

Dogs, maybe not, but old genes can learn new tricks

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Two *Onthophagus taurus* males. Armin Moczek and Debra Rose's study suggests several genes involved in making legs and antennae were co-opted to make the beetles' horns. Horns are a novel trait that is unique to horned beetles. Credit: Alex Wild (<http://www.myrmecos.net>)

A popular view among evolutionary biologists that fundamental genes do not acquire new functions was challenged this week by a new study in the *Proceedings of the National Academy of Sciences*.

Indiana University Bloomington biologist Armin Moczek and research associate Debra Rose report that two ancient [genes](#) were "co-opted" to help build a new trait in [beetles](#) -- the fancy antlers that give horned

beetles their name. The genes, *Distal-less* and *homothorax*, touch most aspects of insect larval development, and have therefore been considered off-limits to the evolution of new traits.

In the two horned beetle species Moczek and Rose studied, the genetic sequences of *Distal-less* and *homothorax* were hardly different, suggesting the two genes have retained their unique identities because of selective pressures not to change. What changed was not the genes themselves, but when and where they are turned on.

"Evolutionary biologists have a good idea of what it takes to change the shape of a wing, the length of a leg, or the anatomy of an eye," Moczek said. "What we have struggled with, though, is how these traits originate in the first place. How do you evolve that first wing, limb or [photoreceptor](#) from a flightless, limbless and blind ancestor?"

To investigate these questions, Moczek and Rose examined three [development genes](#) that are so old, all insects have them: *Distal-less*, *homothorax* and a third, *dachshund*. The genes were first characterized in [fruit flies](#), and are categorized as "upstream" regulatory genes because they influence a wide variety of genetic processes in insect cells, such as the development of legs, antennae and wings. Moczek said that in horned beetles, each of the three genes is likely to have hundreds to thousands of downstream targets.

A tenuous consensus among evolutionary biologists was that such genes -- upon which so many different and important processes depend -- could not be easily modified, because any modification would affect countless aspects of the insect's development, any one of which could be bad for the individual insect, reducing its fitness relative to its peers.

Moczek and Rose's PNAS paper confirms one aspect of this idea. All three genes were sequenced and found to be highly conserved, or

unchanged, not only among the individuals of each beetle species they examined, but also between the two species, *Onthophagus taurus* (Italy) and *Onthophagus binodis* (South Africa), whose lineages diverged about 24 million years ago. But that isn't the whole story.

To understand the effects of the three genes on horned beetle development, Moczek and Rose employed a new and promising technique, RNA interference, which disables the action of specific genes without compromising other genetic processes. Humans are only mimicking nature here; RNA interference is also a natural method of gene regulation in eukaryotes.

Moczek and Rose divided beetle larvae of both species into three treatment groups: no injection, buffer injection with nonsense RNA and buffer injection with RNA interference transcripts designed to disrupt one of three crucial developmental genes.

Moczek and Rose learned that two of the three genes, *Distal-less* and *homothorax*, are used by both *O. taurus* and *O. binodis* in the development of beetle horns. While *Distal-less* was found to affect both the development of thorax horns (which form just behind the head) and head horns, *homothorax* was only found to influence thorax horn development. The gene *dachshund* appears to have no effect whatsoever on horn development in either species.

"The evolution of novel features does not require the evolution of novel genes," Moczek said. "A lot of innovation can grow from within the organism's genetic toolbox."

More importantly, Moczek and Rose learned all developmental genes are candidates for such recruitment, not just the genes whose development functions are considered non-essential or limited in their effects.

Moczek also says the PNAS paper may compel [evolutionary biologists](#) to revisit pleiotropy, the foundational concept of one gene influencing many traits.

"It may be that our understanding of pleiotropy is too simplistic," Moczek said. "Now that we know fundamental development genes can acquire new and diverse functions with relative ease, pleiotropy may not be nearly as constraining as we have thought."

Source: Indiana University ([news](#) : [web](#))

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