

Normal and defective *mariner*-like elements in *Rhynchosciara* species (Sciaridae, Diptera)

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ABSTRACT. Mariner-like elements are widely present in diverse organisms. These elements constitute a large fraction of the eukaryotic genome; they transpose by a "cut-and-paste" mechanism with their own transposase protein. We found two groups of mobile elements in the genus Rhynchosciara. PCR using primers designed from R. americana transposons (Ramar1 and Ramar2) were the starting point for this comparative study. Genomic DNA templates of four species: R. hollaenderi, R. millerii, R. baschanti, and Rhvnchosciara sp were used and genomic sequences were amplified, sequenced and the molecular structures of the elements characterized as being putative *mariner*-like elements. The first group included the putative full-length elements. The second group was composed of defective *mariner* elements that contain a deletion overlapping most of the internal region of the transposase open reading frame. They were named *Rmar1* (type 1) and *Rmar2* (type 2), respectively. Many conserved amino acid blocks were identified, as well as a specific D,D(34)D signature motif that was defective in some elements. Based on predicted transposase sequences, these elements

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encode truncated proteins and are phylogenetically very close to *mariner*-like elements of the *mauritiana* subfamily. The inverted terminal repeat sequences that flanked the *mariner*-like elements are responsible for their mobility. These inverted terminal repeat sequences were identified by inverse PCR.

Key words: *Rhynchosciara*; Polytene chromosome; Transposon; *Mariner*-like element; Transposase; Inverted terminal repeat sequence

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