

DATE: Day 15 Month June Year 2020

SUMMARY of
2019 RESEARCH RESULTS REPORT
For International Collaborative Research with IPR, Osaka University

Research Title		Dynamics of RNA-binding proteins
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<p>Summary</p> <p>Many double-stranded RNA-binding domains (dsRBDs) interact with topologically distinct double-stranded RNAs (dsRNAs) in crucial biological pathways that are pivotal to viral replication, causation and propagation of cancers, neurodegenerative diseases; etc. We hypothesized that the adaptability of dsRBDs is essential to target the pool of dsRNA substrates; thus, it is imperative to comprehend this adaptability for better understanding of such biological pathways. In this study, we employed a model dsRBD and a few topologically distinct dsRNAs to test the systematic shape-dependence of RNA on the binding thermodynamics using Isothermal Titration Calorimetry (ITC) and NMR spectroscopy. Results from ITC-based titrations showed that the binding of dsRBD with topologically distinct dsRNAs is enthalpy-driven; with each dsRNA-dsRBD pair having distinct combination of enthalpy-entropy yielding a similar change in free energy upon RNA-binding. We also show that dsRBD, used in this study, binds to each of the dsRNA in a unique way. Comparison of dynamics in apo- and RNA-bound state yielded important information. While on one hand, intrinsic microsecond timescale dynamics observed in the apo-dsRBD was found to quench, microsecond timescale dynamics got induced at residues that are spatially proximal to quench sites, upon binding with a dsRNA. This apparent relay of conformational exchange from one site to the other site upon dsRNA-binding suggests the importance of intrinsic dynamics to adapt to target a variety of dsRNA-shapes.</p>		

***Deadline: May 15, 2020**

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