INVERSIONS

Chromosomal inversions anchor genes inside the inverted segment by suppressing recombination, effectively "locking" beneficial allele combinations together and preventing them from being reshuffled during meiosis. These genomic regions are often referred to as "Supergenes." A recent study by Akopyan et al. in Science [1] illustrates this principle in a marine fish adapting along a steep thermal gradient. Inversions maintain the advantageous adaptation despite extensive gene flow.

What about humans?

A well-known example is the **17q21.31 inversion**, a large genomic segment common in populations of European descent, described by Stefansson et al. in 2005 [2]. This region exists in two primary forms (H1 and the inverted H2). By suppressing crossover during meiosis, the H2 lineage has remained genetically distinct for over 2 million years. Women carrying the H2 variant tend to have more children, suggesting this inversion is maintained by positive selection on fertility.

Other examples:

High-altitude survival: Inversions on chromosome 2 help preserve clusters of hypoxia-related genes that allow Tibetan populations to thrive in low-oxygen environments [3].

Immune defense: A major inversion on **chromosome 8 (8p23.1)** maintains a high density block of defensin genes, equipping local populations with a specialized genomic toolkit to combat region-specific pathogens [4].

This last inversion at 8p23.1 was described by Giglio et al. [5] as a polymorphism present in ~26% of Europeans, where heterozygosity predisposes to severe chromosomal rearrangements. The same structural variant that locks in immune defensins also carries a genomic cost for the next generation. A perfect example of an evolutionary trade-off that maintains the inversion polymorphism at high frequency in the European population.

1. 10.1126/science.ady6774
2. 10.1038/ng1508
3. 10.1371/journal.pone.0017002
4. https://pubmed.ncbi.nlm.nih.gov/10375637/
5. https://pubmed.ncbi.nlm.nih.gov/11231899/