

## NEWS AND VIEWS

## PERSPECTIVE

**Population genomics fits the bill: genetics of adaptive beak variation in Darwin's finches**

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Darwin's finches are an iconic case of adaptive radiation. The size and shape of their beaks are key adaptive traits related to trophic niche that vary among species and evolve rapidly when the food supply changes. Building on recent studies, a paper in this issue of *Molecular Ecology* (Chaves *et al.* 2016) investigates the genomic basis of beak size variation in sympatric populations of three species of ground finch (*Geospiza*) by performing a Genome-wide association study using RAD-seq data. The authors find that variation in a small number of markers can explain a substantial proportion of variation in beak size. Some of these markers are in genomic regions that have previously been implicated in beak size variation in Darwin's finches, whereas other markers have not, suggesting both conservation and divergence in the genetic basis of morphological evolution. Overall, the study confirms that loci of large effect are involved in beak size variation, which helps to explain the high heritability and rapid response to selection of this trait. The independent identification of regions containing *HMGA2* and *DLK1* loci in a GWAS makes them prime targets for functional studies. The study also shows that under the right conditions, RAD-seq can be a viable alternative to genome sequencing for GWAS in wild vertebrate populations.

**Keywords:** adaptation, Darwin's finch, GWAS, population genomics

Received 2 September 2016; accepted 14 September 2016

The beaks of Darwin's finches are some of the best-studied adaptive traits in natural populations. The size and shape of beaks within and between species in this small radiation on the Galápagos Islands are intimately related to feeding ability (Grant 1999), and also contribute to reproductive isolation (Podos 2001). The three species of ground finch on Santa Cruz Island form a microcosm of evolutionary forces acting on the radiation (Fig. 1). Their beak sizes form a continuum

from small to medium to large ground finches, including a beak size polymorphism in the medium ground finch which is under divergent selection (Hendry *et al.* 2009). Some introgression among the species occurs in the face of assortative mating (De León *et al.* 2010). Chaves *et al.* (2016) obtained data from >32 500 genomewide SNPs in a total of 87 individuals of these species using RAD-seq and performed a GWAS for beak size on the combined data set comprising intraspecific and interspecific comparisons.

From a PCA on the entire SNP data set, PC1 was significantly correlated with beak size, indicating an effect of underlying population structure (presumably due to assortative mating by beak size) and so it was important that population structure was accounted for in the GWAS. As beak size and body size are strongly correlated in the finches, GWAS was performed separately for the two traits. The results are remarkable, with over 90% of the phenotypic variance in both beak and body size accounted for. Using a conservative threshold, 15 SNPs were significantly associated with one or both traits (see Figure 2 in Chaves *et al.* 2016), and the 11 SNPs associated with beak size (with or without body size) were further analysed.

A PCA was performed on these SNPs, and PC1, loaded with six significant SNPs, explained 56.8% of variance in beak size. The six SNPs show significant LD with each other, but do not appear to be physically linked as they are present on different genomic scaffolds. Strikingly, the two most significant SNPs among these six are near loci that have both previously been implicated in beak variation in Darwin's finches. The first is in the *HMGA2* locus, which was shown to be related to beak and body size both across ground and tree finches, and in a population of medium ground finch as it responded to natural selection (Lamichhaney *et al.* 2016a). The second is near the *DLK1* locus that was implicated in beak shape variation in a broad sample of Darwin's finches (Lamichhaney *et al.* 2015). Follow-up studies on these SNPs in a broader range of species confirmed their association with beak size and the strong LD among them, which is possibly due to correlational selection.

It is very encouraging that an independent study has identified the same two genomic regions as there are a number of methodological differences, including different sampling regimes, GWAS methodology and a greatly reduced data set from using RAD-seq rather than whole-genome sequencing. This leads to high confidence that these signals are true positives. Variation in a 500-kb region around *HMGA2* defines divergent haplotypes that are segregating in both medium ground finches and large ground finches (Lamichhaney *et al.* 2016a), and the SNP association uncovered in the present study may relate to this variation. This region, which contains at least four loci, is now a prime candidate for further functional studies elucidating a role in beak size and body size. Somewhat

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**Fig. 1** The three focal species of Darwin's finches studied by Chaves *et al.* (2016): small (left), medium (middle) and large (right) ground finches. (Photograph credit: Andrew Hendry).

surprisingly, there is no overlap among the loci uncovered in genomic studies and those previously implicated in beak size variation in the same species by expression and functional studies (BMP4 and calmodulin; Abzhanov *et al.* 2004, 2006). It seems likely that some of the loci identified by GWAS are acting upstream of BMP4 and/or calmodulin. Joining the dots between these findings is a key priority for future research.

As in other organisms, studies on the genetic basis of adaptation in birds have moved rapidly from single candidate locus studies to the whole-genome level. Fruitful studies on candidate genes typically involve coding variation, which is relatively straightforward to interpret and/or obvious phenotypic polymorphisms such as colour variants (Mundy 2005; Natarajan *et al.* 2015). In contrast, deciphering the genetics of quantitative variation in morphological traits has often been regarded as difficult, because such traits are considered likely to be highly polygenic and to largely involve changes in cis-regulation. There are several factors that account for the success of the GWAS approach in Darwin's finches, including the relatively young age of the Darwin's finch radiation, ongoing gene flow among species and of course that there are some genes of large effect in this system. It remains to be seen to what extent the genomic architecture of beak size variation in Darwin's finches is typical of other morphological traits in birds. This study joins a recent flurry of other papers revealing the genomic basis of reproductive isolation, coloration, co-adapted phenotypes and migration in birds (Poelstra *et al.* 2014; Delmore *et al.* 2016; Küpper *et al.* 2016; Lamichhaney *et al.* 2016b; Toews *et al.* 2016; Tuttle *et al.* 2016). These are indeed exciting times for avian population genomics.

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NIM wrote the paper.

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doi: 10.1111/mec.13868