

*Commentary and Perspective***Participation in 44th Indian Biophysical Society Meeting**Kayo Hibino^{1,2,3}¹ *Laboratory of Genome Dynamics, National Institute of Genetics, ROIS, Mishima, Shizuoka 411-8540, Japan*² *Department of Genetics, School of Life Science, SOKENDAI, Mishima, Shizuoka 411-8540, Japan*³ *PRESTO, Japan Science and Technology Agency, Chiyoda-ku, Tokyo 102-0076, Japan*

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The Biophysical Societies of Japan and the Indian Biophysical Society regularly organize India-Japan joint symposiums and other exchange opportunities for further development of the biophysics field and international exchange of scientists. Here I report on the 44th Indian Biophysical Society Meeting [1] held in Mumbai, India as a hybrid of the online meeting, on March 30-31 and April 1, 2022. The conference theme was "Conceptual Advances in Biophysics and its Applications", and over 300 scientists and students from all over the world participated. The conference hosted five lectures, including the GN Ramachandran Lecture, and 24 invited talks in seven sessions on: 1) Protein-Protein Interactions, 2) Protein Folding, 3) Aggregation & Related Diseases, 4) Molecular & Cellular Biophysics, 5) Structural Biology & its applications, 6) Protein Conformational Dynamics, and 7) Biophysical Techniques & Disease Intervention. It also had a brainstorming panel discussion on the topic entitled "Exploring Integrative Biophysics in Medicine: A less-trodden path?" Moreover, the Young Speakers' Forum and 130 poster presentations were given. All the sessions were very stimulating and lively interactive with discussions. IBS 2022 organizing committee said "The symposium had provided the platform to facilitate networking for scientists crucial for budding collaborations in the field of biophysics and structural biology. It had also shed light on new trends happening in the field of biophysics and increased awareness among the participants."

The annual meeting of the Indian Biophysical Society is relatively tiny compared to the annual meeting in Japan. Therefore, taking advantage of this small size, the schedule was designed by IBS 2022 organizing committee so that we could attend all the lectures, sessions, and poster discussions. In addition, instead of hosting a specific symposium for bilateral exchanges, scientists from various countries presented their latest studies in sessions that suited their research topics, which promoted international exchanges throughout the meeting.

Young scientists from the Biophysical Society of Japan presented three topics using single-molecule technologies, one of the strengths of the Japanese biophysics field. The first is a study on the acting principle of molecular motors by using single-particle analysis with cryo-electron microscopy (cryo-EM). The second is a report on an important issue in innate immunology using single-particle analysis with cryo-EM. The third is a super-resolution and single-molecule imaging study to address the principle of chromosome condensation. The details are as follows.

Jun-ichi Kishikawa (Osaka University) reported structural analysis of V-ATPase during its catalytic cycle by single particle cryo-EM [2]. They found 18 new intermediate structures of the V_1 domain of prokaryotic V-ATPase under different catalytic reaction conditions. The obtained structures indicate that the rotor does not rotate immediately after binding ATP to the V_1 , in contrast to the conventional model that ATP binding induces the rotation. Furthermore, they proposed a ratchet-like mechanism that couples exergonic ATP hydrolysis to the unidirectional rotation of V-ATPase.

Tomoya Kujirai (The University of Tokyo) reported a structure of the human cGAS-nucleosome complex determined by cryo-EM single particle analysis [3]. cGAS plays a central role in the innate immunity system. The cryo-EM structure of the cGAS-nucleosome revealed the DNA binding and the dimerization of cGAS, which are necessary for its activation, are inhibited by the nucleosomes. Based on the structure, they discussed the inhibition mechanism of cGAS for avoiding

autoreactivity.

Kayo Hibino (National Institute of Genetics and SOKENDAI) reported the local motion of nucleosomes in the human mitotic chromosomes during chromosome condensation by using intracellular single-molecule imaging techniques [4]. Their quantitative analysis, in combination with knockdown experiments of related proteins and computer simulation studies, revealed new insights into the chromosome condensation process. Lively discussions followed all talks and presentations. Despite the hybrid of online and on-site meetings, the conference was very well organized and meaningful.

The single-molecule technologies are critical for studying the operating principles of living cells and are now standard tools in laboratories investigating biomolecules' functions in cellular processes. We hope that our topic on these technologies will lead to more accelerated bilateral exchanges.

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