

approach to comparative studies has been the separate isolation of markers for each species, which can be very time-consuming. Pollock *et al.* argue that the time and cost of these projects could be reduced by combining the DNA samples from the different taxa and shotgun sequencing of the mixture. Shotgun sequencing simply involves the random breaking of DNA into pieces, with subsequent cloning of these fragments into vectors. The final step is the random sequencing of the fragments. Given sufficient sequence coverage, the assembly of the individual genomes, from the mix of sequences, will be easy because overlap between the sequence fragments will allow their identification. To illustrate the applicability of this technique, Pollock *et al.*

used published mitochondrial genome sequences from ten species and simulated the 'shotgunning' and assembly of the fragments under assumptions expected to occur in a such a project. The results are promising, with six out of the ten genomes completely and correctly reconstructed, and the other four correctly reconstructed but with short gaps.

So what? Should we start shotgun sequencing mixtures of living creatures? The authors have already started doing this in a pilot project, and propose rapid expansion to sequence 2000 mitochondrial genomes from vertebrates! Given the numbers of described vertebrate species (4000 mammals, 7000 birds, 20 000 fish and thousands of reptiles and amphibians), it is the first time that such extensive data will be

accumulated for comparative analysis, with tremendous benefits for molecular evolutionary studies. The authors believe that the same principle will eventually be applied to whole nuclear genomes and for a range of taxonomic ranks (including intraspecific questions), but nothing beats good ideas like data. Only they will tell if there is grandeur in this view of life...

<sup>1</sup> Pollock, D.D. *et al.* (2000) A case for evolutionary genomics and the comprehensive examination of sequence biodiversity. *Mol. Biol. Evol.* 17, 1776–1788

**Antonis Rokas**

a.rokas@ed.ac.uk

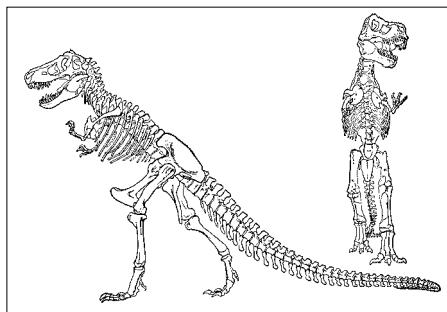
PII: S0169-5347(00)02051-6

## Digit identity and digit number: indirect support for the descent of birds from theropod dinosaurs

The evolutionary origin of birds is the subject of heated debate. As more data are collected, a consensus is emerging in favour of a descent from theropod dinosaurs. However, in 1997, important evidence refuting this hypothesis was put forward by Burke and Feduccia. They provided new data that confirmed old claims that the digit identity of the three fingers of the hand in theropods differs from that of birds (digits I, II and III versus II, III and IV), which implies that there is no homology between the first, second and third digits of the hand of these groups.

In 1999, Wagner and Gauthier subsequently proposed a hypothesis that reconciled the differences in digit homology with an avian descent from theropods. They suggested that changes in digit identity are the cause of homeotic changes (i.e. changes of the identity of one structure into the identity of another structure). Homeotic changes of identity in serial structures are a common occurrence in the vertebral column (e.g. 5% of humans have a thoracic vertebra with a rib instead of the first ribless lumbar one). Also, shifts in identity for an entire group of serial structures, such as that proposed by Wagner and Gauthier, have been amply documented for vertebrae in transgenic mice. There are several different mutations that shift the identity of one vertebra along the entire vertebral column in either the anterior or the posterior direction

(e.g. mutations of the polycomb-group and trithorax-group genes). However, no firm evidence for homeotic changes in digits had been found, although it is plausible that the presence of two opposable digits instead of one in koalas and many tree-dwelling birds represents such a homeotic change (here, a change is the identity of the second digit into that of the first).



In a new paper, Drossopoulou *et al.*<sup>1</sup> now present evidence for the developmental independence of the determination of digit number and digit identity. In an elegant experiment, they demonstrate that the important gene Sonic hedgehog (Shh) is initially involved in the determination of the number of digits and later on in the specification of digit identity via the induction of Bmp genes. This complies with existing knowledge that ectopic expression of Shh induces supernumerary digits (polydactyly). By carefully manipulating the

gene activity of Shh and Bmp2, they produced phenotypes with the same number of (supernumerary) digits but with differences in digit identity (digit 2, 3 or 4), thus showing that the identity of digits can be changed without a change in the number of digits. Evolutionarily, it is important to realize that Shh is not unique in this respect. At present, at least one other gene is known that has an effect comparable to Shh on the development of supernumerary digits – the related Indian hedgehog gene.

Although the evidence is far from complete, these results indirectly support the hypothesis of Wagner and Gauthier. They prove the underlying assumption that homeotic changes in the identity of digits are possible and can occur without a change in digit number. Apart from the relevance to the interpretation of the evolution of birds, Drossopoulou *et al.* have also provided an important piece in the intriguing puzzle of limb and digit development.

<sup>1</sup> Drossopoulou, G. *et al.* (2000) A model for anteroposterior patterning of the vertebrate limb based on sequential long- and short-range Shh signalling and Bmp signalling. *Development* 127, 1337–1348

**Frietson Galis**

galis@rulfsb.leidenuniv.nl

PII: S0169-5347(00)02048-6