

Genome-structural evolution facilitated speciation in nematodes

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Date & Time: Thursday, September 6, 2022; 13:30~15:00 (On-site and Online)

On-site: (Katahira) Life Sciences Project Research Laboratory, Room 103

片平・生命科学プロジェクト研究棟 1階 103会議室

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Abstract:

Speciation, the process by which one species divides into two, is the fundamental cause of biological diversity and completed by reproductive isolation of descendant species resulted from the accumulation of reproductive barriers. In addition to single genes, also genome-wide divergence is involved in this process. Genome-structural evolution (e.g. inversion, chromosome fusions) can affect different genetic processes, such as chromosome segregation, recombination and transcriptional regulation, and may promote the evolution of reproductive isolation. However, while theoretical models predicted a role of genome-structural evolution in speciation long time, empirical studies demonstrating such mechanisms are scarce. I recently developed a new model organism for speciation research, *Pristionchus* nematodes. Nematodes are one of the most diverse animal taxa but the speciation genetics of nematodes has been poorly studied. *Pristionchus* nematodes have great advantages for laboratory experiments. They i) require small cultural space and ii) have short generation time, iii) small genome sizes and iv) the availability of advanced genetic tools (e.g. CRISPR editing). Additionally, one unique ecological feature of *Pristionchus* is their association with arthropods. In the last decade, world-wide collections of beetles resulted in the discovery of 48 *Pristionchus* species, all available as living and frozen stocks. My colleagues and I reported one of the most closely related nematode species groups, the *pacificus*-complex sensu stricto. In this presentation, I introduce projects of closely related species pairs in this species complex. First, we studied the hermaphroditic *P. pacificus* and its closely related sister species, the gonochorist *P. exspectatus*. De novo genome assembly using single-molecular and Hi-C sequencing and cytogenetic analysis indicated two independent chromosome fusions in both lineages. QTL study of hybrid sterility demonstrated that the chromosome fusions accumulated QTLs for hybrid sterility of all three sexes. Subsequent genetic analysis suggested multiple evolutionary mechanisms of chromosome fusions driving speciation. At last, I present karyotype analysis of the 48 *Pristionchus* species, which indicates multiple independent transitions of genome structure, providing a framework for comprehensive studies of speciation genetics in the coming decade.

*This seminar will be held in English.

*単位認定セミナー・イノベーションセミナー(2ポイント)

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