# 多様な昆虫・クモ類における転移因子，マリナー様配列の比較解析：水平伝播とその動態の推測

# 論文要約

論文題目: Comparative sequence analysis of *mariner*-like elements among various insects and spiders: inference of the horizontal transfer and dynamics of these transposons
（多様な昆虫・クモ類における転移因子，マリナー様配列の比較解析: 水平伝播とその動態の推測）

This study presents the comparative sequence analysis of DNA transposons *mariner*-like elements (MLEs) that are prevalent in a wide range of eukaryotic genomes. It is considered that MLEs were inserted into their host genomes via horizontal transfer. As the possible horizontal transfer routes, the special relationships such as host–parasite interactions, have been suggested. However, not only the routes but also their molecular evolution and horizontal transfer dynamics among various species are still not well understood. In order to verify the occurrence of horizontal transfer and their routes among various species, insects and spiders, which have the close relationships such as predator-prey and host-parasite interactions, were chosen as targets. In this study, MLEs obtained from various species of Araneae, Hymenoptera, and Lepidoptera were compared using phylogenetic methods.

In Chapter 2, the distribution of the MLEs belonging to *mellifera* subfamily in the genomes of three orders was investigated. The full lengths of *mellifera* MLEs (approximately 1300 bp) were detected from 33 species. These MLEs were divided into clusters A and B. The incongruence between the phylogenetic relationships of host species and MLEs suggested the occurrence of horizontal transfer among these species.

In the following chapters 3 and 4, I attempted to verify the horizontal transfer, and their routes and modes of the *mellifera* MLEs classified into clusters A and B, respectively.

In Chapter 3, cluster A MLEs were analyzed. The *mellifera* MLEs from 18 species of three order, Araneae, Hymenoptera, and Lepidoptera, were classified into cluster A. This cluster also included the MLEs isolated from four species reported by Lampe et al., (2003), *i.e.*, *A. mellifera* (*Ammar1*), *F. auricularia*, (*Famar1*), *C. capitata* (*Ccmar2*), and *E. funebris* (*Efmar1.1*). These MLEs formed a cluster in the *mellifera* subfamily and showed high sequence similarities (93.23%). The phylogenetic disparity between these MLEs and their respective host species clearly suggests that horizontal transfer occurred across species. Furthermore, MLEs obtained from four distinct species contained an intact or almost intact open reading frame that encoded a putative transposase. However, the phylogenetic tree of these MLEs revealed considerable variation in branch lengths, which indicates differences in their evolutionary, transpositional, and transfer dynamics. The dynamics of these MLEs were inferred from comparative sequence analyses.

In Chapter 4, cluster B MLEs were analyzed. The *mellifera* MLEs obtained from 15 species of three orders formed a novel cluster B within *mellifera* subfamily. These MLEs were further divided into several subclusters. In addition, MLEs from three species, the bee *Amegilla senahai subflavescens* (*Amsmar1*), the wasp *Campsomeris* sp. (*Casmar1*), and the swallowtail butterfly *Pachliopta aristolochiae* (*Paamar1*), contained an intact open reading frame that encoded a putative transposase. These transposases exhibited high similarity of 97.9 % among themselves. In the case of *Casmar1*, the presence of a putative transposase was found in high frequencies. These transposases also showed the presence of a terminal inverted repeat-binding motif, DD(34)D and two

highly conserved amino acid motifs, (W/ L)(I/L)PHQL and YSP(D/N)L(A/S)P. These two motifs differed from previously known motifs, WVPHEL and YSPDLAP. MLEs isolated from these three species may have been inserted into their genomes by horizontal transfer. Furthermore, the presence of an intact open reading frame suggests that they are still active in habitats along these isolated islands.

These MLEs may have been inserted into their genomes by horizontal transfer, and the presence of a putative transposases suggests that they are still active in habitats along these isolated islands. The MLEs in clusters A and B were probably derived from a common ancestral sequence. However, the comparative sequence analyses of these MLEs suggested these MLEs were inserted into the host genomes by the different modes of horizontal transfer. Finally, the final chapter discusses the horizontal transfer modes and dynamics of these MLEs.

The findings of this study are among important steps in understanding the horizontal transfer mode and their dynamics of the *mellifera* MLEs among various insects and spiders. This study is expected to contribute to elucidation of the roles and functions of MLEs in genomes in future studies.

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