

Resilience challenges in agriculture

The climate change threat

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Peter Donaldson/Alamy Stock Photo

Technologies that can support yields of staples like rice in a warming world should be a priority for crop development efforts.



The Joint Research Unit for Genomics Applied to Climate Change

The challenges of climate changes

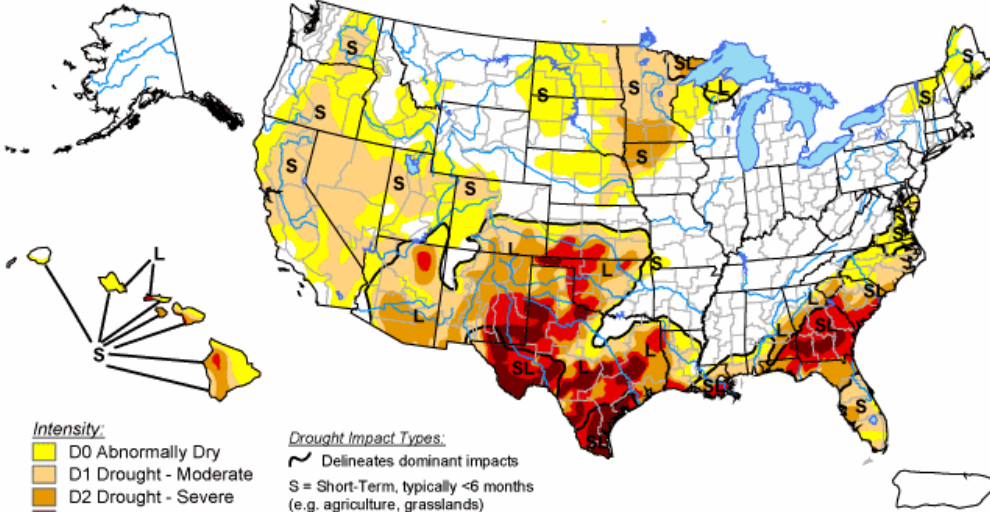
- Global climate change poses a major threat to agricultural production and food security worldwide and especially in the tropics..
- Understanding the dynamics of molecular responses to stresses can be used to develop new stress-resistant genotypes.
- The commercial production of advanced biotechnology plants is concentrated in a few agricultural biotechnology giants. Currently, 3-4 companies control 80% of seed production on a global scale.
- The biotechnology giants operate genetics on an industrial scale, through pipelines of genetic improvement / biotechnology and regulatory issues expertise.
- Modern genome editing technologies that are not susceptible to regulatory barriers open up huge opportunities for the diversification and fragmentation of the seed production sector.
- **There is a need to organize R&D activities to explore genome edited crop improvement to face the challenges of climate change.**



The need for drought tolerant crops

U.S. Drought Monitor

January 31, 2012
Valid 7 a.m. EST



Intensity:
 D0 Abnormally Dry
 D1 Drought - Moderate
 D2 Drought - Severe
 D3 Drought - Extreme
 D4 Drought - Exceptional

Drought Impact Types:
 ~ Delineates dominant impacts
 S = Short-Term, typically <6 months
 (e.g. agriculture, grasslands)
 L = Long-Term, typically >6 months
 (e.g. hydrology, ecology)

The Drought Monitor focuses on broad-scale conditions. Local conditions may vary. See accompanying text summary for forecast statements.

<http://droughtmonitor.unl.edu/>



Released Thursday, February 2, 2012
 Author: Eric Luebehusen, U.S. Department of Agriculture

Impact of drought and heat on corn production in the 2012/13 harvest in the USA:
 Loss of 40 Mt, equivalent to the average annual Brazilian corn production between 2005-2010 (49 Mt)
 Losses estimated at US \$ 12 billion



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Drought and heat tolerance is top priority of the agricultural biotechnology giants



Optimum AQUAmax™

- Marker-Assisted Selection
- Launch in 2011
- 9% increase in productivity under severe drought conditions without adverse effects under normal conditions



Genuity DroughtGard™

- GMO - RNA Chaperone (CspB)
- Pre-commercial launch in 2012
- 10% increase in productivity under severe drought conditions without adverse effects under normal conditions

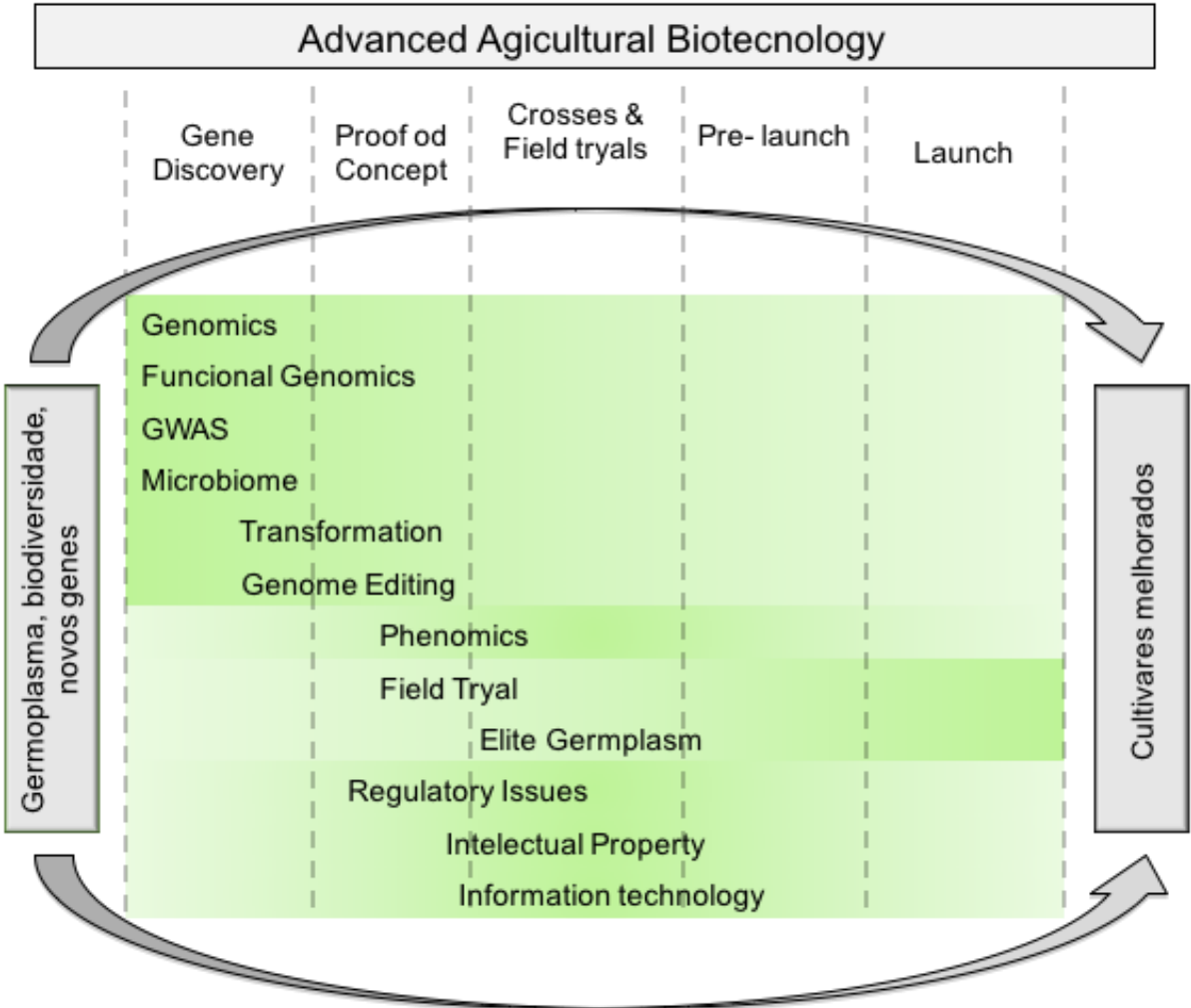


Agrisure Artesian™

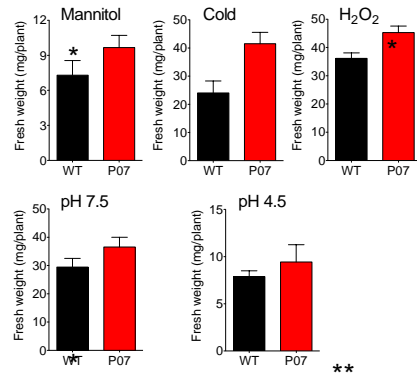
- Marker-Assisted Selection
- Launch in 2011
- 17% increase in productivity under severe drought conditions without adverse effects under normal conditions



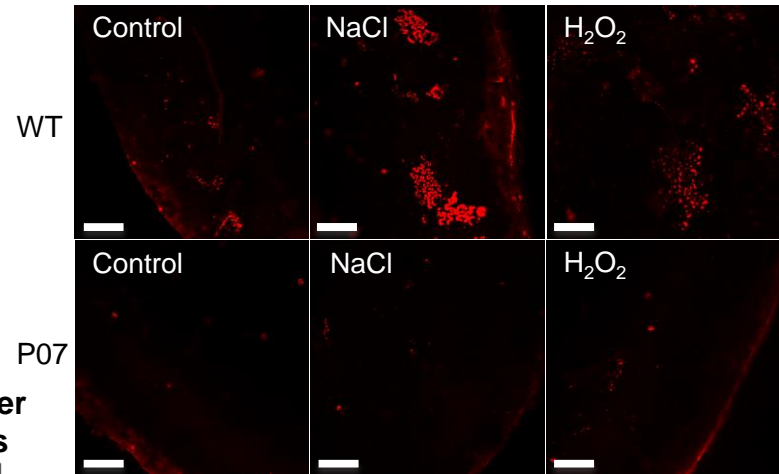
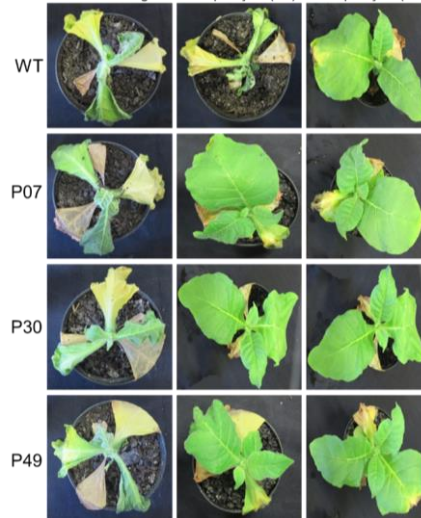
Biotechnology giants operate genetics on an industrial scale



The role of energy metabolism in drought stress resp

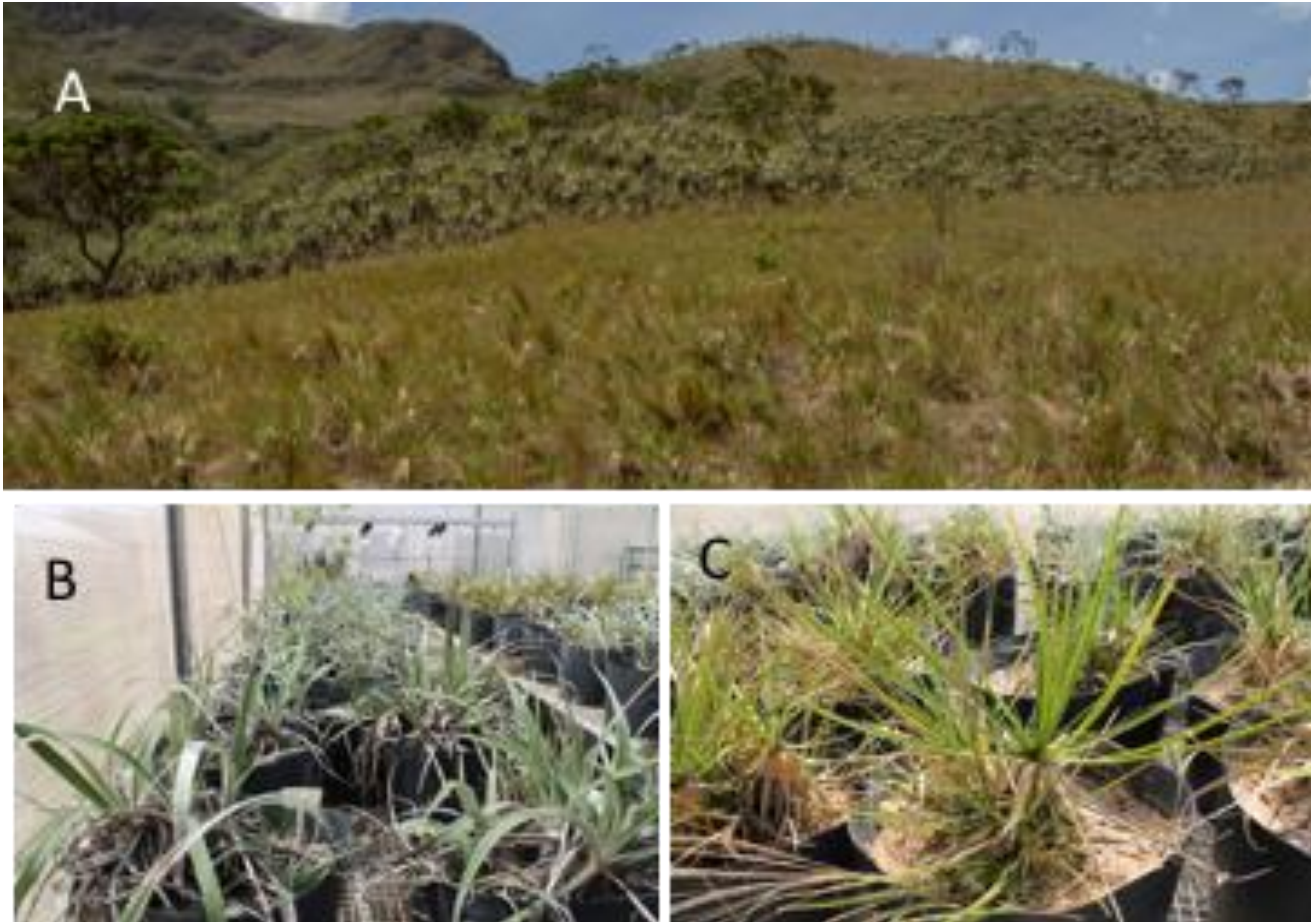


No water 11 days Recover 2 days Recover 4 days



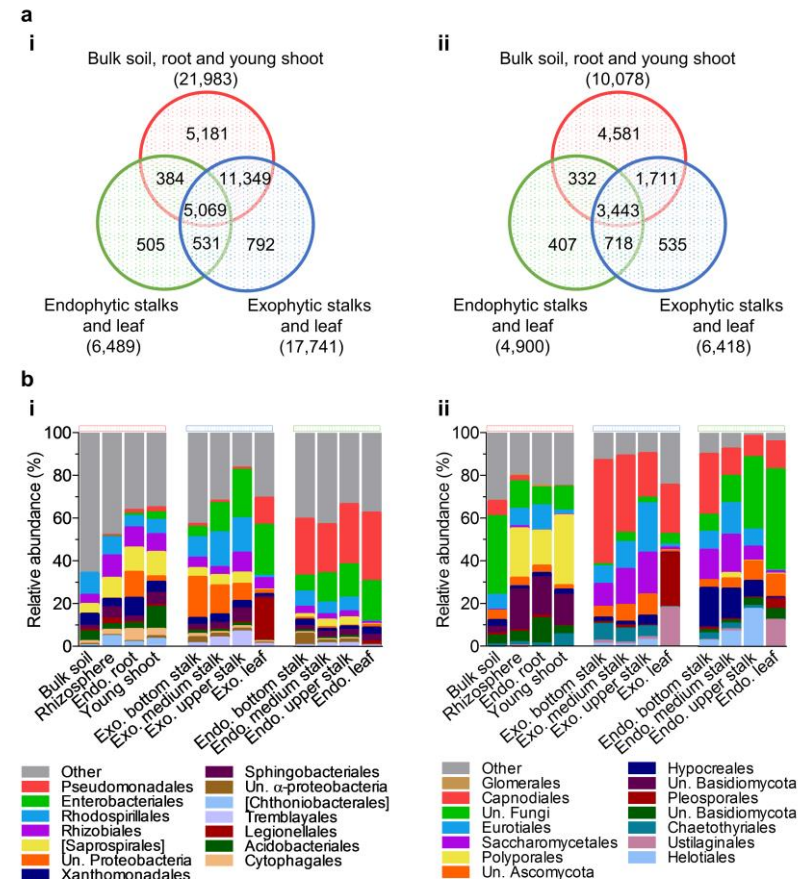
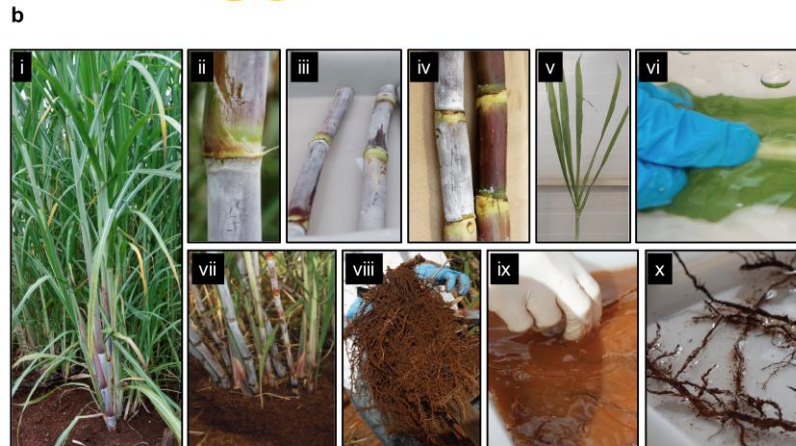
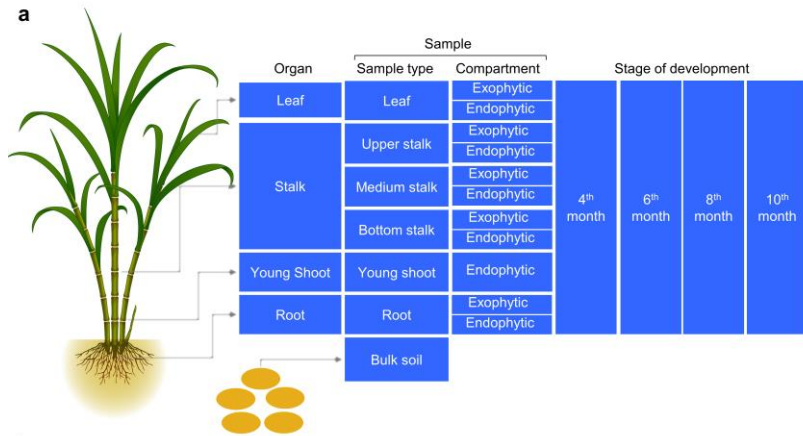
Barreto et al. BMC Plant Biology 2014, 14:144
 Barreto et al. J. Exp. Bot. (2016) 67 (1): 301-313

A look at biodiversity: comparative genomics of wild species



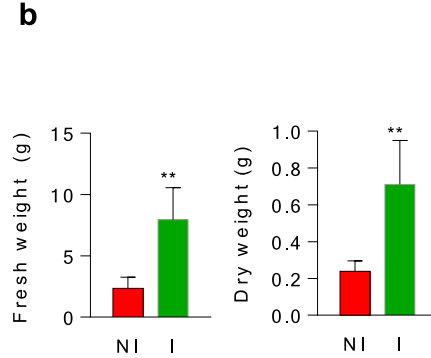
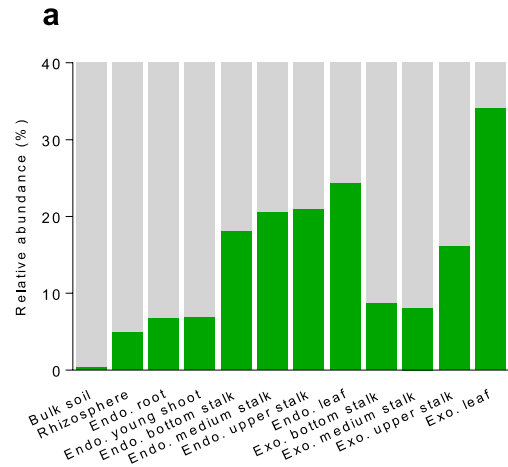
Rock fields and Vellozia species. (A) Plants of *Vellozia intermedia* in rupestre field in Serra da Canastra. (B) *V. nivea* and (C) *V. intermedia* cultivated in greenhouse at the State University of Campinas.

The plant microbiome: a new biology to be explored for stress tolerance mechanisms



de Souza et al. (2016) Scientific Reports 6,
 Article number: 28774, doi:10.1038/srep28774

Community-based culture collection to target plant growth-promoting (PGP) microbes



Drought stress response

Non-inoculated Inoculated



Armanhi et al. (2016) Scientific Reports 6,
Article number: 29543 doi:10.1038/srep29543

Genomic Edition: A revolutionary tool in plant biotechnology

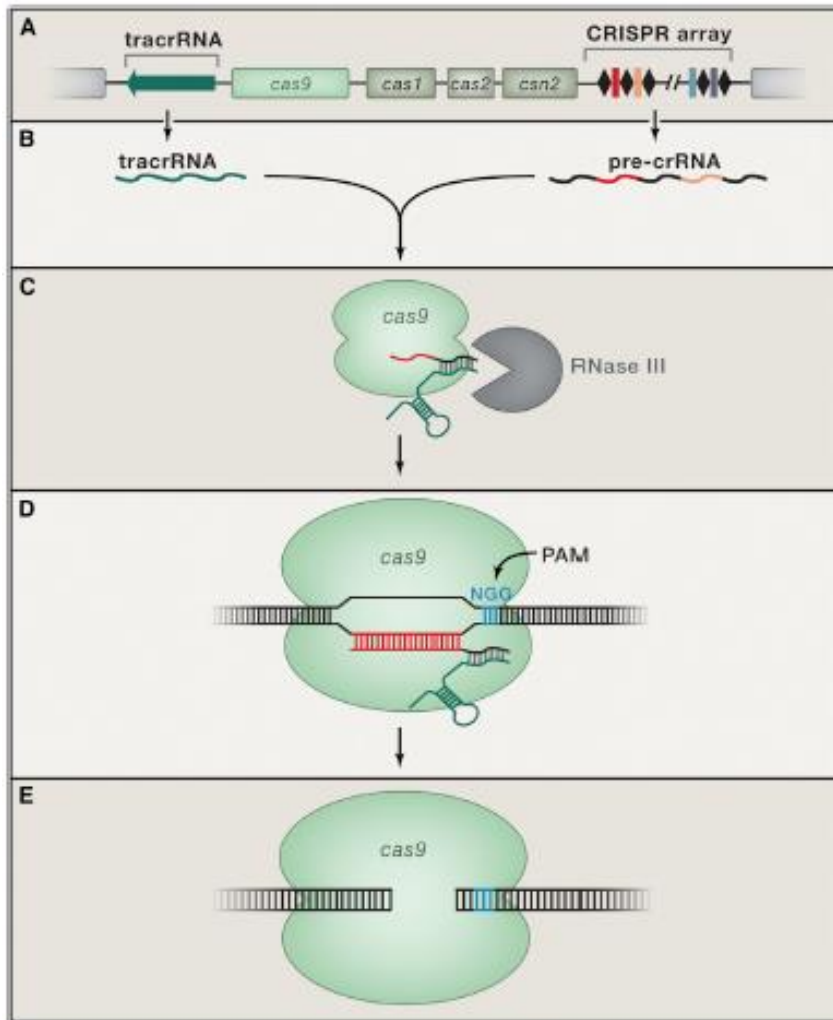


Figure 1. Class 2, Type II CRISPR-Cas9 System from *Streptococcus thermophilus*

(A) The locus contains a CRISPR array, four protein-coding genes (*cas9*, *cas1*, *cas2*, and *cas2*) and the *tracrRNA*. The CRISPR array contains repeat regions (black diamonds) separated by spacer regions (colored rectangles) derived from phage and other invading genetic elements. The *cas9* gene encodes a nuclease that confers immunity by cutting invading DNA that matches existing spacers, while the *cas1*, *cas2*, and *cas2* genes encode proteins that function in the acquisition of new spacers from invading DNA.

(B) The CRISPR array and the *tracrRNA* are transcribed, giving rise to a long *pre-crRNA* and a *tracrRNA*.

(C) These two RNAs hybridize via complementary sequences and are processed to shorter forms by Cas9 and RNase III.

(D) The resulting complex (Cas9 + *tracrRNA* + crRNA) then begins searching for the DNA sequences that match the spacer sequence (shown in red). Binding to the target site also requires the presence of the protospacer adjacent motif (PAM), which functions as a molecular handle for Cas9 to grab on to.

(E) Once Cas9 binds to a target site with a match between the crRNA and the target DNA, it cleaves the DNA three bases upstream of the PAM site. Cas9 contains two endonuclease domains, HNH and RuvC, which cleave, respectively, the complementary and non-complementary strands of the target DNA, creating blunt ends.

Dupont Pioneer develops drought tolerant corn by genomic edition

ARGOS8 variants generated by CRISPR-Cas9 improve maize grain yield under field drought stress conditions

Jinrui Shi*, Huirong Gao, Hongyu Wang, H. Renee Lafitte, Rayeann L. Archibald, Meizhu Yang, Salim M. Hakim, Hua Mo and Jeffrey E. Habben

DuPont Pioneer, Johnston, IA, USA

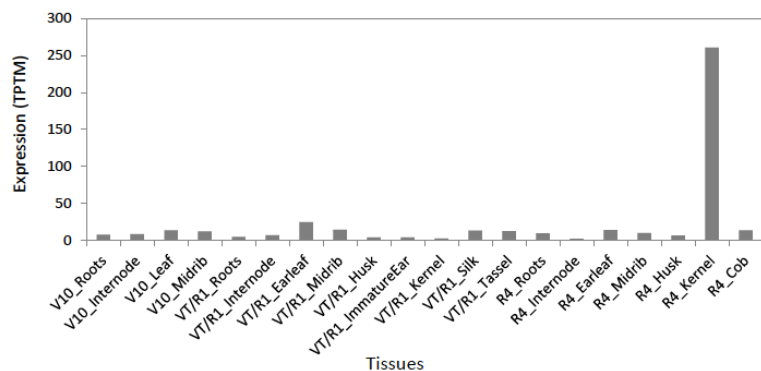


Figure S1. Maize *ARGOS8* gene expression. The transcript abundance of *ARGOS8* in various tissues of maize inbred PH184C was measured by RNA sequencing. Samples were taken from the plants at the developmental stage of V10, VT/R1 and R4. TPTM, transcript per ten million.

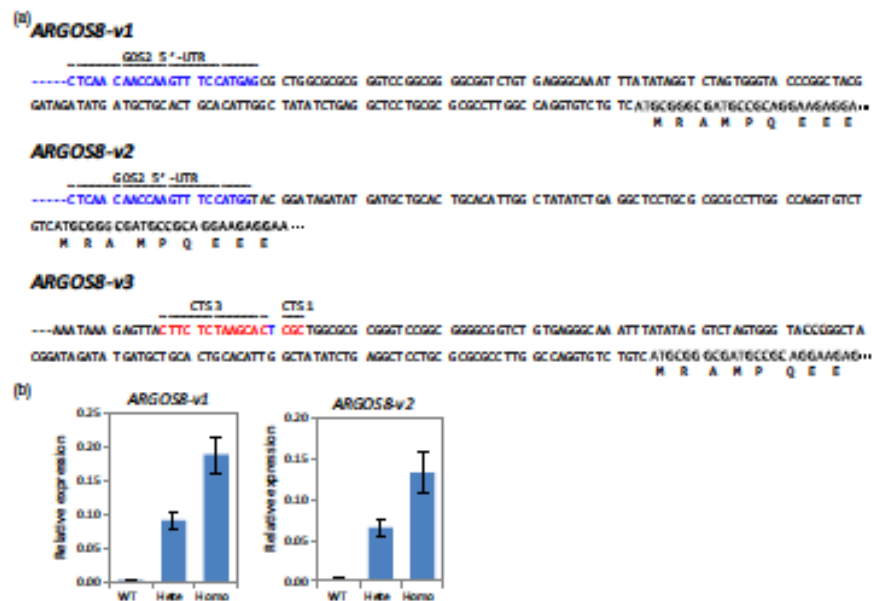


Figure 3 Maize genome-edited *ARGOS8* variants. (a) Genomic sequences upstream of the *ARGOS8* coding region in three genome-edited variants. The entire modification region in homozygous F2 plants was amplified using long PCR, and the PCR products were sequenced. Part of the GOS2 5'-UTR sequence (blue font) and the remaining 5'-UTR of *ARGOS8* as well as the 5'-terminus of *ARGOS8* coding sequence are shown. In the promoter deletion variant *ARGOS8-v3*, the remnant CTS3 and CTS1 sequences are highlighted. (b) Relative expression levels of *ARGOS8* in leaves as measured by qRT-PCR. Means \pm SD are shown for F2 plants of 14-day-old *ARGOS8-v1* and 18-day-old *ARGOS8-v2*; $n = 10-24$. WT, wild-type; Het, heterozygote; Hmo, homozygote.

Table 1 Grain yield of *ARGOS8* genome-edited variants and wild type under flowering stress, grain-filling stress and optimal (well-watered) conditions.

	Flowering Stress	Grain-filling Stress	Optimal
	ton ha ⁻¹ (bushel acre ⁻¹)		
<i>ARGOS8-v1</i>	8.67 (138.0)*	7.67 (119.0)	13.13 (209.0)
<i>ARGOS8-v2</i>	8.67 (138.0)*	7.54 (120.0)	13.19 (210.0)
WT	8.34 (132.8)	7.72 (122.9)	13.01 (207.1)

Data are from two individual genome-edited variants (*ARGOS8-v1*, *ARGOS8-v2*) and wild type tested as one hybrid at eight locations in 2015. Predicted difference for each variant is compared with the wild type. All analyses were implemented using AgrGen with output of the model presented as best linear unbiased predictions (see Experimental procedure).

*Predicted difference significant at $P < 0.1$.

UMiP GenClima team



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