

1 Box 1. Mobile element subfamily evolution.

2 As a genome changes through time, it accumulates retrotransposon insertions in a hierarchical  
3 manner. For example, early in the evolution of a lineage, a single SINE subfamily may be active  
4 (subfamily 1). The master gene produces daughter elements and they are distributed across the  
5 genome. Over time that subfamily becomes quiescent and a second subfamily that is usually derived  
6 from the original master gene or one of its progeny becomes active. This second subfamily retains  
7 similarity with the original element but contains diagnostic mutations that distinguish it. This pattern  
8 recurs with subfamily 3. The end result is a genome with a hierarchical distribution of retrotransposons  
9 that can be characterized both by sequence identity and by time of insertion. Each subfamily is  
10 deposited during a particular time range.

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12 When a speciation event occurs, each daughter species will retain all of the insertions and  
13 lineage specific subfamilies of the ancestor as shared characters. However, each daughter species  
14 immediately starts along its own evolutionary trajectory with regard to SINE accumulation; i.e., it  
15 begins to accumulate its own lineage-specific insertions and mobile element subfamilies.

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17 This pattern has a profound effect on the tactics used to identify elements that might be  
18 informative for a particular research project. By identifying the subfamilies that are active in a taxon or  
19 taxon group that were active at the time of interest, a researcher can identify markers to fit his or her  
20 needs. This process culminates in the most recent insertions, many of which will be polymorphic in the  
21 genome of interest.

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