

Domains of increased genetic polymorphism boost crossover in plant breeding
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Meiotic crossovers, which exchange DNA between homologous chromosomes, are essential for accurate chromosome segregation and generate genetic diversity. In plant breeding, crossovers enable the creation of new haplotypes by combining beneficial alleles. Their distribution along chromosomes is shaped by multiple factors, many of which remain poorly understood. One such factor is local DNA sequence divergence between homologous chromosomes, known as *cis*-acting genetic polymorphism. In most species studied, local polymorphism suppresses crossover formation. However, in the self-fertilizing plant *Arabidopsis thaliana*, crossovers are instead stimulated in heterozygous regions when these are juxtaposed with homozygous regions on the same chromosome.

Here, we report a similar effect in the outcrossing maize. We developed a set of nearly isogenic maize lines carrying distinct patterns of polymorphism and phenotypic markers, enabling precise measurements of recombination frequency. Building on a high-quality PacBio genome assembly combined with high-coverage Illumina sequencing, we discovered that crossover stimulation in heterozygous domains adjacent to homozygous regions occurs even more effectively in maize, reaching up to a threefold increase in crossover frequency. This stimulation occurs in both male and female meiosis and is strongest when heterozygous regions fully span the entire measured interval, consistent with crossover redistribution. Since *Arabidopsis* and maize represent distantly related plant lineages (eudicots and monocots), this shared phenomenon suggests a conserved mechanism.

Enhancing crossover frequency in targeted chromosomal regions remains a major challenge in applied genetics. While global increases can be achieved through mutations in DNA repair pathways, such approaches often compromise chromosomal segregation, particularly in cereals. Directing crossovers to specific chromosomal regions is an attractive alternative, yet no such method currently exists in plants.

Our study demonstrates that a similar outcome can be achieved without genetic modifications, simply by selecting parental lines with defined heterozygosity patterns around genomic regions of interest. Because the effect only manifests when large chromosomal segments are homozygous, this strategy is particularly suited to doubled-haploid technology, which is widely used to generate inbred lines. We envision this as especially valuable when recombination is suppressed between closely linked quantitative trait loci (QTLs). By choosing optimal doubled haploid lines for crossing, breeders can substantially increase the probability of recovering the desired genotype. Moreover, as the effect appears to rely on crossover redistribution from homozygous regions, it may also be exploited to locally suppress recombination, preserving linkage between favorable alleles.

In maize, this approach increased local crossover frequency by up to an unprecedented threefold. Importantly, we did not observe differences between two maize backgrounds differing with the polymorphism density, suggesting that the strength of the effect is not affected by the polymorphism density. We therefore propose integrating this phenomenon into the design of breeding strategies. In the era of high-throughput sequencing, where thousands of fully characterized lines are available, exploiting this juxtaposition effect offers a powerful, non-transgenic tool to accelerate trait introgression and enhance selection efficiency.

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