Dissecting Thermogenic Adipose Tissue from Inside-Out

Yu-Hua Tseng
Joslin Diabetes Center and Harvard Medical School, Boston, MA, USA

Adipose tissue is essential for maintaining metabolic health and functions through two distinct types of fat: white adipose tissue (WAT) and brown adipose tissue (BAT), along with its related beige fat. WAT primarily serves as a storage site for triglycerides, while BAT and beige fat specialize in thermogenic energy expenditure. Although BAT is scarce in humans, these thermogenic adipocytes effectively utilize glucose and triglycerides and function as an endocrine organ by secreting batokines. Consequently, increased BAT activity is linked to improved metabolic health in humans. Growing evidence indicates that the diverse cell types within adipose tissue and their dynamic interactions significantly contribute to its multifaceted functions. We employed single-cell and single-nucleus RNA sequencing analyses of both mouse and human BAT to explore the complex cellular composition of thermogenic adipose tissue. Additionally, we leveraged various computational tools to map cell-cell communications in BAT. Furthermore, we uncovered that acute β3-adrenergic receptor signaling instigates rapid changes in the 3D genome architecture of brown adipocytes, which involves a dynamic reorganization of chromatin loops coupled with the activation of genes involved in thermogenesis. These findings underscore the heterogeneity of BAT and provide insights into the organizational and communicative events that drive adaptive thermogenesis and the associated remodeling of thermogenic adipose tissue.