生命科学在华农—整合生物学前沿论坛

A Structural Basis of RNA Epigenetics and Genetic Control by Riboswitches

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邀请人：殷 平 教授

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第二综合楼 一楼报告厅

报告人简介：David M J Lilley，现任英国邓迪大学教授（Professor of Molecular Biology, University of Dundee），英国癌症研究中心核酸结构研究组组长（Director, CR-UK Nucleic Acid Structure Research Group）。2002 年当选英国皇家学会院士（**F**ellows of the **R**oyal **S**ociety, **FRS**），2003 年当选英国皇家化学学会会士 (**F**ellow of the **R**oyal **S**ociety of **C**hemistry, **FRSC**)，2015 年获得 RNA 学会终身成就奖。Lilley 教授主要从事核酸的化学生物学研究，研究内容包括：染色质和核小体的结构与功能；DNA 超螺旋结构在基因重组以及与酶相互作用中的重要性研究；RNA 折叠以及 RNA 分子催化的起源。已在包括 Nature, Science，Cell 等学术期刊上发表 370 多篇研究论文，H-index 高达 81。

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Abstract: Helical junctions are common elements in the secondary structure of RNA. They have a key role in the folding of small functional RNA molecules such as some of the nucleolytic ribozymes and the HCV IRES element, and are important in larger RNA species, organising the tertiary structure of the molecule. Interestingly, if we take the nucleolytic ribozymes as a representative collection of small autonomously-folding RNA species we find they divide into two groups. The structure of three (the hammerhead, hairpin and VS ribozymes) are based around helical junctions, while the remaining two (the hepatitis delta virus and glmS riboswitch ribozymes) are instead based on complex, nested pseudoknots. For these molecules at least, these two ways to solve the RNA folding appear to be mutually exclusive. In larger RNA species we can dissect the folding problem into the interactions between helices. These will be of two kinds, tertiary interactions, such as between loops and their receptors, and junctions that connect the helical segments. Our philosophy has therefore been to study the conformational properties of RNA junctions in depth.