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Nucleosome positioning by nucleosome inhibitory energy barriers is mediated by Alu element transposition

Transposition potentially disrupts genomic sequence but also modifies the template for chromatin formation. If the consequences of the former have been extensively studied, the interplay between transposable elements (TEs) and chromatin structure has not been fully explored. We compared the respective localization of (i) Alu elements, a very successful primate specific TE that covers about 10% of the human genome with more than one million copies, and (ii) the ~1.9 million nucleosome inhibitory energy barriers (NIEBs) previously described along the human genome using a sequence-based elastic model of DNA bending. NIEBs are short sequences (mean 153 bp) that inhibit the nucleosome formation, with two nucleosomes well positioned at each of their borders.

Alu size and sequence allow them to wrap exactly two histone cores side by side. We found that as much as 70% of Alu are inserted at NIEB borders, in phase with the well positioned nucleosomes. This suggests an association between NIEB chromatin and Alu localisation with a powerful purifying selection of the "out-of-phase" insertions and/or a transposition mechanism favouring "in-phase" insertions. Our analysis of intraspecific insertion polymorphisms in human is in favour of the purifyingselection model. Therefore, the compatibility with the chromatin structure seems to be a key factor for Alu fixation. Moreover, our results indicate that Alu insertions likely generate NIEBs, suggesting a possible role for these TEs in the evolution of NIEBs and in turn chromatin structure at a genome scale. The evolutionary interplay of TEs and chromatin could explain the strong transposition success of Alu in human, but also of other chromatin-compatible TE families in primates and other species.

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