

Insights into the structural evolution of amniote genomes

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We use the complete genome sequences and assemblies of 14 vertebrate species, to infer large regions or synteny of three ancestral genomes: the amniote, therian and boreoeutherian ones. We then infer patterns of genome structural evolution in amniotes: types of rearrangements, long and short branches of the underlying phylogenetic tree, convergent and divergent karyotypic evolution.

We encounter and explore several methodological issues:

- the construction of good conserved orthology blocks among all amniotes;
- the detection of conserved synteny signals between amniotes and teleost fishes based on the principle of Doubly Conserved Synteny (DCS) used in (Jaillon et al. 2004) and taking into account the whole genome duplication in the teleost lineage;
- the construction of large Contiguous Ancestral Regions (CARs) of ancestral genomes (as in Chauve and Tannier, PLoS Comput Biol 2008) and their linkage according to the DCS signal;
- the detection of reliable ancestral genome rearrangements (as in Zaho and Bourque, Genome Res 2009).

The ancestral boreoeutherian genome we infer is in almost complete agreement with previous cytogenetics and computational studies. Therian and amniote ancestral genomes still miss good references, as two previous studies (Nakatani et al. Genome Res 2007, Kohn et al. Trends in Genetics 2004) gave divergent results. Still the amniote ancestral genome is found relatively close to the chicken genome in all studies, including this one. We analyse every karyotypic change in the chicken and therian branches.