**2017 Darwin Finch BMC Evolutionary Biology Summary**

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**Publication**

McNew SM, Beck D, Sadler-Riggleman I, Knutie SA, Koop JAH, Clayton DH, Skinner MK. (2017) Epigenetic variation between urban and rural populations of Darwin's finches. BMC Evol Biol. 17(1):183.

**Summary**

The molecular basis of evolutionary change is assumed to be genetic variation. However, growing evidence suggests that epigenetic mechanisms, such as DNA methylation, may also be involved in rapid adaptation to new environments. An important first step in evaluating this hypothesis is to test for the presence of epigenetic variation between natural populations living under different environmental conditions. In the current study we explored variation between populations of Darwin’s finches, which comprise one of the best-studied examples of adaptive radiation. We tested for morphological, genetic, and epigenetic differences between adjacent “urban” and “rural” populations of each of two species of ground finches, Geospiza fortis and G. fuliginosa, on Santa Cruz Island in the Galápagos. Using data collected from more than 1000 birds, we found significant morphological differences between populations of G. fortis, but not G. fuliginosa. We did not find large size copy number variation (CNV) genetic differences between populations of either species. However, other genetic variants were not investigated. In contrast, we did find dramatic epigenetic differences between the urban and rural populations of both species, based on DNA methylation analysis. We explored genomic features and gene associations of the differentially methylated regions (DMR), as well as their possible functional significance. In summary, our study documents local population epigenetic variation within each of two species of Darwin’s finches.