Nanoscopic Surfactant Behavior of the Porin MspA in Aqueous Media

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ABSTRACT

The mycobacterial porin MspA is one of the most stable channel proteins known to date. MspA forms vesicles at low concentrations from aqueous buffers. Evidence from Dynamic Light Scattering, Transmission Electron Micrography and zeta (ζ) - Potential measurements by electrophoretic light scattering indicate that MspA behaves like a nanoscale surfactant. The extreme thermostability of MspA allows these investigations to be carried out at temperatures as high as 343 K, at which most other proteins would quickly denature. The principles of vesicle formation of MspA as a function of temperature and the underlying thermodynamic factors are discussed. The results obtained provide crucial evidence in support of the hypothesis that, during

vesicle formation, nanoscopic surfactant molecules, such as MspA, deviate from the principles underlined in classical surface chemistry.

INTRODUCTION

The homo-octameric porin MspA from *Mycobacterium smegmatis* is one of the most stable proteins known to date.[1] Due to its size and unique structure[2], resistance to temperature and pH-changes and its stability on non-aqueous solvents[3], MspA has become a versatile tool in bio-nanotechnology. MspA is able to reconstitute within phospholipid double layers[4] and polymer layers on surfaces.[5] This protein can stand alone on surfaces without a supporting polymer or double layer.[6] It is capable of binding gold nanoparticles[6,7] and ruthenium polypridyl complexes.[8] In fact, the binding of so-called "channel blockers" near the constriction zone of MspA has been discussed as a new strategy to fight mycobacterial infections, such as tuberculosis.[8] Although the presence of MspA homo-octamers on surfaces has been unambiguously proven by using TEM (Transmission Electron Microscopy)[5], AFM (Atomic Force Microscopy)[6] and electrochemical techniques[9], only very little is known about the three-dimensional clustering behavior of MspA in aqueous phase. Engelhardt *et al.* have established by using high-resolution TEM that MspA forms micelles and linear aggregates on surfaces showing a zipper-like pattern in the absence of surfactants, and that is able to reconstitute in dimyristoyl phosphatidylcholine (DMPC) vesicles in the presence of HEPES (pH 7.5) / NaN_3 buffer.[10] The formation of this typical zipper-like pattern is achieved through interaction of the strongly hydrophobic docking zones of MspA (Figure 1A), thus shielding the proteins' stems from water.

This study is concerned with the 3D-aggregation behavior of MspA in aqueous buffers, further expanding the pioneering work of Engelhardt *et al.* In 1x PBS (phosphate-buffered saline), MspA is capable of forming vesicles in the absence of added surfactant. Owing to the great thermal stability of MspA[3], we were able to study the influence of ionic strength and especially the temperature on the size of the MspA-vesicles and their zeta-potentials. The influence of temperature on the 3D-aggregation behavior of peptides is rarely discussed, because the temperature is well defined in many living organisms and only a few proteins do not denature at higher temperatures. α-Hemolysin from *Staphylococcus aureus* forms heptameric transmembrane pores that are stable over a wide pH-range and up to 60 °C.[11] However, heptameric α-hemolysin pores are not stable without a stabilizing membrane. Therefore, it can be expected that clusters of monomers (not heptamers) will be formed at higher temperatures in the absence of a membrane. Principally, the same behavior, albeit at lower temperatures (T > 40 °C) can be anticipated for the protective antigen part of anthrax toxin from *Bacillus subtilis / Bacillus anthracis*, which forms heptameric and octameric oligomers.[12] In the near future, designer proteins with tailored biophysical properties are increasingly becoming available[13], and therefore, the influence of temperature on their supramolecular aggregation behavior will become more significant. Recently, the temperature-dependence of the dynamic of several proteins has been studied by FRET (Förster resonance energy transfer).[14,15,16] This study was intended to demonstrate the potential of using dynamic light scattering (DLS) and the measurement of zeta potentials when the studying supramolecular aggregation of proteins.

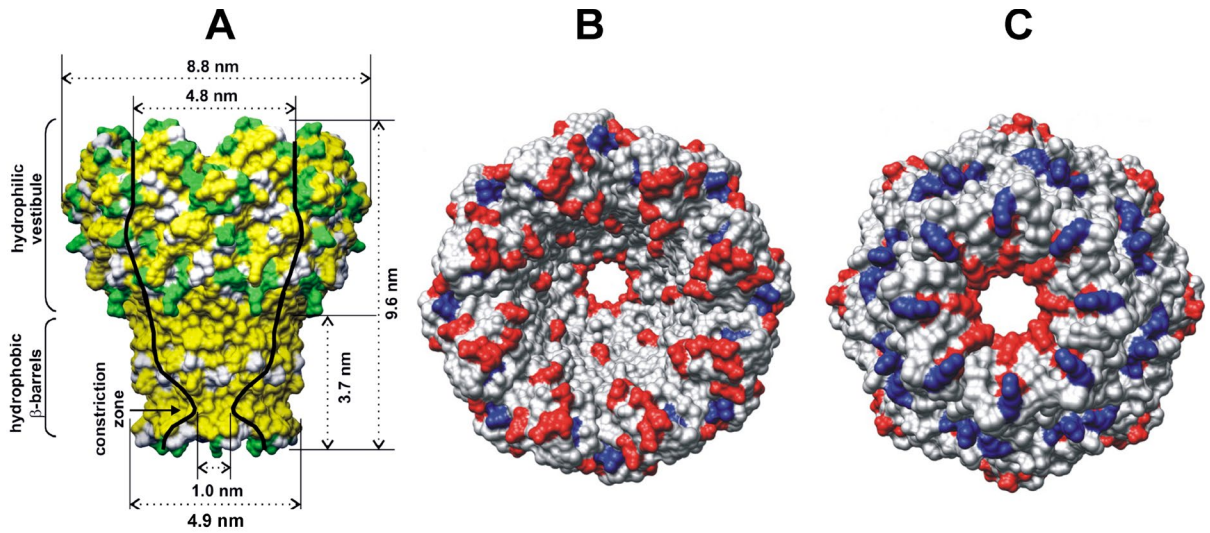


Figure 1: The structure of the homo-octameric mycobacterial porin MspA. A) MspA is 9.6 nm in length and 8.8 nm in width. Its "docking zone", which is formed by hydrophobic □eta-barrels, is located at the "stem". Reproduced with permission from reference 2. B) Structural model of the MspA pore viewed from the top. Negatively and positively charged amino acids are shown in red and blue, respectively. Other amino acids are shown in gray. C) MspA pore viewed from the bottom. B) and C) were adapted from reference 17 using the UCSF Chimera software. Chimera is developed by the Resource for Biocomputing, Visualization, and Informatics at the University of California, San Francisco (supported by NIGMS P41-GM103311).[18]

RESULTS AND DISCUSSION

MspA (porin A from *M. smegmatis*), an octameric channel protein (184 amino acids, M_w = 155,248 Da [19]) is isolated from the outer cell wall of *M. smegmatis*, which is a species of non-pathogenic mycobacteria, commonly found in soil. [20] The structure of MspA has been studied extensively and bares no significant resemblance to any other protein known to date.[2] X-ray studies performed on a mutant MspA strain have provided a complex, detailed structural analysis.[2] Extraction of MspA is carried out using non-ionic detergents and temperatures as high as 90 °C.[21] Remarkably, this porin retains its pore forming ability even after being exposed to harsh physical conditions such as heating to 100 ºC in SDS[22] and being exposed to extreme pH ranges such as 2-14[23]. In fact, high temperature has been a crucial factor in determining the

purity of MspA extracts, as other proteins were denatured and removed by these conditions. Consequently MspA has been classified as the most stable channel forming protein known so far. These findings make MspA especially suited for the study of the influence of temperature on supramolecular aggregation, as it is known to withstand drastic chemical conditions without denaturation.

The MspA-octamer is formed by 160 negatively charged and 64 positively charged amino acids.[2] R165 and E63/E127, as well as R161 and E39, form salt bridges, which greatly stabilize its tertiary structure (R: arginine, E: glutamic acid).[2] As a result, 136 negatively charged and 48 positively charged amino acids are surface accessible. Whereas the negative charges are predominantly found within the interior of the "goblet", positive charges are concentrated in the stem and the periplasmatic loop region of MspA (Figure 1B,C). We have investigated the aggregation of individual MspA in diluted aqueous solutions (5 x 10^{-5} x PBS (phosphate buffered saline) and 1 x PBS) as a function of temperature. MspA shows a distinct tendency to aggregate independent of ionic strength of the surrounding medium.

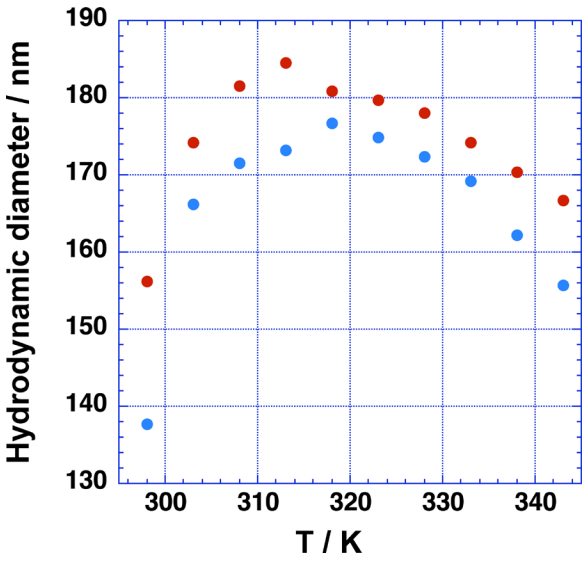


Figure 2: Hydrodynamic diameter of MspA aggregates as a function of temperature, measured by dynamic light scattering (DLS): blue: MspA (1.688 x 10^{-5} mg mL^{-1}) in 5 x 10^{-5} x PBS; red: MspA (1.688 x 10^{-5} mg mL^{-1})) in 1 x PBS. The relative experimental in diameter error has been determined to ±8 nm. Typical polydispersities of the formed supramolecular aggregates is provided in the SI section. PBS (phosphate buffered saline) consists of 8.0 g of NaCl, 0.20 g of KCl, 1.44 g of Na_2HPO_4 and 0.24 g of KH_2PO_4 in 1 L of H_2O, pH=7.40).

The maxima of the supramolecular structures formed were observed at 312 K (standard PBS) and 318 K (diluted PBS). The diameters of these aggregates were in both cases very close to 180 nm and indistinguishable due to experimental error. Since the aggregation proceeds independent of the ionic strength of the medium, it is our paradigm that hydrophobic aggregation is the major mechanism behind the observed aggregation behavior of MspA. In applying a semi-quantitative predictive model of forming supramolecular aggregates to MspA[24], we have calculated the packing parameter P:

$$P = \frac{V_0}{a_0 I_0} \tag{1}$$

V_0: surfactant tail volume, a_0: area at the aggregate interface, I_0: tail length.

Using the geometric parameters of MspA, we have calculated V_0 = 69.7 nm^3 (the geometric dimensions of the "docking region" are 3.7 nm in length (I_0), and 4.9 nm in diameter[2], see Figure 3) and a_0 = 60.8 nm^2.

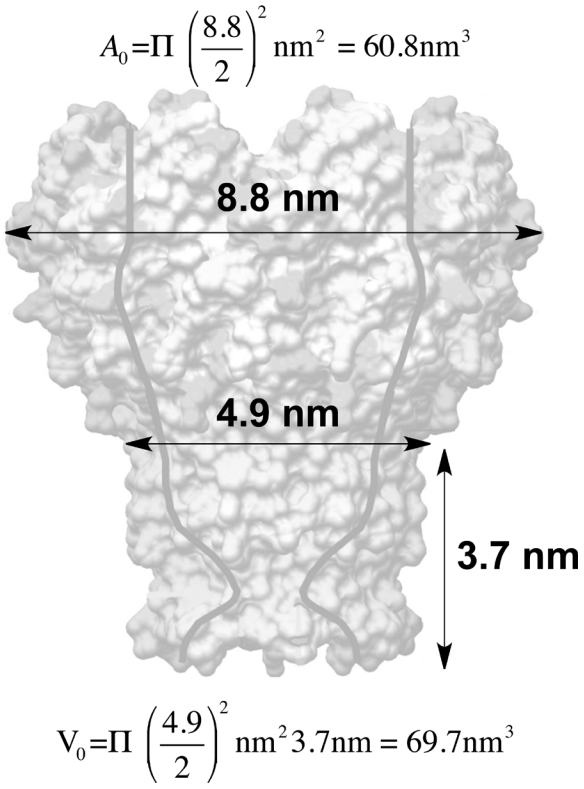


Figure 3: Geometric calculations based on the crystal structure of MspA.[2]

The packing parameter of MspA is 0.31, which is indicative of surfactants forming spherical or ellipsoidal micelles. To our surprise, TEM characterization of MspA aggregates clearly indicated the formation of vesicles (Figure 4). However, typically vesicles are formed by surfactant bilayers featuring a packing parameter in the range of 0.5 to 1.0. [25]

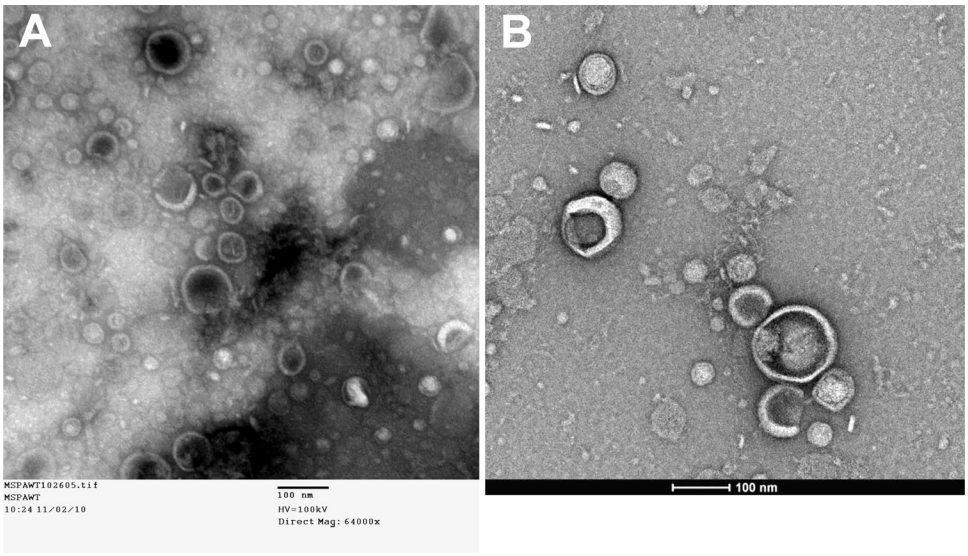


Figure 4. TEM of vesicles formed from MspA on a carbon-coated 200-mesh copper grid. A: MspA vesicles formed in 5 x 10^{-5} x PBS at 312 K (after deposition and in high vacuum on Cu). B: MspA vesicles formed in 1 x PBS under analogous conditions.

This discrepancy requires a discussion. As discussed in the introduction, MspA forms linear aggregates in a zipper-like pattern on surfaces.[10] This behavior is indicative of a packing parameter that is very close to 1.0.[19] Whereas the "docking zone" of MspA is formed by very stable hydrophobic β-barrels, the hydrophilic vestibule (the surfactant's "head") can potentially be deformed when single MspA proteins aggregate. Protein deformation is often observed during crystallization.[26] The formation of a bilayer is evidence for attractive interactions between MspA units. Predicting the geometry of supramolecular aggregates formed by one type of surfactants is assuming that the charged head groups show charge- and/or sterical repulsion.[19] However, the observed formation of vesicles indicates that the interactions of the vestibules are attractive. Furthermore, the formation of vesicles is not a function of ionic strength, as Figure 4AB indicates, as MspA forms vesicles in both diluted and 1X PBS in a similar manner. This

supports the mechanistic assumption that efficient charge-repulsion between the head groups of MspA is not observed.

Aggregation Number as a Function of Vesicle Radius

We have calculated the aggregation number N of MspA-octamers that form a unilamellar vesicle as a function of the vesicles' diameter according to eqn. 2.

$$N = \frac{4\Pi r_e^2}{A} + \frac{4\Pi r_i^2}{A} \tag{2}$$

r_e is the external radius of the vesicle, which is consistent with its diameter divided by 2.

r_i is the inner radius of the vesicle, which is $r_e^2 - 2\ (L_{MspA} - L_{dz})$ (L_{MspA}: length of MspA = 9.6 nm; L_{dz}: length of the docking zone = 3.7 nm, see Figures 1 and 3)

A: Area occupied by one MspA-octamer: 72.4 nm^2. This calculation is based on the assumption that the docking zones are in contact in the vesicles double layer. This interaction causes the centers of MspA within either the external or the internal layer to be 9.6 nm apart from each other, forming a simple packing pattern (see Figure 5). The largest diameter of MspA is 8.8 nm.[2]

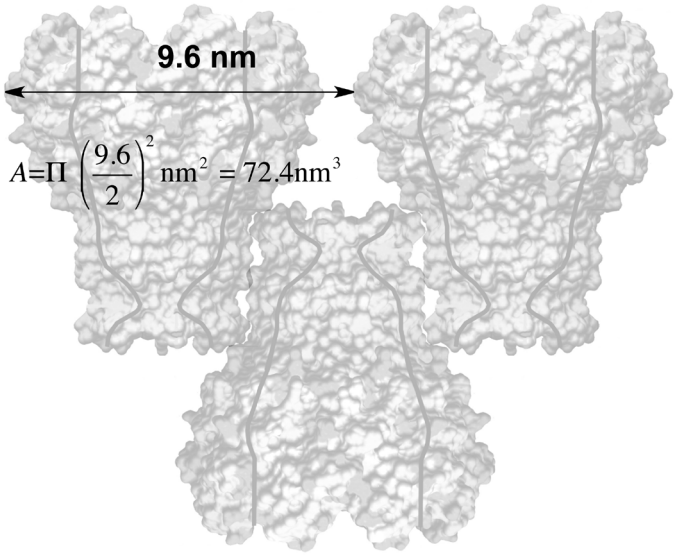


Figure 5: Distance between two neighboring MspA octamer in the outer layer of the vesicle's double layer, and effective size of MspA within that layer.

The inner radius r_i is smaller than the external radius r_e by twice the lengths of MspA minus the extension of the docking zone, because MspA forms aggregates showing a zipper-like pattern in which the hydrophobic docking zones are in contact with each other.[10]

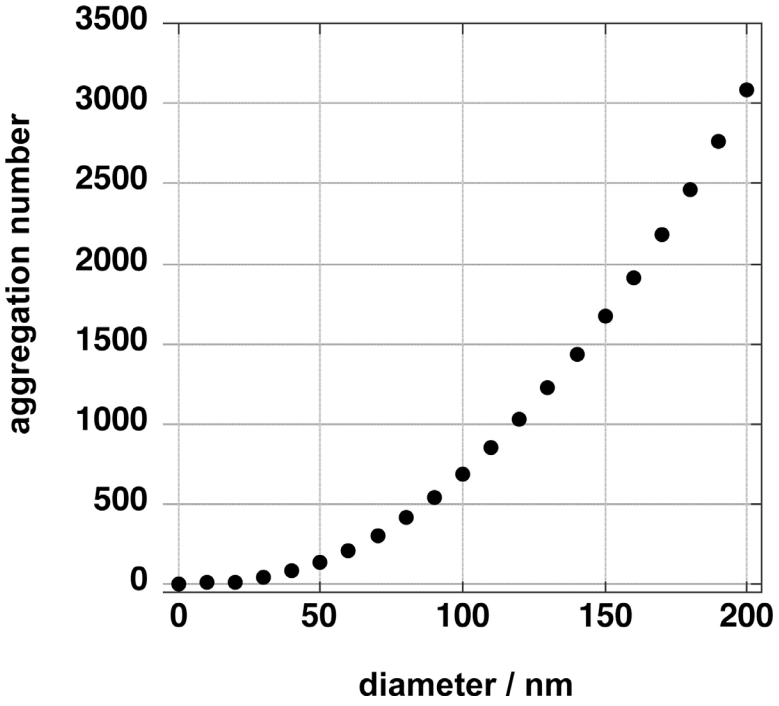


Figure 6: Estimated number of MspA-octamers forming a unilamellar vesicle (the presence of one MspA double layer is assumed) as a function of vesicle radius, according to eqn. 2.

According to eqn. 2 and Figure 6, the aggregation number N varies between N=1395 (d = 138 nm) and N=2470 (d = 180 nm) for the diameters reported in Figure 2.

The Hydrophobic Effect is Responsible for Vesicle Formation by MspA

In describing the self-assembly process by the free energy model originally developed by C. Tanford[27] and assuming that the residual contact of the water with the hydrophobic constriction zone is negligible after vesicle formation, the change in the chemical potential ($\Delta\mu^0$) during

supramolecular aggregation is dependent on the transfer of MspA from the aqueous phase into the MspA-bilayer and the interaction of the head groups.

$$\left(\frac{\Delta\mu^0}{kT}\right)=\left(\frac{\Delta\mu^0}{kT}\right)_{\text{Transfer}}+\left(\frac{\Delta\mu^0}{kT}\right)_{\text{Head Groups}} \quad (3)$$

k: Boltzmann constant. T: temperature in K

$\left(\frac{\Delta\mu^0}{kT}\right)_{\text{Transfer}}$ is negative, because the solvation of extended hydrophobic surfaces has a disruptive effect on water structure. Whereas the hydrogen bond network of water around an alkane of modest length (e.g. C_6H_{14}) is not distorted significantly, the solvation of extended hydrophobic structures has a disruptive effect on water structure because it prohibits the formation of an extended hydrogen bonding network. Huang and Chandler have established that the excess chemical potential decreases monotonically with temperature for structures with radii R > 1 nm, as this is the case with the "docking zone" of MspA (r = 1.85 nm).[28]

$\left(\frac{\Delta\mu^0}{kT}\right)_{\text{Head Groups}}$ is describing the energetic contribution arising from the interactions of the vestibules of MspA in the bilayer. Due to the presence of polar amino acid side chains at the exterior of MspA's "head", hydrogen bonding[29] is most likely responsible for the discrepancy of the calculated packing parameter P = 0.31 and the experimental finding that vesicles are formed, which requires $0.5 < P < 1$.[27] Charge attraction/repulsion[30] is apparently only playing a minor role, since the observed formation of liposomes does not strongly depend on the ionic strengths of the aqueous medium. The anisotropy of the negative and positive charges at the outer surface

of MspA is shown in Figure 1 B) and C). The experimental finding that MspA forms vesicles and not micelles under the described conditions, clearly indicates that there exist additional forces in supramolecular MspA aggregates, which are hydrogen bonding, and, to a significantly lesser extent, charge attraction. Thus, the transfer of MspA from the aqueous phase to the bilayer is driven by the hydrophobic effect, which is the thermodynamic driving force of vesicle formation. The influence of charge attraction/repulsion and hydrogen bonding will be discussed below.

Zeta Potentials of MspA-Vesicles as Functions of Temperature and Ionic Strength

To study the charge of the MspA vesicles as a function of temperature, we have performed a series of zeta potential measurements by electrophoretic light scattering.[31] The results are summarized in Figure 7. The zeta potential is the electric potential between the slipping plane in the interfacial double layer and the bulk solution.[28]

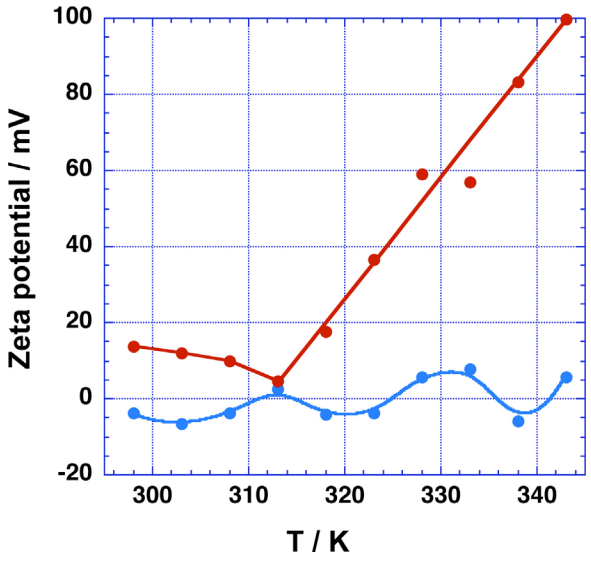


Figure 7: Zeta potential of MspA aggregates as a function of temperature: blue: MspA (1.688 x 10^{-5} mg mL^{-1}) in 5 x 10^{-5} x PBS; red: MspA (1.688 x 10^{-5} mg mL^{-1}) in 1 x PBS.

The zeta potential ζ of MspA vesicles oscillates around the point of zero charge in 5 x 10^{-5} x PBS as the temperature increases. The observed oscillations are reproducible (experimental error ±5 mV at each respective temperature). They are indicative of a complicated interplay between deprotonation of MspA's carboxylic acid groups and increased protonation of MspA's amine functions. Both effects increase with increasing temperature. The enhanced macromolecular motion of MspA with increasing temperature may lead to a changing dynamics of forming and breaking hydrogen bonds as the temperature is increased. We are unable at this point to provide a qualitative analysis of this phenomenon.

The zeta potential ζ of MspA vesicles in 1 x PBS as a function of temperature is completely different. ζ is slightly positive (ζ = 10±14 mV) in the temperature range from 296 to 320 K. Beyond 320 K, a remarkable increase of ζ is observed. At 344 K ζ= 100±12 mV indicates excellent stabilization of MspA-vesicles in PBS. The temperature dependence of the ζ potential is indicative of an endergonic adsorption process of cations (Na^+ and K^+) at MspA. The observed increase of ζ as a function of T is completely reversible. It is noteworthy that the remarkable difference in the surface charges of MspA vesicles in diluted PBS and 1x PBS only results in slightly different diameters, as shown in Figure 2. The size of the MspA vesicles decreases in both media, however, the decrease is stronger in diluted PBS than in 1x PBS, indicating that charge-attraction/repulsion does not contribute significantly to $\left(\frac{\Delta\mu^0}{kT}\right)_{\text{Head Groups}}$, although it is the strongest interactive force (± 5-8 kJ mol^{-1} per bridge/repulsion) in supramolecular binding.[27] The pH of both media (5 x 10^{-5} x PBS and 1 x PBS) was exactly 7.20 at 296 K. Therefore, we assume that the extent of hydrogen bonding events between MspA - "heads" in the bilayer occurs when forming vesicles from both media. Hydrogen bonds between side chains of proteins have a

typical strength of 4-5 kJ mol^{-1} per bridge.[23] At this point we cannot distinguish between the effects of charge-attraction/repulsion and hydrogen bonding on the supramolecular attraction of the vestibules of MspA when forming the bilayer. In addition, different types of attraction/repulsion may exist between MspAs on the same and the opposite side of the bilayer, because the charge distribution at MspA's surface is not isotropic (see Figure 1). The increase of the vesicles' diameters in both, diluted and standard PBS between 296 K and 312 K (1 x PBS) or 318 K (5 x 10^{-5} x PBS) could be caused by a thermal activation step required for vesicle formation. Due to the thermal stability of MspA, it is reasonable to assume that the numbers of vesicles decrease while their diameters increase, because the concentration of free MspA will be very low. Since MspA is a large surfactant, the requirement for thermal activation is comprehensible. It should also be noted that many classic vesicles/liposomes are not in their thermodynamic minimum.[32]

EXPERIMENTAL

MspA was extracted from *M. smegmatis* and purified, adapting from a procedure that was originally developed by Niederweis and coworkers.[21,33] The procedure is described in detail in the SI section.

The hydrodynamic diameter and the zeta potential of the MspA aggregates were measured on a ZetaPALS Zeta Potential Analyzer (Brookhaven Instruments Corporation) by hydrodynamic light scattering and laser Doppler electrophoresis. One drop (50 µl) of wild type MspA extract (~0.6 mg/ml in 1x PBS) was diluted in 2.0 ml of deionized water and the average effective diameter of protein aggregates were recorded while increasing the temperature of the sample. The measurements were taken at increasing temperature values from 25 to 30, 35, 40, 45, 50, 55, 60, 65 and 70 °C. A consistent fluctuation of effective diameter was observed with increasing

temperature. The experiment was repeated using 2.0 ml of 1x PBS buffer solution instead of deionized water. Similarly, zeta potential was measured for wild type MspA extracts in both deionized water and 1x PBS solutions.

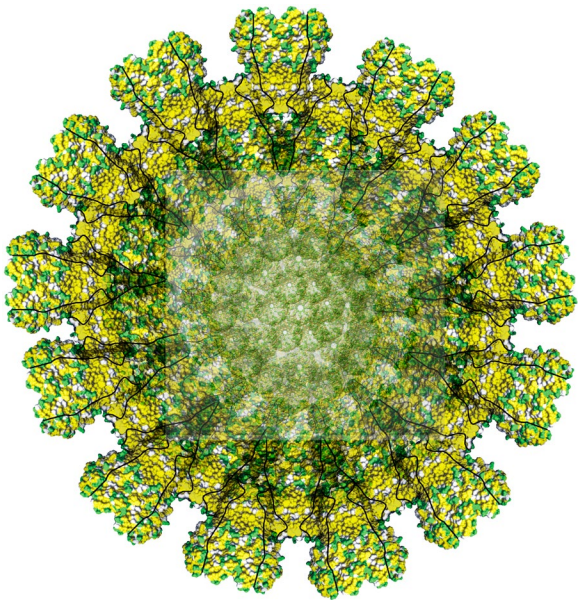
Transmission Electron Micrographs were recorded in the Microscopy and Analytical Imaging Laboratory of the University of Kansas, 1043 Haworth Hall, 1200 Sunnyside Ave, Lawrence, KS 66045. The morphology of MspA aggregates from aqueous buffers was characterized by transmission electron microscopy (TEM). The TEM samples were prepared by immersing carbon-coated 200-mesh copper grids in the aqueous solutions, followed by overnight drying in a desiccator. The dried grids were analyzed by using a Philips CM100 microscope operated at 100 kV.

CONCLUSIONS

TEM has provided experimental evidence that the mycobacterial porin MspA forms vesicles at low concentrations from aqueous buffers. The size of the MspA vesicles is strongly dependent on temperature, but not on the salt content of the aqueous buffer. The hydrodynamic maximum of the vesicles has been determined by dynamic light scattering to approx. 180 nm. It occurs at 312 K (standard PBS) and 318 K (diluted PBS). The occurrence of a temperature maximum is indicative of a thermal activation step required for the formation of bilayers from MspA, which is a rather large surfactant of 9.6 nm in length and 8.8 nm in diameter. Increasing the temperature favors reversible cation (Na^+, K^+) adsorption at MspA in 1 x PBS. It is noteworthy that the corresponding significant increase in ζ does not significantly affect the hydrodynamic diameter of the vesicles. The aggregation number of the vesicles formed by MspA varied between N=1395 and N=2470 for the diameters measured by DLS. Although the aggregation behavior of

MspA as a function of temperature is apparently governed by the hydrophobic effect, we have observed evidence for a strong influence of the ionic strength in the surface charges of MspA vesicles. Our experimental data clearly indicate that temperature is an important experimental variable in this supramolecular system formed by a stable protein. Advances in protein design will lead to increasingly stable supramolecular systems using proteins as biological building elements in functional nanoscopic systems. It is our prediction that the physical properties of these systems will be strongly dependent on their temperature. This is of equal importance for their assembly as well as for their function under operating conditions.

TOC graphic: The mycobacterial protein MspA forms vesicles in aqueous solutions.



ASSOCIATED CONTENT

Supporting Information. The Supporting Information section contains the general formula for calculating the ζ-potentials and representative results from Dynamic Light Scattering. This information is available free of charge via the Internet at http://pubs.acs.org

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Author Contributions

The manuscript was written through contributions of all authors. All authors have given approval to the final version of the manuscript.

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