CBGP
Centre de Biologie pour
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Visioconférence Jitsi Meet

LOCAL ADAPTATION IN BLUE TIT POPULATIONS: INSIGHTS FROM POPULATION GENOMICS

par
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- Understanding the genetic mechanisms underlying local adaptation is a central aim in evolutionary biology. This task notably requires quantitative genomics to understand the genomic architecture of phenotypic variations and population genomics to identify footprints of selection. It is also important to interpret these inferred genomic characteristics in the light of population demography and of the variation in recombination rate along the genome.

- I will present a study of these genomic features in blue tit populations showing strong phenotypic differentiation and putative local adaptations in heterogeneous environments (deciduous versus evergreen forests and in insular versus mainland areas).

- Briefly, while insular and mainland populations have been isolated since the end of the last glaciation, they were only slightly differentiated, as a consequence of historical gene flow and large effective population sizes. We found a few genetic variants showing strong differentiation between these populations, concentrated in genomic regions with low recombination rate, including a large inversion. In contrast, neighboring deciduous and evergreen populations were continuously connected by high gene flow and were almost not genetically differentiated, showing only weak putative footprints of divergent selection. Yet, we found high heritability of several traits significantly differentiated between neighboring contrasted habitats. Such high heritability of phenotypic traits was explained by polygenic architectures including thousands of loci of small effects, but might also be inflated by residual environmental effects.

- These results provide insights into the demographic history and genetic architecture of local adaptation in blue tit populations at multiple geographic scales.