第 178 回　原医研セミナーのご案内

下記のとおりセミナーを開催致します。
多数ご参集くださいますようご案内申し上げます。

記

日時：　平成 **28** 年 **2** 月 **18** 日(木) 午後 **5** 時 **30** 分～

場所：　霞総合研究棟　**6** 階　**604** セミナー室

演題：　Microscopic Studies of the Functional Nuclear Organization

講師：　Department Biology II, Biocenter, Ludwig Maximilians University (LMU), Germany

Dr. Thomas Cremer

We have recently proposed a model for a functionally defined nuclear organization based on two co-aligned three-dimensional networks: an active and an inactive nuclear compartment (ANC and INC) (Cremer et al., 2015. FEBS Letters 589, 2931–2943). Experimental evidence for this model shows that chromosome territories (CTs) are built up from chromatin domain clusters (CDCs), which form still higher networks pervading the nuclear space. Whereas the compacted chromatin core of CDCs, called the INC, is enriched in repressive histone marks, a peripheral peripheral layer of low density chromatin, called the perichromatin region (PR) is enriched in epigenetic marks for transcriptionally competent chromatin and represents the nuclear domain, where transcription, splicing, chromatin replication and DNA repair occur. The PR lines a contiguous channel system, the interchromatin compartment (IC), which starts at nuclear pores, permeates the nuclear space between the higher order chromatin network and serves a role in nuclear import and export functions. The IC carries nuclear bodies and splicing speckles and interacts with the PR. Accordingly, the PR together with the IC is called the ANC. In line with the ANC-INC model we demonstrate that active regulatory sequences are exposed at the outer periphery of CDCs with loops penetrating into the IC. By contrast, inactive regulatory sequences are more embedded within the interior of CDCs, although still excluded from the most compact core.

連絡先：広島大学原爆放射線医科学研究所　　広島大学霞地区運営支援部総務グループ

細胞修復制御研究分野 (内線 5818)　　082-247-1639　　(内線 6279)