GENETICS

REPETITIO EST MATER STUDIORUM

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but repeats in the human genome are not such impressive. Instead they create a lot of trouble when situated in the close proximity to genes. Think of Huntingtons disease, myotonic dystrophy, fragile X or some ataxias. The human genome sequence paper already had a chapter on repeat content (21% are LINES, 13% SINES and 8% other retrovirus stuff) while a new review has some nice figures of replication fork stalling that seems to be responsible for the introduction of repeats. The reasons for the toxicity of these repeats isnÂ´t such clear – as they are dominant a loss of function and haploinsufficiency would be a good explanation. It seems, however, that there is gain of function at the RNA level as repeat containing RNA is more stable by imperfect mismatch hairpins or may get some unwanted siRNA capability, yea, yea.

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