Biased distribution of the nuclear pore complex after second postzygotic nuclear division determine nuclear differentiation in *Teterahymena thermophila*

Fumihide BUNAI[1], Masaaki IWAMOTO[1], Yasushi HIRAOKA[1, 2] and Tokuko HARAGUCHI[1, 3]
([1]Kobe Advanced ICT Research Center, National Institute of Information and Communications Technology, [2]Graduate School of Frontier Biosciences, Osaka University, [3]Graduate School of Science, Osaka University)

SUMMARY

The ciliated protozoan, *Tetrahymena thermophila*, has two functionally and structurally distinct nuclei in a single cell. Although understanding such “nuclear dimorphism” is a central issue, unique to ciliate biology, the molecular bases of nuclear differentiation have remained largely unknown. because of the technical difficulties of monitoring a temporal sequence of highly-dynamic, complex nuclear events in a rapidly moving organism. Here we report a method of live-cell fluorescence imaging to monitor dynamic behavior of specific molecules in living *Tetrahymena* cells undergoing nuclear differentiation. We have also developed a technique of correlative light and electron microscopy by which molecule-specific fluorescence images can be correlated with ultrastructural electron microscopy images. Using these imaging technologies, we examined dynamic behavior of the nuclear pore complex (NPC) and nuclear membranes during sexual reproduction, including nuclear differentiation. We found that the NPCs moved toward the anterior side of the nuclear envelope during the second postzygotic mitosis, generating distinguishable nuclei; one is NPC-rich, and the other is NPC-poor. Live-cell imaging further showed that the NPC-rich and NPC-poor nuclei were destined to become the new macronucleus and micronucleus, respectively. These results suggest that the NPCs, or components of the NPC, may contribute to nuclear differentiation through regulation of selective nuclear transport.