Highlight: "Keeping the Boys in the Conversation: Male Fitness Shapes the Location of Genes that Interact with Mitochondria"

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Several months ago, Devin Drown, Kevin Preuss, and Michael Wade got to talking over coffee and breakfast sandwiches. The men were discussing, as biologists occasionally do, how modes of genetic transmission could give rise to evolutionary patterns. This morning their interest was in mitochondria. Is it possible, they wondered, that the maternal transmission of this one-time symbiont would leave a mark on genetic architecture?

Mitochondria, believed to be once free-living bacteria taken into eukaryotic cells as endosymbionts, operate through interactions that depend on both the mitochondria's own genome and the genome held in the cell's nucleus. In most animals, mitochondria are passed directly from the mother. Drown and his colleagues speculated that, for evolution to work most effectively, genes that work together for mitochondrial functioning should be inherited together.

"If you want to maintain your partner across generations," says Drown, a postdoctoral researcher in Indiana University's biology department, "you should stick with a chromosome you're going to be inherited with."

Specifically, they predicted that nuclear genes involved in mitochondrial complexes would be more often on the sex-linked X-chromosome than the autosomes. Their results, however, which were recently published in *Genome Biology and Evolution* (Drown et al. 2012), give striking evidence for just the opposite trend.

"It is definitely not a random distribution," Drown says. "These genes are under-represented on the X chromosome and over-represented on the autosomes."

After comparing the genomes of 14 mammals and 2 birds, they found mammals keep nuclear–mitochondrial genes off sex chromosomes with a high degree of statistical significance. In birds, where sex is determined differently (males are homogametic), there was no bias in representation.

The authors attribute the pattern seen in mammals to sexual conflict, a genetic "battle of the sexes" in which genes that make one sex more fit are not favored or are detrimental to the other. If mitochondrial genes have traits that are bad for males, the thinking goes, males cannot do anything with it, because only the female's mitochondria but not the male's are transmitted to the next generation. By putting copies of mitochondrial genes on autosomes, males participate in the coevolution of nuclear–mitochondrial gene combinations.

"You could argue that it's a good idea to have all the genes in the nuclear genome and not the mitochondrial genome, from a male fitness point of view," says Nick Lane, an evolutionary biologist at University College London not connected with this study. "For females it might be good to have all the genes retained on the mitochondria."

The authors believe that their data are a strike against the coadaption hypothesis, which they say would facilitate evolution if the nuclear and mitochondrial genes are cotransmitted. Lane, for his part, does not agree. Explaining the pattern based on sexual conflict is, he thinks, over doing it.

"I like the paper. The data are excellent, original, and important. I agree with their interpretation when it comes to sexual conflict," he says. "I would dispute with them that optimal coadaptation would be to have the genes on the X chromosome."

Optimal coadaptation is different for males and females, Lane says. Dispersing genes across the autosome is better for male adaptation, "and it doesn't hurt the females very much." This is a better state for the species because every generation is held to selection pressure.

One of the questions that has occupied Lane's mind in the past is why mitochondrial genes migrate to the nuclear genome. "We've tried to model that in the past but didn't get very far with it," he says. The math needed for the modeling is really hard, the data available were scare, and the student who took on the project became discouraged.

Lane plans to return to that model, based on the data he's seen from Drown, Preuss, and Wade. "This is some of the best evidence I've seen that male fitness is what it's about. . . . I think this is a really important finding. This touches on the whole trajectory of evolution and the differences between males and females."

This study is also, Drown says, one of the growing number that highlights the importance of interactions within and between genomes and the ability of those interactions to shape genomic architecture.

"As we collect more and more genomic data," he says, "we're going to see that this paradigm of one gene, one phenotype is lacking."

In future work, Drown would like to see similar studies done based on a broader range of genomes. "We're demonstrating a remarkable pattern here," he says, "proposing a mechanism that other people have supporting theory for." However, their work samples only two groups of animals. The field is awash in new data, with new genomes, particularly from invertebrates, being sequenced all the time. "It would be great to see some of those examined."

Literature Cited

Drown DM, Preuss KM, Wade MJ. 2012. Evidence of a paucity of genes that interact with the mitochondrion on the X in mammals. Genome Biol Evol., Advance Access published July 19, 2012, doi:10.1093/gbe/evs064.

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