Assessing the Conformational Changes of pb5, the Receptor-binding Protein of Phage T5, upon Binding to Its Escherichia coli Receptor FhuA*

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Background: Little is known about the very first steps of infection of bacterial viruses.

Results: We specifically access the structure of phage T5 receptor-binding protein bound to its membrane receptor using specific techniques in small angle neutron scattering.

Conclusion: There are no large conformational changes.

Significance: Signal transduction within T5 appears different from that of phages binding cell wall saccharides.

Within tailed bacteriophages, interaction of the receptor-binding protein (RBP) with the target cell triggers viral DNA ejection into the host cytoplasm. In the case of phage T5, the RBP pb5 and the receptor FhuA, an outer membrane protein of Escherichia coli, have been identified. Here, we use small angle neutron scattering and electron microscopy to investigate the FhuA-pb5 complex. Specific deuteration of one of the partners allows the complete masking in small angle neutron scattering of the surfactant and unlabeled proteins when the complex is solubilized in the fluorinated surfactant FC-∗DigluM. Thus, individual structures within a membrane protein complex can be described. The solution structure of FhuA agrees with its crystal structure; that of pb5 shows an elongated shape. Neither displays significant conformational changes upon interaction. The mechanism of signal transduction within phage T5 thus appears different from that of phages binding cell wall saccharides, for which structural information is available.

Bacteriophages are the most abundant microorganisms in the biosphere. At the origin of major discoveries in modern genetics, their study is gaining increasing popularity in fields as diverse as ecology, genetics, phylogeny, and nanophysics (1, 2). Phagotherapy is also blooming with the increased multiresistance of human, animal, and plant pathogens to antibiotics (3, 4). Furthermore, deciphering the sophisticated but minimalist phage molecular machineries elaborated for host cell recognition and infection is fascinating. Structural data have revealed horizontal gene transfer, masked at the sequence level by rapid evolution, from phages to bacteria, of machineries developed for bacterial pathogenicity (e.g. Type VI secretion systems, reviewed in Ref. 5).

The vast majority of bacteriophages, Caudovirales, are tailed phages that have an icosahedral protein capsid containing a densely packed double-stranded DNA and a tail with an adsorption device at its end that serves to recognize the cell surface and deliver the phage genome into the bacterium cytoplasm. In the case of lytic phages, the biosynthetic host machinery is then hijacked to transcribe the viral genome and produce new virions. The interaction between the phage receptor-binding protein (RBP)4 and its bacterial receptor is the key signal that leads to capsid opening and cell wall perforation, resulting in the ejection of the DNA from the capsid into the cytoplasm, across the complex host envelope. Our aim is to describe the conformational rearrangements that initially take place between the RBP and its receptor. The coliphage T5 is an excellent model to study phage-host interactions for the following reasons: (i) both its RBP, pb5 (6), and its receptor, the E. coli outer membrane iron-ferrichrome transporter FhuA, have been identified and purified; (ii) the mere interaction between T5 and FhuA, either detergent-solubilized or reconstituted in liposomes, is enough to induce DNA ejection (7); and (iii) the interaction between purified pb5 and FhuA yields a highly stable, stoichiometric complex (8). Furthermore, this complex is

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Currently the only complex biochemically available between an outer membrane receptor and a phage RBP. FhuA is composed of a 22-β-strand barrel, which is obstructed by a globular domain, or the “plug.” Large extracellular loops and loops of the plug form the ligand binding sites (9). pb5 appears to fold as a unique domain, which undergoes secondary structural changes and most probably a rigidification of its structure upon binding to FhuA (10). In parallel to crystallization attempts of the FhuA-pb5 complex, small angle neutron scattering (SANS) and electron microscopy (EM) have been chosen to investigate the conformational changes that occur in pb5 following FhuA binding.

SANS combined with contrast variation and specific deuterium labeling of proteins is a particularly powerful technique to monitor conformational changes undergone by each protein within a complex. The neutron scattering length of the hydrogen nucleus is negative, whereas that of deuterium (and of most of the atoms) is positive. The difference between the scattering of the macromolecule and that of the solvent is proportional to a contrast term that can be modulated by changing the hydrogen content of the macromolecule or of the solvent by deuterium labeling. Very importantly, the contrast term of proteins vanishes in a buffer containing an appropriate H2O/D2O mixture at the contrast match point (CMP), expressed in D2O %. Thus, the signal of a partner within a protein complex can be selectively highlighted or suppressed (11–13).

Purified membrane protein samples comprise at least one additional component, detergent, present as bound detergent and as free micelles. Thus, detergents need to be either matched or modeled, in order to obtain structural information from the non-matched protein partner. Fluorinated surfactants share with detergents their amphipathic structure (Scheme 1). They have been investigated as potential mild surfactants (14–18). F6-Diglu (19, 20) and the chemically related and easier to synthesize F6-DigluM (21) (Scheme 1A) are stabilizing toward membrane proteins and form homogeneous and globular micelles and well defined membrane protein complexes. The CMPs of F6-Diglu (20) and of F6-DigluM (11) are close to that of most proteins (20), making these fluorinated surfactants ideal candidates for SANS study of solubilized membrane protein complexes; both hydrogenated protein partner(s) and surfactant will be matched simultaneously, allowing us to focus on deuterated protein partner(s) only.

Here, we have analyzed the FhuA-pb5 complex solubilized in F6-DigluM by SANS. A contrast matching strategy shown in Scheme 1B was defined to separately resolve each partner alone and within the complex. Hydrogenated proteins and the F6-DigluM micelles were expected to both be contrast-matched at the same D2O %, the observed signal being due to the deuterated partner protein. FhuA low resolution structure in solution, determined by SANS, is in very good agreement with its crystal structure. It remains unchanged upon formation of the complex. pb5 is shown to be an elongated protein, whose structure, at the resolution of the technique, does not show significant conformational changes upon binding to FhuA. The SANS envelopes of the complex and the individual proteins are in excellent agreement with negative stain single particle EM. We propose that the mechanism of signal transduction from the RBP to the rest of the phage within phage T5, and thus other siphophages with straight fibers binding protein receptors, is different from that of siphophages binding cell wall saccharides, for which structural information is available.

EXPERIMENTAL PROCEDURES

Chemicals

F6-DigluM was synthesized by our general procedure consisting of one-pot reduction/alkylation of a thiol-based fluorinated chain onto an acrylamido-type polar head (19) with slight modifications. The 1H,1H,2H,2H-perfluorooctanethiol was directly used instead of its corresponding thioacetate (21), allowing the preparation of F6-DigluM in only three steps. F6-DigluM was purified by flash chromatography on silica gel (AcOEt/MeOH/H2O, 7:2:1, v/v/v), followed by size exclusion chromatography on Sephadex LH 20 (MeOH). The solvent was removed under vacuum; the resulting powder was solubilized in MilliQ water and freeze-dried to give F6-DigluM as a white foam. 300 mg of F6-DigluM was used in this study.

Adaptation, Overexpression, and Purification of dFhuA and hFhuA and of pb5 and dpb5

FhuA was purified from the E. coli strain AW740 transformed with a plasmid encoding the fhuA gene in which a His tag has been inserted in the extracellular loop L5 (22). pb5 was purified from the E. coli strain BL21(DE3) carrying the oad gene encoding pb5 fused to an N terminus His tag in a pET-28 vector.
(8). Cells were grown in LB medium at 37 °C in the presence of 100 μM of the iron-chelating agent dipyridine for AW740 cells, and at 20 °C without induction for BL21(DE3) cells. To produce deuterated proteins, the two strains were first adapted to hydrogenated Enfors minimal medium for 7 days at 37 °C. Strains were then adapted to Enfors minimal medium in 80% D_2O for 5 days. AW740 cells were then grown for 48 h at 37 °C in the presence of 100 μM dipyridine. BL21(DE3) cells were grown at 20 °C, and overexpression of pb5 was induced at A_{600nm} = 0.9 with 0.5 mM isopropyl-1-thio-β-D-galactopyranoside for 24 h. hFhuA, dpb5, and hpb5 purifications were carried out as described (10). For hFhuA, a molecular sieve step was added (SD200 10/300 GL; GE Healthcare; buffer: 20 mM Tris-HCl, 84,061 Da) gives an estimate of 72% exchangeable H only.

Surfactant Exchange, Formation of the FhuA-pb5 Complexes, and Quality Control of the Samples

First Series—SD200 fractions containing hFhuA or dFhuA solubilized in 0.05% LDAO were pooled and concentrated, desalted onto a PG10 column (3 ml; Bio-Rad), and loaded onto a 2-ml nickel-nitrilotriacetic acid home packed column (Qiagen resin) equilibrated in 20 mM Tris-HCl, pH 8.0, 0.05% LDAO. The flow-through, containing some unbound FhuA, was reloaded onto the column (6 cycles). The column was then washed with 10 ml of the equilibration buffer, and surfactant exchange was performed by washing the column with 20 ml of 20 mM Tris-HCl, pH 8.0, 2 mM F_6-DigluM,46% D_2O. The protein was eluted with 20 mM Tris-HCl, pH 8.0, 4 mM F_6-DigluM, and 200 mM imidazole. To avoid excess of one of the partners, different FhuA-pb5 ratios were screened on small volumes and analyzed on SDS gels before formation of the complex on a preparative scale. Except for pb5, all samples were concentrated by ultrafiltration (Centricon 50) and finally dialyzed overnight against 2× 100 ml of 150 mM NaCl, 20 mM Tris-HCl, pH 8.0, 0.7 mM F_6-DigluM,46% D_2O. Final protein concentrations were as follows: hFhuA, 4.5 mg/ml; dFhuA, 4.6 mg/ml; dFhuA-hpb5, 4.9 mg/ml; hFhuA-dpb5, 2.1 mg/ml; dFhuA-dpb5, 3.2 mg/ml. dpb5 was studied in H_2O buffer at 0.5 mg/ml.

Second Series—dFhuA or hFhuA monomer fractions of gel filtration were concentrated by ultrafiltration (30,000 molecular weight cut-off; Millipore) to ~8 mg/ml. Samples were supplemented with 10 mM + 2 g/g F_6-DigluM/protein (total concentration, ~32 mM) and incubated for 30 min. BioBeads (Bio-Rad) were then added (100 mg/ml), and the samples were incubated on a rotating wheel at room temperature for 1 h. BioBeads were removed, and the FhuA/LDAO/F_6-DigluM mixture was submitted to size exclusion chromatography (SEC) (SD200 10/300 GL; buffer: 150 mM NaCl, 20 mM Tris-HCl, pH 8.0, 0.7 mM F_6-DigluM, 46% D_2O). Fractions of the second half of the monomer peak (to avoid any dimer contamination) were pooled and supplemented with 2 mM F_6-DigluM and, for half of the samples, with stoichiometric amounts of dpb5 to form the complexes. dFhuA, hFhuA, hFhuA-dpb5, and dFhuA-dpb5 samples were concentrated by ultrafiltration (molecular weight cut-off 30,000 and 100,000 (Millipore) for FhuA and the complexes, respectively) before another SEC equilibrated in the same buffer. 320-μl fractions were collected, and the most concentrated fractions of the second half of the peak were supplemented with 2 mM F_6-DigluM and directly used for SANS measurements. Final protein concentrations were as follows: hFhuA, 0.9 mg/ml; dFhuA, 0.8 mg/ml; hFhuA-dpb5, 1.0 mg/ml; dFhuA-dpb5, 1.2 mg/ml. dpb5 was also studied in 46% D_2O at 0.4 mg/ml.

In the two series, surfactant exchange was controlled by thin layer chromatography (solvent chloroform/methanol/water, 65:35:5) stained by sulfuric acid and heating (300 °C). No residual LDAO was detected (detection limit <0.005%). To check for the homogeneity of the samples, AUC was performed on the SANS samples, sometimes after a 2-fold dilution in 150 mM NaCl, 20 mM Tris-HCl, pH 8.0, 46% D_2O, using a Beckman-XLI ultracentrifuge at 42,000 rpm and 20 °C, in 3-mm optical path two-channel centrieyes, and analyzed as described (e.g. see Refs. 23 and 24). SEC was also performed for the second series. 10-μl aliquots were loaded onto an analytical SD200 5/150 column (GE Healthcare) in 150 mM NaCl, 20 mM Tris-HCl, pH 8.0, 0.7 mM F_6-DigluM,46% D_2O.

Small Angle X-ray Scattering Experiments

Small angle X-ray scattering experiments were conducted on the ID14-3 beamline at the European Synchrotron Radiation Facility (Grenoble, France). The data were recorded using a two-dimensional Pilatus detector, with a monochromatic x-ray beam (λ = 0.931 Å) and a sample to detector distance of 2430 mm. The concentration of pb5 was 0.48 mg/ml in 25 mM MES buffer, pH 6.0, and 330 mM NaCl. 96 acquisitions (1 s/acquisition) were recorded during 300 s using 100 μl of sample in a continuous flow for both the protein and the buffer. The spectra were corrected individually for the response of the detector and scaled with respect to the incident beam intensity and the absorption of the samples. The averaged spectrum of the buffer was subtracted from the corrected averaged spectrum of pb5. A solution of bovine serum albumin at 4.94 mg/ml was used as a reference for the calibration of the spectra.

SANS Experiments

All samples were measured in Hellma quartz cells 100QS with 1-mm optical path length at the SANS instrument D22 at the Institute Laue-Langevin (Grenoble, France). The sample temperature was kept at 20 °C (first series) and 5 °C (second series) during the exposure times. Scattering data from all samples were recorded at two instrumental detector/collimator
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SANS Data Analysis

At each instrumental configuration, water, the H₂O/D₂O buffers, the empty beam, an empty quartz cell, and a boron sample (electronic background) were measured. Exposure times varied between 20 min (empty cell, boron) and 150 min (dpb5 in 46% D₂O) according to the sample and instrument setup. Transmissions were measured during 2–3 min for each sample. The raw data were reduced (detector efficiency, electronic background, angular averaging) using a standard Institute Laue-Langevin software package (25) and normalized by the scattering of water. When applicable, the corrected scattered intensities from the two different Q ranges were merged \((Q = (4π/λ)sinθ)\) is the modulus of the scattering vector, with 20 being the scattering angle), and in all cases, the respective buffer signals were subtracted. The radii of gyration \((R_g)\) and the intensities scattered in the forward direction \((I(0))\) of all samples were extracted by the Guinier approximation, with \(R_g Q \leq 1.3\), using the program Primus (26). The analysis of \(I(0)\) in terms of molar mass is done according to Ref. 27, \(I(0)/c = (k/N_s)ΣM(∂ρ_N/∂c)^2\), where \(c\) represents the macromolecule weight concentration \((\text{g/liter})\), \(k\) is a geometrical factor, \(N_s\) is Avogadro’s number, \(Σ\) is for the different types of macromolecule in solution, and \(M\) and \(∂ρ_N/∂c\) are their molecular mass and neutron scattering length density increment \((\text{cm}/\text{g})\). For a homogeneous macromolecule, \(∂ρ_N/∂c = Σb/M – ρ_N*\,\bar{v}\), where \(Σb\) is the sum of the scattering lengths of the constituting atoms, \(\bar{v}\) is the partial specific volume \((\text{cm}^3/\text{g})\) of the macromolecule, and \(ρ_N*\) is the solvent neutron scattering length density \((\text{cm}^{-2})\). For a multicomponent complex comprising deuterated and hydrogenated macromolecules, we use the derived equation, \(I(0)/c_d = (k/N_s)M_d(∂ρ_N/∂c_d)^2\), where \(c_d\) is the concentration of the deuterated partner; \(∂ρ_N/∂c_d = (∂ρ_N/∂c)_p + M_p/M_d(∂ρ_N/∂c)_p\), the second contribution being null at 46% D₂O. Numerical values are in Ref. 11.

Low Resolution Models Determined by ab initio Analysis

We used the program DAMMIF (28) to generate low resolution envelopes of FhuA, of pb5 alone or within the complex, and of the complex from the SANS data, and of pb5 from the small angle x-ray scattering data. We used several variations of the input parameters in the default mode to model the data. Data of three types of complexes were measured during 2–3 min for each sample. The raw files were generated using the program GNOM (29), imposing distance distribution function \((p(r))\) curve. As a quality control, the radii of gyration determined from the pair distribution analyses were compared with the ones determined by the Guinier analysis. 10–30 DAMMIF models were averaged using DAMAVER (30). The experimental curve for the SANS data was compared with the Protein Data Bank structure 2FCP of FhuA using CRYSON (31), applying a 72% deuteration degree of the protein, as determined by mass spectrometry.

Transmission Electron Microscopy and Image Processing

Samples were diluted at 0.01 mg/ml in 20 mM Tris-HCl, pH 8.0, 150 mM NaCl, 0.05% LDAO. Aliquots of 5 μl were adsorbed onto a glow-discharged carbon film-coated copper grid, washed with three droplets of pure water, and subsequently stained with 2% uranyl-acetate. Images were recorded using a Philips CM10 microscope operating at 80 kV on a Veleta 2000 × 2000 CCD camera (Olympus).

Reference-free alignment was performed on manually selected particles from digitized electron micrographs using the EMAN image processing package (32). After using a reference-free alignment procedure, particle projections were classified by multivariant statistical analysis. The class averages with the best signal/noise ratio were selected and gathered in a gallery.

RESULTS

F₆-DigluM in SANS Can Be Matched Homogeneously in the Whole Q Range—F₆-DigluM scattering was measured at 10.0 mg/ml in H₂O and at 3.2, 6.4, and 9.7 mg/ml in 100% D₂O. It displays a very near, linear Guinier plot (Fig. 1A), indicative of well defined globular particles. The derived radii of gyration \((R_g)\) are \(1.87 ± 0.02\ nm (H₂O)\) and \(2.05 ± 0.01\ nm (D₂O)\). An estimate of the critical micellar concentration \((0.7\ mM)\) in D₂O can be obtained from the change of the forward scattering (\(I(0)\)) with the total concentration, \(c\), of surfactant. This value is close to the value determined from tensiometry and analytical ultracentrifugation (AUC) measurements (0.38 and 0.48 mM, respectively) (21). From an absolute calibration of \(I(0)\), a molecular mass of \(64 ± 2\ kDa\) can be calculated in D₂O for F₆-DigluM micelles, close to the value of 47 kDa from AUC, considering a globular shape, the difference being most probably related to the inaccuracy of the partial specific volume. A match point of 46% D₂O is derived from the \(\sqrt{[(I(0))/c – cmc]}\) plot, with \(cmc\) the critical micellar concentration and \(T\) the sample transmission, close to the calculated one of 49% (11). The \(R_g\) critical micellar concentration, molar mass, and match point are close to those measured by SANS for the very similar F₆-Diglu (20). Neutron scattering was measured for F₆-DigluM at 17.6 mg/ml (20 mM) in 150 mM NaCl, 20 mM Tris-HCl, pH 8.0, 46% D₂O. Fig. 1B shows that the scattering of F₆-DigluM is indistinguishable from that of the solvent. Thus, F₆-DigluM not only is globally matched at the forward direction \((Q = 0)\) but displays no structural features in the investigated Q range. This is not common for surfactants, for which hydrophobic tail and hydrophilic head do not have the same chemical composition (11). The match point of F₆-DigluM, as for F₆-Diglu, corresponds roughly to that of hydrogenated proteins, which is highly interesting for SANS studies of membrane protein complexes in combination with specific deuteration.

Production and Quality Control of the SANS Samples—In view of our strategy (Scheme 1B), pb5 and FhuA were individually overproduced and purified, according to published protocols for the hydrogenated protein. Deuterated proteins were purified from E. coli stains adapted to 80% D₂O in minimal medium, with slight modifications in the purification (see “Experimental Procedures”), leading to the purification of 1.5 mg of dpb5 and 2 mg of dFhuA per liter of culture. The deu-
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FIGURE 1. SANS of F$_6$-DigluM and validation of SANS strategy. A. Guinier plot of F$_6$-DigluM (10 mg/ml) in 0% (triangles) or 100% D$_2$O (squares). B and C, scattering curves, before buffer subtraction, of F$_6$-DigluM (17.6 mg/ml; B, triangles) and hFhuA (4.5 mg/ml; C, triangles) in F$_6$-DigluM (8 mg/ml free micelles from AUC), measured in 46% D$_2$O buffer, compared with the scattering curve of the 46% D$_2$O buffer (squares in B and C) and dFhuA in F$_6$-DigluM (circles in B and C). dFhuA was at 4.6 (B) and 0.8 (C) mg/ml, and AUC estimated 9 (B) and 2.3 (C) mg/ml free micelles. Insets, enlargements of the buffer curves.

FIGURE 2. AUC and SEC quality control for dFhuA and dFhuA-pb5 sample following SANS. A and B, superposition of experimental and fitted sedimentation velocity profiles obtained in 3-mm optical path length cells during 2 h at 42,000 rpm at 20 °C (top subpanels) and their differences (bottom subpanels), at 284 nm (A) and using interference optics (B), for dFhuA SANS sample in 46% D$_2$O (second protocol) after 4-day storage at 4 °C. C, Sedimentation coefficient distributions c(s). The distributions are normalized to the main protein peak value. D, SEC of the dFhuA-pb5 SANS sample (second protocol), loaded after the SANS measurements onto an SD200 5/150 column in 20 mM Tris-HCl, pH 8, 150 mM NaCl, 0.7 mM F$_6$-DigluM, 46% D$_2$O, run at 0.45 ml/min. Void volume ($V'_0$) = 1.12 ml; total volume ($V'_t$) = 2.83 ml.

teration rate, estimated for dFhuA using mass spectrometry, was ~72%.

Two series of SANS experiments were performed with surfactant and solvent exchange following two different protocols: (i) affinity chromatography, mixture of the partners, dialysis, and concentration, and (ii) incubation with BioBeads, SEC, concentration, mixture of the partners, and SEC. These protocols led to sample concentrations of 2–4 and ~1 mg/ml, respectively. In the first protocol, some of the samples contained aggregates, detected by SANS and AUC, and satisfactory samples were found only for hFhuA, dFhuA, and dFhuA-hpb5. The second protocol, avoiding final concentration steps, was thus designed to fulfill the requirements of full surfactant exchange, taking into account the limited availability of F$_6$-DigluM, control of the D$_2$O content, and sample homogeneity, with protein concentrations compatible with SANS analysis. Sample homogeneity was checked after SANS experiments by AUC and analytical SEC. Fig. 2 shows sedimentation velocity AUC analysis for dFhuA. F$_6$-DigluM micelles are detected mainly using the interference optics at 5.3 ± 0.2 S, at a concentration, from fringe shifts, of ~3 mM (for the second protocol) in the SANS samples. The main species is detected at 10.7 S for dFhuA. Similar results were obtained for hFhuA, hFhuA-dpb5, dFhuA-hpb5, and dFhuA-pb5, with main peaks obtained at 10.4, 11.5, 11.8, and 11.9 ± 0.2 S, the variation in the s values being logically related to the deuteration level, deuterated molecules being more dense than hydrogenated ones. The combined analysis of the absorbance and interference signals gave an identical amount, in mol/mol, of bound F$_6$-DigluM of 130 ± 15 and 130 ± 45 for FhuA and FhuA-pb5, respectively. The derived frictional ratio of 1.28 for dFhuA and 1.35 for the complexes considered as monomer are close to that of 1.25 expected for a globular compact shape. Larger species were also detected in limited amounts (~5%) in both protocols, the second one, however, leading to more homogeneous samples. In the case of the complexes, aggregates are detected in AUC in larger amounts, a feature probably related to pb5 sensitivity to pressure and propensity to aggregate at a concentration above 0.5 mg/ml, because they were undetected in SEC (Fig. 2D) and in the SANS analysis.

Hydrogenated Proteins Are Masked in SANS at the CMP of F$_6$-DigluM—Because the CMP of F$_6$-DigluM is close to that of most proteins (~44% D$_2$O), it is expected that both surfactant and hydrogenated proteins can be matched in the same buffer condition. Fig. 1C shows the scattering curve of hFhuA solubilized in F$_6$-DigluM at 46% D$_2$O. It clearly shows that both hFhuA and F$_6$-DigluM are indeed indistinguishable from the
buffer, showing no structural feature in the investigated Q range.

The Low Resolution SANS Structures of FhuA Alone and in Complex with pb5 Are Identical to the Crystal Structure—Fig. 3A shows the scattering curve of isolated dFhuA solubilized in F6-DigluM (triangles) or in complex with hpb5 (diamonds). Inset, Guinier analysis of the two data sets. C, scattering curves of dpb5 alone (crosses) or in complex with hFhuA solubilized in F6-DigluM (squares) measured in 46% D2O. Inset, Kratky representation of the dpb5 sample. D, pair distance distribution function, p(R), calculated using Gnom, of hFhuA-dpb5 (squares), dFhuA-hpb5 (diamonds), and dFhuA-dpb5 (circles) samples measured in a 46% D2O buffer.

In order to detect conformational changes induced upon formation of a complex with pb5, scattering data of dFhuA solubilized in F6-DigluM at 46% D2O were recorded. As shown in Fig. 3B, the data are superimposable, suggesting that the FhuA structure remains unchanged upon binding of pb5. The Guinier analyses of the two data sets (Fig. 3B, inset) allow the extrapolation of the forward intensities, which, normalized by FhuA concentration, are insignificantly different for dFhuA and for dFhuA-hpb5 samples, and correspond to FhuA as a monomer with 85% deuteration. The derived Rg are 28.1 ± 0.3 and 27.8 ± 0.2 Å for dFhuA and for dFhuA-hpb5, respectively. Both results corroborate the complete masking of hpb5 and the absence of conformational changes in the structure of FhuA upon formation of the complex. As expected from the nice superpositions of the curves, ab initio modeling of the dFhuA and dFhuA-hpb5 at 46% D2O shows very similar cylindrical volumes, ~75 Å long and ~50 Å wide, in which the Protein Data Bank structure of FhuA fits very well (Fig. 4A).

SANS Structure of pb5 Alone and in Complex with FhuA—pb5 has a strong tendency to aggregate whenever concentrated or dialyzed or at concentrations above 0.5 mg/ml. Thus, sample preparation had to be optimized without protein concentration, and the most concentrated fraction of the cation exchange chromatography was recovered and immediately diluted to 0.5 mg/ml if exceeding this concentration. However, even at these relatively low concentrations, interpretable SANS data of the dpb5 samples could be recorded (Fig. 3C), in particular for dpb5 in H2O buffer, where contrast is maximal. A Kratky representation of the data displays a bell shape, suggesting that pb5 is a compact protein, showing no sign of unfolding or structural disorder (Fig. 3C, inset) (33). Neutron diffraction curves of dpb5 measured either in 46% D2O or in H2O or x-ray diffusion curves
of pb5 were superimposable, modulo the hydration shell, and so were their derived pair distance distribution functions (not shown). *Ab initio* modeling reveals an elongated, scamorza-shaped molecule (Fig. 4A), with a maximum distance of 90 Å and a width of 20–60 Å. Fig. 3C shows the scattering curve of dbp5, alone or in complex with hFhuA, both in a 46% D₂O buffer, where hFhuA and F₆-DigluM are masked. The two curves, like their derived pair distribution functions (not shown), are very similar, indicating that pb5 does not undergo important conformational changes upon binding of FhuA. Radii of gyration of 28.0 ± 1.2 and 29.6 ± 0.9 Å were extracted for dbp5 and hFhuA-dbpb5, respectively, suggesting a slight elongation of pb5 within the complex. However, it cannot be excluded that this small difference is due to residual contributions from the hFhuA-F₆-DigluM moiety of the complex.

*SANS Structure of the Complex*—The overall structure of the complex can be obtained by measuring SANS data on a dbp5-dFhuA complex solubilized in F₆-DigluM in a 46% D₂O buffer. A molar mass of 196 ± 41 Da (i.e. compatible with a 1:1 complex of 151 kDa) and an Rₑ of 49.2 ± 0.9 Å are extracted from the Guinier plot, and GNOM allows determination of D_max = 150 Å (Fig. 3D). *Ab initio* modeling reveals an elongated particle, with a socklike shape (Fig. 4C). The shape and dimensions of the dFhuA-dbpb5 complex are compatible with a longitudinal organization of the individual FhuA and pb5 proteins. Without further constraints in the SANS data, the resolution (~30 Å) is, however, too low to allow fitting of the individual proteins within the envelope.

*EM Negative Stain Data Structure of the FhuA-pb5 Complex*—FhuA, pb5, and the complex were analyzed by EM and single particle analysis of negatively stained sample, the particles being too small to be visualized by cryo-EM. Fig. 5 shows the overall projection structure of FhuA, pb5, and the complex. The dimensions of FhuA are in agreement with the crystal structure (height of 70 Å). pb5 protein has an elongated shape, 80 Å long and 50 Å wide, and presents a slightly sharp extremity. There is a good agreement between pb5 structures determined by SANS and by EM (Fig. 6). The dimensions and overall shape of the complex are also similar between SANS and EM data, with an elongated shape of 150 Å long, even if the reconstituted volumes do not perfectly coincide. The slight differences may be attributed to the differences in the techniques (see “Discussion”). The localization of each protein within the EM complex projection is facilitated by the substructures within each protein (Fig. 5B). The peaked side of pb5 is recognizable at the extremity of the complex. Even if the different partners within the complex are not distinguished individually, the EM data strongly suggest that, at this resolution and in agreement with SANS data, there are no noticeable conformational changes of pb5 upon complex formation.

**DISCUSSION**

In this study, we validate the use of F₆-DigluM for low resolution studies of individual protein partners within a membrane protein complex using SANS. Conformational changes, if occurring, can be monitored. For all practical purposes, F₆-DigluM (34) can be considered as homogeneous, matched on the whole Q range. Therefore, sophisticated modeling of deter-
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gent residuals and very careful control of detergent concentra-
tion in the sample can be avoided. Usually, hydrophobic tails
and hydrophilic heads have different CMPs (due to their differ-
ent chemical composition) and will contribute to the scattered
signal (see Ref. 11 and references therein). Only a very limited
number of other detergents, such as Foscholine12 (35), can be
considered as homogeneously matched in practice. However,
$F_c$-DigluM has the particular property of very similar scattering
length densities, for both head and tail on the whole $D_2O$ %
range, similar to hydrogenated proteins (11). This allows
specific investigation of a protein subunit, if deuterated,
within a membrane protein complex. A similar achievement
was obtained by combining partial protein deuteration and
appropriate mixing of deuterated and hydrogenated SDS (36).
The advantage of $F_c$-DigluM is that it can be used with a wide
range of membrane proteins and that it is potentially less dena-
turating than most commonly used detergents (15). Impor-
tantly, in our study, $F_c$-DigluM provided samples of required
homogeneity for SANS.

In this study, we have determined for the first time, using
SANS and EM, the low resolution structure of the receptor-
binding protein of a Siphoviridae infecting Gram-negative bac-
teria. From both techniques, pb5 appears to be elongated and
compact with a maximum dimension of $\sim 80-90$ Å. This is in
agreement with the limited proteolysis results suggesting that
the protein folds as a unique and compact domain (10).

SANS, combined with the use of $F_c$-DigluM and specific deu-
teration of one of the partners, shows no large structural reu-
arrangements of either partner upon formation of the complex
(Figs. 3 and 4). Note that even at low resolution, rather minor
conformational changes can be distinguished by small angle
scattering. For example, in the two multidomain proteins,
adénylate cyclase (23.5 kDa) and lactoferrin (78.2 kDa), a small
domain (17 and 22% of the protein mass) undergoes $\sim 60-70\degree$
rotation with respect to the rest of the protein upon ligand
binding. These conformational changes are reflected by very
distinguishable scattering curves (36). The absence of struc-
tural rearrangements in FhuA is consistent with its crystal
structure alone or bound to different ligands showing only lit-
tle, rigid body, conformational changes of extracellular loops
(see Ref. 9 for a review). A dynamic behavior of the plug has
recently been reported from destabilization by urea (37). How-
ever, our results definitely rule out the possibility of the plug
domain of FhuA or part of it being removed from the barrel
upon pb5 binding (e.g. to allow the DNA through the barrel of
FhuA, a mechanism already eliminated from electron micros-
copy studies) (38). Concerning pb5, the invariance of its shape
upon binding to FhuA from SANS and EM analysis was instead
unexpected because binding information needs to be transmit-
ted to the rest of the phage (see below).

The overall envelope and projection of the FhuA-pb5 com-
plex determined by SANS and EM are similar (Fig. 6), even if the
SANS envelope of the complex presents a slightly curved shape
that is not apparent in the EM projection. We should keep in
mind, however, that both techniques sample different objects;
the EM projections result from stained, possibly oriented and
dried particles that are picked individually and averaged. We
cannot rule out that staining induces slight distortions of the
particle. SANS, on the other hand, is a mean of all particles
present in the solution sample, including aggregates (if present)
and averaging conformations in dynamic equilibrium. Signifi-
cant differences in EM and small angle x-ray scattering enve-
lopes were, for example, observed in subcomplexes of the type 6
secretion system (39). Furthermore, in the EM structure of our
membrane complex, the detergent could contribute to the sig-
nal, whereas it does not for the SANS data. Thus, the two enve-
lopes do not represent exactly the same object. However, using
both techniques, the complex appears as an elongated particle,
with a maximum dimension of $150$ Å, corresponding to juxta-
position of the two partners along their longer axis. Although
pb5 can be clearly recognized within the complex in the EM
projection, it is not possible to fit the isolated proteins into
the FhuA-pb5 SANS envelope at this resolution without fur-
ther restraints. In agreement with our data, pb5 was recently
unambiguously localized by immunolocalization at the tip of
the straight fiber, and EM images show a similar structure of
pb5 whether isolated, bound to FhuA (Fig. 5), or within the
phage.\(^5\) The comparison of EM images further suggests that
monomeric pb5 has its long axis parallel to the straight fiber
and that one extremity binds to the straight fiber protein,
whereas the interaction with FhuA occurs via the other
extremity.

Although this is the event that commits the phage to infec-
tion, little is known about the irreversible interaction between
phage RBPs and their receptors at the surface of the host and
subsequent signaling for cell wall puncturing and DNA ejec-
tion. An increasing number of structures of caudovirales RBPs
(also named tail spikes) that bind cell wall polysaccharides and
that are present in multicity within the phage are now available
(for a review, see Ref. 40). A more complete picture of the
molecular mechanisms that signal binding to the rest of the
phage comes from the resolution of larger baseplate assemblies.
The structures of these host recognition apparatus are available
for the Myoviridae coliphage T4 (41) and the Siphoviridae lac-
tococcal phage p2 (42) and TP901.1 (43) at high resolution and
for the Bacillus siphophage SPP1 at lower resolution (44, 45).
The T4 and p2 baseplates, whose structure has been solved before
and after DNA ejection, experience large conformational
changes after irreversible binding of the phage to the host,
resulting from low affinity but multiple attachments of receptor
binding domains (18 copies in p2) to polysaccharides. For
TP901-1, the irreversible and “avid” binding mediated by 54
flexible RBPs is thought to induce minor mechanical deforma-
tions or reorientations of the baseplate components. These
large or minor conformational changes within the baseplate
will trigger DNA ejection. Other structural information comes
from the study of the short-tailed Podoviridae e15 (46), BPP-1
(47), and P-SSP7 (48). It is worth noting that for all of these
phages, the structures of the isolated RBPs, when available, fit
into the density of the low resolution phage structures, indicat-
ing that these proteins have an autonomous fold, irrespective of
whether they are isolated or integrated in the phage structure.

\(^5\) Y. Zivanovic, L. Confalonieri, L. Ponchon, R. Lurz, M. Chami, A. Flayhan, M.
Renouard, A. Huet, P. Decottignies, A. R. Davidson, C. Breyton, and P. Bou-
langer, submitted for publication.
This is also what we observe for pb5. However, T5 differs from the phages for which structural data are available. It does not have a baseplate with multiple copies of the RBP but bears a single copy of pb5 that is located at the distal end of a central straight fiber. This RBP folds as a unique domain and binds with extremely high affinity a protein receptor (8, 10, 49).

T5 shares some structural features of its tail tip with the other well described siphophages λ and SPP1, which bear a central spike-like fiber formed by a trimer of the proteins gpJ and gp21, respectively. gpJ binds the E. coli porin LamB (50), and gp21 binds the Bacillus subtilis protein YueB (44, 45, 51), and in both cases, it is the C-terminal part of the protein that forms the RBP. In all three phages, the host recognition and binding strategy is different from phages bearing a baseplate whose structure is known. Their sophisticated adsorption mechanism relies on two types of receptors: low affinity receptors for saccharides of the LPS (T5), tectoic acids (SPP1), or the porin OmpC (λ) that accelerate adsorption, and high affinity RBP, present in low copy number, that binds a protein receptor. As for T5, the mere interaction of λ (53) and SPP1 (51) with their respective receptor is enough to trigger DNA ejection. The structures of the SPP1 tail before and after DNA release show very nicely how the conformational switch is propagated as a domino-like cascade along the tail. At the level of the spike, gp21N-ter opens to allow DNA transit out of the tail. The rest of the spike is not visible on EM pictures, probably due to the disordering of the receptor DNA transit out of the tail. The rest of the spike is not visible on EM pictures, probably due to the disordering of the receptor.

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