

Highlight—Small Genomes for the Swift: Of Flight and Intron Size

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Six years ago skeptics asked Fyodor Kondrashov whether the future held anything new for the field of genomics. The thinking was, he says, “we already had a few genomes so we already knew everything just from a few examples. Those asking didn’t think that, given 100 genomes instead of 10, we would learn anything new about life.” Scott Edwards and Qu Zhang, two Harvard evolutionary biologists, give a resounding answer to this question in a new study published in *Genome Biology and Evolution*.

“This shows that, with more genomes, you can get qualitatively different understandings of genome evolution,” says Kondrashov of the Centre for Genome Regulation in Barcelona, who was not involved in the research. “It’s a good example of quality coming from quantity.”

Edwards and Zhang compare the sizes of introns, noncoding stretches of DNA, within three data sets to ask whether flying animals with high metabolic rates are more likely to have small introns. And indeed, they find, they are.

Edwards has spent most of his career as an ornithologist, asking questions about the evolution of birds. Phylogenetics and biogeography are his normal preoccupations. Nearly 10 years ago, however, his attention was caught by a report from Austin and Marianne Hughes of Pennsylvania State University that chicken introns are smaller than comparable human introns. Their proposed explanation? Less DNA might help a bird fly.

“[The idea] was provocative at the time,” Edwards says, “but it didn’t look at enough species to see if the relationship between flight and genome size was viable. In this work we were able to use the most recent databases to once again address this question.”

Revisiting this question with the latest data and informatics tools confirmed some old patterns and outlined some new ones.

“For the first time we were able to look at two groups of flying lineages in vertebrates: birds and bats. Both of those lineages have introns that are smaller than those lineages that don’t fly.”

The satisfaction in this finding is only partial, however. The meat of the matter, what “causes” this link, is what everyone would like to know.

“The mechanism is still an outstanding question,” Edwards says. The seminal Hughes and Hughes article holds that flight is energetically expensive, requiring great respiratory and metabolic feats. Small cells and slimed-down genomes, they say, make that easier. Although the link between small genomes and cells is well established and few, says Edwards, would question it, the notion that diminutive cells can enhance metabolism is more controversial.

“It’s not clear exactly which selection forces are acting on the introns,” says Kondrashov, echoing the same concern. “It would be nice to know which parameter is being optimized. ‘Metabolism’ is sort of a general easy target. The way to go forward on this is to go deeper on a molecular level.”

It would be interesting to know, he says, how much ATP is needed for intron transcription and how long that transcription takes. As an analogy for how natural selection could act on the system, Kondrashov suggests thinking of an office setting. Offices requiring extremely tight turnaround times cannot handle any slack in processing paperwork. Clerks who take minutes or hours longer than their colleagues to do the same work will soon be out of a job. Offices with a more relaxed pace, however, can afford to keep the employee who turns in his forms 20 min later than his colleagues.

Edwards is quick to point out that the patterns he and Zhang found could just be correlates or a surrogate. Other factors could select for small genomes as well. In fact, it is likely that they do.

In 2007, Edwards’s team tried to reconstruct genome sizes for extinct dinosaur ancestors of birds. The best estimates, they found, were small genomes, similar in size to modern birds.

“That tells that flight can’t be the whole story. Lots of these non-flying dinosaurs still had small genomes.”

It is also possible, however, that the pattern can be explained by theories not involving natural selection, such as the “neutral theory” of genome evolution. Members of this camp thinking (e.g., Michael Lynch) believe that species with

large effective population sizes are able to purge from their genomes bad things more easily than species with small effective population sizes. The prediction of this hypothesis would hold that birds and bats have larger population sizes than their nonflying relatives. This study, however, does not thoroughly test this hypothesis.

“I think the Lynch idea needs to be looked at in more detail,” Edwards says. “We should see if there is a relationship between population and genome size.”

Edwards still believes that the demands of flight and high metabolic rates are acting on genome sizes. He points to the comparison between bats and other mammals as evidence. Intriguingly, bats have significantly smaller introns.

“To be honest, I was really surprised the signal came out in bats,” Edwards says. “I didn’t expect it to be as clear as in the birds, but there it is.”

Nonetheless, he finds metabolic rate the most compelling explanation so far for the correlations he and Zhang found,

“as skeptical as I was of Hughes’s original paper in 1995,” he says.

He would also love to do more mechanistic experiments, by manipulating the metabolic and watching what direction evolution takes the genome, for example. (At this point, he is not sure how to do that.) He is planning also to look at the genome sizes of flightless birds, the ratites, a group including emus and ostriches. The prediction? Their genomes should be extravagantly plumed with noncoding information, compared with their swifter cousins.

Literature Cited

Zhang Q, Edwards S. Forthcoming 2012. The evolution of intron size in amniotes: a role for powered flight? *Genome Biol Evol.*, Advance Access published August 28, 2012, doi: 10.1093/gbe/evs070.