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Scientists Map Hop Genome and Find Breeding Barriers

The study shows European and North American chromosomes often stay distinct, complicating efforts to breed better beer hops.

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Scientists have built the most detailed genome maps yet of hop, the plant that gives beer much of its bitterness and aroma, and found that European and North American chromosomes can remain strikingly distinct even after generations of breeding.

The study, published Wednesday in Nature Communications, analyzed the hybrid hop cultivar Apollo at chromosome scale and traced which parts of its genome came from European hop and which came from North American hop. The researchers found that some chromosomes from the two lineages recombine poorly, if at all, a result that helps explain why hop breeding has been difficult and why desirable traits such as bitter acid content can be hard to predict.

Hop is one of the key ingredients in beer. Its alpha acids shape bitterness, while other compounds contribute aroma and help preserve the drink. For decades, breeders have crossed European and North American hops to combine traits from both lineages, but the genetic basis for those improvements has remained unclear.

The new work gives breeders a reference they did not have before: phased, chromosome-level assemblies that separate the two sets of chromosomes in a hybrid plant and identify their ancestry. That matters because most modern hop cultivars are not pure European lines but complex hybrids descended from repeated crosses between European and North American plants.

Using long-read sequencing and Hi-C data, the researchers assembled the Apollo genome and then used repeat-based markers to assign ancestry across the chromosomes. They found that some chromosome pairs were entirely European or entirely North American, while others carried mixed ancestry or large introgressed segments. In several cases, the two ancestral lineages remained highly divergent, with sequence identity around 75% to 78%, far below what would be expected if recombination had freely mixed them over time.

The team also tested recombination in three breeding populations. In two of them, they saw little or no recombination between European and North American chromosomes, making it impossible to build conventional linkage maps. In the third population, recombination was present but still limited. The pattern suggests that in some hop crosses, breeders may be moving whole chromosomes or large chromosome blocks

rather than reshuffling genes in a fine-grained way.

That finding could change how hop breeding is done. If recombination is suppressed across large parts of the genome, then selecting for bitterness, aroma or disease resistance may require genomic tools that can track chromosome ancestry directly instead of relying only on visible traits in the field.

The researchers also reported that beneficial alleles from both European and North American hops can have additive effects on alpha-acid content, the main bittering compound used in brewing. That gives breeders a clearer path to developing varieties with more predictable chemistry.

The work comes as hop growers face pressure from climate change. Earlier studies have projected declines in yield and alpha-acid content in Europe by midcentury, raising concern for beer production and for farmers who depend on stable hop crops. The new genome resource could help speed the development of varieties better suited to warmer conditions while preserving the flavor profiles brewers want.

Hop breeding has long depended on trial and error because the plant’s genetics are unusually complex. Female plants produce the cones used in brewing, but hop is dioecious, meaning male and female flowers grow on separate plants. That complicates breeding programs and slows selection. The new genome assemblies should make it easier to identify useful genes linked to bitterness, aroma and resistance to mildew.

The study also adds to a broader effort to understand how domesticated plants retain or lose genetic diversity as they are crossed across continents. In hop, that diversity appears to be both a strength and a constraint: it has helped create productive modern cultivars, but it may also limit how easily breeders can combine traits through ordinary crossing alone.