Spread of endogenous retrovirus K is similar in the DNA of humans and rhesus monkeys

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According to paleontologic and molecular studies, the chimpanzee (Pan troglodytes) is the closer relative to the humans (Homo sapiens) and that both lineages had a common ancestor at 5 to 7 million years ago. Moreover, the human-chimp lineage split from that of the rhesus monkey (Macaca mulatta) around 25 million years ago.

However, by studying the population dynamics of complete copies of primate endogenous retrovirus family K (ERV-K) in the genomes of humans, chimpanzee and rhesus monkey, a surprising pattern was observed.

The study by Romano and colleagues being published this week on PLoS ONE revealed that human ERV-K had a similar demographic signature to that of the rhesus monkey, both differing greatly from that of the chimpanzee. The data suggested that the humans and rhesus have been purging ERV-K copies from their genomes while the chimpanzee ERV-K population kept the signature of increasing numbers of ERV-K amplification in the genome of ancestral primates during the last 20 million years.

Hominins have been moving out of Africa for the last 2 million years and the modern humans (Homo sapiens) spread around almost the entire globe during the last 100 thousand years. Moreover, Macaca is the most specious primate genus and it is believed to have originated around 2.5 million years ago and became widely dispersed within a short period of time, from the West in Afghanistan to the Eastern coast of China. It is also known that speciation events partition and restrict flow among genetic pools.

As a consequence, both Homo and Macaca by colonizing new environments and undergoing successive population fluctuations that caused severe genetic bottlenecks, possible purged ERV-K from their genomes in a similar fashion. On the other hand, populations chimpanzee have been restricted to Eastern and Central Sub-Saharan Africa, ever since and crucially, are also known to have a greater genetic diversity than humans (due to a greater effective population number Ne), even when humans have a far greater sensus population.

While the population size fluctuations due to dispersal or speciation may have had impact on genome architecture, the several expansion and bottlenecks experienced by Homo and Macaca may have played an important role in shaping ERV-K dynamics.

Because Pan did not suffer severe bottlenecks since their separation from the Pan – Homo (human) common ancestor, they not only show a greater genetic diversity but also they preserved a greater number of complete ERV-K copies in their genomes.

The most remarkable result was that for the first time we could observe that genetic fluctuations caused by bottlenecks and expansion in host species play a fundamental role not only in their genetic diversity but also in the interaction with latent parasites that leave their genome copies in our DNA.

Source: Public Library of Science