# Structural variation in closely related songbird species

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Structural variants, i.e. mutations altering the position, orientation, or number of copies of longer (> 50 bp) regions within the genome, represent a rich source of variation in the evolution of species. These genomic rearrangements can lead to the development of novel adaptations and act as key factors in the establishment and maintenance of reproductive barriers between species, although direct evidence linking structural variants to speciation remains scarce. In our research, we focus on structural variation in two closely related songbird species, the common nightingale and the thrush nightingale, which diverged approximately 1.8 Mya, but still occasionally hybridize in their secondary contact zone spanning Central Europe. We employed a combination of bioinformatic approaches to detect structural variants in these species, comparing and integrating their results to gain an insight into the rearrangements that differentiate the nightingales’ genomes. Through bioinformatic analyses, we were able to identify events that remained undetected in previous karyotype analyses. Among those, there were also 13 species-specific inversions ranging in length from 100 kbp to 2.4 Mbp, many located in the pericentromeric region. We hypothesize that these pericentric inversions might amplify the recombination suppression effect of centromeres and thereby reduce the rate of interspecific recombinant genotypes. This mechanism could facilitate speciation despite ongoing gene flow between the species.