Gene syntenies conserved on very large genetic distances

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Conserved synteny genes are homologous genes that map to the same chromosome in two or more species. We set up to characterize the syntenies conserved on very large genetic distances (billions of years). We used orthologous sets of genes from human, fruit fly *Drosophila melanogaster*, worm *C. elegans* and yeast *S. cerevisiae* and compared the number of conserved syntenies for all pairs of organisms. As controls, we used random genomes generated by permutations of the orthologous relationships and counted conserved syntenies in the same way as for the real sets.

The number of conserved syntenies in all the pairs of animal genomes (human-fly, fly-worm, human-worm) was significantly higher than in the random genomes, while the number of syntenies involving the yeast genome was similar to the control. Among the animal genomes, we also identified chromosomal combinations enriched for genes of conserved synteny. The most significant combination (P<0.00001) was for chromosomes 14 (human), V (*C. elegans*), and 3R (*Drosophila*). The combinations 14-V, 14-3R, and V-3R were also significant in pairwise genome comparisons (P<0.00001, P<0.007, P<0.00001, respectively). In parallel, we have also identified several sets of chromosomes depleted for conserved syntenies.

We show that synteny in animal genomes is more conserved than expected from random genomes. We aim to characterize the genes involved in conserved syntenies in order to identify additional factors contributing to the non-random gene order.

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