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

メタデータ	
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論文要旨

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

Mariner-like elements (MLEs) are DNA transposons 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 the molecular evolution and transfer dynamics of MLEs are still not well understood. To verify the horizontal transfer of MLEs and their routes among various species, the MLEs belonging to *mellifera* subfamily obtained from Araneae, Hymenoptera, and Lepidoptera were compared using phylogenetic methods. The full lengths of *mellifera* MLEs (approximately 1300 bp) were detected from 33 species of three orders. These MLEs were divided into clusters A and B within the *mellifera* subfamily. The *mellifera* MLEs obtained from 18 species were classified into cluster A and showed high sequence similarities. 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. On the other hand, the MLEs obtained from 15 species formed a novel cluster B within *mellifera* subfamily. These MLEs were further divided into several subclusters. In addition, MLEs from three species that inhabit the Southwest Islands of Japan, 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 considerably high similarity (97.9 %). 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, I discuss the horizontal transfer modes and dynamics of these MLEs.

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