Thermal stability of a helical conformation in bee venom melittin

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A single molecule of melittin, a protein of bee venom with 26 amino acid residues, takes a monomeric and helical conformation in methanol solution at room temperature, in contrast with an aggregated conformation (tetramer) in water [1]: this suggests the helix is stabilized mainly by the hydrogen bonding in the intra-molecule, but the aggregation is caused by hydrophobic interaction (and/or van der Waals force) between inter-molecules. We have investigated the helix-coil transition of melittin in methanol solution to clarify the thermal stability of hydrogen bonding, the finite size effect and the degree of the transition (1st or 2nd) by using 500MHz proton nuclear magnetic resonance (NMR) spectroscopy. In order to detect the NMR signals of the labile (hydrogen bonding) protons, melittin molecules were dissolved in partially deuterated methanol "CD3OH" (1wt. locally with increasing temperature up to 62B°C (below boiling temperature of methanol (65B°C)). However, no latent heat was observed in differential scanning calorimetry (DSC) measurement. [1] R. Bazzo, et al., Eur. J. Biochem., 173,139-146,(1988).

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