



Diverse Assets & Applications International LABoratory Classroom for Advanced & Frontier Education SERIES 101

Sat�e Obuchi
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Series - 101

Date and Time - 21 May 2025 (Wednesday) (3:30 PM JST | 12:00 IST)
Venue - Zoom
Speaker - Sat�e Obuchi
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Dynamic Analysis of Protein Structures for Synovial Sarcoma Drug Development

Synovial sarcoma is a malignant soft tissue tumor that predominantly arises around the joints of the limbs, especially in young adults. It carries a high risk of recurrence and metastasis to the lungs and lymph nodes. The prognosis is poor, with a 5-year survival rate of only 60% in adults. As a rare cancer, research progress has been limited, and many aspects of its molecular pathogenesis remain unclear. Current treatments options include surgical resection, chemotherapy and radiotherapy. However, metastatic cases are highly refractory, making the development of new therapeutic strategies an urgent need.

Nearly all cases of synovial sarcoma harbor chromosomal translocations that generate aberrant fusion genes. The resultant pathogenic protein bind to nucleosomes* and disrupt normal transcriptional regulation, thereby promoting tumorigenesis. Thus, inhibiting the interaction between the pathogenic protein and nucleosome holds promise as an effective therapeutic approach. In this study, we aimed to obtain essential structural information for developing such inhibitors through structure-based drug design (SBDD). We performed structural analysis of the pathogenic protein-nucleosome complex via cryo-electron microscopy (cryo-TEM) single particle analysis and molecular dynamics (MD) simulations.

Our single particle analysis results suggest that binding of the pathogenic protein to nucleosome leads to nucleosome dissociation, contributing to transcriptional dysregulation. Furthermore, mutations at two residues W164 and R167 of the pathogenic protein are promising new targets for inhibitor binding.

*: the fundamental units of chromatin, in which DNA is wrapped around proteins called histones. In addition to compactly storing DNA, their dynamic structure also plays a key role in regulating gene functions such as transcription, replication and repair.

43 participants
Thanks Everyone!

Research objective

How to design the inhibitor?



Research Objective

Structure analysis of oncogenic driver protein-nucleosome complex
for Structure Based Drug Design (SBDD)

① Formation of the complex and single particle analysis



How to bind?

② MD simulation



find optimal inhibitor binding site



- RW Renu WADHWA (Host, me)
- SO Sat�e Obuchi
- Hv Harini velayudham
- AK Ajalkumar Kunnumakkara
- AM Anamika Mishra
- AA Anchal Agarwal
- AK Aviral Kumar
- DI Dr Intiaj Hasan
- DM Dr M V Jali
- DM Dr Mahamudul Hasan Khan
- J Jaspreet
- KH Kazumi Hirano
- MH Mangala Hegde
- MN Myat Nyein Khine (カイ)
- NW Nalaka Wijekoon
- o ochishitomoyo
- P Pampila
- SJ SHIRISTY JHA
- Shiweta Shinde
- KIST 이수환 Soohwan Lee
- SK Sunil KAUL (AIIST, Japan)
- U Upasana
- YT Yuji Teramura
- YS Yuya Sato
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