

Hybridization in Natural Populations

Jochen B. W. Wolf

Division of Evolutionary Biology, Faculty of Biology, Ludwig-Maximilians University of Munich

Speciation can be conceptualized as process during which reproductive barriers accumulate in the genomes of diverging populations. During the early stages of this process, reproductive barriers are generally incomplete allowing for gene flow that is mediated by first generation hybrids backcrossing into the parental populations. Hybridization thus is a natural component of species divergence with varied impact. It may slow down or reverse divergence, accelerate it via adaptive introgression, induce instantaneous isolation by allopolyploidization or open novel niche space to transgressive genotypic combinations. Whole genome sequencing data of natural populations allows insight into the evolutionary processes acting upon hybridization and may eventually help identify the reproductive barriers promoting species divergence. I will here present two examples of population divergence with gene flow from our own research. First, I will share some insights from a long-standing research program on the Eurasian crow superspecies complex forming two distinct hybrid zones in Europe and Russia. Second, I will describe the consequences of hybridization in natural populations of fission yeast. Though very different at first sight, these systems share a history of hybridization which they still carry in their genomes today.