

Technology is plenty for the Plant under Abiotic and Biotic Stress

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ABSTRACT

Plants also suffer adverse environmental conditions such as abiotic stresses which dramatically change the distribution of plants within ecological niches and reduce crop yields. Biotic and Abiotic stresses are among these causes, one of the most significant factors that modify the physiology of plants significantly and help to reduce crop productivity. They caused inhibit plant growth, and most crop plants cannot be properly cultivated except in the event of death. In order to improve them, we will need to update our future technologies. Abiotic and biotic typically play an important role in damaging crop growth. Most Plant research focuses on development although there is often a direct link to the functionality of technology in plant tolerance development. Technologies can allow the maintenance of abiotic and biotic stress. This analysis focuses on whether we can develop our technology. So maybe we can solve these crop-damaging issues to a significant extent and we can get healthy plants to feed these populations.

Keywords: Technology, Biotic and Abiotic stress

INTRODUCTION

In areas where agricultural production is drastically reduced, crop plants typically undergo either one or two biotic and/or abiotic stresses leading to large yield gaps. Soil salinity is one of the stresses which dramatically reduce agricultural production. The World FAO / UNESCO Soil Map (1970-80) has shown 20% of land to be irrigated with salt, with around 2,one percent of all dry land farms affected by salt. The current salinity-impacted area is unknown, but over one-third of the total irrigated area is estimated. With increased irrigation, soil salinization often rises steadily semi-arid and arid zones. Furthermore, about 805 million people suffer from chronic undernourishment despite global hunger-reduction⁶. In addition; the world's population has grown so exponentially that 9.5 billion is expected to be reached by 2050⁷. Roots are able to sense the physical and chemical parameters of the soil and to change their efficiency and growth accordingly play a critical function in sustaining the plant's nutritional and developmental functions under abiotic stress¹. Roots are more vulnerable to abiotic stress than the aerial parts of the plant, for example, dryness, water supply and salt stress, as the interface between plant and soil². Root plasticity under salinity stress is the secret

to handling stressful environments, since root surfaces are first exposed to environmental stress³. The stress of salinity is often known as hypertonic stress. Na⁺ and Cl⁻ ion accretion in plant tissues exposed to soils with high NaCl concentrations are one of the most adverse effects of salinity stress. Entering both Na⁺ and Cl⁻ in cells causes serious ion imbalances and excess uptake can lead to major physiological disorder(s). High Na⁺ inhibits the absorption of K⁺ ions which is an important element for growth and development, leading to reducing efficiency and even death⁴. The formation of salt-induced ROS can lead to oxidative damage in various components of the cell, such as proteins, lipids, and DNA, which can disrupt plant essential cellular functions. Genetic variations in salt tolerance are present and the degree of salt tolerance varies among plant species and species. Barley (*Hordeum vulgare*) is more resistant to salt than rice (*Oryza sativa*) and wheat (*Triticum aestivum*) among major crops. Dicotyledons ranging from highly sensitive *Arabidopsis thaliana* to halophyte salinity like *mesembryanthemum crystallinum*, *Atriplex* sp. and *Thellungiella salina* (formerly known as *T. halophila*) have an even greater degree of variation⁵. In this review, we will concentrate on our technology which we use to handle major

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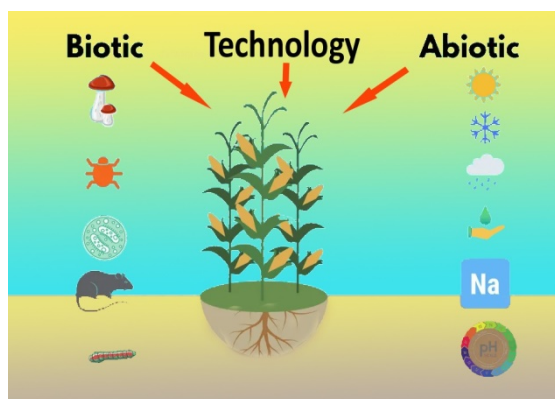
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plant problems in the future by means of this technology, but we need to develop our technology even further

GENE APPROACH CANDIDATE

Since basic processes, like plant growth and mechanisms for a Stress reaction, follow similar paths in different plant species, model species, genes can be expressed directly in non-model plant breeding species and/or serve as candidate genes for the recognition of orthologs. Species that are non-model⁸. Several salt stress-responsive researchers were able to classify approaches through both forward and reverse genetic approaches at a genome-wide scale. Genes in different models and non-model species, for example, Wu and colleagues use the forward genetics approach⁹. The primary protective response in plants that retards the toxic effects of high cytoplasmic Na^+ is root cell exclusion. The comparison between unidirectional Na^+ absorption streams and the rate of Na^+ net accumulation in the root indicates that the great majority of the Na^+ absorbed in the root symplast is returned to an apoplastic and soil solution. In both *Arabidopsis thaliana* and her relative halophytic *T. Salsuginea*, this Na^+ cycling is like 77–78 per cent of Na^+ roots taken up¹⁰. The main differences in Na^+ tolerance between *A* were concluded. *Thaliana* and *Salsuginea* was due to a significantly higher Na^+ influx in *Arabidopsis thaliana*. This observation is consistent with the findings of other parties that *SOS1* is necessary for Na^+ but *SOS1* is overexpressed by either *Arabidopsis thaliana* or *T. Salsuginea* does not improve the Na^+ tolerance significantly¹¹. The Na^+/H^+ plasma membrane *Arabidopsis* genome sequence was used to identify *AtNHX1* utilizing sequence homology with the characterized animal Na^+/H^+ exchanger (NHE) family and *ScNHX1* yeast¹². *AtNHX1*, the heterologous overexpression, suppressed the salt-sensitive phenotype in a mutant yeast *nhx1* and gave *Arabidopsis* as well as tomato and *Brassica* salt tolerance¹³. This underlines the preserved essence of the salinity response, not only the 'candidate gene' approach to identifying orthologs is therefore highly important genomics' method for gene identification/discovery in different genes. Figure 1.

Figure1: Here we see how affect abiotic and biotic can can be for plants. If we can't control it with the help of technology, it may become a problem in the coming time. There is an urgent need to control technology.



RNA

RNA-mediated silencing is one of the most common approaches to gene accessibility. In this case, gene silencing generally includes gene expression downregulation, mediated by small RNAs (sRNAs) divided into two classes: small interfering RNAs (siRNAs) and microRNAs (miRNAs), by targeted downregulation of the accumulation of transcripts¹⁵. Silencing by transgenic expression of sRNAs was also widely used in gene characterization. For example, by RNAi interference, *OsNAC5* knockdowns¹⁶. *OsNAC5* demonstrated positive regulation of abiotic stress response in rice. Likewise, Ouyang and colleagues grow transgenic RNAi rice¹⁷. Rice tocopherolcyclase had a constructive regulatory function in resisting salt stress¹⁸. The *Thellungiella salsuginea* *SOS1* gene's RNAi knockdown has been shown to result in increased salt sensitivity and halophytism loss in salt stress transgenics, confirming *ThSOS1* function as an integral halophyte salt tolerance regulator. Various methods have been developed for silencing sRNA-mediated genes, and the mechanisms and discrepancies between them and applications are beyond the scope of this paper but have been extensively reviewed elsewhere¹⁹. Most methods include post-transcription silencing, however, DNA methylation (RNA-directed DNA methylation) or chromatin modifications may be used to suppress gene expression²⁰. Hence, RNAi is a valuable method for determining gene function in crop plants. Compared to mutagenesis, it's a concentrated approach with little background effects noise. Crossing back to wild plants, therefore, is not acceptable. Furthermore, sRNA-mediated gene silencing is a specific sequence, so it is possible to simultaneously delete multiple redundant genes from the family simply by targeting retained regions of the gene family. With awareness on endogenous sRNAs exponentially increasing due to the contribution of NGS technologies, RNA-mediated gene silencing has also evolved tremendously. Additionally, artificial microRNAs (amiRNAs) have added more traction to the field. Computational tools such as the Web MicroRNA Designer (WMD) and the PsRNA Target were advance that greatly simplified amiRNAs design, particularly for model plant species such as rice, *Arabidopsis*, poplar, etc²¹.

CRISPR/CAS9

The CRISPR / Cas9 system has been developed in recent years to ensure accurate, convenient and efficient genome editing²². In order to increase the crop resistance and to improve tolerance of major abiotic strains, such as drought and salinity, CRISPR / Cas9 based genome editing was used. Below is a description of CRISPR's use the genome editing

RICE

Rice (*Oryza sativa*), a major staple food crop for over half the world's population, is well studied and, due to its small genome size, serves as a model crop for monocots. Recent trials have illustrated the use of the CRISPR approach to genome editing, and very few studies have reported the use of genome editing to increase biotic and abiotic stress for rice cultivation.

The genome of rice has a profusion of possible PAM sites (1 in 10 bp)²³. Therefore, CRISPR technology will theoretically be used to target any rice genome interest in the near future²⁴. The genomic modification of three genes, the phytoenadesaturase (OsPDS), and the betain aldehyde of hydrogenase (OsBADH2) of the gene with mitogen-activated protein kinase (OsMPK2) genes, have been demonstrated in sequence-specific CRISPR and Cas9 for the first time in any crop plant using both protoplast and particle-bombed rice calli systems. Nearly 9% and 7% of the OsPDS and OsBADH2 editing Level respectively²³. A demonstrated approach to RNA genome editing by developing two vectors suitable for the rice genome editing pRGE3 and pRGE6. For targeted mutagenesis, OsMPK5 selected three gRNAs, a negative regulator for rice stress, and abiotic stress, and tested in rice protoplasts recorded a lower off-target amount using a more accurate gRNA process.

CRISPR / Cas9 evaluated the efficiency and heritability of selective mutation induction systems for a variety of genes such as OsDERF1, OsPMS3, OsEPSPS, OsMSH1, OsMYB525. A significant variance in mutation rates (21–66%) was observed in T0 generation with no or 1 bp off-target mutation and in T2 generation up to 11% of homozygous mutants. Targeted editing of the herbicide foundation, C287 rice with activation-induced cytidine deaminase (Target-AID) was made possible²⁶. D-Cas9 fused with cytidine deaminase was used without DSBs for simple editing²⁷. Precise genome editing in rice, wheat, and maize²⁸. Base editing with the BE3 Reference Editor of OsPDS and OsSBEIIb genes and BE3 base editor is an improved genome-editing tool that incorporates nicked cas9 (9-D10 mutation), a cytosine deaminase (D10), and an inhibitor of uracil glycosylase (UGI), which prevents the repair of base-excision. This study has shown that rice base editing is effective. CRISPR / Cas9 also enables multiplex genome editing of possible genes that are unregulated²⁹ and previously observed in Arabidopsis and rice.

ARABIDOPSIS

CRISPR / Cas9-based target genome editing was first illustrated in Arabidopsis³¹. CRISPR / Cas9 Five A genome editing. PDS3 (PHYTOENE DESATURASE), AtFLS2 (FLAGELLIN Responsive 2), CYCD3 (CYCLIN D-TYPE 3), RACK1 (RECEPTOR FOR ACTIVATED C KINASE 1-AtRACK1b and AtRACK1c) were examined in protoplasts³². The variability in mutational output may be attributed to the binding strength of sgRNA or chromatin structure. This study also showed the efficiency of many GRNAs in gene editing. As the floral dip in Arabidopsis is the preferred mode of transformation, tissue-specific promoters and terminators are used to obtain germinal mutants³³. The germ-line-specific Cas9 (GSC) the system was developed for Arabidopsis via 5' regulatory sequences of three genes (SPOROCTELESS, DD45 and LAT52) from Arabidopsis, targeting Cas9 expression-driving floral organs. The proportions of heritable mutations were significantly increased, the proportion of chimaera decreased, and the diversity of mutations increased in aT2 generation provided for the CRISPR / Cas9 system's specific genetic screening of mortal or other predicted mutations of Arabidopsis. The

TUMV virus is a destructive viral disease in field-grown crops. Loss-of-function mutations in the eukaryotic translation factor, eIF4F translation complex, are associated with stable resistance to many potyviruses. In the Arabidopsis eIF(iso)4E region, CRISPR / Cas9 genome editing was implemented to successfully create sequence-specific deleterious point mutations to ensure maximum TuMV resistance.³⁴ CRISPR / Cas9 is more effective than traditional breeding since only mutations are produced in the target gene without altering other genes. Negative regulatory genes with the desired function and the need for PAM (-NGG) CRISPR / Cas9 system sequence type restriction are, however, uncommon. Conventional root growth has the advantage of enhancing the complex characteristics, while CRISPR / Cas9 have the benefit of mutagenesis of the main genes. This study, therefore, shows that combined with traditional root growth in CRISPR/Cas9 technology could be a very effective new method for improving crops.

COMPUTER SOFTWARE AND DATABASES

Genome sequences for a wide variety of plant species including tomatoes, potatoes, barley, maize, and wheat were compiled using NGS technologies, but the characteristics and coverage of those genomes differ depending on the consistency and coverage of Arabidopsis and rice³⁵. This increase in sequenced genomes created a large number of web-based databases for sequenced genome organisms. These databases became an important resource for global plant biologists³⁶. Databases provide a quick and determined method for identifying putative genes involved in the response to stress through the sequence and structure homology in salinity stress-related studies, as well as similar patterns of expression with known salinity-sensitive genes of the same or other species. Note, however, that data collected from databases are merely estimates and must be verified by biological tests. However, based on observations prior to target gene recognition studies, these databases can provide a starting point for experiments or may be used as tools for determining selections³⁷. Rearing for abiotic stress tolerance such as salinity can be the remedy for can growth in stressed areas. Since plant responses to abiotic stress, such as salinity, are complex, multigenic in nature, usually involving hundreds of genes, breeding approaches to stress tolerance and plant stability have proven challenging. Using marker-assisted breeding / marker-assisted breeding helped simplify things to this point.

MARKER ASSISTED SELECTION

Marker Assisted Selection (MAS) uses markers such as a certain phenotype, chromosome bandage, a specific DNA or RNA motive, or a chemical tag incorporating the desired feature³⁸. NGS, association genetics, and other innovations have become a standard for marker breeding support. New breeding practises including gene pyramidization, QTL pyramidization, recurrent marker-assisted selection (MARS), and genome-wide selection are typically performed using MAS. Marker helped breed to grow crops with biotic stress tolerance and increase grain quality in cereals³⁹. With complex features like salinity tolerance, MAS wasn't as successful. A genome-wide selection,

however, seems a promising approach to breeding salinity tolerance with high-density maps available. Cultivation with exotic wild relatives can seem another way to achieve tolerant salinity lines. Exotic wildlife has evolved to withstand several stresses concurrently with yield costs. Exotic wildlife species breeding is also an interesting way to learn. The possible success of this strategy can be seen by developing a highly salt-tolerant rice variety in wild relative *Oryzacoarctata* with elite variant *Oryza sativa*-IR5640. While it can be challenging and time-consuming with a very low likelihood of success, the attempt to achieve the extraordinarily high salinity tolerance seems worthwhile in this case.

CONCLUSION

The effect of climate change on plants is profound. These include biotic and abiotic strains that can seriously damage plants. It is necessary to recognize the current obstacles and to develop suitable solutions. Via current Modern technology, we can better manage these obstacles. We can understand the plant better and we can be effectively monitored. The high cost of technology will continue to be a major obstacle to the adoption in the near future of some crop and plant breeding species in developing countries. Specific technology techniques can need

to be adapted to particular crops, characteristics and budgets. New technology could reduce the obstacle to the plant. If the feasibility of new technologies is confirmed and the crop can be easily obtained, technology can become more widely applicable to crop breeding programs.

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