

Local variation of the mutation rate across the primate phylogeny

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Mutation rate is not uniform across the human genome. Variation of the mutation rate could be partially explained by DNA features: time of replication¹, DNase-hypersensitive sites (DHSs)², *etc.*, but most of variation remains cryptic³. The knowledge of regions of elevated and reduced mutation rate is of high importance and could facilitate the identification of genes involved in *de novo* diseases. We observed that the correlation between human and chimp divergence in 1 Mb genomic windows is 95% and it becomes less by ~30% when we compare human with the new world monkeys. Although the landscape of genomic features is quite sustainable it accumulates changes with time of million years. We found the excess of explained variance by some genomic features such as recombination rate and DHSs for regions in which mutation rate has changed recently. Landscapes of genomic features accumulate fewer changes compared with the landscape of the mutation rate, however shifts in distributions of genomic features correlate significantly with the changes in the local mutation rate between species in 1 Mb windows. In this study we re-analyzed the heterogeneity of mutation rate across primate species in a profound way with the more species genome sequences became available since last investigations. These findings shed light on the determinants of the mutation rate evolution and should be taken into account in biomedical studies and future essays.

1. Y.H. Woo, & W.-H. Li (2012) DNA replication timing and selection shape the landscape of nucleotide variation in cancer genomes. *Nat Commun* **3**: 1-12.
2. R.E. Thurman, *et al.* (2012) The accessible chromatin landscape of the human genome. *Nature* **489**: 75-82.
3. B. Schuster-Bockler & B. Lehner (2012) Chromatin organization is a major influence on regional mutation rates in human cancer cells. *Nature* **488**: 504-508.