

論文 / 著書情報
Article / Book Information

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論文要旨

THESIS SUMMARY

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要旨 (英文 800 語程度)

Thesis Summary (approx.800 English Words)

The termites in the family Rhinotermitidae, except the genus *Reticulitermes*, obligately harbor the cellulolytic gut protist *Pseudotrichonympha*, which nestedly harbors the bacterial endosymbiont “*Candidatus Azobacteroides pseudotrichonymphae*” (order Bacteroidales) in its cytoplasm. These termites, protists, and endosymbionts have cospeciated and established a tripartite symbiosis (Noda *et al.*, 2007, *Mol Ecol* 16: 1257-66). Although both “*Ca. A. pseudotrichonymphae*” and its host *Pseudotrichonympha* protists are as-yet uncultivable, the complete genome sequence of “*Ca. A. pseudotrichonymphae*” phylotype CfPt1-2 genomovar CFP2 from the Formosan termite *Coptotermes formosanus* has previously been obtained and analyzed, using the whole genome amplification (Hongoh *et al.*, 2008, *Science* 322: 1108-9). The genome consisted of a single chromosome (1.1 Mbp) and four plasmids, and encoded gene sets responsible for nitrogen fixation, nitrogen recycling, and biosynthesis of various amino acids and cofactors. These functions should critically contribute to the nutrition of the termite hosts, which feed exclusively on nitrogen-poor, dead wood.

In my thesis, I newly obtained complete and draft genome sequences of “*Ca. A. pseudotrichonymphae*” from eight termite species in six genera (*Coptotermes*, *Heterotermes*, *Prorhinotermes*, *Termitogeton*, *Schedorhinotermes*, and *Parrhinotermes*) of the Rhinotermitidae family, and compared them, including genomovar CFP2 from *C. formosanus*. All of the “*Ca. A. pseudotrichonymphae*” genomes were small (0.9-1.4 Mb) and AT-rich, and showed massive rearrangements, indicating an ongoing reductive genome evolution.

The genes encoding nitrogenase-nitrogenase reductase complex (NifHDK) that are essential for nitrogen fixation were found in the genomovars from *C. acinaciformis* and *H. paradoxus* as well as in genomovar CFP2 from *C. formosanus*; however, surprisingly, the *nif*-operon is pseudogenized or missing in other rhinotermitid termite genera. Although genomovars from *Pro. japonicus* retained

apparently intact *nif*-operon, its promoter region is missing. These results are congruent with the results of acetylene reduction assay (ARA) that indirectly indicates dinitrogen-fixing activity. In ARA, termites of *Proterhinotermes* and *Schedorhinotermes* showed only a low level of nitrogen-fixing activity, and *H. paradoxus* exhibited much but still three-fold less activity than *C. formosanus*. This difference between *C. formosanus* and *H. paradoxus*, where “*Ca. A. pseudotrichonymphae*” from both termites possess intact *nif*-operon, may be attributable to the loss of F_0F_1 -ATP synthase genes in the genomovars from *H. paradoxus*, which has possibly lead to less ATP supply required for nitrogen fixation.

Although all “*Ca. A. pseudotrichonymphae*” genomovars retained genes for biosynthesis of 19 proteinaceous amino acids and various cofactors, genes required for nitrogen recycling, *i.e.*, urease and urea transporter, are missing or pseudogenized except in *Coptotermes* and *Heterotermes* termites as seen in genes for nitrogen fixation. These results apparently coincided with the feeding preference of the termite hosts. *Coptotermes* termites can ingest low-nitrogen, sound wood, whereas *Heterotermes* termites prefer decayed wood and other genera generally inhabit more decayed, damp, rotten wood in forests, which should contain much nitrogen compounds than sound woods. The present study showed an example how symbiotic microorganisms evolve in harmony with the ecology of their host animals.

During the genome analysis of “*Ca. A. pseudotrichonymphae*” phylotype ProJPt-1 from *Pro. japonicus*, I obtained the complete circular genome sequence (99,517 bp) of a bacteriophage, designated as ProJPt-Bp1. The phage is a member of the crAss-like phage family (order *Caudovirales*) that may be mainly associated with the phylum Bacteroidetes (Yutin *et al.*, 2017, *Nat Microbiol* 3: 38-46). The ProJPt-Bp1 phage encoded a tRNA-Gln (CAG), which shared a high sequence identity with tRNA-Gln (CAA) of the host “*Ca. A. pseudotrichonymphae*”, and also contained regions showing high similarities to the host plasmid sequences. Sequences similar to ProJPt-Bp1 were also found in “*Ca. A. pseudotrichonymphae*” phylotype ProIPt-1 from *Pro. inopinatus*; thus, this phage and its relatives may be common in “*Ca. A. pseudotrichonymphae*”, at least from the *Proterhinotermes* genus. This is the first discovery of a bacteriophage from a mutualistic, obligate intracellular symbiont of eukaryotes.

Although it is useful to compare genomes between endosymbiotic bacteria and their closely related, free-living species, “*Ca. A. pseudotrichonymphae*” has no close relatives cultured. Among distantly related, cultured genera of the order Bacteroidales, *Dysgonomonas* is yet closest to “*Ca. Azobacteroides*”. For example, the *nif* genes of “*Ca. A. pseudotrichonymphae*” showed the highest

sequence similarity to those of *Dysgonomonas capnocytophagoides* and *Dysgonomonas gadei*. I therefore characterized the physiology of *Dysgonomonas* sp. strain N-10, which has been isolated from the gut of the Japanese termite *Reticulitermes speratus* (family Rhinotermitidae). I described this strain as a novel species, *Dysgonomonas termitidis*, the first representative of this genus from the termite gut. I will analyze the genome of *D. termitidis* in future, for comparative genomics with “*Ca. A. pseudotrichonymphae*”.

備考：論文要旨は、和文 2000 字と英文 300 語を 1 部ずつ提出するか、もしくは英文 800 語を 1 部提出してください。

Note: Thesis Summary should be submitted in either a copy of 2000 Japanese Characters and 300 Words (English) or 1 copy of 800 Words (English).

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