Stress-Induced Cell Reprogramming. A Role for Global Genome Regulation?

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Virtual Biology Aims to Mimic Stress Reactions in Plants and Needs Adequate Data

Stress adaptation in crops is an important and timely topic in basic and applied biology. Interest in the issue is ambiguous. On the one hand, it is fascinating to understand interaction between plants and environment. On the other hand and in view of the needs of human life, we want to create crop plants that are able to confront successfully unfavorable natural conditions. The main goal in plant breeding is to obtain plants that combine high yields and reliable yield stability over years and locations. Simultaneously, plant products must have a high quality in terms of nutritional value, if used as food or feed, and/or of other characteristics of commercial interests. However, in addition to biotic stress factors, disturbances of extreme or even mild abiotic stress are supposed to account for a high amount of unachieved potential in plant production all over the world. Diverse forms of abiotic stress may occur, including drought, heat, cold and freezing, salinity, nutrient deficiency, toxic concentration of heavy metals, oxidative stress as well as oxygen shortage, and mechanical stress. Although it is known that diverse environmental stress factors never act alone, experimental study of plant responses on abiotic stress is normally restricted to plant reactions on isolated stress factors. However, it has to be considered that stress always occurs as a complex of various interacting environmental factors that contribute in varying degrees to the overall stress. Consequently, plants always respond to a unique complex of growth conditions. Stress inducers from the abiotic as well as biotic world have some common signal and response pathways in plants and thereby have the potential to modulate the effect of each other through cross-talking. Further, plants, as sessile organisms, have to get along with the dynamics of transiently changing environmental conditions, and this has to be achieved at the various stages of plant development (see Amzallag, 2001, for the meaning of developmental windows in stress adaptation).

Virtual experimentation is currently thought to offer the best potential for future research on stress adaptation because the complexity of plant reactions and stress factors may be taken into account simultaneously. Therefore, a global, multidisciplinary initiative to establish systems biology in plant sciences is very promising. Systems biology aims to collect and manage the huge amount of data available at any level of plant life to enable modeling of an artificial plant organism, the in silico plant. Confronting the artificial plant by computer simulation with real-life obstacles, such as abiotic stress through nutrient depletion or water deficit, will help to improve our understanding of how plants work and how to improve the capacity of plants in terms of increased ''fitness for stress.'' Combining computational skill and interest in natural sciences to the benefit of humanity, environment, and remunerative intersectorial applications covers the most fascinating areas for younger researchers in biology and has the potential to attract students to a scientific career. Therefore, the field of systems plant biology will especially promote the potential of young scientists and promises to advance science a significant step forward.

However, crucial to the success of this challenging idea of in silico experimental studies on stress adaptation will be the quality and completeness of the data used. Modeling the potential of plants requires a maximum of input of regulatory networks working in plants to cover the high adaptability of plants to environmental conditions and the plasticity of plant reactions. Therefore, it is of outstanding importance to understand all levels of regulatory mechanisms. This includes sequence analysis of genes and non-gene DNA, and studies of transcriptomes and posttranscriptional regulation, of proteomes and posttranslational regulation, as well as of metabolomes. Besides, profound knowledge on the functioning of regulatory genes, like transcription factors, seems to be critical to understanding general and specific expression control mechanisms in plant responses. But of equal importance for future progress will be our understanding of the details of chromatin and nuclear organization. In medicinal research and research on plant development, global mechanisms to organize genome structure and nuclear territories are discussed as superimposed instruments for the regulation of concerted gene activities. Nevertheless, in plant research on stress adaptation, the significance of this kind of global regulation of expression is still more or less ignored.

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This article will first illustrate how plants can adapt in a complex and coordinated manner to transient changes of abiotic environmental conditions and why cellular reprogramming is considered as a key process in stress adaptation. As an example, recent knowledge on both physiological and molecular adaptive reactions by plants to phosphorus (P) deficiency will be pointed out. Then, the factors involved in global genome regulation will be presented, and their possible contribution for adaptive reprogramming in target cells will be brought to attention.

STRESS ADAPTATION: A COMPLEX PHENOMENON

Adaptation to Abiotic Stress Requires Coordinated Actions at the Whole-Plant Level and Cell Redifferentiation in Target Tissues: P Deficiency as an Illustration

Nutrient deficiency may seriously interfere with normal plant growth and development. Nutrient efficiency is therefore thought to be an important goal in plant breeding. This might refer to macronutrients, such as nitrogen and P, and/or microelements, such as iron or zinc. Phosphorus is especially critical in terms of crop productivity. Access to this nutrient may be hampered by soil characteristics and water availability. Bioavailable anionic phosphate may be excluded from soil solutions and, thus, from mobility in the soil by the strong tendency of P to form insoluble inorganic compounds or to convert to organic forms.

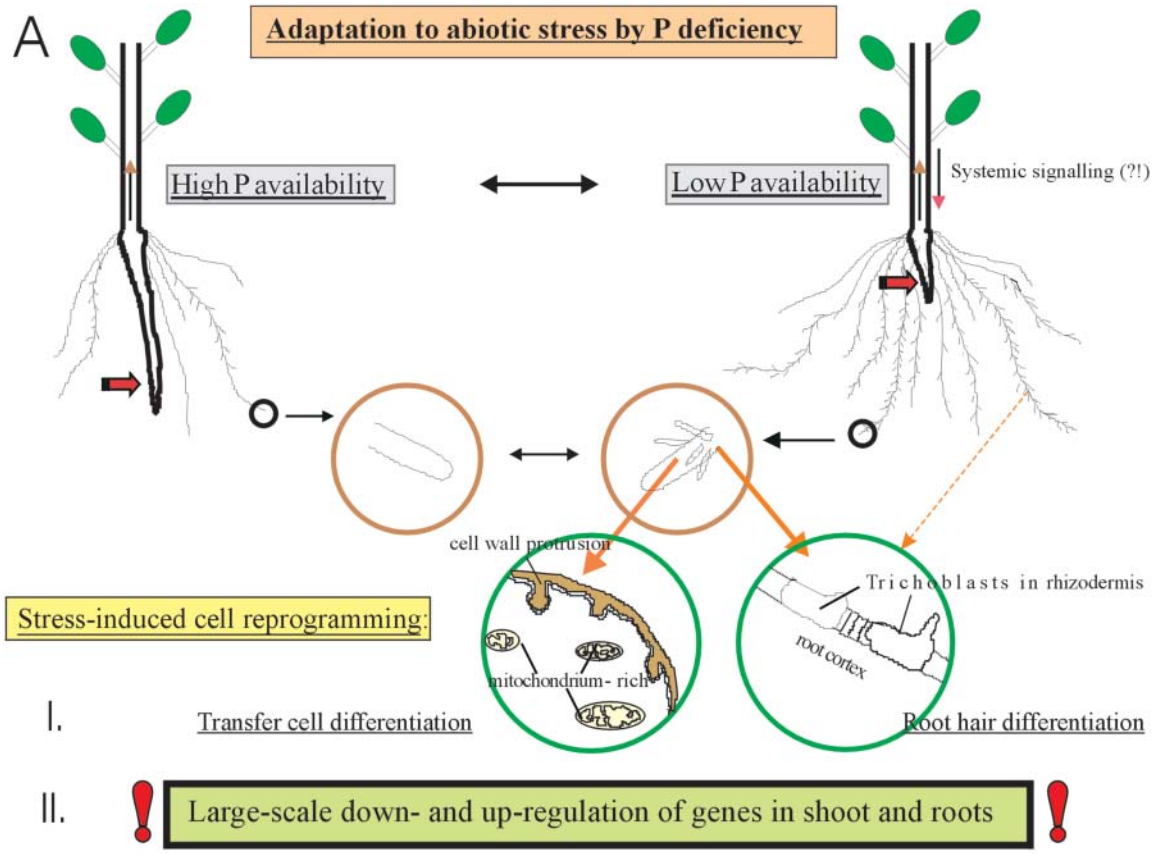
Low concentrations of available P in the rhizosphere can be sensed by plants as a cue for the induction of adaptation to this stress. Surprisingly, the sensing of low available P concentrations in the rhizosphere seems to occur mainly in the shoot (Föhse and Jungk, 1983; Burleigh and Harrison, 1999; Williamson et al., 2001). Available P will be taken up by the root system, then transferred to xylem and further transported via xylem flow to the shoot. A low concentration of P in the shoot obviously induces a systemic signaling cascade that initiates signal transduction pathways in the root meristems and epidermis with dramatic consequences on root architecture (Fig. 1A) involving mainly auxins and ethylene as signaling compounds (Dolan, 2001; Schmidt, 2001; Williamson et al., 2001; López-Bucio et al., 2002). In any case, under P deprivation, the density and length of lateral roots are increased by initiating preformed lateral meristems while primary root growth is restricted, displaying a reduced number of cells within the elongation zone of the root tip (Williamson et al., 2001). Obviously, a change in auxin concentration and altered sensitivity to auxin play important roles for this kind of adaptive change in the developmental pattern (López-Bucio et al., 2002). Additionally, when P availability is low, a significant increase in the number and length of root hairs can be observed as a fascinating morphological sign of adaptation. Molecular analyses have revealed that these root hairs normally demonstrate a higher density of inward-directed transporting molecules with a high affinity for P. These reactions in plant adaptation may be found throughout the plant kingdom, though the level of modification and certain morphological arrangements will depend on the genetic background. The family Proteaceae, for example, demonstrates induction of typically clustered roots, named proteoid roots. These roots are normally covered with high numbers of long root hairs.

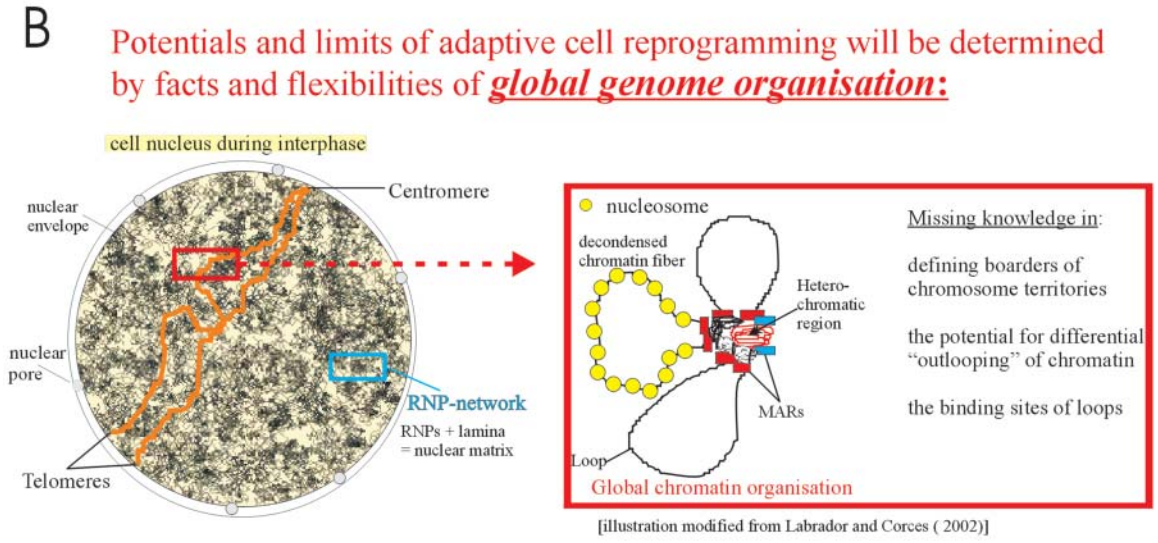
The amount of P taken up into the root system is about proportional to the percentage of root hairs (Jungk, 2001). Therefore, root hairs are discussed as a breeding trait for high nutrient efficiency in crop plants. Taking into account that induction of root hairs by environmental conditions demands redifferentiation of existing root epidermal cells to trichoblasts, it was recommended by Michael (2001) to calculate this trait in studies of environmental effects on plants as ''percentage of hair-forming cells in the rhizodermis'' rather than ''hair density per unit root length'' (p. 118), as it is used for studies on mineral uptake.

Another kind of significant cell redifferentiation response to P deficiency is typically observed in the rhizodermis near the root apex next to the zone of differentiation, where root hair initiation takes place. Here, so-called transfer cells are formed. These cells rarely occur under ordinary conditions and demonstrate two outstanding characteristics: strong enlargement of the cell surface due to ingrowths of secondary cell wall material extending into the cell lumina and a high increase in the number of mitochondria pointing to a high turnover of energy and carbon. Although the specific function of transfer cells in the rhizodermis remains to be further elucidated, in general they are thought to strengthen the flux of solutes at the boundaries of symplast and apoplast.

Along with these environmentally induced changes in cell differentiation during adaptation, the rhizosphere of P-depleted plants is found to be enriched by plant excretion products, including protons and organic acids such as citrate and malate. Excreted acidic phosphatases as well as ribonucleases are also reported to occur due to P deficiency. These compounds are appropriate to initiate the conversion of immobile P in the soil to bioavailable forms by chemical and biochemical reactions or promotion of the proliferation of associating microorganisms and fungi, including also mycorrhizae.

Taken together, adaptive phenotypic expression as response on P deficiency is primarily directed to avoid or minimize forthcoming stress by increasing P uptake. This is achieved by different strategies: (1) through the enlargement of the surface of the root system to reach a wider area of the environment; (2) by intensifying excretion of plant compounds to influence the bioavailability of the nutrient actively; and (3) by enhancing the potential of the uptake system. To realize these adaptive reactions to low amounts of bioavailable P, interaction of organs and targeting of tissues and cells for differential regulation is required.





Flexibilities in genome organisation are related to:

- Acetylation of histones
- Methylation of histones and DNA
- DNA arrangements
- Looping and packaging of chromatin
- Size of loops
- differential attachment binding sites (?!)

Figure 1. Adaptation to abiotic stress. The figure emphasizes typical phenotypic and epigenetic changes at the whole-plant as well as the cell level in response to phosphate deficiency (A) and indicates factors involved in global genome regulation (B). For details, refer to the text.

Reprogramming of Target Cells Is Fundamental for Stress Adaptation

Highly efficient methods are available now to study complex alterations at the level of transcripts, proteins, and metabolism, completing our current knowledge due to genomics. A wealth of data has been recorded recently for changes caused by various abiotic stress inducers and is ready to be analyzed by bioinformatics. All these data show that numerous genes and pre- as well as posttranscriptional and/or -translational factors and processes are involved to achieve appropriate plant responses to environmental circumstances, including mechanisms for stress avoidance as well as tolerance. Related to P depletion, for example, Wu et al. (2003) performed microarray studies in shoots and roots of Arabidopsis that covered transcription analysis of 6,172 genes. About 30% of these genes, i.e. 1,835 genes, have been transiently up- or down-regulated by 2-fold or more within the first 72 h under P deprivation. These genes cover a wide range of functions, including more than 100 genes each for transcription factors as well as cell signaling proteins. In the roots, 296 genes were specifically repressed and 141 specifically up-regulated. In the shoot, the number of differentially regulated genes was significantly higher and accounts for 617 down-regulated and 488 up-regulated genes. A further 293 genes were found to be up- or - down-regulated in the shoot as well as in the roots. It is noteworthy that adaptive reprogramming obviously requires a higher number of down-regulated genes than up-regulated genes.

Alteration of complex expression patterns needs to be coordinated at the cell level. During recent years, a driving force to gain new insights in basic knowledge on how plants function at cellular levels has been the powerful search for transgenes that might enable efficient molecular breeding on abiotic stress tolerance. Three levels in cell biology have been mainly envisaged as tools for analyses and manipulation: (1) the level of target proteins, which are involved directly in metabolism or structure; (2) the level of regulatory proteins, namely the transcription factors and their target sequences to affect gene activity; and, evidently, (3) the level of signal transduction, including e.g. calcium and activated oxygens as signals, as well as signal cascades like the mitogen-activated protein kinase system. However, regulation of gene expression also requires superimposed organizational structures to realize coordinated transient access to the binding sites of regulating factors.

GLOBAL GENOME REGULATION

What Is Meant by Global Genome Regulation?

In eukaryotes, accessibility of DNA sequences to the transcription machinery is crucially determined by the degree of packaging of the DNA into condensed and open chromatin domains. Additionally, recent studies have been undertaken to unravel the role of non-randomly positioning of genes in the nucleus for gene expression during the interphase of the cell cycle. Global genome regulation refers to the structural and compositional organization of chromatin in the nucleus that defines coordinated accessibility to the DNA. The importance of factors involved in global genome regulation is currently highly acknowledged as critical for genetic as well as epigenetic programming in plant development. Environmentally induced reprogramming of cells during adaptation points to developmental plasticity as a typical characteristic of plants. This suggests a significant role of global genome regulation also in adaptive plant cell biology.

Chromatin Organization during Interphase of the Cell Cycle: Facts and Flexibilities

Linear DNA is packaged into a condensed higher-order structure, the chromatin. Organization to a first-order condensation is achieved by wrapping the DNA around a globular octamer of histone proteins in a 1.8 turn according to 146 bp. The octamer consists of two tetramers of the histones H2A, H2B, H3, and H4. The DNA/protein complexes are called nucleosomes. Nucleosomes are linked to each other by a linear DNA stretch of 20 to 200 bp, giving the impression of beads on a string in electron microscopy. This 10-nm-diameter fiber is referred to as decondensed or open chromatin, which is ready to get directly into contact with regulatory factors, e.g. of the transcription or replication machinery. A higher degree of condensation will render access to the DNA more difficult or even impossible, leading finally to the silencing of underlying sequences.

To further condense the 10-nm-diameter fiber to a solenoid structure, histone H1 links coils consisting of 6 nucleosomes to the famous 30-nm-diameter fiber. These chromatin structures are typically addressed to the fraction of euchromatic domains, whereas heterochromatic domains demonstrate highly compact structures that are generally inaccessible to DNA-binding factors and transcriptionally silent. Heterochromatic regions are thought to have an important impact on the realization of cell programs during development and differentiation and, hence, are of high interest related to future research on plant stress responses. Large heterochromatic domains are found at the centromeric and telomeric regions of the chromosomes and contribute to proper chromatid cohesion and chromosome segregation. However, additional smaller heterochromatic domains are distributed throughout the chromosomes. Current studies reveal that many factors and processes are involved in the assembly of heterochromatin, including, most importantly, the targeting of initiation sites by help of repetitive sequences or silencers as well as the post-translational modifications of histones (see Grewal and Moazed, 2003).

A flux from a decondensed to a more condensed state and vice versa is crucial for all kinds of cellular

differentiation. This flexibility in chromatin structure is termed chromatin remodeling and may be defined as ''any event that alters the nuclease sensitivity of a region of chromatin'' (Aalfs and Kingston, 2000, p. 548). Chromatin remodeling can be achieved by many different mechanisms and might refer exclusively to nucleosomes or may be involved in the inhibition of transcription-repressing complexes, such as the polycomb group complex identified in Drosophila. This last described mechanism is also found in Arabidopsis. VRN2, a plant chromatin remodeling factor from Arabidopsis, is environmentally inducible by temperature and mediates the initiation of reproduction after vernalization due to its interference with a flowering repressor (Gendall et al., 2001). Stress-mediated effects on chromatin remodeling are known also from research on yeast mutants. The stress-activated protein kinase cascade, a well-conserved pathway in eukaryotes, activates chromatin remodeling as response to nitrogen starvation in a region related to recombination hotspot activity (Mizuno et al., 2001).

Especially important events in chromatin remodeling are histone modifications by enzymatic acetylation or deacetylation of Lys residues that modulate DNA/histone interactions and correlate with activation or deactivation of transcription. Evidence for a link to stress-induced effects is coming from medicinal research. Gilmour et al. (2003) found that oxidative stress from environmental particles enhanced acetylation of histone 4 in lung alveolar epithelial cells, regulating thereby interleukin expression. Shear stress in human vein endothelial cells was shown to affect histone acetylation and chromatin remodeling in the promoter region of target genes (Illi et al., 2003). Differential histone acetylation is also reported for plants as response to environment. Chua et al. (2003) showed that light-dependent transcriptional up-regulation of the pea plastocyanin gene is related to histone acetylation. The results suggest that the responsible enhancer associates with the nuclear matrix and activates transcription by increasing acetylation of the promoter and the nearby 5′ coding region, leading to an altered local chromatin structure. Besides acetylation, also methylation of histones may interfere with transcription. Methylation at Lys-4 of H3 [Met(K4)H3] was currently reported to be generally enriched in euchromatin of various plant species. By contrast, methylated Lys-9 residues at H3 were found to be binding sites for the heterochromatin protein HP1/Swi6 in Drosophila during assembly of silencing heterochromatin. Consequently, in regions of constitutive heterochromatin of various plant species, strong methylation of Lys-9 of H3 was observed, whereas [Met(K4)H3] was not present (Houben et al., 2003). Homologs of HP1 that are involved in the regulation of flowering time in response to environmental signals were recently described for Arabidopsis (e.g. Gaudin et al., 2001).

Methylation at sites of previously deacetylated Lys-9 of H3 is obviously linked to methylation of cytosines in the DNA. In most of the cases observed, DNA methylation was found to correlate to the inhibition of transcription. Whereas methylation of the protein-coding region is often associated with post-transcriptional gene silencing, silencing of genes due to a blockage of transcription (transcriptional gene silencing) is usually related to methylated sites in the promoter region (Okamoto and Hirochika, 2001). Modifications on histone proteins or DNA are generally thought to be involved in both local regulation of gene expression as well as global regulation across chromatin domains. Global DNA methylation has long been known to occur in a tissue-specific manner. The degree of overall methylation of the genome was shown in *Daucus carota* to be linked to the differentiation state of a defined tissue rather than to the background genotype, age, or secondary growth of the plant (Arnholdt-Schmitt et al., 1995).

Chromatin remodeling might also be affected by ATPases that alter conformation and positioning of the nucleosome. Recently, such complexes have also been described for plants (see Wagner, 2003). The chromatin remodeling ATPase DDM1 of Arabidopsis is probably involved to make DNA accessible to methyltransferases (Jeddeloh et al., 1999). Loss of DDM1 by mutation results in the activation of retrotransposons and transposons. The activity of transposons in terms of transcription as well as transpositioning is often found to correlate with methylation of the DNA. In maize, most transposable elements that were present in a high number of copies were restricted to methylated heterochromatin regions (San Miguel et al., 1996; Rabinowicz et al., 1999). Transposing sequences play a key role for rearrangement in genomes. Their potential to define dynamically a site of structural silencing makes them an especially hot topic in the research on developmental plasticity in plants. Retrotransposons have been shown to be specifically activated by environmental stress signaling (Grandbastien, 1998). The link between retrotransposon activation and stress is best characterized for the tobacco retrotransposons Tnt1 and Tto1 (Mhiri et al., 1997; Takeda et al., 1999; Beguiristain et al., 2001). Responsiveness was demonstrated through transcriptional induction and was related to diverse forms of stress, including elicitors, pathogen attacks, salicylic acid, wounding, protoplast isolation, cell subculture, 2,4-dichlorophenoxyacetic acid, methyl jasmonate, $CuCl_2$, and oxidative stress. From the results with the three Tnt1 subfamilies, it is highly suggested that the variable U3 region of the retrotransposons is crucial for nonrandom stress responses. Different stress factors induced different RNA populations of the Tnt1 subfamilies that could be distinguished by U3 sequence differences. For example, whereas Tnt1B was preferentially induced after onset of cell subculture, Tnt1A transcripts were strongly activated by the elicitor cryptogein and methyl jasmonate, and differential induction of Tnt1C RNA populations were observed by salicylic acid and 2,4-dichlorophenoxyacetic acid. Additionally, although induced Tnt1C RNA populations still differ in relation to their U3 sequences, the same

promoter element could be identified within this region. These results point to a direct link between stress factors and the activation of specific retroelements through defined promoter elements. Future studies may now involve targeted knockout of retrotransposon expression to evaluate its significance for stress adaptation.

In plant genomes, up to 85% of the nuclear DNA may consist of mobile elements (Kumar and Bennetzen, 1999), depending on the size of the genome (Arabidopsis contains about 14%), and a large portion thereof is dispersed as repetitive sequences throughout the genome. There is vast literature available from the past, demonstrating the high variability in repetitive DNA in relation to plant development and stress, including especially tissue culture experiments (see Arnholdt-Schmitt, 1995; Schaefer et al., 2000). Also, environmentally induced DNA polymorphisms were reported for several species (Shatters et al., 1995; Lerner, 1999).

Dynamics in the Nucleus: A Crucial Role of Flexible Gene Positioning for Coordinated Expression Profiles?

During interphase of the cell cycle, the chromosomes are polarized due to opposite positions of centromeres and telomeres in the nucleus mainly occupying a distinct area, called territory (Fig. 1B, left). Chromosome territories basically correspond to reproducible positions within the nucleus, as can be inferred by chromosome painting. This technique refers to the visualization of entire chromosomes by fluorescence in situ hybridization. However, current insights in studies on human and mouse genome organization reveal that many genomic regions may also be found outside these territories uncovered by chromosomal painting. These regions have been characterized preferentially as gene rich and/or actively transcribing (Mahy et al., 2002). Additionally, there is consensus that chromatin fibers are anchored at nuclear structures due to defined sites of the DNA, called insulator sequences, and matrix or scaffold attachment regions (MARs or SARs). These sequences are arranged in such a way, that looping of open chromatin fibers results (Fig. 1B, right). Loops vary in size and are thought to form units for transcription as well as replication. Whereas replicons in plants are known to range between 20 and 100 kb, actively transcribed, undermethylated, and gene-rich loops in association with acetylated histones are described in Arabidopsis to consist of 200 to 2,000 kb (Fransz et al., 2002). Current debate is on the precise functioning of three-dimensional structuring for genetic as well as epigenetic control of gene and transgene expression and the factors and binding sites involved.

Attachment sequences and their binding sites are thought to have a special role in differential expression. Potential candidate sites for tethering chromatin are the nuclear envelope, the nuclear matrix, which consists of a lamina and the ribonuclear protein network, nuclear pore complexes, nucleoli, and insulator bodies (Nickerson, 2001; Labrador and Corces, 2002; Marshall, 2002). The so-called boundaries or insulator elements or bodies are large structures that are supposed to contain various individual insulator sites. Through interaction of involved insulator DNA sequences and proteins in the boundaries, rosette-like structures are formed. The more compact kernel includes chromatin remodeling and histone-modifying proteins as well as silenced chromatin. From this center, outlooping of decondensed chromatin is organized. Insulating sequences are generally supposed to cover the following functions: (1) separation of condensed and decondensed chromatin structures, thereby inhibiting the spreading of regulatory mechanisms between neighboring regions; (2) enabling localized, topologically independent control of domains; (3) positioning of chromatin in defined areas of the nucleus to enable nonrandom interactions and control also from different chromosomes; and (4) realization of developmental programs by binding to differentially expressed MAR-binding proteins, which may force differential looping in terms of length and position of the loop and subsequent differential control of expression. Recently, a central structural role was proposed for MARs for early recovering from transient cadmium stress. Fojtová et al. (2002) observed maintenance of full cell viability despite extensive fragmentation of DNA into pieces of chromatin loop size, leading to apoptosis in prolonged stress. Further efforts are urgently needed to characterize insulating sequences and the binding tools, as well as how differential positioning of loops and/or chromatin domains is precisely achieved. At the DNA level, repeated sequences may play an important role. At least, the well-characterized gypsy element of Drosophila is known to include a retrotransposon. However, research on links between stress-induced cell redifferentiation in plants and differential positioning of chromatin loops and the significance of MARs in this context is still lacking. Nevertheless, it is of interest that recent studies on growth-induced tobacco cells revealed differential expression of a MAR-binding protein (Fujiwara et al., 2002).

Hot News from the Ever-Surprising World of RNAs: RNAi Suggests a Pivotal Role Also in Global Genome Regulation

Double-stranded noncoding RNAs are currently known to be involved in epigenetic silencing of genes in eukaryotes. Such regulatory dsRNAs are processed in ribonucleoprotein complexes to the tiny interfering RNAs (RNAi), small interfering RNA, and microRNA of about 21 to 25 nucleotides that target mRNA sequences for subsequent cleavage according to post-transcriptional gene silencing or also translational repression in case of microRNAs. Current results also points to their biological significance in targeting DNA methylation as well as heterochromatin formation (see

Volpe et al., 2002). Additionally, increasing evidence suggests that heterochromatin formation and small RNAs are involved in programmed elimination of DNA in the ciliate Tetrahymena (Mochizuki et al., 2002; Taverna et al., 2002). It remains to be seen whether regulatory RNAs may also be responsible inducers of physiologically determined losses of repeated DNA sequences in plants, as was observed in systematic analyses on *D. carota* in relation to growth phases, differentiation, and aging (Arnholdt-Schmitt, 1995; Schaefer et al., 2000; Schaffer and Arnholdt-Schmitt, 2001).

FINAL REMARKS

Adaptation of sessile plants to varying and complex abiotic conditions requires plasticity in development and reprogramming of target cells. Global genome regulation mechanisms have recently been recognized as important factors of epigenetic programming. Updating current knowledge of the mechanisms involved in global genome regulation with special consideration of environmentally induced responses intends to help advance future interdisciplinary research on plant stress adaptation.

Traditional breeding on environmental stress tolerance succeeded by ingenious selection procedures at the population as well as single-plant level in various environmental backgrounds (years and locations), and by calculating genetic as well as environmental components. These methods automatically considered the complexity of plant organisms (selection at the whole-plant level), as well as the complexity of stress phenomena (testing above years and locations), and have been very successful, although limited by nature. If modern breeding on abiotic tolerance wants to exceed natural limits, a better understanding of the complex interaction between plant and environment is urgently required and has to include research on the adaptive and coordinating capacities of global genome regulation.

Successful transgene strategies to improve abiotic stress have been rare so far, although obviously straightforward. The presence of a transgene sequence in the plant genome cannot be expected to account solely for success or failure in molecular breeding on abiotic stress tolerance. Nevertheless, investigation of all factors involved in global genome regulation of both successful and failing transgenic plants could certainly improve our understanding of complex molecular mechanisms. In this sense, creation of transgenic plants could prove, once again, its worth in leading basic research a significant step forward. Additionally, transgene RNAi knockout plants will help to understand causal links between global genome regulation and stress adaptation.

Future progress in systems biology and virtual experiments will no doubt help us to understand how plants work to overcome abiotic stress. However, since models always carry the danger of multiplying underlying minor errors according to the rules of chaos, it will be wise to remember limitations and the potential for misleading. An interdisciplinary glimpse at globally applied computer simulations and their limitations in reliably predicting future perspectives in economy, though based on very well-studied data of the economy markets, may serve as a powerful warning.

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