

Sequence Comparison of *Cecropia*-ITR-MLEs among some Invertebrate including Lepidopteran Insects Inhabiting Japan Islands

Yumiko Nakajima^{1*}, Hirofumi Fujimoto^{2,3}, Tsutomu Negishi¹, Kazuo Hashido², Teiichiro Shiino⁴, Kozo Tsuchida², Michio Hidaka⁵, Naoko Takada² and Hideaki Maekawa²

¹Division of Functional Genomics, Center of Molecular Biosciences (COMB), University of the Ryukyus, Nishihara, Okinawa 903-0213, Japan, ²Institute of Genetic Resources, Graduate School of Bioresource and Boenvironmental Sciences, Kyushu University, 6-10-1 Hakozaki, Higashi-ku, Fukuoka 812-8581, Japan, ³Division of Radiological Protection and Biology, National Institute of Infectious Diseases, 1-23-1 Toyama, Shinjuku-ku, Tokyo 162-0052, Japan, ⁴Laboratory of Insect Genetics and Bioscience, Department of Agricultural and Environmental Biology, Graduate School of Agricultural and Life Sciences, The University of Tokyo, 1-1-1 Yayoi, Bunkyo-ku, Tokyo 113-8657, Japan

Mariner-like elements (MLEs) were amplified by PCR against genomic DNAs from several Japanese lepidopteran species, using the inverted terminal repeats (IR) of the *Hyalophora cecropia* MLE as a primer. Clones thus obtained clones named *Cecropia*-ITR-MLEs were approximately 1.3 kb length, and expected to contain the full-length of MLE. A 1.3-kb band was also amplified against genomic DNA from the grasshopper, *Traulia ornate*, and from a coral allocated to the *Fungia* family. All of the 1.3-kb bands were cloned and analyzed for nucleotide sequence. Multi-alignment analyses of the results indicated that the clones were highly similar to each other and classified into the *cecropia* subfamily of MLEs. The coral MLE was also found to have a complete ORF coding for transposase, a situation similar to that previously found in the Emperor moth, *Attacus atlas*, from a Ryukyu island (Nakajima *et al*, 1998). These findings, together with the fact that all of the insect and coral species that exhibited a positive signal for the full-length MLE were collected in relatively close regions around Japan, indicated that horizontal transfer of MLEs among the phylogenetically remote organisms has taken place at relatively recent evolutionary periods.