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A new approach to estimate genomic GC content equilibrium

The equilibrium of genomic GC content was estimated under assumption that per base pair rate of GC->AT (u) and AT->GC (v) mutations are temporally constant (the constant model). However, this assumption may be unrealistic. We propose a simple mathematical model to estimate the equilibrium GC content based on temporal per base pair rate of mutations (the variable model). In this model, u and v vary depending on temporal GC content. We estimated the equilibrium GC contents of the human genome by using extensive SNP data and the chimpanzee genome as outgroup. In the constant model, the equilibrium GC content values are significantly different to each other depending on each initial GC content value, while they clearly show a tendency of homogenization in terms of GC-rich isochore. In the temporal model, under certain conditions, GC content converges on the same equilibrium independent from initial GC content values. Meanwhile, under the other conditions, the temporal model theoretically shows a chaotic behavior in terms of temporal GC content. This may explain the origin and evolution of isochore.

CV

Education

Ph.D.	The Graduate University for Advanced Studies	1998
M.Sc. in Information and Computer Science		
	Japan Advanced Institute of Science and Technology	1995
B.L.A.	The Open University of Japan	1993

Employment Background

2004-Present	RIKEN, Researcher
2001-2004	Japan Science and Technology Agency, Post-doctoral fellow
1999-2001	University of Chicago, Post-doctoral fellow
1998-1999	National Institute of Genetics, Post-doctoral fellow