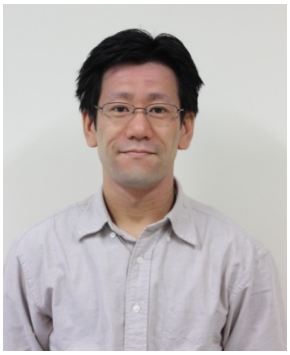
Dr.
Kosuke Teshima

The graduate university for advanced studies
Kamiyamaguchi 1560-39
Hayama, Kanagawa 240-0193, Japan
Phone: +81-46-858-1576, Fax: +81-46-858-1544
E-mail: kteshima [at] soken.ac.jp



Evolution of duplicated genes under the pressure of gene conversion

Gene duplication is considered to be a source of genome evolution. It is considered that duplicated genes can obtain a new functional mutation because of their redundancy. This neofunctionalization process is one of the main process for genome evolution.

Although the importance of gene duplication has been well recognized, the evolutionary process is not fully understood yet because the process is so complicated that the traditional population genetics theory is infeasible. Thus, we performed simulation to study the evolutionary process.

Our simulation study brought out very unique aspects of duplicated genes: the violation of the molecular clock and the distinctive distribution of divergence. Because gene conversion between duplicates suppresses two regions to diverge, the amount of mutations between duplicates are not proportional to time. Instead, two regions keep high homology for a very long time.

If an functional mutation arises on one gene and if the combination of the original and the neofunctional alleles provides selective advantage, the combination of two functional alleles prevails in a population. Gene conversion event on the neofunctional site is suppressed because such conversion event erases selective advantage. As a result, a distinctive spacial distribution of divergence are observed around the neofunctional mutation. Because this distribution is distinctive and limited to the neighborhood of the neofunctional mutation, the pattern can be used as a good indicator to find neofunctionalization event. We confirmed the pattern of polymorphism on human opsin gene agrees with the pattern expected from our simulation study.

CV

2006-present:	Research Associate, Graduate University for Advanced Studies. Advisor: H. Innan
2004-2006:	Research Associate, Brown University (2004-2005) and University of Chicago (2005-2006). Advisor: M. Przeworski
2002-2004:	Postdoctoral Fellow, University of Cincinnati. Advisor: R. Chakraborti
1997-2002	Ph.D., University of Tokyo. Major: Biological Sciences. Advisor: F. Tajima
1993-1997	B.Sc., University of Tokyo. Major: Biological Sciences.

Publications

(1) Takahashi Y., Teshima KM., Yokoi S., Innan H. and K. Shimamoto, Variations in Hd1 proteins, Hd3a promoters, and Ehd1 expression levels contribute to diversity of flowering time in cultivated rice. Proc Natl Acad Sci USA. (accepted)

(2) Blekhman R., Man O., Herrmann L., Boyko AR., Indap A., Kosiol C., Bustamante CD., Teshima KM., Przeworski M., Natural selection on Genes that underlie human disease susceptibility. Curr Biol. 2008 18: 883-889

(3) Teshima KM., Innan H., Neofunctionalization of duplicated genes under the pressure of gene conversion. Genetics 2008 178: 1385-1398

(4) Teshima, KM., Coop, G., and Przeworski, M., How reliable are genomic scans for selective sweeps? Genome Res. 2006 16: 702-712

(5) Teshima, KM. and Przeworski, M., 2006, Directional Positive Selection on an Allele of Arbitrary Dominance. Genetics 2006 172: 713-718

(6) Teshima, KM. and Innan, H., 2003, The effect of gene conversion on the divergence between duplicated genes. Genetics, 166: 1553-1560

(7) Teshima, KM. and Tajima, F., 2002, The effect of migration during the divergence. Theor. Popul. Biol., 62: 81-95