

The genetic code of adaptation in collared flycatcher

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The collared flycatcher (*Ficedula albicollis*) is a passerine bird species, which is even smaller than sparrows. These birds migrate from sub-Saharan Africa to Europe every summer for breeding and fly back every autumn to spend the winter in warm African habitats. In northern Europe, the only breeding site for collared flycatchers was the Baltic Sea island of Gotland until 60 years ago when these small black-and-white birds started to be also observed on the neighbouring island called Öland, located closer to the Swedish mainland.

The colonization of Öland started around the town Löttorp in the early 1960ies and today most of the suitable habitat sites on Öland have become inhabited by collared flycatchers. How do collared flycatchers adapt to the different habitats on Öland at this very edge of their breeding distribution? This is an interesting question due to both the short colonization history and due to the small spatial scale of this Öland population. In view of the huge time scale of the evolutionary history of most species (usually counting by Mya, i.e. million years ago), 60 years is a really short period. That means the various demographic events which will leave footprints in the genome are less likely to happen in this brief of time. Therefore, any evidence of adaptation found in the birds' genome will be less liable to be confounded by demographic factors. On the other hand, the latitude variance of 100 km of the Öland breeding sites is small compared to most of the other adaptation studies, which generally include populations that are thousands of kilometers apart. However, this short spatial scale in fact increases the likelihood of finding genetic variation specifically associated with local adaptation since gene flow is expected to homogenise neutral genomic variance quickly across spatially closely located populations.

To answer that question, I applied a method called genome-wide association study (GWAS). GWAS can identify single-nucleotide polymorphisms (SNPs) – they are variants on genome representing the genetic difference between individuals – that are associated with the phenotypic traits of interest. As a result, I found 20 SNPs associated with the latitude of the location of the nest of collared flycatchers in this study. My results suggest an early-stage adaptation of collared flycatchers on Öland. I also found the birds which carry lower-frequency SNPs present in the south of Öland more frequently. That may correlate with the habitat quality variance across a latitude gradient on Öland. Southern habitats contain more deciduous forest which produces more food, i.e. caterpillar larvae, while north habitats are mostly consist of coniferous forest and have fewer food resource for collared flycatchers. On the other hand, other factors such as population density, demographic structure, and parasite vectors could also co-occur with latitude. Thus, do collared flycatchers adapt to different habitats on Öland, their new breeding site, in only 60 years? The answer is yes, and the adaptation is associated with the latitude of their nest boxes. But how does latitude work in adaptation? The answer is still not clear enough. In the future, we could do more experiments to clarify this question better. For example, a functional test of these genetic variants could be done to investigate the functional role of the SNPs found in this study, and that may be a way to find out the primary adaptive trait which is related to the latitude of the nesting site of collared flycatchers.

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