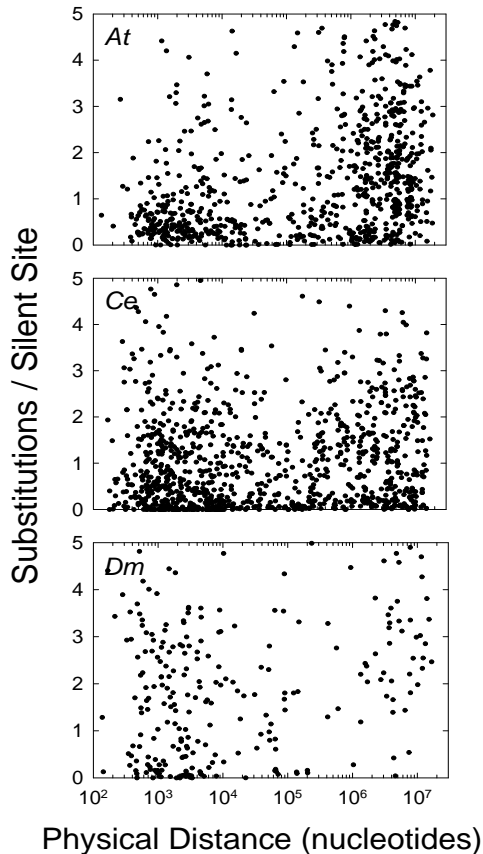


## Supplement

The following figure is a supplement to:

Lynch, M. and Conery, J.S. The evolutionary fate and consequences of duplicate genes.  
*Science* 2000 Nov 10;290(5494):1151-1155.



The relationship between the number of substitutions per silent site ( $S$ ) and the number of nucleotides separating the two members of a duplicate pair on the same chromosome. The data for *Arabidopsis thaliana* (*At*) are derived from the complete sequences of chromosomes 2 and 4; those for *Caenorhabditis elegans* (*Ce*) are derived from the complete genomic sequence; and those for *Drosophila melanogaster* (*Dm*) are pairs of duplicates contained within the same scaffolds. Least-squares regression involve the natural logarithm of physical distance. For *At*, slope = 0.111 (0.003),  $r^2 = 0.115$ ,  $n = 811$ ; for *Ce*, slope = 0.091 (0.003),  $r^2 = 0.028$ ,  $n = 1027$ ; for *Dm*, slope = 0.183 (0.009),  $r^2 = 0.031$ ,  $n = 250$ . All regressions are significant at the  $P = 0.01$  level, although the proportion of the variance explained by the model ( $r^2$ ) is very low in all cases. In no case is the intercept significantly different from zero.