



Changes to the Imprint Related to the Culture of the Vegetation

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Abstract

Inbreeding is the mating of closely related species in nature, on plantations, or in self-pollinated plants that produce highly homozygous plants. This process can reduce the genetic diversity of offspring and reduce heterozygosity, whereas inbreeding inhibition (ID) can often reduce survival. Inbreeding suppression is widespread in plants and animals and has played an important role in evolution. The overview aims to show that inbreeding affects gene expression through the action of epigenetic mechanisms, leading to metabolic and phenotypic changes in organisms. This is especially important in plant breeding. Epigenetic profiles can be associated with degradation or enhancement of agriculturally important traits.

Keywords: Inbreeding; Epigenetic mechanisms; Inbreeding depression; epiRIL

INTRODUCTION

Diversity in agronomically and evolutionarily important traits (yield, flowering time, insect resistance, drought, etc.) is usually explained by the occurrence of DNA sequence polymorphisms and the interaction of environmental factors. Inheritance of complex traits is now believed to be based not only on the transmission of stable DNA sequence variants to offspring, but also on the transmission of specific patterns of chromatin modifications. H. Second, epigenetic changes are linked from generation to generation. Examples include specific DNA methylation patterns that are reflected in phenotypes. B. Characteristics such as flower shape and size and fruit pigmentation.

Inbreeding can lead to reduced genetic diversity in offspring due to restricted and reduced heterozygosity, which can lead to decreased survival associated with suppression of inbreeding. Despite genetic diversity and low evolutionary potential, self-pollinated plant lineages are widespread even among invasive species. This suggests that certain phenotypes are better adapted to specific environmental conditions, and if this is maintained by inbreeding, adaptation to specific environmental conditions may be associated with reduced genetic variation. suggesting.

Epigenetic mechanisms play an additional role here, as they are involved in regulating many processes within the genome.

Epigenetics includes numerous mechanisms that act not only at the transcriptional level by altering chromatin structure, but also post-transcriptionally by modulating gene expression activity. Chromatin structure affects DNA accessibility of transcription factors and is regulated by epigenetic mechanisms such as DNA methylation, histone variant exchange, post-translational histone modifications, chromatin remodeling, and interaction with noncoding RNAs (ncRNAs). The development of new techniques, especially state-of-the-art sequencing techniques, allows a deeper understanding of epigenetic mechanisms. Research over the past two decades has demonstrated the importance of epigenetic mechanisms in plant adaptation to new and changing environmental conditions and in plant breeding. Epigenetic mutation through so-called epiBreeding can be used to optimize plant breeding and improve crop resilience. An important source of phenotypic variability is the epiallele, which is less common in nature. Identification of epialleles requires epigenome analysis (map-based gene cloning, genome-wide methylome analysis) to identify the association between epigenetic changes and phenotypic

alterations. For the same purpose, recombinant inbred lines (RILs) from germplasm with high epigenetic diversity are used. Another source of natural epigenetic changes is stress-induced changes. One strategy for conserving epigenetic mutations is to use systems such as TALE, ZF proteins, or CRISPR-Cas9 to edit the epigenome and alter gene expression through targeted epigenetic changes. That's it. It's a genetic change. B. To improve agricultural properties. To reduce the need to use plant transformation systems, virus-induced transcriptional gene silencing (VITGS) can be used to obtain epigenetic modifications in plants. That said, the changes achieved are not always stable and inherited. Epigenetic recombinant inbred lines (epiRIL) – created by crossing wild plants with hypomethylated mutants – are also commonly used in epibreeding (*met1* and/or *ddm1*). Equipped with various functions such as B. Plant height, flowering time, yield and plant stress tolerance. Our collaboration with epiRIL has so far focused on *Arabidopsis*, but the potential of this strategy is enormous. The development of epiRILs in *Arabidopsis thaliana* has also enabled the mapping of quantitative epigenetic trait loci (epiQTLs), enabling the analysis of the role of epigenetic diversity in the regulation of agronomic traits. Because crops lack DNA methylation variants, pharmacological strategies involving DNA MTase inhibitors or the MSH1 system are used, resulting in altered DNA methylation that affects plant yield and tolerance. An example of such "epimutogenesis" is the development of *Oryza sativa* strains resistant to *Xanthomonas oryzae* after treatment with 5-azacytidine. Iterative selection of isogenic lines allows us to obtain stable epigenotypes and identify epigenetic elements that influence agronomic traits that can be used for epibreeding. Epigenome studies can provide a basis for building phenotypic prediction models. B [1]. epiRIL was used to obtain a predictive model of plant height and predict gene expression levels. Epihybrids (resulting from crossing epigenetically dissimilar inbred strains), which often exhibit heterosis, can be used to reveal novel epiallels associated with adaptation to new environmental conditions. Epigenetic alterations can be biomarkers indicating beneficial or detrimental phenotypes regulated by epiallele data and can be used to learn more about the molecular regulation of agronomic traits in plant breeding [2].

Epigenetic mechanisms

Cytosine methylation in DNA is a conservative chromatin modification in which a methyl group (CH₃) is attached to the 5-carbon position of cytosine (5 mC - 5-methylcytosine) [3]. Cytosine methylation plays an important role in regulating gene expression and ensuring genome integrity. B. Silence of mobile elements. It is also directly involved in genome imprinting and epigenetic memory across generations. In plants, DNA methylation occurs in three sequence contexts, is initiated and maintained by separate enzymatic pathways, and is strongly correlated with methylation of histone H3 lysine 9 (H3K9me) [4]. The most common is

symmetric methylation of CG dinucleotides (CpG) catalyzed and maintained by DNA methyltransferase 1 (MET1), which corresponds to DNMT1 (DNA methyltransferase 1) in animals. Cytosine methylation remains symmetrical in the context of CHG and may be asymmetrical in CHH (H=A, C, or T) (cytosine methylation is [remote] TGS at the transcriptional level). silence). (plays an important role in silencing). Sequences are conserved that ensure the stability of the plant's own genome. DNA methylation also usually results in inactivation or reduction of gene transcription, especially when it affects promoter regions. In this case, it prevents the recruitment of transcriptional activators and allows the binding of repressors of this process. In contrast, gene body methylation (gbM) is not always associated with silencing [5].

Chromatin contains numerous post-translational histone modifications (PTMs). They form the histone code and allow the recruitment of specific proteins that determine the transcriptional capacity of specific genes. PTMs include methylation, acetylation, ubiquitination, sumoylation, phosphorylation, carbonylation, and glycosylation. These modifications can be dynamically altered by the activity of protein and histone modification complexes involved in binding, maintaining, or removing these markers. The most important PTMs include histone acetylation and methylation. In general, histone acetylation reduces the electrostatic interactions between histones and DNA, thereby improving access to DNA [6]. Histone methylation can have both repressive (H3K9me_{2/3}, H3K27me₃, H4R3me₂ - symmetric) and activating (H3K4me₃, H3K36me_{2/3}, H4R3me₂ - asymmetric) effects on transcription. The presence or absence of post-translational histone modifications alters chromatin structure and alters interaction with the corresponding 'histone decoding proteins', altering gene expression in this region. Histones can also be exchanged with histone variants, altering nucleosome stability and directly affecting DNA availability to a variety of proteins, including transcription factors. This alters the activity of genes in specific chromatin regions, allowing or inhibiting their transcription. For example, the histone variants H2A.Z or H3.3 are characteristic of euchromatin regions, especially loci with moderate to high transcription levels [7].

Epigenetic recombinant inbred lines

Natural epiallels are rare. Therefore, inbred populations, so-called epigenetic recombinant inbreds, were developed to study and understand the contribution of epiallels to intergenerational inheritance, transposable element activation, and phenotypic changes. EpiRIL was generated by crossing *A. thaliana* wild-type (WT) plants (ecotype; Columbia-0, Col-0) with *met1* or *ddm1* mutant lines. The resulting progeny were repeatedly self-pollinated until homozygous epiRILs with specific DNA methylation patterns were obtained [8].

Studies of epiRIL from *A. thaliana* have shown that the

development of epigenetic mutations can increase the productivity and stability of plant populations and increase their evolutionary potential. *A. thaliana* populations consisting of epiRIL monocultures and populations consisting of 2, 3, or 16 different epiRILs were analyzed. He observed that epigenetically distinct populations produced more biomass than epigenetically uniform plant populations. A specific increase in biomass of up to 40% was observed in the presence of competitors and pathogens [9]. Analysis of its DNA methylation mutations in near-isogenic lineages of the *Arabidopsis* population shows that epigenetic mutations can lead to functional diversity at the same level as genetic variation. Examples include fluctuations in flowering time and fluctuations in epiRIL populations associated with increased resistance to pathogens [10].

CONCLUSIONS

Natural epialls are rare. Therefore, inbred populations, so-called epigenetic recombinant inbred lines, were developed to study and understand the contribution of epialls to intergenerational inheritance, transposable element activation, and phenotypic changes. EpiRIL was generated by crossing *A. thaliana* wild-type (WT) plants (ecotype; Columbia-0, Col-0) with *met1* or *ddm1* mutant lines. The resulting progeny were repeatedly self-pollinated until homozygous epiRILs with specific DNA methylation patterns were obtained.

Inbreeding is associated with many genetic and epigenetic alterations. A number of studies have shown differences in DNA methylation patterns between the inbred parental line and her F1 hybrids. Literature data presented in this review illustrate several aspects of epigenetic alterations associated with the inbreeding process, with a particular emphasis on environmental factors that influence the formation of epigenetic variation and phenotypic plasticity. is placed. EpiRILs, obtained by crossing isogenic parental strains characterized by distinct DNA methylation profiles, are of paramount importance in understanding epigenetic variability, or environmental influences on epiall formation and inheritance. Comparative studies of epiRIL and recombinant inbred lines (RIL) have shown that both epigenetic and genetic variability have similar phenotypic potential. However, it should be noted that such conclusions may not be absolutely true: epiRIL exhibits high epigenetic variability and very low genetic variability, mainly due to TE activity. Because the genomes of RILs contain high genetic variability because of their characterization, they exhibit epigenetic variation. There are some genetic mutations that may not. Therefore, further studies should be conducted

to investigate the impact of epigenetic mechanisms on phenotypic design in natural populations.

Epigenetic analysis allowed us to understand the changes that occur during inbreeding and explain the phenomenon of inbreeding suppression. These studies have also made it possible to explain the changes in gene expression that underlie heterosis. Further research and understanding of the regulation and interplay between DNA methylation, histone modifications, sRNA, and transcription will enable broader use of inbred strains in future epibreeding. Appropriate selection of inbred lines has proven important for producing hybrids with expected agronomically important traits. Epigenetics and epigenomics contribute to our understanding of the mechanisms of plant phenotypic variation, epialls, epiQTLs, epihybrids, and epiRIL analyzes, and may lead to the development of effective strategies for future crop improvement.

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