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Trypanosome mitochondrial genome: the mechanism of inheritance

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Trypanosomes are haemoflagellates found in various vertebrates. They represent a group of early branched eukaryotes, with numbers of diverged characteristics from mammalian cells. The most obvious one is that they contain a specialized mitochondrial genome, termed a kinetoplast. The kinetoplast forms a disc shape of interlocking DNA circles of two types, maxicircles and minicircles. Maxicircle is generally over 20 kb, and encoding some typical and more encrypted mitochondrial genes, which are decrypted only using hundreds of keys from minicircles. Concerning this structure, there are some very interesting questions to be answered. 1) How do they maintain this complex mitochondrial genome? 2) How does this complex mitochondrial genome work? 3) How does this complex mitochondrial genome evolve from and to? To address these questions, the authors investigated the model organisms of *Trypanosoma brucei*, *T. evansi*, *T. equiperdum* and *T. lewisi* and found that the maintenance of kinetoplast was via basal body, and identified novel protein of BBLP. The authors revealed that the transcriptome patterns of kinetoplast, and identified new structure of minicircles. In addition, the authors described the distinct features of various kinetoplasts, and proposed evolutionary scenery of kinetoplast. Altogether, kinetoplast is a distinct and complex structural mitochondrial genome, which is also an excellent example to show the diversity of eukaryotic cells and stupidity of designer if presents.

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