The *Shigella flexneri* OmpA amino acid residues 188EVQ190 are essential for the interaction with the virulence factor PhoN2

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**A B S T R A C T**

*Shigella flexneri* is an intracellular pathogen that deploys an arsenal of virulence factors promoting host cell invasion, intracellular multiplication and intra- and inter-cellular dissemination. We have previously reported that the interaction between apyrase (PhoN2), a periplasmic ATP-diphosphohydrolase, and the C-terminal domain of the outer membrane (OM) protein OmpA is likely required for proper IcsA exposition at the old bacterial pole and thus for full virulence expression of *Shigella flexneri* (Scribano et al., 2014). OmpA, that is the major OM protein of Gram-negative bacteria, is a multifaceted protein that plays many different roles both in the OM structural integrity and in the virulence of several pathogens. Here, by using yeast two-hybrid technology and by constructing an *in silico* 3D model of OmpA from *S. flexneri* 5a strain M90T, we have shown that the OM protein residues 188EVQ190 are likely essential for PhoN2-OmpA interaction. The 188EVQ190 amino acids are located within a flexible region of the OmpA protein that could represent a scaffold for protein-protein interaction.

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1. Introduction

Proper protein localization and protein–protein interaction are central to all cellular processes. Therefore, the unraveling of these complex phenomena is of fundamental importance for many areas of biochemical and biomedical research. *Shigella flexneri* is a Gram-negative facultative intracellular pathogen that causes bacillary dysentery by invading the epithelial cells of the large intestine of human hosts [2]. *S. flexneri* harbors a virulence plasmid that encodes a type III secretion system (T3SS) and the majority of T3SS-secreted effector proteins are responsible for *S. flexneri* pathogenesis [3]. After cell invasion, *S. flexneri* spreads intra- and intercellularly through the expression of the virulence factor IcsA. This protein is localized and exposed at the old bacterial pole and, by interacting with the eukaryotic proteins vinculin and neuronal Wiskott-Aldrich syndrome protein (N-WASP), induces actin polymerization with the formation of typical long F-actin comet tails [4].

Thus, proper protein localization and protein–protein interactions are central to the expression of *S. flexneri* virulence. In this respect, we have previously shown that *phoN2*, a gene located on a highly conserved region of the virulence plasmid of *S. flexneri*, encoding a periplasmic ATP-diphosphohydrolase (apyrase), participates, at least indirectly, to proper localization of IcsA at the bacterial surface [1,5]. By generating *phoN2::HA* fusions in the wild-type *S. flexneri* 5a strain M90T, we have shown that periplasmic PhoN2 strictly localizes at the bacterial poles, with a strong preference for the old pole, just beneath IcsA [1]. To evaluate whether PhoN2 and IcsA may interact for the correct exposition of IcsA, we conducted two-hybrid assays in yeast and cross-linking experiments. Both experimental approaches failed to find evidences supporting the existence of a PhoN2-IcsA interaction. Surprisingly, a strong interaction of PhoN2 with the OM protein *A* (OmpA) was found. Sequence analysis indicated that OmpA binds PhoN2 through its periplasmic-exposed C-terminal domain (minimal interaction region, amino acid residues 166–250) [1]. OmpA is the major OM protein of Gram-negative bacteria principally involved in the structural integrity of the OM [6]. Moreover, it has been recently shown that OmpA represents an important virulence factor for several pathogens, including *S. flexneri* [7,8]. By using independent *ompA* mutants of the *S. flexneri* strain M90T we have shown that all invariably displayed IcsA exposed across the entire bacterial surface and that a functional OmpA protein is required and sufficient for proper IcsA exposition, plaque and protrusion formation [7]. Furthermore, we...
hypothesized that the PhoN2–OmpA interaction may be necessary for proper lcsA exposition and thus for full virulence expression of S. flexneri [1].

Here to further characterize OmpA domains involved in the interaction with PhoN2 two two-hybrid screens in yeast were conducted. In the first screen we used four different PCR-generated ompA fragments. This screen allowed us to identify a new minimal region, encompassing amino acids 132–190, required for PhoN2–OmpA interaction. Furthermore, basing on the available sequences and resolved structures of OmpA of Escherichia coli, Klebsiella pneumoniae and Salmonella enterica, a 3D model of OmpA from S. flexneri strain M90T was built using the SWISS model workspace. The second two hybrid screen was conducted using this structural model in order to generate twelve independent ompA encoded peptides (from residue 136–325) in turn devoid of selected secondary structure elements. Our results indicated that the OmpA residues 188EVQ190 are likely essential for PhoN2–OmpA interaction.

2. Materials and methods

2.1. Bacterial/yeast strains, plasmids and growth conditions

Bacterial/yeast strains and plasmids used in this study are listed in Table S1. The yeast Saccharomyces cerevisiae strain AH109 (Clontech) was used for two-hybrid assays as recommended by the manufacturer. E. coli and S. flexneri strains were grown at 37°C either in Luria broth (LB) with aeration or on tryptic soy agar plates (TSA) containing 0.01% Congo red (Sigma), unless indicated otherwise. Antibiotics (Sigma), when appropriate, were added at the following concentrations: 100 μg ml⁻¹ ampicillin (Ap); 30 μg ml⁻¹ kanamycin (Km); 100 μg ml⁻¹ streptomycin (Sm).

2.2. DNA manipulations

DNA extraction, isolation of plasmids, restriction digestion, electrophoresis, purification of DNA fragments, construction of recombinant plasmids, transformation, and immunoblotting were performed by standard methods [9]. The primers used for PCR amplifications are listed in Table S2. Primers were designed to amplify ompA fragments based on the available S. flexneri genome sequence (Accession number CM001474). DNA sequence data were compared to known nucleotide sequences using the BLAST Server (National Centre for Biotechnology Information, Bethesda, Md).

2.3. Preparation of total protein extracts

Total protein extracts were prepared from yeast cells grown in minimal medium (OD₆₀₀=0.4–0.6). Briefly, 20 ml of yeast cell cultures were centrifuged at 3,000 × g for 20 min at 4°C and resuspended in 1 ml of a solution containing 2 M NaOH and 5% β-mercaptoethanol (lysis buffer). Proteins were concentrated by TCA (50%) precipitation. Precipitated proteins were washed with 90% acetone, centrifuged and resuspended in 2x Laemmli buffer (100 mM Tris–HCl pH 6.8, 4% SDS, 20% glycerol % and 5% β-mercaptoethanol) and stored at −20°C. Equal amounts of proteins were separated on 12.5% SDS-PAGE, transferred to PVDF membranes (Hybond-P, Millipore) and analyzed by immunoblotting. A protein molecular weight marker (Pierce) was included in each electrophoresis run in order to determine the molecular weight of the proteins. Immunoblotting was carried out with mouse monoclonal anti-HA (Sigma) antibody. Anti-mouse antibody were used as secondary antibody and the signals were detected with enhanced chemiluminescence (GE Healthcare).

2.4. Yeast two-hybrid assay

OmpA domains interacting with PhoN2 were identified using the two-hybrid technique in yeast (Matchmaker TwoHybrid System Protocols; Clontech). The bait recombinant plasmid pGBK7/phoN2 (phoN2 full length) was constructed as previously described [1]. Four different ompA regions were PCR-amplified using M90T total DNA as template and the primers listed in Table S2. Each fragment was cloned into the polyclonal multiple cloning site of prey plasmid pGADT7 (Table S1 and Fig. 1). Each prey plasmid was transformed independently into the yeast strain AH109 carrying the bait plasmid pGBK7/phoN2 and plated on synthetic drop-out (SD) medium lacking Leu and Trp (SD/-Leu–Trp). The bait-prey interaction was detected by plating 250 well isolated colonies, obtained from each transformation, on solid SD medium lacking His, Ade, Leu, and Trp (SD/-His–Ade–Leu–Trp). The ability of the four different OmpA regions fused to the GAL4 AD domain to activate the reporter genes expression (the so-called self-activation) was tested. Each AH109 strain carrying one of the four prey plasmids was plated on solid SD/-Leu, SD/-His–Leu and SD/-Ade–Leu media. AH109 transformed with the empty vector pGADT7 was used as negative control. The toxic effect of the four different encoded OmpA regions was evaluated by comparing the growth rate of AH109 carrying the different prey plasmids. The AH109 strain carrying the void plasmid pGADT7 was used as control. Strains were grown in SD minimal broth medium without Leu for 18 h. Inserts were considered non-toxic if the yeast strains reached an OD₆₀₀ ≥ 0.8 after the incubation time. To determine the expression levels of the four encoded prey proteins, yeast cells were grown in SD minimal broth medium without Leu (OD₆₀₀=0.4–0.6) and used for total protein extraction preparations. Equal amount of whole cell extracts were subjected to Western blot analysis using the
monoclonal anti-HA antibody (Sigma).

For the identification of the OmpA amino acid residues involved in the interaction with PhoN2, twelve different forward primers were used in combination with a single reverse primer to generate twelve independent ompA amplicons (Table S2). Then, amplicons were purified from 1% agarose gel electrophoresis. Each amplicon was flanked by the specific sequences for homologous recombination with the Smal linearized pGADT7 prey plasmid. AH109 pGBKTT7/phi2OmpN was transformed with a mixture of pooled amplicons, the linearized pGADT7 plasmid and plated as described above. DNA plasmid preparation from selected positive colonies was used to transform E. coli DH10b competent cells in order to determine the insert sequence.

2.5. Homology modeling of OmpA from S. flexneri strain M90T

Secondary structure of OmpA (GenBank EID61499.1) from S. flexneri strain M90T was built by using SWISS-MODEL workspace, applying default parameters [http://swissmodel.expasy.org; 10]. The OmpA sequence of S. flexneri strain M90T was compared via BLAST against non-redundant protein sequences database to determine the protein type. BLAST search was performed again against Protein Data Bank (PDB) to search suitable templates for the prediction of OmpA secondary structures. A total of 7 templates (PDB id: 2k01 [11], 1qjp [12], 2ge4 [13], 1g90 [14], 1bxv [15], 2jmm [16] and the deposited structure PDB id: 4erh; Table 1 and Fig. 2) were used to build the secondary structure.

3. Results

We have recently shown that the OM protein OmpA of the S. flexneri strain M90T is required for proper virulence expression and that the interaction with the virulence-associated periplasmic protein PhoN2 is likely required for proper IcsA expression at bacterial surface [1]. A minimal DNA region of ompA, encoding residues 166–250, was identified to be involved in PhoN2-OmpA interaction. Residues 166–250 represent part of the OmpA C-terminal domain known to be exposed into the bacterial periplasm, the same bacterial compartment which hosts mature PhoN2 [1].

3.1. Identification of the OmpA region interacting with PhoN2

Here, to confirm and extend our previous results in order to precisely identify the OmpA region interacting with PhoN2, a first yeast two-hybrid screen was conducted by using four different PCR-generated ompA fragments encoding: i) the entire mature OmpA protein (residues 1–325) as positive control; ii) the OmpA N-terminal region known to be embedded into the OM (residues 1–131), as negative control; iii) the OmpA C-terminal region exposed into the periplasm (residues 191–299), that includes part of the minimal region of interaction previously identified (residues 166–250); and iv) the OmpA region that includes the N- and part of the C-terminal OmpA domain (residues 1–299) and the linker sequence (residues 173–190) (Fig. 1). The four ompA DNA fragments were cloned individually into the pGADT7 prey vector thus generating prey plasmids pOAI–325, pOAI–131, pOAI–299, and pOAI191–299, respectively (Table S1 and Fig. 1). Prey plasmids were then transformed separately into the S. cerevisiae strain AH109 harboring the bait plasmid pGBKTT7/phi2OmpN (Table S1). The ability of the four different OmpA derived domains to activate the reporter genes (self-activation), the toxicity, and their expression levels were evaluated. No evidence of self-activation, differences in the expression of the four different ompA fragments or toxicity was detected (Figs. S1, S2, and data not shown, respectively).

Then, the interaction between PhoN2 and the four different prey plasmids was evaluated by plating transformed yeast cells on minimal SD-/His–Ade–Leu–Trp plates. As expected, AH109 pGBKTT7/phi2OmpN transformed with pOAI–325 (full length) was able to grow on SD-/His–Ade–Leu–Trp medium, confirming the PhoN2-OmpA interaction. Conversely, AH109 pGBKTT7/phi2OmpN strain transformed with pOAI–131 did not grow on minimal medium. Plasmid pOAI–131 was selected as negative control since it encodes for the N-terminal β-barrel embedded into the OM (Fig. 1). Surprisingly, AH109 pGBKTT7/phi2OmpN transformed with pOAI191–299 did not grow on minimal medium. The OmpA191–299 region was selected since it forms the C-terminal periplasmic OmpA domain and includes part of the minimal interaction region previously identified (residues 166–250) [1]. On the other hand, the OmpA1–299 fragment, containing the N-terminal, part of the C-terminal OmpA domains and the linker sequence, grew on SD-/His–Ade–Leu–Trp- medium minimal medium, indicating that amino acid residues 132–190 are necessary for PhoN2-OmpA interaction (Fig. 1).

3.2. Secondary structure model of OmpA of S. flexneri strain M90T

To search for the OmpA critical amino acids involved in the PhoN2-OmpA interaction, a secondary structure prediction of OmpA of S. flexneri strain M90T was built using the SWISS-MODEL workspace. The sequence of the OmpA protein of M90T (accession number EID61499.1) was then blasted to search the database for suitable templates among Gram-negative bacteria containing OmpA homologues whose structure has been resolved (Fig. 2A and C). Among these, a total of 6 templates presenting 82–92% sequence identity (PDB id: 2k01, 1qjp, 2ge4, 1g90, 1bxv, and 2jmm) were selected to model the N-terminal structure of OmpA of M90T (Table 1). OmpA of S. enterica (PDB id: 4erh), which presented 95% sequence identity with the OmpA C-terminal 152 residues of S. flexneri strain M90T, was selected as template for predicting the C-terminal structure (Table 1).

The structural model indicated that OmpA of M90T is a double domain protein presenting an N-terminal β-barrel domain (residues 1–172) composed by 8 β-strands connected by 4 extracellular and 3 periplasmic loops (Fig. 2A and B) while the C-terminal region is a globular domain (residues 191–325) which consists of 4 β-sheet, 5 α-helices and 6 connecting loops (Fig. 2C and D). These two domains are connected by the short linker sequence with no resolved structure (residues 173–190).

3.3. Identification of OmpA critical amino acids involved in the interaction with PhoN2

Basing on the structural model of OmpA of S. flexneri strain M90T, a set of twelve DNA fragments of different size were PCR-generated from the C-terminal domain of ompA (from encoded

| PDB Identification | Organism       | Sequence/identity similarity % | Coverage (%) |
|--------------------|----------------|--------------------------------|--------------|
| 2k01               | Klebsiella pneumoniae | 82.80                          | 57           |
| 1qjp               | Escherichia coli    | 93.49                          | 52           |
| 2ge4               | Escherichia coli    | 92.40                          | 53           |
| 1g90               | Escherichia coli    | 92.40                          | 53           |
| 1bxv               | Escherichia coli    | 92.40                          | 53           |
| 2jmm               | Escherichia coli    | 84.83                          | 45           |
| 4erh               | Salmonella enterica | 95.07                          | 42           |

Table 1 Templates from BLAST against PDB with OmpA from S. flexneri strain M90T.
residue 136–325) (Fig. 3 and Table S2). The twelve ompA encoded peptides were challenged for their ability to interact with PhoN2 by the two-hybrid assay. Each fragment was generated in order to exclude in turn secondary structure elements, namely β-strands, α-helices or loops (Fig. 3). Competent cells of S. cerevisiae strain AH109 carrying the bait plasmid pGBKT7/phoN2 were simultaneously transformed with the pooled DNA fragments and the SmaI linearized pGADT7 prey plasmid. The interactions between PhoN2 and the different OmpA peptides was screened by plating the transformation mixture on SD/-His–Ade–Leu–Trp minimal medium. Positive colonies were streaked again on the same medium and the prey plasmids DNA was extracted from competent cells of S. cerevisiae strain AH109 carrying the bait plasmid pGBKT7/phoN2 were simultaneously transformed with the pooled DNA fragments and the SmaI linearized pGADT7 prey plasmid. The interactions between PhoN2 and the different OmpA peptides was screened by plating the transformation mixture on SD/-His–Ade–Leu–Trp minimal medium. Positive colonies were streaked again on the same medium and the prey plasmids DNA was extracted from
positive colonies, and used to transform E. coli DH10b competent cells to determine the insert sequence. Each sequence was identified by BLAST analysis. Remarkably, the great majority (79%) of peptides encoded by the prey plasmids corresponded to the OmpA residues 188–325. A low number of sequenced inserts (21%) corresponded to the 136–325, 162–325 and 173–325 OmpA peptides. The OmpA188–325 amino acid sequence contains part of the minimal region (residues 166–250) that we have previously identified as responsible of the PhoN2-OmpA interaction [1].

Comparing the results obtained, we evidenced an amino acid stretch, _188EVQ190", which is included in the OmpA188–325 interacting peptide and absent in the OmpA191–299 domain. Since we did not observe interaction between the OmpA191–299 domain and PhoN2 we concluded that the amino acid stretch _188EVQ190" is required for PhoN2-OmpA interaction.

We hypothesized that the low efficiency of interaction detected for the 136–325, 162–325 and 173–325 peptides could be due to the characteristic of the fused peptides. Indeed, it is known that the GAL4 AD domain of the prey plasmid and the prey protein are separated by a linker region that is critical to ensure proper flexibility of the fused protein in order to facilitate protein-protein interaction [17]. Thus it might be possible to envisage that the amino acids _188EVQ190" directly fused to the GAL4 AD linker are accessible for the binding to PhoN2.

4. Discussion

OmpA is a 35 kDa protein embedded in the bacterial OM as a β-barrel protein, highly conserved among Gram-negative bacteria [18,19]. Recent studies have suggested that OmpA has to be considered a pleiotropic protein that plays different roles in the mechanism of virulence of different bacterial pathogens [8]. Furthermore, OmpA of _S. flexneri_ 2a has been identified as a novel molecule coordinating the innate and adaptive immune response, indicating that OmpA may also represent a promising antigen for vaccine development [20,21]. In spite of its relevance in the immune response the secondary structure of OmpA of _S. flexneri_ has not been determined yet and, to date, few data are available on the role of OmpA on the virulence of this bacterial pathogen [7]. In this context, we have recently shown that the virulence-associated periplasmic protein PhoN2 interacts with the C-terminal domain of OmpA of _S. flexneri_ strain M90T and that null-mutants of either gene influence bacterial virulence by altering proper IcsA exposition at the bacterial surface [17]. To further characterize the OmpA domains essential for PhoN2-OmpA interaction, we built a secondary structural model of OmpA of _S. flexneri_ strain M90T by using the SWISS-MODEL workspace (Fig. 2B and D). By in silico analysis we compared the secondary structure of several OmpA proteins (Fig. 2A and C). The overall architecture of the built model shows that _S. flexneri_ OmpA is a double-domain protein where the C-terminal globular domain (the OmpA-like domain) represents a conserved structural motif in several OmpA-related proteins [22–24]. It has been reported that the OmpA-like domain interacts with the peptidoglycan through two conserved amino acid residues that bind diaminopimelate acid [25] and that is essential for dimer formation [24,26]. Although, the biological function of dimerization is not well understood yet, it has been proposed that it could be involved in OmpA-mediated bacterial virulence. It was also shown that the periplasmic domain of OmpA might increase folding efficiency functioning as a chaperone-like structure, important for proper OmpA insertion into the OM [27].

We have previously shown that the C-terminal domain of OmpA of _S. flexneri_ strain M90T interacts with the PhoN2 protein (OmpA minimal interaction region residues 166–250) [1]. To confirm and extend our previous results, we performed two-hybrid experiments using prey plasmids pOA1–325, pOA1–131, pOA191–299 and pOA1–299 (Table S1 and Fig. 1) and the bait plasmid pGBK7/PhoN2 (Table S1) [1]. As expected, the results of the two-hybrid assay confirmed that the full length OmpA (plasmid pOA1–325), interacted with PhoN2, while the OmpA N-terminal region that forms the β-barrel, (plasmid pOA1–131) did not (Fig. 1). Interestingly, the C-terminal OmpA region, (plasmid pOA191–299), that forms part of the periplasmic domain of the protein, did not interact with PhoN2, while the 1–299 fragment, (plasmid pOA1–299), that includes both the N- and part of the C-terminal domains of OmpA and a short flexible linker sequence, interacted with PhoN2. Overall, these results indicated residues 132–190 as the minimal region essential for the interaction with PhoN2 (Fig. 1). To refine our analysis we used the predicted secondary structure of OmpA of _S. flexneri_ to generate a set of OmpA fragments. As outlined above, the overall architecture of the built model suggests that OmpA of _S. flexneri_ strain M90T is organized into two domains. In particular, the N-terminal beta-barrel domain (residues 1–172) is composed of 8 anti-parallel beta strands (Fig. 2B), while the C-terminal OmpA-like globular domain (residues 191–325) is composed of 4 beta sheets, 5 α-helices and 6 connecting loops (Fig. 2D). The N- and the C-terminal domains of OmpA are connected by a short region (residues 173–190) with unresolved structure that forms a flexible linker [28]. Basing on our tridimensional model, a set of twelve OmpA fragments were PCR-generated (Fig. 3). Thus, each fragment was designed to exclude in turn selected secondary structure elements encompassing the C-terminal domain of OmpA (from residue 136–325; Fig. 3). The interaction between PhoN2 and the different OmpA fragments was assayed using the two-hybrid assay. In this second screening, the OmpA encoded 188–325 peptide was detected as a major PhoN2 interactor. Comparing the results obtained by the two screening, we evidenced a specific amino acid sequence, _188EVQ190", that is present in the PhoN2 interaction-positive 188–325 peptide and absent in the interaction-negative 191–299 peptide (Figs. 1 and 3). These results led us to conclude that the three amino acids _188EVQ190" are likely essential for the PhoN2-OmpA interaction. The _188EVQ190" amino acids are located within the linker flexible region of OmpA, that could represent a scaffold for protein-protein interaction.

In conclusion our results extend our previous results on the PhoN2-OmpA interaction [1]. Experiments are underway to introduce point mutations into the OmpA _188EVQ190" stretch in order to precisely establish the role of the three amino acids in the PhoN2-OmpA interaction.

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Transparency document

Supporting information

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Appendix A. Supplementary material

Supplementary data associated with this article can be found in the online version at http://dx.doi.org/10.1016/j.bbrep.2016.08.010.
References

[1] D. Scribano, A. Petrucca, M. Pomplii, C. Ambrosi, E. Bruni, C. Zagaglia, G. Proseda, L. Nencioni, M. Casalino, F. Polticelli, M. Nicoletti, Polar localization of PhoN2, a periplasmic virulence-associated factor of Shigella flexneri, is required for proper IcsA exposition at the old bacterial pole, PLoS One 9 (2014) e90230.

[2] N. Carayol, G. Tran Van, Nhieu, The inside story of Shigella invasion of intestinal epithelial cells, Cold Spring Harb. Perspect. Med. 3 (2013) a016717.

[3] C. Sasakawa, A new paradigm of bacteria-gut interplay brought through the study of Shigella, Proc. Jpn. Acad. Ser. B Phys. Biol. Sci. 86 (2010) 229–245.

[4] C.J. Kuehl, A.M. Dragoi, A. Talman, H. Agaisse, Bacterial spread from cell to cell: beyond actin-based motility, Trends Microbiol. 23 (2015) 558–566.

[5] D. Santapaola, F. Del Chierico, A. Petrucca, S. Uzzau, M. Casalino, B. Colonna, R. Sessa, F. Berlutti, M. Nicoletti, Apyrase, the product of the virulence plasmid-encoded phoN2 (apy) gene of Shigella flexneri, is necessary for proper unipolar IcsA localization and for efficient intercellular spread, J. Bacteriol. 188 (2006) 1620–1627.

[6] R.N. Reusch, Insights into the structure and assembly of Escherichia coli outer membrane protein A, FEBS J. 279 (2012) 894–909.

[7] C. Ambrosi, M. Pomplii, D. Scribano, C. Zagaglia, S. Ripa, M. Nicoletti, Outer membrane protein A (OmpA); a new player in shigella flexneri protrusion formation and inter-cellular spreading, PLoS One 7 (2012) e49625.

[8] A.W. Confe, S. Ayalew, The OmpA family of proteins: roles in bacterial pathogenesis and immunity, Vet. Microbiol. 163 (2013) 207–222.

[9] J. Sambrook, D.W. Russel, Molecular Cloning: A Laboratory Manual, third ed., Cold Spring, 2001.

[10] M. Renault, O. Saurel, J. Czaplicki, P. Demange, V. Gervais, F. Löhrr, V. Réat, T. Cierpicki, B. Liang, L.K. Tamm, J.H. Bushweller, Increasing the accuracy of proteomics and characterization of an immunogenic outer membrane protein of Shigella flexneri 2a, Vaccine 27 (2009) 5855–5864.

[11] D. Pore, P. Chowdhury, N. Mahata, A. Pal, S. Yamasaki, D. Mahalanabis, M. K. Chakrabarti, Purification and characterization of an immunogenic outer membrane protein of Shigella flexneri 2a, Vaccine 27 (2009) 5855–5864.

[12] D. Pore, N. Mahata, M.K. Chakrabarti, Outer membrane protein A (OmpA) of Shigella flexneri 2a links innate and adaptive immunity in a TLR2-dependent manner and involvement of IL-12 and nitric oxide, J. Biol. Chem. 287 (2012) 12589–12601.

[13] R. Koebnik, K.P. Locher, P. Van Gelder, Structure and function of bacterial outer membrane proteins: barrels in a nutshell, Mol. Microbiol. 37 (2000) 239–253.

[14] S. Khalid, P.J. Bond, T. Carpenter, M.S. Sansom, OmpA: gating and dynamics via molecular dynamics simulations, Biochim. Biophys. Acta 2008 (1778) 1871–1880.

[15] J. Marcoux, A. Politis, D. Rinehart, D.P. Marshall, M.I. Wallace, L.K. Tamm, C.V. Robinson, Mass spectrometry defines the C-terminal dimerization domain and enables modeling of the structure of full-length OmpA, Structure 22 (2014) 781–790.

[16] J.S. Park, W.C. Lee, K.J. Yeo, K.S. Ryu, M. Kumarasiri, D. Hesek, M. Lee, S. Moabashery, J.H. Song, S.I. Kim, J.C. Lee, C. Cheong, Y.H. Jeon, H.Y. Kim, Mechanism of anchoring of OmpA protein to the cell wall peptidoglycan of the gram-negative bacterial outer membrane, FASEB J. 26 (2012) 219–228.

[17] C. Zheng, L. Yang, M.R. Hoopsmann, J.K. Eng, X. Tang, C.K. Weisbrod, J.E. Bruce, Cross-linking measurements of in vivo protein complex topologies, Mol. Cell Proteom. 10 (2011), M110.006841.

[18] E.J. Danoff, K.G. Fleming, The soluble, periplasmic domain of OmpA unfolds as an independent unit and displays chaperone activity by reducing the self-association propensity of the unfolded OmpA transmembrane β-barrel, Biophys. Chem. 159 (2011) 194–204.

[19] H. Ishida, A. Garcia-Herrero, H.J. Vogel, The periplasmic domain of Escherichia coli outer membrane protein A can undergo a localized temperature dependent structural transition, Biochim. Biophys. Acta 14 (1838) 3014–3024.