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Genetics and epigenetics-role in development of climate resilient crops

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Abstract

Today's era, Recent advancements in the area of -omics of crops have facilitated effect on plant response to environmental stresses and identification of epigenetic marks. As climate change effects the crop growth, so there is need to develop climate resilient crop variety. As germplasm plateau occur in many crops so there is need to examine genes from wild variety, which are high yielding and resistant to climate change. As global warming occur temperature fluctuation rate is very high. To better adapt genetics and epigenetics transiently or lastingly to stimuli from the surrounding environment, the chromatin states in plant cells vary to allow the cells to fine tune their transcriptional profiles. Conceptually genetics deals with gene function and genes whereas epigenetics deals with gene regulations. Modifications in chromatin states include a wide range of histone post-transcriptional modifications, histone variants, DNA methylation and non-coding RNAs, which can arrange various chromatin states that epigenetically determine specific transcriptional outputs. Specifically genetics focuses on how DNA sequences changes in the cell while epigenetics focuses on how DNA is regulated to achieve those changes. This has paved the way to exploitation of epigenetic variation in crop breeding. That helps to develop climate resilient crop varieties.

Keywords: Omics, genetics and epigenetics

Introduction

Epigenetic has emerged as an valuable research field for crop improvement under the present climatic changes. Epigenetic phenomenon Plant response to abiotic stresses is complex and involves multiple mechanisms, activated and controlled by massive changes in gene expression and nuclear organization (Budak *et al.*, 2015) [4]. Epigenetic diversity provide additional sources of variation within a species that could be captured and created improvement in crops. Evidence found from model plants indicates that epigenetic modifications, some of them inherited to the next generation, play an important role in this response. However, the role of epigenetic variation in adaptation of crops to abiotic stress is still not well understood (Niederhuth and Schmitz, 2014) [16]. It is important to keen understand the sources of epigenetic variation and the stability of newly formed epigenetic variants from one generation to another to use potential of epigenetic variation for improvement of crops. Epigenetics is new and fascinating field of genetics, completely meddling with classical knowledge of interaction between the hereditary material and the phenotype. Plant breeding has relied on combining the genetic diversity and variation present within species to develop various combinations of alleles which provide desired traits. If we talk about the epigenetics, It is "the study of mitotically and/or meiotically heritable changes in gene function that cannot be explained by changes in DNA sequence" (Russo *et al.*, 1996) [22]. Epigenetic changes, which include histone modifications, DNA methylation, chromatin remodelling and small RNAs, are thus heritable, but do not follow the known patterns of inheritance (Bräutigam *et al.*, 2013) [2].

Genetics and Epigenetics

In plants, active maintenance mechanisms are enable to transfer of epigenetic information throughout gametogenesis, then fertilization and early embryogenesis (Rival and Jaligot, 2012) [21]. However, epigenetic states may often be unstable. Therefore, to achieve plant improvement that may persist over generations to generations, there is need to learn more which epigenetic state can be stably transmitted (Kinoshita and Seki, 2014) [10]. The application and development of methods for widespread epigenome profiling and engineering may generate new avenues for using the potential of epigenetics in crop improvement.

It is well known fact that abiotic stresses negatively impact plant growth and development with severe effects on crop yield leading to huge economic losses. Since most epigenetics studies have been carried out in model plants, particularly *Arabidopsis* (Pechinka *et al.*, 2019) ^[19]. All knowledge accumulated on the role of epigenetic regulation response to the environment has led to an increased interest in the role of epigenetics in crop resilience to abiotic stress. Epigenetic mechanisms and marks Chromatin conformation influences the accessibility of DNA sequences, such as regulatory DNA sequences and coding, to the transcriptional machinery thus intervening in regulation of gene expression (Li *et al.*, 2008) ^[13]. For transcription DNA accessibility is mediated by nucleosome positioning, each core nucleosome is made up by a histone octamer comprised of 146 DNA base pairs in two turns and two copies of each histone H2A, H2B, H3, and H4. DNA Unpackaged between nucleosomes, with different varying length depending on the nucleosome's compaction level, is associated to H1, the linker histone. Interaction of histones with DNA is influenced by reversible covalent posttranslational modifications (PTMs) of the histone tails protruding the nucleosome core particle. The suite of PTMs that regulate the level of chromatin condensation and DNA accessibility is known as the histone code (Wei *et al.*, 2017) ^[26]. Histone methylation and demethylation and Histone acetylation and deacetylation are the two reversible well-characterized plant histone modifications. Acetylation marks, such as histone 3 lysine 14 acetylation (H3K14ac), histone 3 lysine 9 acetylation (H3K9ac) and histone 3 lysine 36 acetylation (H3K36ac) are associated with gene activation. Histone deacetylation at the same residues is associated to transcriptional repression.

Histone methylation can have a repressing role or gene activating, depending on the site of modifications: histone H3 lysine 4 (H3K4) and H3K36 methylation are related to gene expression, while H3K9 and H3K27 methylation are related to gene repression and heterochromatin formation. In plants, both repetitive sequence-enriched heterochromatic regions and transposable elements are marked by histone H3 lysine 9 monomethylation and dimethylation (H3K9me1 and H3K9me2). Chromatin are modified in plants at the level of DNA sequence by DNA methylation that occurs in CHG, CG, and CHH (H = A, T or C) contexts through various pathways. METHYLTRANSFERASE 1 (MET1) and CHROMOMETHYLASE 3 (CMT3) are plant enzymes that are responsible for the maintenance of CG and CHG methylation, respectively (Zhang *et al.*, 2018) ^[31]. Chromatin states are vary in response to environmental stimuli, allowing plant cells to fine tune their transcriptional profiles are to better adapt transiently or lastingly to the surrounding environment condition.

Epigenetics response to climate and temperature

As the climate change is very frequent, Plants are constantly exposed to various environmental biotic and abiotic stresses, including nutrient availability, low water, extreme temperatures and light intensities etc. such as salinity or heavy metal content. To cope with various climate change conditions and increasing occurrences of unpredictable environmental conditions, plants have to developed various mechanisms controlled by genetics and epigenetics that enable them to withstand single or combined stresses and their interactions (Shanker and Venkateswarlu, 2011) ^[23]. And

also there is need of developing such varieties which are climate adaptive, so, understanding this condition in crops requires knowledge of genetic and epigenetic bases of responses to environmental changes. Adaptation to climate changes transmitted through generation to generation Creating climate-smart crops also requires knowledge of how epigenetic changes are transmitted through generations.

It is widely accepted that important part of these epigenetic modifications includes priming or memory involved in improved capacity to withstand future stresses, even if not primed by the same stress. Since priming can affect plant growth and development, this phenomenon is not always observed. Thus, plants may employ mechanisms to elucidate whether to memorize or to forget (Baier *et al.*, 2018; Crisp *et al.*, 2016; Mozgova *et al.*, 2019) ^[1, 5, 19]. In *Arabidopsis*, it has been observed that progeny plants preserve an adaptive epigenetic memory of several environmental conditions of their ancestors (Whittle *et al.*, 2009) ^[27]. Zhong *et al.* (2013) ^[29] showed clear associations between increase in plant epigenetic system, ambient temperature, and siRNA biogenesis. This warmth-induced epigenetic memory was maintained for at least three different generations, with declining strength over further generations. Opposite to this, trans generational epigenetic memory as a response to pathogen showed slower decrease in strength over many generations (Molinier *et al.*, 2006) ^[15]. In *Arabidopsis* exposure to abiotic stress during many generations can induce heritable and potentially adaptive phenotypic changes, that were maternally and paternally inherited.

Climate change and frequent occurrences of both biotic and abiotic stresses have become a constant threat for global production of maize (*Zea mays* L.) which is a principal cereal crop cultivated worldwide. Epigenetics responses to drought and temperature stresses in agronomically important crops, In Maize Low water availability is an important environmental factor affecting maize yield. In order to evaluate how maize modulates its response to drought and recovery from drought stress, transcriptomic and genome-wide chromatin data were integrated (Forestan *et al.*, 2018) ^[6]. Epigenetics represents accepted set of mechanism by which organism respond to the environment by regulating phenotypic plasticity and transitions.

Future Prospects

Climate-smart crop breeding several applications, as climate change is expected to increase the prevalence of extreme environmental conditions, improved stress tolerance has become a major breeding target of epigenetics. In field conditions, crops are often simultaneously challenged by different biotic and abiotic stresses. So, understanding of shared mechanisms contributing to one or more simultaneously occurring stresses also become an important aspect in improvement of crop productivity under complex stress situations (Ramu *et al.*, 2016) ^[20]. Heritable epigenetic changes may arise independently of DNA sequence alterations and have been associated with gene expression. By modulating plant development and response to environmental conditions, epigenetic diversity, chemically, genetically or environmentally induced may help to optimize crop traits in an era challenged by global climate change. Knowledge and use of epigenetic mechanisms and variation could potentially help plant breeders to generate new and innovative, flexible varieties through the exploitation of the natural phenotypic

variation in existing crop plants. Also, environmental changing effects of epigenetic mechanisms should be exploited to find yield stability in a fast-changing climate. There is growing evidence and fact that epigenetic mechanisms may have a role in increasing crop resilience to different specific stresses and therefore may be an important tool in climate-smart crops breeding. For example, methylation of histone H3 lysine 4 (H3K4) is involved, persistent expression of high temperature responsive genes, as well as hyper-induction of genes during repeated heat stress treatments (Lämke *et al.*, 2016) [12].

Perhaps, the seeds from the drought stressed plants find faster shoot emergence due to abundance of cytokinin ribosides (Surdonja *et al.*, 2017) [24]. In rice, it was found that large proportion of the drought-induced epimutations (DNA methylation changes) maintained their altered methylation pattern in next generations exposed to drought at the tillering to the grain filling stages suggesting the presence of possible epi-marks that are drought inducible and heritable across generations (Zheng *et al.*, 2017) [30]. The DNA sequence variation, the epigenetic modifications can contribute to breeding by providing useful markers and allowing the use of epigenome diversity to predict performance of crop production. Various epigenetic mechanisms has arise for transferring the knowledge from model plant to crop.

It is obserb that multigenerational drought exposure, improved the adaptability of rice plants to drought conditions, various findings suggested that epigenetic modifications can play important roles in the response to drought and the longterm adaptation of rice crop, and perhaps other plants, to adverse environmental conditions (Zhang *et al.* 2017) [26]. The key challenge that agriculture faces in this century is to increase crop production by speeding up the breeding of resilient crop species. Therefore information about the epigenetics provide fundamental molecular level conditions with potential direct applications in crop enhancement, tolerance and adaptation within the context of climate change

Conclusion

The climate change impact can be one of the greatest threats facing all life on Earth today. Around the world, extreme weather patterns and rising temperatures are already affecting the habitats of several organism. Undoubtedly, their fate will depend on their ability to either migrate away from or adapt to the new environment, and eventually evolve as a species. There is valuable excitement about the potential for epigenetic information to contribute to remarkable heritable variation in various crop species. Our keen understanding of the molecular mechanisms of epigenetic inheritance is improving fastly and now it is possible to sum up the profile of the epigenome at high resolution. several possibilities are there, which should be taken in consideration to improve crop stress tolerance. The identification of epigenetic regulatory systems and epialleles, that have functional impacts on various agronomic traits can lead to a range of different approaches for epigenetic breeding of crop plants, such as the use of mutant lines (Yang *et al.*, 2015) [28], hybrid mimics (Wang *et al.*, 2015) [25], recurrent epi-selection (Hauben *et al.*, 2009; Greaves *et al.*, 2015) [7, 8], epigenome editing (Park *et al.*, 2016; Lämke and Bäurle, 2017) [11] and epigenomic selection (Jonas and de Koning, 2013; Oakey *et al.*, 2016) [9, 17], as well as exploitation of stress priming mechanisms to induce a constitutively primed state and increase the crop's ability to

tolerate various stress without the reduction of biomass accumulation and yield (Lämke and Bäurle, 2017) [11]. Epigenetic information plays a role in developmental gene regulation, response to the environment, and in natural variation of gene expression levels. Due to these important and beneficial roles, there is potential for epigenetics to play a role in crop improvement strategies to play a role in crop improvement strategies including the selection for favourable epigenetic states, creation of novel epialleles, and regulation of transgene expression. Conserved and remarkable role of epigenetics in responding to temperature change, that appears to an element of temperature and species specific. The various specific effects of temperature change on epigenetic modification resulting phenotypic response.

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