NEWS AND COMMENTARY

Uncovering the genomic signatures of species differences in flycatchers

Speciation genetics

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Understanding how new species arise—speciation—is one of the most fascinating areas of evolutionary biology. A well-known, long-lasting debate asks whether speciation can only occur in geographical isolation (for example, Mayr, 1963) or whether selection is strong enough to promote the evolution of reproductive isolation through assortative mating even in the face of gene flow (for example, Bush, 1969). We are now experiencing a boom in speciation research—culminating a few years ago with the 150th anniversary of the publication of *On the Origin of Species* (Darwin, 1859)—and it is generally acknowledged nowadays that focusing on single factors is too simplistic and that several mechanisms need to be considered for understanding speciation (Butlin *et al.*, 2012).

One particularly active area of speciation research concerns the genetics of divergence, speciation and species differences (for example, Nosil and Schluter, 2011). A recent study by Ellegren *et al.* (2012) pushes the research frontier a significant step forward and with a notable sequence and bioinformatics effort in two closely related, sometimes hybridizing species—the collared and the pied flycatcher (*Ficedula albicollis* and *F. hypoleuca*)—the authors uncover the genomic footprints of speciation with paramount precision.

In brief, the 1.13 Gb flycatcher genome was assembled *de novo* using modern sequencing techniques, and large chunks of sequence ('scaffolds') were linked to chromosomes using an available linkage map (Backström *et al.*, 2008) and—under the reasonable assumption of high degree of synteny in birds—the zebra finch genome sequence (Warren *et al.*, 2010). In the next phase of

analyses, the authors re-sequenced the genomes of 10 unrelated males of each of the two flycatcher species. They detected ∼8 million polymorphic sites in each species of which 45% were shared—a reflection of their close relatedness. In contrast, there were 240 000 sites with fixed differences. Of these, 1500 were located within protein-coding regions and some of these may represent the genetic basis for key phenotypic differences between the two species or even speciation genes (that is, loci contributing to reproductive isolation). Interestingly, the genomic landscape of species divergence was highly heterogeneous and ∼50 substantially diverged regions—referred to as 'genomic islands of divergence'—were pinpointed. These regions, identified with sliding window analyses, were characterized by skewed allele-frequency spectra, reduced proportions of shared polymorphisms and reduced levels of nucleotide diversity in both species. The divergence islands were non-randomly distributed across the genome and highly over-represented towards chromosome ends.

The Z chromosome showed a seven-fold higher mean divergence than the autosomes and an overall uniform divergence. The higher background divergence and a lower proportion of shared polymorphisms on the Z indicate that sex chromosomes and autosomes are at different stages of speciation in these flycatchers. Previous findings of a large X effect on hybrid sterility and reduced introgression of sex-linked genes have suggested that sex chromosomes have a particularly important role in speciation (Qvarnström and Bailey, 2009). For example, in flycatchers, both male plumage and species recognition have been shown to be sex-linked (Sæther *et al.*, 2007). Ellegren *et al.* (2012) propose that the Z chromosome-wide divergence that is observed today could have been initiated by natural and/or sexual selection at

multiple loci associated with reproductive isolation and that high background divergence happened over time due to linkage. The high Z chromosome divergence in flycatchers is a fascinating observation *per se*, but will impede localizing Z-linked genes of particular importance in this model system. Studies evaluating more recent speciation events may turn out even more informative in this respect.

So how did the collared flycatcher and the pied flycatcher diverge? A plausible scenario is that the divergence happened in allopatric glacial refugia during the Pleistocene (<3 MYA); this fits with the mitochondrial cytochrome *b* sequence divergence of c 4% (see for example, Sæther *et al.*, 2001). It is further reasonable to assume that gene flow was possible during interglacial periods when populations came into secondary contact. Indeed, hybridization and gene flow occur today in areas of sympatry, for instance in the Czech Republic and on the Swedish Islands Öland and Gotland (Sætre *et al.*, 1997). This could have allowed reinforcement, that is, enhancement of prezygotic isolation in sympatry by natural selection, which would have strengthened the reproductive isolation and decreased gene flow. Accordingly, a complex scenario could be suggested, where allopatric divergence may have been followed repeatedly by genomic homogenization in sympatry in most parts of the genome, with the exceptions being the more strongly divergent genomic islands now detected.

An interesting observation is the substantially reduced diversity in the divergence islands within both flycatcher species which may suggest that the same loci, or closely linked loci, have been subject to directional selection in both lineages independently. For instance, this pattern may reflect historical selection for key adaptations unique to each

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of the species. The reduced intra-species diversity in divergence islands may also, to some extent, be an inherent outcome of the definition of the islands, as low within-population genetic variation will contribute to a high divergence. Many of the cases of extreme divergence were found to be associated with gaps in the genome assembly, which indicates that regions that were difficult to assembly are drivers of speciation. Centromeres and other heterochromatic regions, as well as large multigene families, are candidates for such regions. The potential link between species divergence and repetitive elements of chromosomes detected in flycatchers is in line with a rarely discussed hypothesis—the 'meiotic drive model of speciation'—that proposes strong selection on centromeric alleles for the ability to be deposited into the female oocyte, which can lead to rapid divergent evolution of repeat regions and proteins involved in chromosome segregation during meiosis (Henikoff and Malik, 2002; Malik and Henikoff, 2009). Ellegren *et al.* (2012) call '... for a shift in (research) focus, with the quest for genetic basis of reproductive isolation extended to include sequences other than protein-coding genes'. Several mechanisms may act in concert to push apart the divergent taxa during the early stages of speciation and future genomic and ecological work in flycatchers and other radiations are necessary to tease apart their relative importance (see for example, Butlin *et al.*, 2012).

CONFLICT OF INTEREST

The author declares no conflict of interest.

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