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RIKEN

The molecular origins of morphological diversity

A research team at RIKEN has clarified details of key mechanisms driving the emergence of functional novelty in genes of eukaryotes. In a paper to appear in *PLoS Genetics*, the researchers analyze the molecular-level mechanisms of functionalization in duplicate genes, shedding light on their relationship to morphological evolution.

Gene duplication, a process whereby a region of DNA containing a gene is duplicated as a result of cell division errors, plays a major role in eukaryotic evolution. Over time, mutations in duplicate genes induce a novel evolutionary paths potentially leading to functionalization, an important source of diversification in complex organisms.

The researchers investigated two mechanisms believed to play a role in such functionalization: divergence of gene expression and of protein function. A set of 492 gene pairs associated with morphological diversification in the model organism *Arabidopsis thaliana* were examined and classified according to their level of morphological diversification.

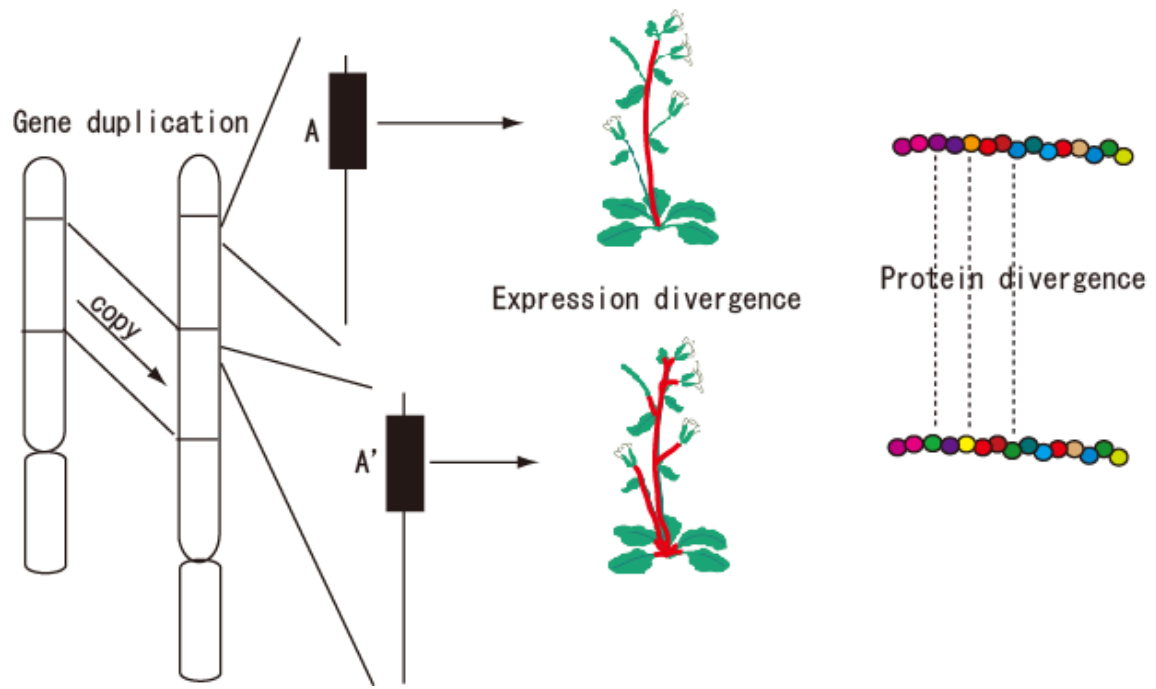
Results indicated that in gene pairs with high and low morphological diversification, divergence rates are significantly higher than in pairs with no diversification. Analysis also suggested that whereas protein function plays a major role in such diversification, gene expression plays a minor one. At the genome level, instances of either mechanism leading to diversification were found to be extremely rare, indicating that only a few duplicate genes are crucial to morphological evolution.

While making up as much as one fifth of all genes in the eukaryotic cell, duplicate genes have eluded functional analysis due to their redundancy. The success of the current research demonstrates a novel approach, promising fundamental advances in our understanding of genetic function.

For more information, please contact:

Dr. Kosuke Hanada
Gene Discovery Research Group
RIKEN Plant Science Center
Tel: +81-(0)45-503-9578 / Fax: +81-(0)45-503-9580

Ms. Saeko Okada (PI officer)
Global Relations Office
RIKEN
Tel: +81-(0)48-462-1225 / Fax: +81-(0)48-462-4715
Email: koho@riken.jp



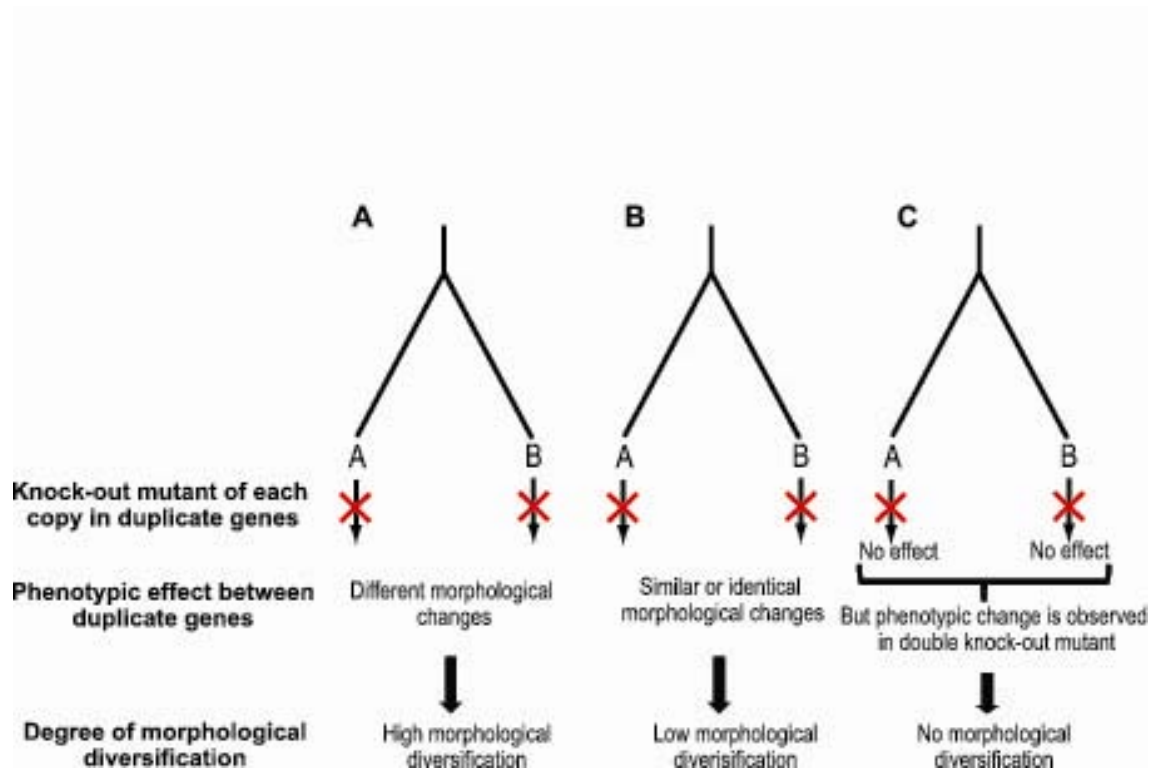


Figure 1: Paralogous gene pairs with high, low and no morphological diversification.

A. Paralogous gene pairs with different knock-out phenotypes are defined to have high morphological diversification. B. Paralogous gene pairs with similar or identical knock-out phenotypes are defined to have low morphological diversification. C. Paralogous gene pairs in which morphological changes are observed only upon the deletion of multiple paralogous genes but not by the deletion of each gene individually are defined to have no morphological diversification.

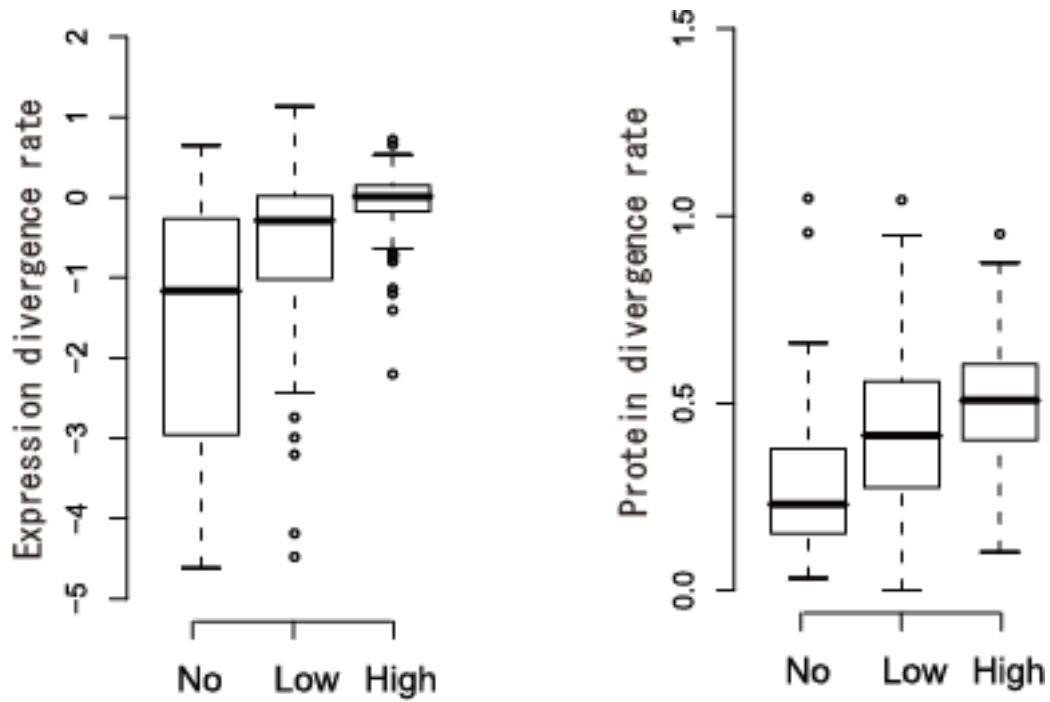


Figure 2: Divergence rate of expression and protein sequence in paralogous gene pairs.

A. Relationship between expression divergence (E_d) and morphological diversification. E_d is $\log((1 - R) / (1 + R)) / K_s$, where R is the correlation coefficient of paralogous gene pairs among different experimental conditions and K_s is synonymous distance. B. Relationship between ratio of K_a (nonsynonymous distance) to K_s in paralogous gene pairs and morphological diversification. C. Relationship between ratio of K_r (radical nonsynonymous distance) to K_c (conservative nonsynonymous distance) and morphological diversification. The random sample included 1000 pairs of paralogs. The distributions of E_d , K_a/K_s ratio and K_r/K_c ratio are shown as box plots with the solid horizontal line indicating the median value, the box representing the inter quartile range (25%–75%), and the dotted line indicating the first to the 99th percentile.