A Quadrupole/Time-of-Flight Mass Spectrometry Study of Trp-Cage's Conformation

Mingxiang Lin, Zeeshan Ahmed, Christopher R. Taormina, and Kasi V. Somayajula*

Department of Chemistry, University of Pittsburgh, Pittsburgh, Pennsylvania, USA

Trp-cage is a synthetic 20-residue miniprotein that uses tertiary contacts to stabilize its native conformation. NMR, circular dichroism (CD), and UV-resonance Raman spectroscopy were used to probe its energy landscape. In this quadrupole/time-of-flight study, electrospray ionization charge state distribution (CSD) and solution-phase H/D exchange are used to probe Trp-cage's tertiary structure. The CSDs of Trp-cage and its mutant provide spectra showing a pH-dependent conformation change. Solution-phase H/D exchange in 30% deuterated trifluoroethanol solution of the wild type shows increased protection of one labile hydrogen in the native state. Together, CSDs and solution-phase H/D exchange are demonstrated to constitute a simple but effective means to follow conformation changes in a small tertiary protein. (J Am Soc Mass Spectrom 2007, 18, 195–200) © 2007 American Society for Mass Spectrometry

Trp-cage is a synthetic 20-residue miniprotein of sequence $N_1LYIQWLKDG_{10}GPSSGRPPPS$, which resulted from a de novo design effort [1]. The effort began with an examination of a poorly folded 39 residue long saliva protein of a Gila monster. Using an iterative design effort with selective mutations and truncations, Neidigh et al. [1] created different variants and characterized their folded states using NMR and circular dichroism spectroscopy (CD). Trp-cage, originally referred to as Tc5b, exhibited the most structure in terms of the cage motif. It was found to be 95% folded under physiological conditions.

Trp-cage consists entirely of natural amino acids and has been shown to exhibit elements of tertiary structure in the absence of disulfide bridges, metal ion chelation, or stabilization through oligomerization [2]. NMR and CD data of Neidigh et al. [1] suggest a simple two-state unfolding mechanism. Using the intrinsic fluorescence of Trp, Qiu et al. [3] determined the folding time to be $4 \ \mu s$, which makes Trp-cage the fastest folding polypeptide to exhibit a tertiary structure.

Several groups previously reported theoretical simulations of Trp-cage's folding [4–11]. Simmerling et al. [4], in their all atom molecular dynamics simulation, calculated a native-state topology consistent with the NMR structure reported by Neidigh et al. [1]. Their simulation at 325 K, which modeled the folding of Trp-cage, found that it converges to a native-state topology within 20 ns. Snow et al. [6] carried out stochastic dynamics simulations over a total modeled folding time of 100 μ s and found that the unfolded state retains features resembling the native-state topology.

Ahmed et al. [12] recently°used°UV-resonance°Raman spectroscopy (UVRR) to examine the thermal unfolding behavior of Trp-cage. The authors demonstrated that at physiological pH, Trp-cage initially melts to a more compact intermediate state as temperature is increased from 4 to 20 °C, while retaining its nativestate secondary structure. Increasing the temperature to 70 °C results in partial unfolding of this maximally compact intermediate, although it still retains some native-like features even at high temperatures, as suggested by the invariance of the trytophan's χ^2 dihedral angle°[12].

Recently, °Adams°et°al.°[13]°applied°electron°capture dissociation mass spectrometry to examine the conformation of different charge states of Trp-cage. The authors propose that the +2 state retains the solutionphase native conformation, whereas the +3 charge state, dominated by ionic hydrogen bonds, adopts a more open gas-phase conformation. Furthermore, Adams° et°al.°[13]° demonstrated° that° D-Tyr° substitution denatures Trp-cage's native structure. The D-isomer prevents stabilization of the tryptophan side chain that destabilizes the hydrogen-bond network and increases the°interior°solvent°accessibility°[13].

Published online October 24, 2006

Address reprint requests to C. Taormina, Department of Chemistry, University of Pittsburgh, Pittsburgh, PA, 15260, USA. E-mail: crtst7@pitt.edu * Present address: The Coca-Cola Company, 1 Coca-Cola Plaza, Atlanta, GA 30313.

In this study, we use the conformational dependency of protein charge state distributions (CSDs) in electrospray ionization mass spectrometry (ESI-MS) to examine the pH dependency of Trp-cage's conformation. Well documented for over a decade, protein CSDs in ESI-MS show a shift toward higher charge state values upon protein unfolding [14°-17]. Through this marker, we can discriminate between different global conformations of Trp-cage as the solvent pH is varied. Furthermore, we also probe Trp-cage conformation by solution-phase hydrogen/deuterium exchange, which is an established mass spectrometric technique for protein conformation and dynamics tudies [18].

Experimental

Mass spectrometry measurements were performed on a hybrid quadrupole time-of-flight mass spectrometer (Q-ToF MS, API-US, Micromass UK Ltd., Manchester, UK), equipped with a Z-spray electrospray source. The typical instrument operation parameters at the source region for this study were: capillary voltage 3.5 kV, cone voltage 40 V, source temperature 80 °C, desolvation temperature 150 °C, cone gas flow 60 L/h, and desolvation gas flow 600 L/h. Sample solutions were injected from the embedded syringe pump at a flow rate of 10 μ L/min. Argon was used as the collision gas with a pressure of 5×10^{-5} bar at the analyzer pressure. The collision energy was kept at 10 V in the ToF MS mode. The instrument was calibrated externally by a cesium iodide solution up to 2500 amu. Spectra were accumulated at 1 s per scan at reflectron V mode with a full-width half-maximum resolution of 10,000. Data acquisition and processing were performed by use of MassLynx V4.0 software (Waters Corp., Milford, MA).

Trp-cage peptide was obtained at >95% purity from the Pittsburgh peptide synthesis facility and was used at 40 μ M concentrations. D-Tyr substituted Trp-cage peptide was provided by Dr. Zubarev at Uppsala University and was used at 18 μ M concentrations. The pH in all of the experiments was adjusted using glacial acetic acid (Aldrich, St. Louis, MO) and NH₄OH (Aldrich).

Charge state distribution analysis was carried out by measuring the intensity differences of the ToF spectrum of Trp-cage aqueous solutions at pH 3 and pH 7. A complete deuterium-exchanged Trp-cage spectrum was obtained from a 100% D₂O Trp-cage solution buffered at pH 7 using deuterated acetic acid and ammonium hydroxide (Sigma Chemical, St. Louis, MO). By dissolving Trp-cage directly in 70% D₂O and 30% deuterated trifluoroethanol, CF₃CH₂OD (d-TFE, Sigma Chemical), we examined the amide hydrogen protection against hydrogen–deuterium (H/D) exchange in a 30% TFE (Aldrich) solution by continuously monitoring the temporal dependency of the spectrum up to 30 min.

Results and Discussion

Trp-cage charge state distributions were obtained at pH 3° and° pH° 7.° As° shown° in° Figure° 1a,° the° ESI° mass spectrum of the wild-type Trp-cage at pH 7 shows three peaks corresponding to the +1, +2, and +3 charge state, with +2 being the dominant state. The intensity ratio of charge state +2/charge state +3 is 2.0. The intensity ratios obtained at different solvent conditions and° pH° values° are° summarized° in° Table° 1.° As° the solution pH is decreased from pH 7 to pH 3, the CSD shifts from the +2 to the +3 state and the intensity ratio of +2 to +3 charge states decreases from 2.0 to 0.3. The weak +1 state observed at pH 7 is no longer observed at pH 3. Our results indicate that at low pH Trp-cage denatures, adopting a more open conformation results in a CSD shift to the +3 charge state. Contrary to the behavior of wild-type Trp-cage, the D-Tyr substituted mutant shows a dominant +3 state at either pH with the intensity ratio of +2 to +3 charge states being 0.2 at pH 3 and 0.6 at pH 7. The spectrum obtained at pH 7 is shown°in°Figure°2b.°The°difference°in°intensity°ratio°at the two pH values likely arises from charge repulsion. The D-Tyr substituted mutant adopts a more open conformation at either pH value compared to that of the wild-type Trp-cage at pH 7. Our results offer further support°of°the°proposal°introduced°byAdams°et°al.°[13] that the substitution with the D-Tyr isomer within Trp-cage denatures the native Trp-cage conformation.

We further probed the Trp-cage by examining its conformation in an aqueous solution of 30% TFE. Helixstabilizing effects of aqueous TFE are well documented [19].°Extensive°work°on°helix-stabilizing°effects°of°TFE indicate that 30% vol/vol is the optimum concentration of°TFE'heeded°tor'helical°stabilization°[1,°19]. Neidigh°et al.° [1]° showed° that° Trp-cage° exhibits° a° pronounced resistance to thermal denaturation in 30% vol/vol aqueous TFE solution. They reported an increased amide protection of Leu HN and Trp H ϵ 1 hydrogens in TFE solution, which indicates a more stable native state. Based on this evidence Neidigh et al. argued that the addition of TFE led to increased "nativeness" of the protein.

Figure 2°shows ESI-ToF spectra°of $40^{\circ}\mu$ M Trp-cage in 30% TFE and 70% H₂O solution at pH 3 and pH 7. The intensity ratio of +2 and +3 charge states at pH 7 is 2.5 and the value is comparable to the value of 2.0 observed in aqueous solution. The stabilizing effect of TFE can be seen from the intensity ratio of +2 and +3 charge states at pH 3. The ratio is 0.3 in pure water, whereas the ratio changes to 1.3 in 30% TFE aqueous solution. This signifies an increase in "nativeness" or compactness of Trp-cage in aqueous TFE solutions. Our conclusions agree°with°the°observations°of°Neidigh°et°al.°[1].

We further probed the Trp-cage conformation by examining the H/D exchange protection of labile hydrogens. The spectrum of Trp-Cage in 100% H₂O is shown'inFigure³a°and'in¹00% D₂O, obtained within 1 min° after° dissolution,° is° shown° in° Figure° 3b.° The



Figure 1. ESI-ToF spectrum of (a) 40 μ M Trp-cage in H₂O at pH 7; (b) 18 μ M D-Tyr substituted Trp-cage in H₂O at pH 7.

 Table 1. Intensity ratio of charge state +2/charge state +3 of Trp-cage and D-Tyr substituted Trp-cage under different solvent conditions

Experimental conditions	Intensity of charge state +2 Intensity of charge state +3
Trp-cage in H ₂ O, pH 7	2.0
D-Tyr substituted Trp-cage in H_2O , pH 3	0.2
D-Tyr substituted Trp-cage in H ₂ O, pH 7	0.6
Trp-cage in 30% TFE and 70% H_2O , pH 3	1.3
Trp-cage in 30% TFE and 70% H_2O , pH 7	2.5



Figure 2. ESI-ToF spectrum of 40 μ M Trp-cage in 30% TFE and 70% H₂O solution at (**a**) pH 3 and (**b**) pH 7. Some minor fragments arising from in-source fragmentation are observed.

number of labile hydrogens in Trp-cage is 34, including two N-terminal hydrogens, 15 backbone amide hydrogens, one C-terminal hydrogen, and 16 side-chain hydrogens. The number of labile hydrogens on each side chain is indicated below:

A total of 34 labile hydrogens are observed from comparing isotopic distribution of singly charged Trp-cage peak at 100% H₂O°and°100%°D₂O°(Figure°3a°and°b). Note that a 35-mass-unit shift is observed as a result of the addition of a deuterium atom, instead of a proton, in the singly charged Trp-cage ion electrosprayed from 100% D₂O. Likewise, an 18-mass-unit shift is observed in the doubly charged Trp-cage ion obtained from 100% D₂O as a result of the addition of two deuterium atoms.

The isotopic distribution of singly charged Trp-cage ions in 70% D₂O and 30% d-TFE is shown at 1- and 20-min°intervals°after°dissolution°in°Figure°3c°and°d. After 20 min, the isotopic distribution showed an increase of m/z value by 1 amu and is identical to the spectrum obtained from Trp-cage in 100% D₂O°(Figure



Figure 3. Isotopic distribution of singly charged Trp-cage in (a) 100% H₂O, pH 7; (b) 100% D₂O, pH 7; (c) in 30% d-TFE D₂O solution pH 7 after 1-min incubation; (d) in 30% d-TFE D₂O solution pH 7 after 20-min incubation.

3b).° Beyond° the° 20-min° mark° the° spectrum° remains unchanged. The isotopic distribution of doubly charged Trp-cage ion obtained at 1 and 20 min yields the same result. Thus the time-dependent spectra of Trp-cage show increased H/D exchange protection of only one labile hydrogen atom. This increased protection against H/D exchange supports the TFE's stabilizing effect on Trp-cage's native state. The fact that native Trp-cage does not show any significant protection of the labile hydrogens in a water solution indicates that the native and nonnative unfolded conformations are separated by a small energy barrier. This allows for rapid interconversion between the folded and unfolded conformations. In 30% TFE solution, the rate of interconversion is sufficiently slowed down to afford some protection of the protein's labile hydrogen.

In this work we successfully applied ESI-MS CSD methodology to Trp-cage, which is one of the smallest known peptides to show conformationally dependent CSD°shifts°[15-17,°20].°Our°results°indicate°that°Trpcage conformation is pH sensitive and has maximum stability at around physiological pH. The lowering of the pH beyond the pH 6-7 region disrupts ionic interaction in the native conformation leading to denaturation of Trp-cage. TFE solutions are shown to stabilize the native conformation and provide resistance against acid denaturation. This study demonstrates the utility of ESI-MS CSD in determining the compactness of tertiary proteins/polypeptides in a rapid and efficient manner.

Acknowledgments

The authors gratefully acknowledge NIH shared instrument grant 1S10RR017977-01 and NIH grant 8 RO1 EB002053201 for financial support, Professor Asher for providing the wild-type Trp-cage, and Professor Zubarev for providing the D-Tyr substituted Trpcage.

References

- Neidigh, J. W.; Fesinmeyer, R. M.; Anderson, N. H. Designing a 20-residue protein. *Nat. Struct. Biol.* 2002, *9*, 425–430.
 Gellman, S. H.; Woolfson, D. N. Mini-proteins Trp the light fantastic. *Nat. Struct. Biol.* 2002, *9*, 408–410.
- Qiu, L.; Pabit, S. A.; Roitberg, A. E.; Hagen, S. J. Smaller and faster: The 3. 20-residue Trp-cage protein folds in 14 microseconds. J. Am. Chem. Soc. 2002, 124, 12952-12953.
- 4. Simmerling, C.; Strockbine, B.; Roitberg, A. E. All-atom structure prediction and folding simulations of a stable protein. J. Am. Chem. Soc. 2002, 124, 11258-11259

- 5. Simmerling, C.; Strockbine, B.; Roitberg, A. E. Personal communication.
- Similariting, C., Strockine, D., Kolberg, A. E. Personal continuindation: Department of Chemistry, University of Florida, 2004.
 Snow, C.; Zagrovic, B.; Pande, V. S. The Trp cage: Folding kinetics and unfolded state topology via molecular dynamics simulations. *J. Am. Chem. Soc.* 2002, *124*, 14548–14549.
- 7. Chowdhury, S.; Lee, M. C.; Xiong, G.; Duan, Y. Ab initio folding simulation of the Trp-cage mini-protein approaches NMR resolution.) Mol. Biol. 2003, 327, 711–717.
- Zhou, R. Exploring the protein folding free energy landscape: Coupling replica exchange method with P3ME/RESPA algorithm. J. Mol. Graph. Model. 2004, 22, 451–462.
- Zhou, R. Trp-cage: Folding free energy landscape in explicit water. *Proc. Natl. Acad. Sci. USA* **2003**, *100*, 13280–13285.
- 10. Chowdhury, S.; Lee, M. C.; Xiong, G.; Duan, Y. Characterizing the C. Chowiniting, S., Lee, M. C., Molig, S., Duai, D. Characterizing the rate-limiting step of Trp-cage folding by all-atom molecular dynamics simulations. J. Phys. Chem. B 2004, 108, 13855–13865.
 Pitera, J. W.; Swope, W. Understanding folding and design: Replica-exchange simulations of "Trp-cage" miniproteins. Proc. Natl. Acad. Sci. USA 2002, 100, 7527, 7529.
- USA 2003, 100, 7587-7592.
- Ahmed, Z.; Beta, I. A.; Mikhonin, A. V.; Asher, S. A. UV-resonance Raman thermal unfolding study of Trp-cage shows that it is not a simple two-state miniprotein. *J. Am. Chem. Soc.* 2005, *127*, 10943–10950.
 Adams, C. M.; Kjeldsen, F.; Zubarev, R. A.; Budnik, B. A.; Haselmann, K. E. Electrone reprinted description of distinguishes a sincel of amino acid
- K. F. Electron capture dissociation distinguishes a single d-amino acid

in a protein and probes the tertiary structure. J. Am. Soc. Mass Spectrom. 2004, 15, 1087–1098.

- 14. Grandori, R. Origin of the conformation dependence of protein chargestate distributions in electrospray ionization mass spectrometry. J. Mass Spectrom. 2003, 38, 11-15.
- 15. Grandori, R. Electrospray-ionization mass spectrometry for protein conformational studies. *Curr. Org. Chem.* **200**, 7, 1589–1603. 16. Samalikova, M.; Matecko, I.; Mueller, N.; Grandori, R. Interpreting
- Chamanova, M., Matecko, L., Mucher, N., Grandon, K. Interpreting conformational effects in protein nano-ESI-MS spectra. *Anal. Bioanal. Chem.* 2004, *378*, 1112–1123.
 Lin, H.; Dass, C. A mass spectrometry investigation of the conforma-tional changes in adrenocorticotropic hormones. *Eur. J. Mass Spectrom.* 2020, 297.
- 2002, 8, 381-387.
- 18. Kaltashov, I. A.; Eyles, S. J. Studies of biomolecular conformations and conformational dynamics by mass spectrometry. Mass Spectrom. Rev. 2002, 21, 37-71
- Lednev, I. K. K.; Anton, S.; Sparrow, M. C.; Asher, S. A. Alpha-helix peptide folding and unfolding activation barriers: A nanosecond UV resonance Raman study. J. Am. Chem. Soc. 1999, 121, 8074– 8086.
- 20. Alomirah, H.; Alli, I.; Konishi, Y. Charge state distribution and hydrogen/deuterium exchange of α -lactalbumin and β -lactoglobulin preparations by electrospray ionization mass spectrometry. J. Agric. Food Chem. 2003, 51, 2049-2057.