

P038 Structural and sequence analysis reveals multiple group I intron lineages among subgroup IE

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As a large family of catalytic RNAs, group I introns share a relatively conserved secondary structure in the core region but greatly vary in the nucleotide identities of the core and the peripheral structures. These difference affects the folding pathway, and very possibly introduce variations in the three-dimensional structure of group I introns. The large number of currently available group I intron sequences in the public databases raise an opportunity for large-scale analysis of the conservations and variations of structural motifs of group I introns. Here we present our study of 211 group I introns in the subgroup E using a manual-auto combined strategy. Detailed secondary structure was predicted for each intron, and reliable alignment was obtained according to the secondary structures. Analysis of the sequence conservation in the core structure unambiguously classifies these introns into 3 minor subgroups, namely IE1, IE2 and IE3. Meanwhile, multiple motifs found in the peripheral elements co-vary with core sequences; some potential tertiary interactions among these motifs are found. Interesting, these minor subgroups are both host- and insertion site-specific. The intersection of intron structures, insertion sites in rRNA and their host phylogeny suggests transfer of group I introns depends on insertion site and host. This strict selection may be due to the necessity of guarantying an efficient RNA folding in vivo, which is affected by the folding context (exon sequence) and folding factors (environment).