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From Folding to Sweet Taste: NMR, Circular Dichroism and Fluorescence Studies on Sweet Protein, Monellin

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A sweet protein monellin was originally isolated from the berries of the West African plant *Dioscoreophyllum cumminsii*. The studies for molecular interaction of different sweeteners with receptor as well as receptor binding model have been proposed previously. The high-resolution solution structure of single-chain monellin (SCM) has been determined to investigate structural origin of sweet taste by NMR spectroscopy and simulated annealing calculations. Solution structure of SCM revealed that the long α-helix is folded into the concave side of a six-stranded antiparallel β-sheet. The side chains of both Tyr63 and Asp66 which are common to all sweet peptides show opposite orientation to H1 helix, and they are all solvent exposed. Circular dichroism, fluorescence, and NMR data have reveled that SCM as well as its mutant proteins are excellent targets for probing folding mechanism of protein by their unusual stability for acidic and high temperature environments. Here, we report the structure-functions of SCM as well as spectroscopic characterization of the unfolding intermediate by fluorescence, far-UV CD, and two-dimensional NMR spectroscopy.