海外特別講演

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Research Summary

Satchin Panda's major scientific achievements include discoveries of key molecules, mechanisms and principles underlying the diurnal rhythms in metazoans. He discovered the role of a novel blue-light sensitive photopigment melanopsin in adapting mammalian circadian clock and non-image forming behavior to ambient lighting condition. This has led to public policy and commercial products aimed at dynamically managing lighting in built environment to optimize human health. His research identified genome-scale circadian regulation of thousands of genes in a tissue specific manner, which led to the subsequent discoveries of several core clock components, and molecular mechanisms. Recently, his lab demonstrated that the feeding-fasting cycle is a dominant determinant of diurnal rhythms in gene expression and function in peripheral organs independent of ambient lighting. Health relevance of this finding was demonstrated in a pre-clinical animal model that a robust feeding-fasting cycle without altering nutrient quality and quantity can prevent several chronic metabolic diseases. Based on a feasibility study in humans, his lab is currently carrying out a smartphone based study (www.mycircadianclock.org) to assess the extent of circadian disruption among adults.

Education, Positions and Honors

1996–2001	Graduate Student, The Scripps Research Institute, La Jolla, California
2001–2004	Postdoctoral Fellow, Genomics Institute of Novartis Research Foundation, San Diego
2003	Finalist for Science-Eppendorf Prize in Neurobiology.
2004–2011	Assistant Professor, The Salk Institute for Biological Studies, La Jolla, CA
2006	Pew Scholar in Biomedical Research
2011–present	Associate Professor, The Salk Institute for Biological Studies, La Jolla, CA
2014	The Julie Martin Mid-Career Award in Aging Research

Interactions among diet, eating pattern, and gut microbiome contribute to host metabolism

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Background: The gut microbiome influences host metabolic processes and can contribute to obesity and dysmetabolism. However, many fundamental characteristics are still unknown, such as how the microbiome responds to normal feeding/fasting cycles.

Purpose: We wanted to test how different diet types and eating pattern affect the dynamic composition of gut microbiome in the mouse model.

Methods: To test the nature of the dynamic relationship between the host and the gut microbiome, we subjected male C57B6 mice to different diet and eating pattern; mice ate normal chow ad libitum (NA), high fat diet ad libitum (FA) or high fat diet in a time restricted regime (FT; food access for 8 h every night). Both groups of mice eating high fat diet consumed the same amount of calories daily, but differed in the temporal eating pattern. Surprisingly, the diet induced obesity (DIO) that results in the FA group was not observed in FT group, even though both groups consumed the same amount of calories from high fat diet. We assessed the composition of the gut microbiome at different time of the day to assess how gut microbiome composition correlates with health outcomes of eating pattern modulation.

Results: We discovered that the gut microbiome in NA group is highly dynamic with daily cyclical fluctuations. This dynamic environment is perturbed in diet induced obesity (DIO), with obliteration of many cyclical fluctuations in the gut microbiome. Time restricted feeding (TRF), where feeding is consolidated to the nocturnal phase, partially restores cyclical fluctuations in the microbiome. Furthermore, TRF, which protects against obesity and metabolic disease, restores cyclical fluctuation in some families that have been hypothesized to be important to metabolism. Cyclical changes in the gut microbiome from feeding/fasting rhythms and diet contribute to the diversity of organisms and likely underlie the mechanism by which the gut microbiome affects host metabolism.

Implications: Hence, feeding pattern and the time at which gut microbiome is harvested can affect the measured results for those seeking to determine its composition. Furthermore, we cannot rule out the possibility that the eating pattern also affects the functional state of the gut microbiome by affecting gene expression and protein function of the gut microbiome.