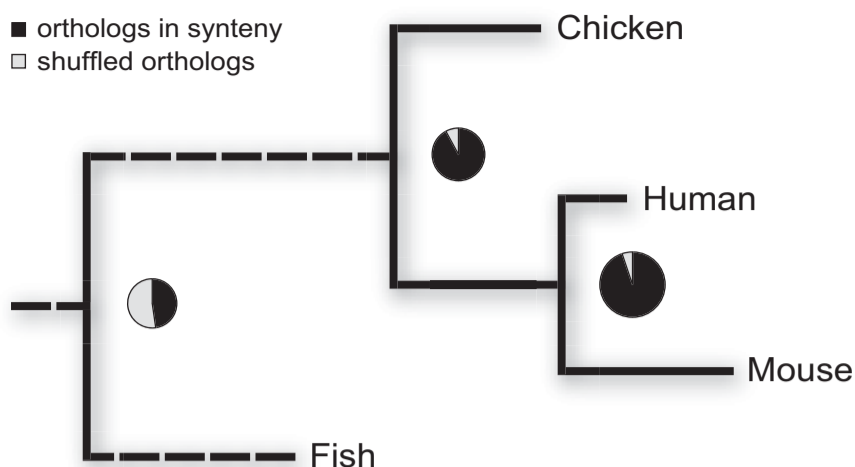


A) Synteny breaks



B) Inter-chromosomal shuffling

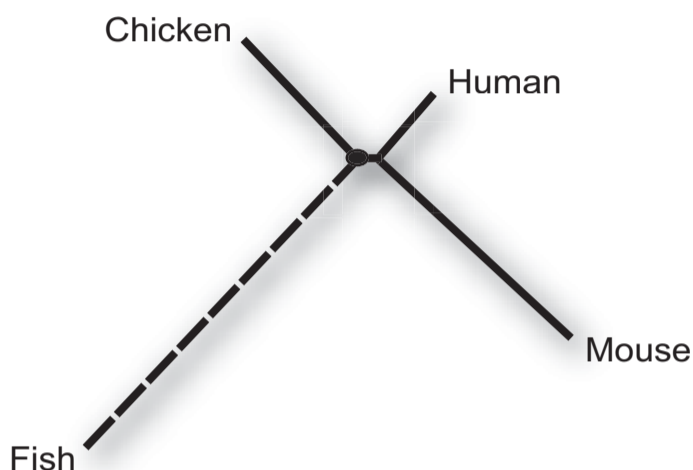


Figure ST.

A) Synteny breaks.

The quantitative genome synteny divergence tree of chicken, human and mouse. The relative length of each branch was estimated counting the number of synteny breaks where ancestral state is supported by synteny to an outgroup species, e.g. if there are two neighboring genes in synteny between chicken and human that are found in different synteny blocks in mouse we counted a genome break on rodent lineage. Thus we measured the length of the synapsid branch (leading to mammals) and sauropsid branch (leading to birds) using Tetraodon fish as the outgroup. Measuring the relative branch length leading to human and mouse using chicken as the outgroup allowed us to resolve the branch length before human and mouse split. The pie-charts show the fraction of orthologous genes that have retained their genomic neighborhood and their relative sizes indicate the number of recognizable orthologous genes.

B) Inter-chromosomal shuffling.

The chromosomal similarity tree of chicken, human and mouse, estimating minimum number of exchanges between different chromosomes. The quantitative estimation of the branch lengths was derived from all pair-wise measures, counting the number of inter-chromosomal relations with at least one synteny block spanning more than 3 genes except number of 1:1 ancestral chromosomal relations determined by the total number of orthologous genes.

some text:

Maps of conserved synteny between chicken, human, mouse and Tetraodon fish were constructed on the level of orthologous gene pairs as described earlier [Zdobnov et al. Science. 2002 Oct 4], which are tolerant to micro-rearrangements inside synteny blocks and to variable gene density.

The analysis clearly shows that:

A) the chicken genome is more stable than the mammalian one, accumulating less rearrangements than the human and mouse ancestor,

B) the genome in the rodent lineage is nearly three times more dynamic than in the human one, accumulating more rearrangements since the human and mouse split than the whole chicken branch.

In general we observe a remarkable conservation between chicken and mammalian genomes revealing that roughly 85% of genes retained their genomic neighborhood during about 300 MYA of independent evolution while less than 50% of orthologous genes in fish genomes of Tetraodon and Fugu retained their neighborhood during about 500 MYA of evolution (Figure ST. A).

On the other hand counting the number of inter-chromosomal rearrangements confirms an earlier observation [XX] that human is closer to chicken than to rodents in terms of chromosomal content (having fewer inter-chromosomal rearrangements) (Figure ST. B).

The analysis revealed that the human lineage encountered twice less inter-chromosomal exchanges than the chicken branch and only one third that of rodents, which is consistent with the observed numbers of all synteny breaks. The surprising similarity of chromosomal organization between chicken and human comes from an apparent lack of inter-chromosomal shuffling during early mammalian evolution (before the mouse and human split).