INSERTION-DELETION POLYMORPHISMS AS INDICATION OF MECHANISMS OF TANDEM REPEATS EVOLUTION IN HUMAN GENOME.

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Introduction

Mutation pattern in tandem repeats is different from that in non-repeated genome regions. For microsatellites the most common mutations are insertions or deletions of one or several repeated units, although other mutations are also possible [1]. Mutations in minisatellites have not been yet in comparable detail.

Material and Methods

Human polymorphisms have been identified in large numbers and stored in databases like dbSNP. Mutation patterns in genome segments can be assessed via characteristic distributions of polymorphisms of different types. Although many polymorphisms were obtained on microarrays and thus are subject to experimental biases they can be used for comparative studies; new data on individual genome sequencing allows obtaining more precise data on genome variants distributions. Particularly interesting is comparison of frequencies of insertions/deletions of different lengths in genome tandem repeats like micro- and minisatellites.

Results

Statistical properties of mutations are dramatically different for tandem repeats with the length of repeated unit longer or smaller than 5-7 b.p., which accurately corresponds to the length separating microsatellites from minisatellites. In microsatellites insertion/deletion SNPs of one or several repeated units are very frequent, whereas for minisatellites such block indels are rather rare. We believe that such block indels in microsatellites are likely to appear stepwise coming from series of sequential mutations.

Indels in minisatellites are usually shorter than the length of the repeated unit. Such indels mostly come from microsatellites, which are included into a microsatellite repeated unit. Such events is a very common one [2], with more than 50% of indel SNP in minisatellites are actually related to microsatellites found within those minisatellites. A high frequency of such indels appears to be the main reason of fast degradation of minisatellites in the genome; the majority of minisatellites contains a very small number of repeated units, often less than two. Even "young" minisatellites often contain truncated repeated units [3]. This does not agree with polymerase slippage mechanism of minisatellite generation, which brings about multiplication of the intact repeated units. Other mechanisms of minisatellite generation are also far from being convincing. Probably, the origin of minisatellites can be elucidated by analysis of genomic segments with frequent SNPs in minisatellites

References

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