

What Do a Bat, a Pig, a Mouse, and an Opossum Have in Common?

You've seen the diagram below a thousand times—different vertebrate limbs colored in a way so that you recognize their similar pattern: one bone close to the body, then two bones, then many bones, then digits (fingers or toes). This arrangement of bones is an example of a homologous trait. Homologous traits were inherited from a common ancestor and are shared among the ancestors' descendant species. But the *differences* in the structures and functions of vertebrate limbs are just as remarkable as their similarities. And although we know why they're similar, we didn't, until recently, have too many clues as to exactly why they are different.

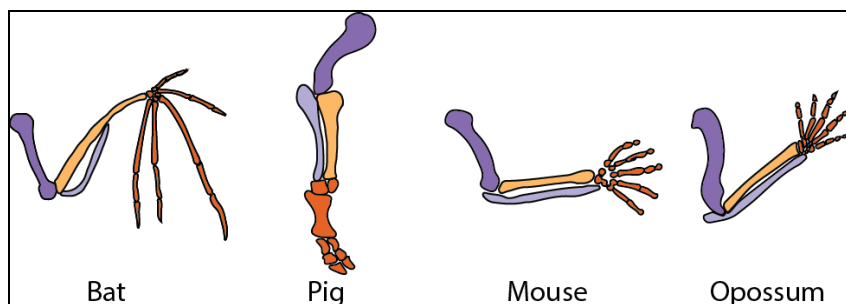


Figure 1. Bones In the Forelimb (Arm) of a Bat, Pig, Mouse, and Opossum.

In search of answers, researchers at the University of Chicago compared not the

bones, but **gene expression** (where and when in development the genes are turned into mRNA) of four mammals: a bat, a pig, a mouse, and an opossum. To do this, they needed to figure out which genes are associated with limb development, which is not an easy task! The researchers sequenced every single mRNA in the forelimbs and hindlimbs of a bat, a pig, an opossum, and a mouse at different time points as they developed. What they found is that as the limbs develop, the same genes are expressed at similar times in all four species. This should not, perhaps, be surprising since genes underlie traits and are passed from parent to offspring.

But we know there are important differences in the limbs of a bat, a pig, a mouse, and an opossum (see **Figure 1**). What underlies these differences if it's not the genes, or when the genes are expressed in development? The researchers wondered if the answer could be in *where* the genes are expressed.

To determine where genes are expressed, scientists use a technique called *in situ* hybridization. ("*In situ*" is Latin for "in position.") *In situ* hybridization lets researchers see a gene's pattern of expression within a developing organism. **Figure 2** shows a developing frog (from a different study) in which *in situ* hybridization has been used to indicate where a particular gene is being expressed. A molecule binds to the mRNA for the gene and stains it purple. The researchers studying the bat, pig, mouse, and opossum limbs use similar techniques to find out where different mRNAs are expressed at different stages of development.

Using *in situ* hybridization, the University of Chicago researchers found that the *where* was indeed important! The mRNA expression pattern of the homologous genes differed among the species, especially in later stages of development. These results suggest that what look like big

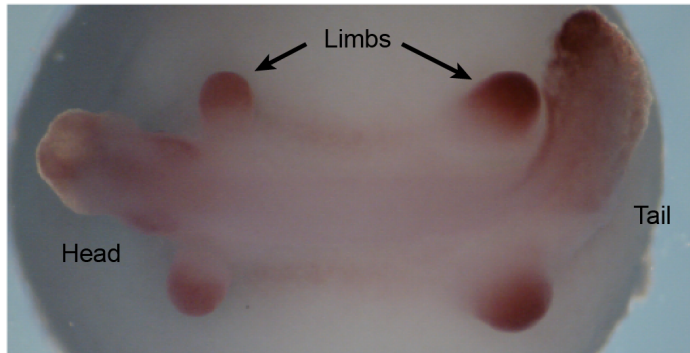


Figure 2. *In Situ* Hybridization of a Developing Frog. The dark purple stain shows where the mRNA of the gene *wnt5a* is expressed: in the tail, forelimbs, and hindlimbs, and also a little bit in the head. *Source:* Used with permission of J. Gross.

differences to us—the difference between a pig’s hoof and a bat’s wing for example—are actually the result of relatively small changes in the location of homologous gene expression in development.

These results suggest that even the ancestor of all *animals*, which lived about 600 million years ago, might have had the same set of homologous genes (the “genetic toolkit”) we see in living mammals. For 600 million years, evolutionary forces slowly acting on these genes and their mRNA expression patterns have generated the diversity of animal limbs represented on our planet today.

Reference

Maier, Jennifer A., Marcelo Rivas-Astroza, Jenny Deng, Anna Dowling, Paige Oboikovitz, Xiaoyi Cao, Richard R. Behringer, Chris J. Cretekos, John J. Rasweiler IV, Sheng Zhong, and Karen E. Sears. “Transcriptomic Insights into the Genetic Basis of Mammalian Limb Diversity.” *BMC Evolutionary Biology* 17, no. 1 (2017): 1–18. doi:10.1186/s12862-017-0902-6.

BiteScientist Profiles



At the Harvard Museum of Comparative Zoology, **Mara Laslo** studies the evolution of endocrine systems and life cycles in frogs. Her dissertation investigates how a frog could skip the tadpole stage—as almost a third of all frogs do! She also works with the Harvard Museum of Natural History to share her research and make museum collections available to teachers and citizen scientists.

As a student at Williams College, **Kaitlin Dinett** discovered her love of the complex world of living things and decided that she wanted to share this with other students as a teacher. After teaching middle school life science for three years, Kaitlin earned an advanced degree from Harvard Graduate School of Education. She is now a high school biology teacher, where she loves challenging her students to apply their knowledge to real life scenarios.

