東京大学 グローバル COE『統合生命学』特別セミナー

東京大学大学院 理学系研究科 生物化学専攻

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演題：Transcriptome Profiling of the Rodent Pineal Gland:
The Impact

日時：平成 21 年 6 月 1 日（月）17：30～19：00

場所：東京大学理学部 3 号館 4 階 416 号室

The pineal gland is characterized by a 24-hour activity cycle, which is best represented by the daily rhythm in melatonin production. The rhythm in circulating melatonin provides an indicator of time and is used in a variety of ways to coordinate physiological processes with daily and seasonal changes in environmental lighting. A recently completed study (1) of gene expression in the pineal gland has revealed the highly expressed genes in this tissue and has identified genes which exhibit daily changes in expression, including >600 genes with 2-fold or greater night/day differences. In some cases, the night/day differences are ~100-fold. These changes appear to be due primarily to adrenergic-cyclic AMP signaling. The findings of this effort have triggered investigations of a broad nature, including those related to development, to the molecular nature of pineal/retina similarity, to signal transduction, to the role of the thyroid hormone in pineal signal transduction and to the role of the pineal gland in the immune/inflammatory response. Current work is directed at identifying the conserved genetic features of the vertebrate pineal gland, based on studies of the transcriptomes of the zebrafish, mouse, rhesus and human pineal glands.

Reference

1) Bailey MJ *et al.* (2009) Night/day changes in pineal expression of >600 genes: Central role of adrenergic/cAMP signaling. ***J. Biol. Chem.*** *284*: 7606 – 7622.

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