

## **Genomic signals of adaptation after a population range expansion**

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Range expansions have occurred in many species including our own, and their effect on the genetic diversity of populations colonizing new habitats has been well described. A frequent consequence is the phenomenon of “gene surfing”, where variants located near the expanding front can reach high frequencies or even fix in newly occupied territories. Although gene surfing events have been characterized thoroughly for a specific locus, their effects on linked genomic regions and on the overall patterns of genomic diversity have been little investigated. Here I report results from recent theoretical and simulation studies describing the shape and the distribution of regions of very low diversity, or troughs, often interpreted as a signal of selective sweeps, but more generally indicative of fixation events. These troughs have a shape that can exactly match those expected after a selective sweep, and they are found to occur frequently during a range expansion. Importantly, their density and average size are similar in 1D or 2D expansions, irrespective of the exact demographic conditions of the expansions. They rather depend on the average genomic recombination rate and the amount of diversity lost since the beginning of the expansion, and they tend to be over-represented in regions of low recombination. These results show that range expansion can mimic all signals usually attributed to past episodes of positive selection, and suggest that evidencing adaptation in recently expanding populations from genomic diversity alone is hard.