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## The songbird and the chicken

how a song can change a genome Laura Dean, MD Created: May 3, 2010.

The zebra finch is a tiny Australian songbird. Only the males sing, and they learn a particular song by listening to their fathers.

As in all songbirds, there is a discrete area of the forebrain called the "song control center". When the young finch is learning to sing, he almost "babbles" like a human baby would. During this time, nuclei in the song control center change in size and organization, and during adulthood, the act of singing alters the expression of genes. Listening to a song also activates many genes in their auditory centers, also located in the bird's forebrain.

The zebra finch recently had its genome decoded by Warren et al. Once they identified the positions of the song-responsive genes, they looked for similar genes in the chicken, the only other bird to have its genome fully sequenced. The chicken does not sing, it merely clucks, and its clucking is instinctive, not learned. Therefore by comparing the genomes of the two birds, the scientists could identify the genes that are most likely to be important in singing and learning to sing.

Warren et al. also compared complimentary DNA from a juvenille songbird (learning to sing) and an adult one (able to sing). The finch's communication system turned out much more complex than previously thought. Singing changes expression for over 800 genes in the song control center, including ones that alter the expression of transcription factors and their targets.

Recent research by Dong et al. found that RNAs in the finch's auditory centers respond in different ways as the bird learns a song. Warren et al. found that many of the RNA transcripts (40%) are non-coding, and of the RNAs that are suppressed in response to song, the majority are non-coding. Noncoding RNAs (ncRNAs) were once thought to be "junk", but they have increasingly been found to have important functions in regulating other genes. It has even been proposed that these molecules aid the evolution of complexity in humans. It is therefore fitting that ncRNAs are so extensively involved in the complex ability of the songbirds learning to communicate.

Hearing song also activates small ncRNAs called microRNAs. These regulate gene expression by binding to target messenger RNAs. A potential site of action for the microRNAs aligns to an area in a human gene, NR4A3, that encodes a transcription factor protein. The fact that this transcription factor appears to be conserved in humans and songbirds suggests it has an important function in microRNA regulatory pathways.

Learning to sing is crucial for the finch. Without a song, he is unable to attract a mate and reproduce. The unique neurobiological apparatus that enables the finch to sing developed after the lineage of the zebra finch and chicken diverged, about 100 million years ago. It is likely that the genes involved, which include genes that encode neuronal ion channels, have been subject to a positive selection pressure leading to an accelerated evolution of genetic changes. Another possible channel of evolution is gene duplications. For example the genes PHF7 and PAK3 are found in mammals, but in the zebra finch, these genes have been duplicated and many variants are present in the finch's brain.

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This tiny songbird has shown us how a behavior, such as learning a song, can change a genome. Studying these changes may bring us closer to understanding how babies learn to speak by listening to their parents, and ultimately provide insights into speech disorders, autism, and neurological disorders such as Parkinson's disease.

This Coffee Break was reviewed by Wes Warren, Ph.D.



## Taeniopygia Guttata (zebra finch).

The zebra finch is the second bird to have its genome sequenced, the first being the chicken. Studying and comparing these two avian genomes may help us understand how humans learn to speak their first words.

## References

- 1. Warren Wesley C, Clayton David F, Ellegren Hans, Arnold Arthur P, Hillier Ladeana W, Künstner Axel, Searle Steve, White Simon, Vilella Albert J, Fairley Susan, Heger Andreas, Kong Lesheng, Ponting Chris P, Jarvis Erich D, Mello Claudio V, Minx Pat, Lovell Peter, Velho Tarciso A F, Ferris Margaret, Balakrishnan Christopher N, Sinha Saurabh, Blatti Charles, London Sarah E, Li Yun, Lin Ya-Chi, George Julia, Sweedler Jonathan, Southey Bruce, Gunaratne Preethi, Watson Michael, Nam Kiwoong, Backström Niclas, Smeds Linnea, Nabholz Benoit, Itoh Yuichiro, Whitney Osceola, Pfenning Andreas R, Howard Jason, Völker Martin, Skinner Bejamin M, Griffin Darren K, Ye Liang, McLaren William M, Flicek Paul, Quesada Victor, Velasco Gloria, Lopez-Otin Carlos, Puente Xose S, Olender Tsviya, Lancet Doron, Smit Arian F A, Hubley Robert, Konkel Miriam K, Walker Jerilyn A, Batzer Mark A, Gu Wanjun, Pollock David D, Chen Lin, Cheng Ze, Eichler Evan E, Stapley Jessica, Slate Jon, Ekblom Robert, Birkhead Tim, Burke Terry, Burt David, Scharff Constance, Adam Iris, Richard Hugues, Sultan Marc, Soldatov Alexey, Lehrach Hans, Edwards Scott V, Yang Shiaw-Pyng, Li Xiaoching, Graves Tina, Fulton Lucinda, Nelson Joanne, Chinwalla Asif, Hou Shunfeng, Mardis Elaine R, Wilson Richard K. The genome of a songbird. Nature. 2010;464:757–762. PubMed PMID: 20360741.
- 2. Dong Shu, Replogle Kirstin L, Hasadsri Linda, Imai Brian S, Yau Peter M, Rodriguez-Zas Sandra, Southey Bruce R, Sweedler Jonathan V, Clayton David F. Discrete molecular states in the brain accompany changing responses to a vocal signal. Proceedings of the National Academy of Sciences of the United States of America. 2009;106:11364–11369. PubMed PMID: 19541599.