



POPULAR ARTICLE

Beyond DNA: How plant epigenetics could shape the crops of tomorrow

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Intricacies of the subject

For decades, crop improvement has been described mainly as a search for better genes. Breeders cross parents, select useful plants and advance generations until desirable traits are combined in a new variety. But plants do not read their DNA in a simple on-or-off manner. The same DNA sequence can behave differently depending on how it is chemically marked, how chromatin is arranged and how environmental signals influence gene activity. This additional layer of biological information is broadly known as epigenetics. Plant epigenetics is therefore opening an exciting new chapter in crop improvement. It does not replace conventional breeding, genomics or gene editing. Instead, it adds another layer of information that may help breeders understand why genetically similar plants can respond differently to drought, temperature, nutrients, pathogens and other stresses. The long-term promise is a more precise approach to selecting plants that are productive and resilient under changing environments.

Introduction

The word epigenetics refers to changes in gene activity that occur without changing the underlying DNA sequence. One of the best-known mechanisms is DNA methylation, in

which chemical groups are added to DNA and can influence whether nearby genes are active. Histone modifications and changes in chromatin structure provide additional control. Small regulatory RNAs can also influence gene expression. A simple way to understand this is to think of DNA as the instruction manual of a plant and epigenetic regulation as a system of bookmarks, switches and annotations. The letters of the manual may remain the same, but the plant can control which instructions are used, when they are used and how strongly they are expressed. This distinction is especially important in plants because they cannot move away from unfavorable environments. Their growth and development must continuously adjust to changes in water availability, temperature, light, soil nutrients and biological threats. Epigenetic regulation is one of the mechanisms that helps plants make these adjustments.

Why should plant breeders care?

Traditional breeding generally focuses on observable variation and the genetic differences that control it. Epigenetic variation can add another source of information. In some cases plants with similar, even identical DNA sequences can show differences in flowering, plant architecture, stress responses



or other traits because of differences in gene regulation. This does not mean that every environmental response is inherited epigenetically, nor that epigenetic marks are always stable across generations. Their stability varies with the type of modification, tissue, developmental stage and environmental conditions. This is one reason why epigenetics should be viewed as a complementary tool rather than a shortcut around genetics. For breeders, the most useful question is practical: can reliable epigenetic signatures help identify superior plants earlier or under conditions where conventional selection is difficult? Research is increasingly exploring this possibility.

Epigenetics and climate-resilient crops

Climate change is making breeding targets more complex. Farmers need varieties that can maintain yield under heat, drought, irregular rainfall, salinity and emerging pest and disease pressures. A plant's response to these stresses is not determined by a single gene. It involves networks of genes that must be activated or suppressed at the right time. Epigenetic regulation can influence these networks. Stress exposure may alter DNA methylation and chromatin states, which can in turn affect gene expression. In some systems, stress-associated epigenetic changes have been observed to persist for a period after the original stress is removed. Scientists are investigating whether some of these changes can contribute to stress memory or improved responses to repeated stress. The idea of stress memory is particularly interesting for agriculture. If a plant can 'remember' an earlier environmental challenge through molecular changes, breeders may eventually be able to identify or exploit such responses. However, translating laboratory observations into stable field performance remains a major research challenge.

From epigenetic marks to breeding decisions

The future value of epigenetics will depend on connecting molecular information with useful agronomic traits. A possible breeding workflow could begin with diverse germplasm exposed to contrasting environments. Researchers could then measure DNA methylation patterns, gene expression and phenotypic performance. Statistical and machine-learning approaches could be used to identify molecular patterns associated with drought tolerance, heat resilience, flowering time, seed quality or yield stability. Such information could complement genomic selection. Instead of predicting performance from DNA markers alone, breeders could potentially combine genetic markers with epigenetic and transcriptomic information. This multi-layer approach may provide a more complete picture of plant performance. For example, two lines carrying similar alleles at a candidate locus might express a trait differently. If their regulatory states also differ, an epigenetic measurement could help explain the phenotype. The practical challenge is determining which epigenetic signals are reproducible enough to support selection.

The role of modern technologies

Rapid advances in sequencing and molecular biology are making epigenetic research more accessible. Bisulfite sequencing and related methods can profile DNA methylation, while chromatin-based approaches can examine regulatory states. RNA sequencing helps researchers connect these molecular patterns with gene activity. High-throughput phenotyping can then measure plant responses at a much larger scale. The integration of these computational pipelines are needed to identify meaningful associations while avoiding false signals caused by tissue, developmental stage or environmental differences. Artificial



intelligence may further assist by detecting complex relationships among genotype, epigenetic state, environment and phenotype. The goal is not to replace the breeder but to turn large biological datasets into information that can support better selection decisions.

Can epigenetic breeding become a routine tool?

Several hurdles must be solved before epigenetic information becomes routine in breeding programmes. First, many epigenetic marks are tissue-specific and can change with development. A mark detected in a young leaf may not be present in seed tissue or reproductive organs. Second, environmental conditions can strongly influence epigenetic states, making it difficult to distinguish inherited information from temporary environmental effects. Third, breeders need robust markers with predictable relationships to field performance. A molecular signal is valuable only when it can be measured consistently and contributes to a meaningful selection decision. Finally, large-scale epigenetic profiling can be expensive and technically demanding compared with conventional marker assays. These limitations are not reasons to dismiss the technology. They simply indicate that the strongest applications are likely to emerge from carefully designed combinations of genetics, epigenetics, physiology and field phenotyping.

What could the crop of tomorrow look like?

Imagine a breeding programme in which a young seedling is evaluated using several layers of information. Its DNA markers indicate the alleles it carries. Its epigenetic profile provides clues about gene regulation. Gene-expression data show which pathways are active. Automated phenotyping measures growth and stress response. Environmental

data describe the conditions in which the plant is growing. A prediction model then estimates its likely performance across target environments. This vision is still developing, but it illustrates the direction of modern crop breeding: moving from selection based mainly on visible traits toward selection informed by multiple biological layers. Epigenetics could become one important component of this approach. The most exciting possibility is not simply producing a crop with a particular epigenetic pattern. It is understanding how plants regulate their existing genetic potential and using that knowledge to breed varieties that perform more reliably in real farming environments.

The road ahead

Plant epigenetics reminds us that the genome is not a static script. How genes are regulated can be just as important as which genes are present. As climate variability increases and breeding programmes generate increasingly large datasets, this additional layer of information may help explain variation that conventional genetic analysis cannot fully capture. The next generation of crop improvement is therefore likely to be integrated rather than dominated by a single technology. Conventional crossing, molecular markers, genomics, gene editing, transcriptomics, epigenomics, phenotyping and artificial intelligence can work together. Epigenetics may not replace DNA-based breeding, but it can help breeders look beyond the DNA sequences and understand how plants use their genetic information. For farmers, the ultimate measure will remain simple: higher and more stable productivity, better quality and greater resilience under changing conditions. If epigenetic discoveries can be translated into reliable selection tools, they may become another valuable instrument in achieving that goal.



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