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Biophysical Study of Intrinsically Disordered Proteins: Their Solubility, Hydration and Resistance to Salting-Out

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Summary

In recent years, the new concept of intrinsically disordered protein (IDP) is proposed, which draws many attention of researchers. Usual proteins adopt into certain structures that are specified in their primary structures through folding processes. The specific functions of proteins are then exhibited based on their structures. IDP is believed to adopt into a specific structure under physiological conditions. The genome project showed that many IDP was found in genomes of higher-eukaryotes rather than prokaryotes. Especially, neuron-specific genes and nuclear-specific genes contain much more IDPs, the elucidation of the physiology function is hurried. Since many hydrophilic amino acid residues are contained, IDP's solubility was expected to be higher than the usual protein. Also, it was predicted that IDP may show resistance against salting-out. In this study, we examined whether a characteristic interaction with salt of IDP would be observed by measuring and comparing ^{1}H-^{15}N 2D-NMR with and without high concentration salt. At the same time solubility of some IDP samples are also examined.

Herein, we succeeded in obtaining enough amount of ^{15}N-labeled IDP samples for NMR measurement, by refining conditions of the N^{pro} autoprotease fusion protein expression system. As a result of solubility experiments, we revealed that many IDP's do not necessarily show high solubility. Although some certain IDPs contain many charged amino acids, some were never solved into the buffer solution at neutral buffer. The ^{1}H-^{15}N 2D-NMR spectra of IDP with and without salt were measured. Almost all the residues showed downfield chemical shift changes. However, induction of the α-helical structure was not observed alpha by addition of salt. With many residues, ^{15}N chemical shift did not change but only ^{1}H showed changes. Moreover, the amount of change was larger than folded proteins. Some of them also showed a relatively large chemical shift changes in ^{15}N axis.