

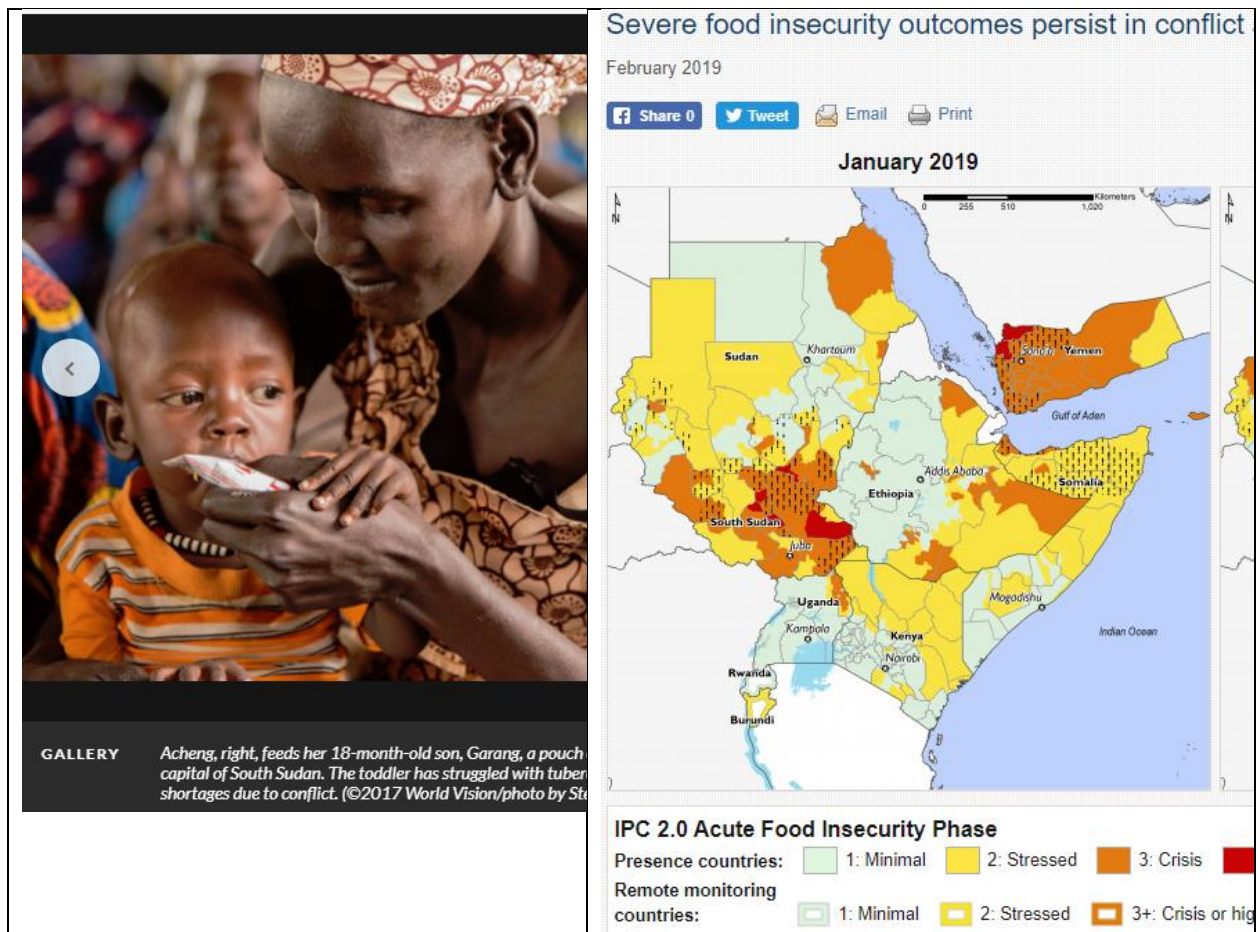
A Study of DREB2A Drought Tolerance on Maize Crop

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Background and Significance

Some countries in Africa such as South Sudan, Kenya and Ethiopia are plagued with chronic hunger. Setting political conflict aside, recurring severe drought is a major abiotic contributor to food shortage in this part of the world. Climate change significantly affects Africa crop production and consequently livelihood of most the population who heavily depend on agriculture [1].

With the advancements made in the last few decades, genetically modified crops that can tolerate drought can be introduced to alleviate hunger and revitalize the eco system in the vulnerable regions.



Studies have shown that transcription factors (TFs) dehydration-responsive element-binding protein (DREB), abscisic acid (ABA)-responsive element-binding (AREB), NAM (no apical meristem), ATAF (Arabidopsis transcription activation factor) and CUC (cup-shaped cotyledon) play an important role in

regulation of stress responses and tolerances [2]. The overexpression of these key genes can enhance the stress of tolerance of certain crops. The drought avoidance (Osmotic Stress) and drought tolerance (Heat/Cold Stress) network are shown in in Figure 1.

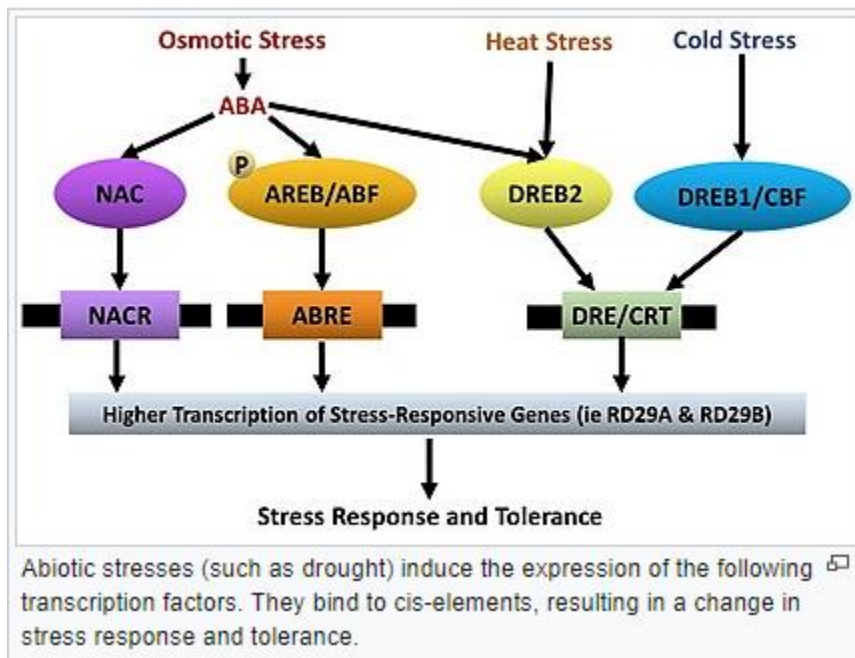


Figure 1 - Transcriptional network for environmental stress condition in plants

Proposal

It has been shown that gene DREB2A encodes a transcription factor (TF). The TF binds to the DRE/CRT cis elements responsive to drought. The overexpression of the DREB2A is an effective drought stress tolerance [5].

This study proposal is to enrich DREB2A drought resistant gene and use epigenetic mechanism on DNA binding to histones to alter the gene expression of maize which is a main staple crop in Africa. Though there are several amino acids that can be used to modulate histones and DNA packing. This study is focused on the acetylation of lysine. The Acetyl-Coenzyme A [4] is used catalyze in the lysine acetylation. The enzyme is added at different rates to the lysine group, and the effectiveness can be analyzed visually and RNA-Seq from Illumina NGS platform [6]. Ultimately the collected information can be used to determine the most effective genetic variant of maize that can be cultivated for the drought nations.

Scope and Methodology

Considering the environmental conditions including soil composition, it is best that the study can be done locally in a greenhouse - perhaps with a government partner of the impacted country. The greenhouse should be equipped with heating control to induce drought stress.

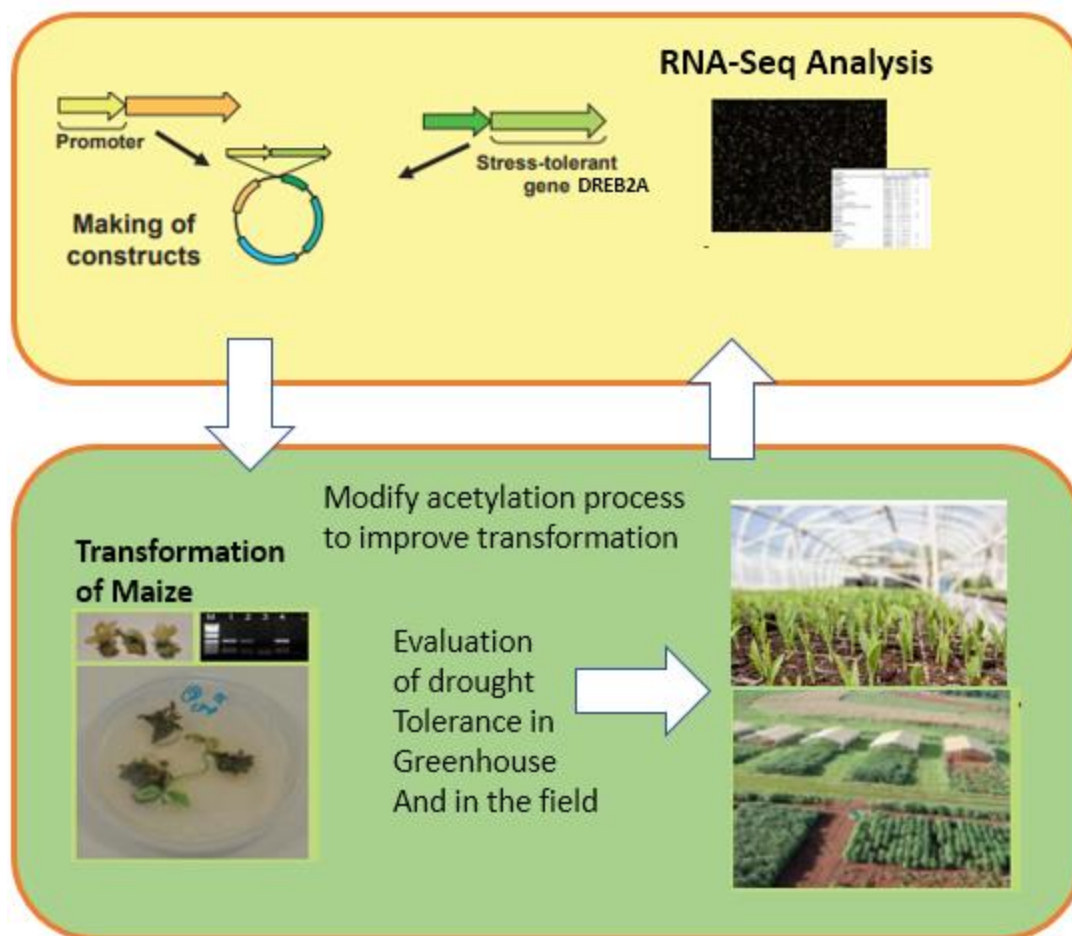


Figure 2 - Overview of maize genetic modification for drought tolerance

Figure 2 shows the process steps of the genetic modifying maize for optimal drought tolerance. The process includes a schedule of enzyme A with different amount added to catalyze the reaction on DREB2A gene histones for each cycle. Acetylation is designed to modulate the histones removing the negative charges making them more loosely packed with the DNA. This would enable the transcription machinery to turn on gene expression.

The shoot and root samples can be harvested for analysis preparing for the next cycle. RNA sequencing can provide insights into changing expression levels as drought condition is introduced leading to adjustments to the enzyme amount added or reduced in the next cycle. The process can be repeated to for optimization.

To speed up the process, multiple setups with different enzyme rates can be run in parallel. The results including the RNA-Seq can be clustered and analyzed. Subsequent runs can be optimized from previous data sets.

The end goal is to achieve the optimal DREB2A gene expression with the right chemistry for acetylation on the histones and DNA packing.

Risk Factors

There are other factors that can affect drought tolerance such length of drought, severity, temperature, and soil water depth [3]. Controlling a combination of drought-tolerance from osmotic and temperature sensitive genes would be more viable than a single gene.

Another risk factor would be the specific environmental conditions for each area considering the vast size of Africa. The soil and climate conditions for example in Ethiopia may be quite different than of Kenya making the modified seeds less effective if the conditions deviated from those of targeted location.

References

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