage in the P. fluorescens oprF (De Mot et al., 1992) and recA (De Mot et al., 1993) genes into consideration to reduce the extent of degeneration. The C-terminal parts were amplified with OLIPCR5: 5' ATTAGGATTCGCGGTGTTTAGATTCGGGGT 3'; and OLIPCR6: 5' ATTAGGAATTCYYAYTKNGCYTSNGCYTCN-AC 3' (where K = G, T; and S = G, C). The consensus sequence GLGVNFGG for the six strains deduced from the respective N-terminal PCR products was used to design the forward primer OLIPCR5, whereas the reverse primer OLIPCR6 corresponds to the C-terminal consensus sequence VEA[W,Q,E][A,Q,K] plus stop codons. After a hot start at 94°C, 25-30 cycles of amplification were performed with template denaturation at 94°C for 1 min, primer annealing at 50°C for 2 min, and elongation at 72°C for 3 min, concluded with a final 10 min elongation step at 72°C. Pfu polymerase (Strategen) was preferred over the Taq enzyme for its higher fidelity in DNA synthesis (Arnein & Erlich, 1992). Appropriate PCR fragments were purified from agarose gels by the double GeneClean protocol (BIO101), digested with EcoRI and BamHI to generate cohesive ends within the incorporated primer tags (shown in italic), and cloned in plasmid pUC19. Double-stranded DNA sequencing was carried out using the AutoRead Sequencing Kit (Pharmacia Biotech) on an automated ALF sequencer (Pharmacia Biotech). For each strain, at least three independent clones were analysed. Sequence data were processed using the ASSEMBL program (PC Gene: IntelliGenetics). The PC Gene software was also used for multiple alignments of DNA and protein sequences (CLUSTAL; Higgins & Sharp, 1988). **Electrophoretic techniques.** Protein extracts for one- or two-dimensional electrophoresis were prepared by phenol extraction of whole cells or outer-membrane preparations (De Mot & Vanderleyden, 1989). SDS-PAGE was carried out in a vertical Laemmli system with a 15% gel to generate cohesive ends within the incorporated primer tags. Two-dimensional PAGE was carried out as described previously (De Mot & Vanderleyden, 1989). For semi-dry blotting at alkaline pH onto polyvinylidene difluoride (PVDF) membranes (Millipore) the procedure of Matsudaira (1989) was used.

**Proteolysis of membrane-associated OprF.** OprF-enriched outer-membrane fraction (30 μl) from strain OE 28.3, prepared as described previously (De Mot & Vanderleyden, 1991), was suspended in 1 ml 30 mM Tris/HCl, pH 8.1, or 30 mM Na₂HPO₄/NaH₂PO₄ buffer, pH 6.2. Digestion with pronase E (100 μg ml⁻¹; Sigma), proteinase K (100 μg ml⁻¹; Sigma), both at pH 8.1; and papain (50 μg ml⁻¹; Sigma) at pH 6.2 was carried out at 37°C for 2 h. PMSF was then added to 2.5 mM. The outer membranes were reisolated and washed twice in 30 mMTris/HCl buffer, pH 8.1, by ultracentrifugation (50000 g) for 30 min at 4°C. The remaining membrane-associated peptides were then electrophoretically separated and blotted onto PVDF membranes for N-terminal microsequencing by automated Edman degradation using a 477A Protein Sequencer (Applied Biosystems). In a similar experiment, washed P. fluorescens cells were resuspended in 0.1 M sodium phosphate buffer, pH 6.2, at about 10^8 cells ml⁻¹ and incubated with papain (500 μg ml⁻¹) for up to 1 h at 25°C. Subsequently, outer membranes were isolated from the protease-treated cells in the presence of PMSF and analysed as described above. Identification of OprF-derived peptides was facilitated by the protein’s relative abundance in the outer-membrane preparations. Low molecular mass calibration proteins (Fluka) were used to estimate the size of the different peptides.

**RESULTS**

**Isolation of OprF-specific monoclonal antibodies for P. fluorescens OE 28.3.**

The specificity of the four monoclonal antibodies isolated (MA-28B9, MA-29A6, MA-40D1 and MA-8F5) was investigated by Western blotting of total cell proteins from several P. fluorescens strains and a number of related or more distant species (data not shown). These antibodies displayed a highly similar pattern of reactivity for the strains tested (listed in Table 1). Since no qualitative differences in reactivity were observed with peptides generated by different proteases (see below), it appeared that the respective epitopes, if not identical, are all confined to a limited area of the protein.

The banding pattern of P. fluorescens OE 28.3 was detected in all the P. fluorescens strains tested, except for the non-reacting strain PGSB 7941. Among the other Pseudomonas species representing the five rRNA homology groups, a weak cross-reactivity was only observed with P. aeruginosa and P. syringae, both producing a band of slightly higher apparent molecular mass, as expected for their OprFs (Duchêne et al., 1988; Ullstrom et al., 1991). No epitopes were recognized in more distant rhizosphere bacteria from the genera Agrobacterium, Azospirillum, Erwinia, Phyllobacterium and Rhizobium.

Whole-cell ELISA for the strains listed in Table 1 indicated a weak reactivity of the above positive strains with the monoclonal antibodies. However, these results could not be confirmed by flow cytometry, indicating that the epitopes are weakly surface-exposed or inaccessible in intact cells. The presence of lipo- or exopolysaccharides may interfere with antibody binding to the outer-membrane protein in the intact cells.

**Protease treatment of membrane-embedded OprF**

Digestion of membrane-associated OprF from P. fluorescens OE 28.3 by papain, proteinase K and pronase E, produced only a limited number of peptides (Fig. 1a). The differences in band intensities probably reflected differences in relative rates of hydrolysis and/or accessibility of the respective sites. N-terminal sequence analysis of these peptides enabled unambiguous identification of several cleavage sites, since the amino acid sequence of OprF from strain OE 28.3 is known (see Fig. 3 for the sequence). The data compiled in Table 2 and Fig. 1(c) show that primary cleavage sites for the three proteases were located between amino acids 187 and 191 of the mature protein,
right behind the peculiar proline-rich repeat of OprF. After cleavage, both the N- and C-terminal parts remained associated with the membrane. The larger N- and C-terminal peptides of 20 kDa (band 1) and 14 kDa (band 7), respectively, accounted for the full-size OprF protein (32104 Da). The smaller (18 kDa) N-terminal peptide (bands 2, 4 and 6) was probably generated by a second cleavage of the 20 kDa peptide (band 1) a few amino acids ahead of the first site, presumably located just in front of the proline-rich stretch (calculated size: 17.5 kDa). The presence of additional cleavage sites closer to the C-terminus of the 14 kDa peptide (band 7) can explain the appearance of the smaller minor bands of about 13 kDa (bands 3 and 5), 12 kDa (band 8) and 9 kDa (band 9), having the same N-terminal end. The latter peptide was only poorly visible upon Coomassie blue staining but was clearly demonstrated by Western blotting (Fig. 1b). Sequence analysis of band 3 (pronase E) and band 5 (proteinase K) revealed some microheterogeneity due to cleavage at adjacent positions within the QVVRVE sequence (Table 2).

From this it can be concluded that the regions around residues 165 and 191 constituted exposed domains, whilst the rest of the molecule, especially the N-terminal region, was well protected by the outer-membrane environment. It appeared that this accessible region did not face the periplasmic space but was located at the cell surface, since a similar peptide pattern was obtained with papain-treated whole cells (Fig. 1c). Under these conditions, however, an additional cleavage product was detected containing the proline repeat at its N terminus (band 10). The apparent molecular mass of the latter peptide (about 23 kDa) was unexpectedly high. Assuming that no additional cleavage had occurred in the C-terminal part, the molecular mass calculated from the amino acid sequence is much lower (14.6 kDa). This discrepancy may be due to the presence of the unusual proline-rich stretch at its N-terminal end which imposes an extended coil structure (De Mot et al., 1992) and may have reduced the electrophoretic mobility of the peptide. Since this fragment was not generated from protease-treated outer membranes, the accessibility of this region may differ in the native configuration.
**Table 2.** Survey of outer-membrane-associated peptides generated by protease treatment of OprF from *P. fluorescens* OE 28.3 present in outer-membrane preparations or in whole cells (the latter with papain only)

<table>
<thead>
<tr>
<th>Enzyme</th>
<th>Peptide</th>
<th>N-terminal sequence†</th>
<th>Molecular mass (kDa)</th>
<th>Immuno-reactivity‡</th>
</tr>
</thead>
<tbody>
<tr>
<td>Pronase E</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>1</td>
<td>1QGQG</td>
<td>20</td>
<td>—</td>
<td></td>
</tr>
<tr>
<td>2</td>
<td>1QGQ</td>
<td>18</td>
<td>—</td>
<td></td>
</tr>
<tr>
<td>3</td>
<td>108RVEL§</td>
<td>13</td>
<td>+</td>
<td></td>
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<tr>
<td></td>
<td>191VELD</td>
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</tr>
<tr>
<td></td>
<td>189VRVE</td>
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</tr>
<tr>
<td>Proteinase K</td>
<td></td>
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<td></td>
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</tr>
<tr>
<td>4</td>
<td>1QGQGAVEGELF</td>
<td>18</td>
<td>—</td>
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</tr>
<tr>
<td>5</td>
<td>88VRVELDVKFD†</td>
<td>13</td>
<td>+</td>
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<td>Papain</td>
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</tr>
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<td>6</td>
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<td>18</td>
<td>—</td>
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<td>9</td>
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</tr>
<tr>
<td>10§</td>
<td>166APAPTP</td>
<td>23</td>
<td>+</td>
<td></td>
</tr>
</tbody>
</table>

* Same numbering as in Fig. 1.
† The superscript at the N-terminal amino acid refers to its position in mature OprF.
‡ A similar immunoreactivity pattern was obtained with MA-28B9, MA-29A6, MA-40D1 and MA-8F5.
§ Predominant peptide in band 3.
|| Equal amounts present in band 5.
¶ Only detectable with whole cells.

(whole cells) as compared to its configuration in isolated membrane fragments.

All immunoreactive bands contained C-terminal peptides, the smallest being the minor 9 kDa fragment (Fig. 1b and Table 2). Given this size, the epitopes should be located somewhere between position 188 and 270. To gain insight into the relative susceptibility of the respective target sites, the time-course of OprF hydrolysis by papain in whole cells was analysed by Western blotting (Fig. 1d). After 5–15 min, the main immunodetectable product was band 7, whereas only a low amount of band 10 was visible. At this early stage, two intermediate degradation products were generated (located between OprF and band 10), most likely by C-terminal cleavage. Their further degradation coincided with the appearance of the 9 kDa peptide (band 9). The minor 12 kDa peptide appeared only upon prolonged incubation.

**Strain-dependent differences in isoelectric point of OprFs**

Two-dimensional electrophoresis of cellular proteins from the immunoreactive strains showed that they contained a major protein with a similar relative molecular mass to OprF from strain OE 28.3. However, Fig. 2 clearly shows a difference in isoelectric point (pI) between the OprF from strain OE 28.3 (type A; Fig. 2a) and the more acidic OprF from strain NRRL B-15132 (type C; Fig. 2c). The type A OprF was also present in strains OE 46.1 and PGSB 8472, whereas type C also occurred in strains VA 2.1, ZA 4.1, PGSB 7828, PGSB 8059, PGSB 8273, NRRL B-15134 and PGSB 7861 (data not shown). Strain PGSB 7941 contained a less acidic OprF-like protein (type B; Fig. 2b) which did not react with our monoclonal antibodies. Surprisingly, this was also the case for the mushroom pathogen *P. tolaasii* CH 36. Confirmation that the major spot obtained from *P. tolaasii* cells represented an authentic OprF protein was obtained by N-terminal sequence analysis: the first 38 amino acids were identical to the N-terminus of strain OE 28.3 OprF.

**PCR amplification and sequencing of oprF genes**

To compare the differences in primary structure between the three types of OprF identified above, the oprF genes of six representative strains (two of each pI type) were cloned after PCR (see Methods) and sequenced. PCR primers were based on conserved regions present in the OprF proteins from *P. aeruginosa, P. fluorescens* and *P. syringae*. This enabled cloning of almost the entire oprF coding regions from *P. fluorescens* strains OE 46.1 and PGSB 8472 (type A), NRRL B-15132 and PGSB 8059 (type C), PGSB 7941 (type B), and *P. tolaasii* CH 36 (type B). The in vitro amplified DNA fragments included the signal peptide region (except for the first two amino acids), but not the six C-terminal amino acids (Fig. 3). For
corresponding part of the unprocessed OprF from *P. syringae* (Ullstrom *et al.*, 1991). For the mature OprFs, the seven sequences showed 83.3% identity over 275 residues, and 27 of the 46 non-conserved residues contained at least one substitution with a dissimilar residue. From Fig. 3 it is also apparent that the extent of primary sequence variation differed along the length of the OprFs. The overall inter-strain variability appeared to be lower in the C-terminal half. The best conserved region was found between residues 142 and 219 and contains the proline-rich sequence (residues 167–184). Substitutions of charged residues by non-charged ones and vice versa were spread throughout the sequences and appeared not to be confined to well delineated regions of the three OprF types.

In the C-terminal region spanning residues 221–230, the OprFs from strain CH 36 and PGSB 7941 (KQYPQTT- TTVVE) differed substantially from the other five proteins with their consensus sequence AQYP[A,D]TNV-EVA (Fig. 3). Actually, in this part these two type B OprFs were more similar to the corresponding OprF sequence from *P. aeruginosa* (KQYPSTSTTVE) and of *P. syringae* (QQYPQTTTTTVE). This region, located within the boundaries of the 9 kDa immunoreactive peptide, is a likely candidate for the epitope of the monoclonal antibodies, since the OprFs from strains CH 36 and PGSB 7941 were non-reactive, whereas the OprFs from *P. aeruginosa* and *P. syringae* showed a weak cross-reactivity (see above). In the model proposed for the membrane topology of *P. aeruginosa* OprF, the equivalent region of this putative epitope is located on the periplasmic side of the outer membrane (Wong *et al.*, 1993). Assuming a similar topology for this region of *P. fluorescens* OprF, this may explain the lack of reactivity of the monoclonal antibodies with whole cells (see above).

In the OprF-based dendrogram, strains CH 36 and PGSB 7941 clearly constitute a separate cluster (Fig. 4). Since strain CH 36 is a virulent strain of *P. tolaasii* causing toxin-mediated disease symptoms (brown blotch) on mushroom caps and producing the highly specific white-line reaction with *Pseudomonas reactans* (Wong & Preece, 1979; Goor *et al.*, 1986), *P. fluorescens* PGSB 7941 was also tested for, but was found not to express these phenotypes (data not shown). The clustering of the five other strains of *P. fluorescens* did not completely reflect the differences observed in pI of their respective OprFs: strain OE 46.1 (type A) clustered with PGSB 8059 (type C) but was less closely related to strains OE 28.3 and PGSB 8472 (both type A). Fig. 4 also clearly illustrated the relative distance between the *P. fluorescens* strains and *P. aeruginosa*/ *P. syringae*.

The primer combination OLIPCR1–OLIPCR3 was used to amplify oprF-like sequences from other members of the *Pseudomonas* rRNA group I, including *P. stichorii*, *P. chlororaphis* and *P. viridiflava* (data not shown). This is not unexpected since earlier reports based on cross-reactivity of antibodies (Mutharia & Hancock, 1985) and on DNA hybridization (Ullstrom *et al.*, 1991) indicated the occurrence of oprF-like genes and their products in several species of this group.

Fig. 2. Two-dimensional electrophoresis of total cell proteins from *Pseudomonas* strains containing an OprF protein (marked by arrow) with a pI higher (b; CH 36) or lower (c; NRRL B-15132) than *P. fluorescens* OE 28.3 OprF (a). The pH gradient extends from left (basic) to right (acidic). The migration distances of the molecular mass calibration proteins (kDa) are indicated on the right.

the PGSB 8059 OprF, 21 additional residues at the C-end were lacking because of the presence of a BamHI site in the oprF gene.

Fig. 3 shows that the signal peptides of the different OprF proteins were highly similar and strongly resembled the
### Homology of OprF with OmpA and OmpA-related proteins

Previously, we and others pointed out that several outer-membrane proteins bear considerable sequence homology in their respective C-terminal parts to the corresponding domains of OmpA proteins from Enterobacteriaceae: the Neisserial protein III and class-4 proteins (Gotschlich et al., 1987; Klugman et al., 1989), the OprFs from *Pseudomonas* species (Duchhe et al., 1988; Ullstrom et al., 1991; De Mot et al., 1992) and a 21 kDa protein from *Bordetella avium* (Gentry-Weeks et al., 1992). A further database search for additional related sequences revealed that the peptidoglycan-associated lipoproteins (PALS)
from Escherichia coli (Chen & Henning, 1987), Haemophilus influenzae (Deich et al., 1988; Nelson et al., 1988) and Legionella pneumophila (Engleberg et al., 1991) should be added to this list, as well as a putative lipoprotein from E. coli (Byström et al., 1983). Recently, three additional Haemophilus outer-membrane proteins with C-terminal sequence homology to OmpA were described: a haemolytic 31 kDa protein from 'Haemophilus somnis' (Won & Griffith, 1993) and two H. influenzae proteins sharing 92% identity, namely protein P5 (Munson et al., 1993) and a non-typeable fimbril protein (GenBank L08448).

Strong sequence homology in the C-terminal part of the major outer-membrane protein CD of Branhamella catarrhalis with the OprF proteins from Pseudomonas species was reported by Murphy et al. (1993).

A multiple alignment was performed for these sequences, including the data from Lawrence et al. (1991) deduced from PCR-amplified and sequenced ompA genes from several additional enterobacterial species, and the data presented in this paper for OprF proteins from several Pseudomonas strains. A striking local sequence homology was apparent in the C-terminal part of the aligned sequences and the following consensus sequence was deduced: GX[T,A][D,N,S]X₃[G,S][X₃.6][Y,F,A][NX₄-L-[S,G][E,Q,L]]XRAXⱽV (where X denotes more variable positions) (see positions 231-253 in Fig. 3). In the SwissProt 26 database, no additional proteins were found which contained the sub-motif [Y,F,A][NX₄-L-[S,G]-[E,Q,L]]XRAXⱽV. Therefore, this region may be useful as a fingerprint for identification of OmpA-related proteins. In P. fluorescens OE 28.3, this region is contained within the 9 kDa peptide (band 9) and so appears inaccessible to proteases (Table 2 and Fig. 3).

**DISCUSSION**

Proteolysis of membrane-bound OprF from P. fluorescens OE 28.3 revealed that most of the protein's domains were not accessible to pronase, proteinase K and papain, and that the N-terminal half of the protein had no cleavage site. However, these enzymes all cleaved OprF at one or more sites adjacent to the proline-rich repeat in both isolated membranes and whole cells. Therefore, this region appears to be freely exposed to the cell surface. Based on its particular amino acid composition, we previously proposed that this region may reside outside the outer membrane (De Mot et al., 1992). The observation that the exposed proline-rich sequence itself is not proteolytically cleaved, is not surprising since such activity is limited to specific proteases acting on short peptides only (Szwajcer-Dey et al., 1992). Three additional protease sites were demonstrated in the C-terminal half but apparently these were less frequently cleaved, probably because of steric hindrance. Also for the OprF from P. aeruginosa, evidence suggested that surface-exposed regions were present in the C-terminal part (Finnen et al., 1992; Hughes et al., 1992). The role of the conspicuous proline repeat in the P. fluorescens OprF remains to be elucidated and some functional importance may be anticipated from its high degree of inter-strain conservation. In general, exposed loops of outer-membrane proteins are the more variable regions. Remarkably, such an extended proline stretch is absent from the otherwise closely related OprFs from P. aeruginosa and P. syringae, and is replaced with a larger disulphide-stabilized domain (Finnen et al., 1992). This cysteine domain is thought to be exposed on the bacterial surface (Wong et al., 1993). In the OmpA proteins of at least ten enterobacterial species a similar though shorter proline stretch is very well conserved, albeit the topology of the adjacent C-terminal region appears to be quite different from the one assigned to OprF (see below). Furthermore, such a proline-rich sequence is also present in the OmpA-related proteins from Neisseria species (Gotschlich et al., 1987; Klugman et al., 1989). Attempts to elucidate the role of the four-fold alanine–proline repeat in E. coli OmpA by mutagenesis, have shown that its elimination does not impair incorporation into the outer membrane (Klose et al., 1988a), but no function was assigned to it.

Our data indicate that the OprF protein from P. fluorescens OE 28.3, including most of the C-terminal part, is embedded in the outer membrane. This is in agreement with the model proposed for P. aeruginosa OprF (Finnen et al., 1992; Wong et al., 1993). Considering the extent of homology between OmpA and OprF in the carboxy halves of these proteins, this membrane topology for the *Pseudomonas* proteins is quite intriguing. Indeed, there is ample evidence that the OmpA carboxy half rests in the periplasm and is not essential for membrane insertion (Morona et al., 1984; Vogel & Jähnig, 1986; Klose et al., 1988a, b; Surrey & Jähnig, 1992). Both models could be reconciled assuming that the highly conserved C-terminal region plays a role not in membrane incorporation but in the interaction with the peptidoglycan layer. This would then account for the high level of localized sequence conservation between widely different species of a set of proteins, apparently quite diverse in size, function and topology.

The identification of surface-exposed loops in outer-membrane proteins not only contributes to a better understanding of their topology and function, but also
offers new perspectives for the engineering of Gram-negative bacteria. Indeed, such surface domains can be used to target heterologous proteins or parts thereof to the outer membrane, thereby anchoring novel polypeptides onto the bacterial surface. Potential applications of such surface-targeted expression have been highlighted in recent reviews (Georgiou et al., 1993; Little et al., 1993).

Sequence analysis of in vitro amplified genes encoding outer-membrane proteins has already proven its value to pinpoint inter-species and inter-serovar differences at the amino acid level among strains of human pathogens, such as Chlamydia and Neisseria species (Butt et al., 1990; Hayes et al., 1990; Maiden et al., 1991; Dean et al., 1992; Kaltenboeck et al., 1993; Lampe et al., 1993). Lawrence et al. (1991) showed that such sequence data are quite useful for phylogenetic analysis of closely related bacteria such as enterics. Application of this approach to the oprF genes from several fluorescent Pseudomonas strains, revealed a close relationship of the mushroom pathogen P. tulaasii with typical rhizosphere isolates of P. fluorescens, including the well known biocontrol strain NRRL B-15132 (= 2-79) (Weller & Cook, 1983; Mazzola et al., 1992). These molecular data strongly support the view that P. tulaasii is a typical member of the Pseudomonas RNA homology group I (Rainey et al., 1992; Stead, 1992). Clearly, it can be anticipated that an oprF-based comparative analysis of the members from the rRNA homology group I of Pseudomonas, including the numerous P. syringae pathovars, will provide an improved insight into their phylogenetic relatedness.

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