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Letter to the editor

t-SINE or simple SINE? Can be both

A typical SINE includes a tRNA-related region, a tRNA-unrelated region, and an A-rich tail, which suggests their origin from tRNA (Daniels and Deininger, 1985; Sakamoto and Okada, 1985). The mammalian genomes harbor tens of copies of tRNA pseudogenes with or without A-rich tails (Lander et al., 2001; Schmitz et al., 2004). Such retropseudogenes can be considered as evolutionary precursors of SINEs (Deininger and Daniels, 1986). However, SINEs differ from retropseudogenes by a great number of copies in the genome (tens and hundreds of thousands).

Recently we (Borodulina and Kramerov, 2005) and Churakov et al. (2005) described a new SINE Das-1 with an unusual structure including only a $tRNA^{Ala}$-related region and an A-rich tail. 30,000 copies of this short (90 bp) SINEs are present in the genome of armadillo *Dasypus novemcinctus*. We noticed that two more $tRNA^{Ala}$-derived SINEs have similar structures: ID from rodents (Kim et al., 1994) and Vic-1 from camels (Lin et al., 2001). Considering the simplicity and shortness of these efficient SINEs, we proposed the term 'simple SINEs' (Borodulina and Kramerov, 2005).

Piskurek et al. (2003) as well as Schmitz and Zischler (2003) described another SINE (CYN) from the genome of flying lemur, composed of a tRNA-related region and an A-rich tail. Okada et al. designated such structure as 't-SINE' (Piskurek et al., 2003). However, 37 out of 38 sequenced CYNs included two or three tRNA-derived monomers and were accordingly long (190–230 bp). The only copy (AF543574) annotated as monomeric (Schmitz and Zischler, 2003) has no flanking sequences, which questions its monomeric structure. Thus, the putative monomeric CYN seems by far less efficient than the di- and trimeric counterparts, which distinguishes it from efficient ID, Vic-1, and Das-1.

Piskurek and Okada claimed that the structure of ID and Vic-1 does not correspond to a simple SINE. We believe that the presence of several non-A nucleotides in the A-rich tail is irrelevant for their recognition as simple SINEs, the more so since a considerable fraction of ID and Vic-1 copies lack such conserved motifs.

Generally, we consider the acquirement of tRNA-unrelated sequences by typical SINEs as well as di- and trimerization (observed in CYN) as a progressive advancement, which can sharply increase their retropositional efficiency. High-copy-number ID, Vic-1, and Das-1 are amazing exceptions; although they can also combine with other DNA sequences to yield even more efficient retroposons (Kramerov and Vassetzky, 2001; Churakov et al., 2005; Kramerov and Vassetzky, 2005).

In conclusion, 'simple SINE' applies to very short but efficient SINEs, while 't-SINE' outlines the presence of tRNA-related region and absence of tRNA-unrelated one in a SINE. These terms highlight different structural features of short retroposons and can be used both.

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