



第 234 回 つくば分子生命科学セミナー

TSUKUBA MOLECULAR LIFE SCIENCE SEMINAR

演題 : Coordination of functionally related mRNAs
by RNA-binding proteins
(RNA 結合タンパク質による機能的に相関
した mRNA 群の協調的制御)

演者 : André P. Gerber 博士

Swiss Federal Institute of Technology、スイス

日時 : 2007 年 1 月 9 日 (火) 17:00-18:30

会場 : 筑波大学医学学群棟 4A411

Gerber 博士は、DNA マイクロアレイの開発者である Patrik Brown 教授 (スタンフォード大学、米国) の研究室でポスドクとして活躍した DNA マイクロアレイ解析のエキスパートです。本セミナーでは、DNA マイクロアレイを用いたゲノムワイドな解析手法の例として、mRNA の安定性制御や翻訳段階での制御など遺伝子発現の転写後制御 (post-transcriptional regulation) に関する RNA 結合タンパク質の全標的 mRNA の網羅的同定とその解析について紹介していただきます。

Post-transcriptional regulation of gene expression plays important roles in diverse cellular processes such as development, neurogenesis and cancer progression. This regulation is often mediated by specific RNA-binding proteins (RBPs) that bind to elements in the untranslated regions (UTRs) of mRNAs and regulate the stability, translation, or localization of the mRNA. Whereas many classical studies explored the cellular role of RBPs with specific mRNA substrates, the recent development of genome-wide analysis tools enables systematic identification of the mRNA substrates of RBPs, and the study of post-transcriptional gene regulation on a global scale. For instance, mRNAs targeted by specific RBPs can be identified by combining biochemical purification of RBPs followed by the analysis of associated RNAs with DNA microarrays. As exemplified for the Pumilio-Fem-3-binding factor (PUF) proteins, for which we have systematically identified the mRNA targets in yeast and *Drosophila* (1,2), the groups of RNAs associated with RBPs often encode functionally or cytologically related proteins which act in the same biochemical pathway, are parts of a macromolecular complex or localize to the same subcellular structure. Moreover, the global approach enabled the discovery of conserved sequence elements in the RNA which specify protein binding. I will further talk about our ongoing analysis of RNAs associated with more than thirty RNA-binding proteins in yeast and which allows to further define common principles of the RNA-protein network. In conclusion, these studies suggest extensive coordinate regulation of RNAs by RBPs being part of a highly organized and versatile post-transcriptional regulatory system.

1. Gerber, A.P., Herschlag, D., Brown, P.O. (2004) *PLoS Biol.*, 2(3), E79.

2. Gerber, A.P., Luschnig, S., Krasnow, M.A., Brown, P.O., Herschlag D. (2006) *Proc. Natl. Acad. Sci. USA.* 103, 4487-4492.

連絡先 : 人間総合科学研究科 入江 賢児 (内線 3066)

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