African Journal of Food Science and Technology (ISSN: 2141-5455) Vol. 12(10) pp. 01-02, November, 2021
DOI: http:/dx.doi.org/10.14303//ajfst.2021.051
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Commentary

Temperature and chemical denaturation investigation of protein stability on a global scale

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Abstract

The stability of a protein is a basic feature that controls whether or not the protein is functional under certain conditions. Equilibrium unfolding with denaturants necessitates many sample preparations and only gives the free energy of folding when performed at a single temperature. The usual protein requirement for a sample is 0.5–1 mg. If the stability of a large number of proteins or protein variations needs to be assessed, large amounts of protein may be required. Using of a combination of temperature and denaturant unfolding to test the stability of acyl-coenzyme a binding protein at pH 5.3 and chymotrypsin inhibitor 2 at pH 3 and pH 6.25.

Keywords: Acyl-coenzyme, Hydrophobic, Hyperthermopile, Monomeric.

INTRODUCTION

Protein is a macronutrient that helps the body's tissues develop, maintain, regulate, and repair itself. Protein has several important activities in the body, including: acting as enzymes to catalyse reactions in processes including metabolism, DNA replication, and digestion (Duy and Fitter, 2005).

- Acting as a source of some hormones and antibodies.
- Maintaining the acid-base balance by regulating key bodily activities such as water distribution, nutrient transport, and muscle contractions.
- Supplying an energy source (about 4 calories per gramme).
- Promoting healthy skin, hair, and nails.
- Food's role in providing body proteins.
- Food's role in providing body proteins is to offer amino acids from which the body may produce its own proteins. A cell must have all of the necessary amino acids available at the same time in order to generate body protein. Dietary protein must contain all of the required amino acids as well as enough nitrogen to allow for the synthesis of other amino acids.
- Proteins that is complete and incomplete.
- Complete and incomplete proteins are two types of proteins. A complete protein has all of the essential amino acids, whereas an incomplete protein lacks one or more of them (Shire et al., 2004).

Proteins' tertiary structures, which are important for their physiological functions, are linked to amino-acid sequences and are stabilised by thermodynamic laws. Obtaining the thermodynamic characteristics of protein denaturation as a function of temperature is vital for elucidating the mechanisms of protein folding and protein stability. One challenge in examining the stabilisation process of proteins with denaturation temperatures above 100°C is that heat denaturation of proteins is usually irreversible at temperatures above 80°C because proteins tend to cluster following heat denaturation under these conditions. As a result, the thermodynamic characteristics of protein stabilisation at temperatures exceeding 100 °C are unknown. One key concern in this subject is whether the hydrophobic interactions that contribute the most to protein stability still exist at temperatures higher than 100°C. Thermodynamic investigations of salt bridges in proteins with denaturation temperatures above 100°C are therefore required, because the quantity of ion pairs produced by charged residues appears to stabilize many hyperthermophile proteins (Wang et al., 2007).

With a denaturation temperature (Td) of over 150°C at pH 7.0 and a large amount of charged residues, the CutA1 protein from the hyperthermophile Pyrococcus horikoshii (PhCutA1) is unusually stable. CutA1 proteins from Thermus thermophilus (TtCutA1), Oryza sativa (OsCutA1), Homo sapiens (brain) (HsCutA1), and Escherichia coli were also studied for their stability and architectures at different growing temperatures (EcCutA1). Td values of 113.9°C for

TtCutA1, 98.9°C for OsCutA1, 96.2°C for HsCutA1, and 89.9°C for EcCutA1 are likewise exceptionally high in comparison to each species' growth temperatures: 113.9°C for TtCutA1, 98.9°C for OsCutA1, 96.2°C for HsCutA1, and 89.9 PhCutA1 has an X-ray crystal structure that is very similar to other CutA1 proteins. Three helixes and five strands make up the monomeric structure. By interacting between the edges of three -strands, three monomers are formed into a trimer. The stabilization of trimer formations is aided by this intricate interplay. The CutA1 proteins' trimer structures are stabilized as a result of this densely entwined relationship (Harn et al., 2007).

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