Digest

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Digest: Positive selection and recombination shape the genomic landscape in flycatchers

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Footnote: This article corresponds to Chase, M. A., Ellegren, H., & Mugal, C. F. 2021. Positive selection plays a major role in shaping signatures of differentiation across the genomic landscape of two independent Ficedula flycatcher species pairs. *Evolution*. doi:10.1111/evo.14234. https://onlinelibrary.wiley.com/doi/10.1111/evo.14234

Abstract: Whether background selection is sufficient to explain observed genomic differentiation is a long-standing debate. Using four species of flycatcher, Chase et al. (2021) addressed this issue and found that the effect of background selection may not be as great as previously thought. Instead, both positive selection and recombination were shown to have a significant effect on genomic differentiation.

Main Text:

Genetic diversity and differentiation within and between species is not uniformly distributed across the genomic landscape. Instead, there are "differentiation islands", genomic regions that show high levels of differentiation. Speciation with gene flow is usually considered an important driver of heterogeneity of overall genomic differentiation (Nosil 2008). Natural selection may also contribute to genomic differentiation.

Natural selection can be classified into three categories based on its effects on allele frequency (Fig 1A). The first, positive selection, increases the allele frequency of a beneficial variant while reducing the surrounding neutral genetic diversity via linked selection (also known as a selective sweep) (Hermisson & Pennings 2005). The second category, negative selection, removes the deleterious variants from the population while maintaining a low surrounding genetic diversity via linked selection (also known as background selection) (Charlesworth, et al. 1993). The third category, balancing selection, maintains an intermediate allele frequency.

Of the three categories, background selection is thought to play a key role in generating differentiation islands. Gene density and recombination rate determine the intensity of this type of selection. If gene density and recombination rate are conserved between certain species, background selection should behave similarly in these species and persist over a long evolutionary timescale, resulting in reduced genetic diversity, reduced divergence, and elevated shared F_{st} peaks. This proposed process is known as the recurrent selection model. But empirical and simulated data suggest that this model alone is not sufficient to explain the existence of differentiation islands, and that there are additional evolutionary forces involved in their creation and maintenance.

In this issue, Chase et al. (2021) compared the genome-wide genetic diversity(π), F_{st}, and divergence (D_{xy}) within four species of *Ficedula* flycatcher to test whether positive selection could generate lineage-specific and/or shared signatures of differentiation, and whether recombination rate change could be a reason for lineage-specific differentiation.

First, the authors found that the four species exhibited a similar level of genetic diversity but distinct levels of D_{xy} and F_{st}. Then, by using Fay and Wu's H and a composite likelihood ratio (CLR), they identified the genomic regions of selective sweep and found that these tended to overlap with F_{st} peaks, which suggests that positive selection results in genetic differentiation. Third, they found a decreased correlation of π with increased species differentiation and a reduction in D_{xy} in shared F_{st} peaks compared with that found in lineage-specific F_{st} peaks (Fig 1C). This provides support for a recurrent selection model. Lastly, by examining the distribution of recombination rate and gene density in different F_{st} regions, they concluded the changes in recombination rate may be responsible for the lineage-specific F_{st}.

Whether background selection is sufficient to explain genetic differentiation remains controversial in evolutionary biology. By ruling out the confounding effects resulting from incomplete lineage sorting (ILS) and gene flow (Fig 1B), the results of Chase et al. (2021) provide insights into the generation of differentiation islands in flycatchers and highlight the critical role of positive selection and recombination in shaping the genomic landscape.

References

Charlesworth, B., Morgan, M. T., & Charlesworth, D. 1993. The effect of deleterious mutations on neutral molecular variation. *Genetics, 134*(4), 1289-1303.

Chase, M. A., Ellegren, H., & Mugal, C. F. 2021. Positive selection plays a major role in shaping signatures of differentiation across the genomic landscape of two independent Ficedula flycatcher species pairs. *Evolution*. doi:10.1111/evo.14234

Hermisson, J., & Pennings, P. S. 2005. Soft sweeps: molecular population genetics of adaptation from standing genetic variation. *Genetics, 169*(4), 2335-2352. doi:10.1534/genetics.104.036947

Nosil, P. 2008. Speciation with gene flow could be common. *Molecular ecology, 17*(9), 2103-2106. doi:10.1111/j.1365-294X.2008.03715.x