Dynamics of genomic islands of divergence during the speciation process of whitefish

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While knowledge on the ecological causes of adaptive divergence and speciation has made substantial leaps over the last decades, that pertaining to the genetic basis of ecological speciation is still in its infancy. Among the many unresolved questions, those pertaining to the size, distribution and nature of genomic islands of divergence maintained in the face of gene flow have attracted particular attention in the recent literature. Namely, theory predicts that divergence hitchhiking may sometimes create large regions of differentiation around a selected site, although specific conditions for this to occur appear relatively strict. Moreover, empirical evidence in support of this concept is still scant and of mixed nature. In this paper, we first provide empirical evidence showing that sympatric whitefish species pairs are good candidate to investigate the dynamics of genomics islands of divergence in the early step of the speciation process. Secondly, combining QTL mapping and genome scan methods revealed that highly significant relationships between genetic divergence vs. chromosomal distance from QTL outliers may extend over very large regions. Moreover, results suggest that the number, size and height of genomics islands of divergence tend to increase with the intensity of selection driving adaptive divergence in different species pairs. We thus conclude that the concept of genomic islands of divergence in its general form provides a useful means to investigate the genomic basis of adaptive divergence in this group of fish.