

Estado da arte da biotecnologia agrícola frente aos desafios impostos pelas mudanças climáticas

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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

A Biotecnologia avançada e os desafios das mudanças climáticas

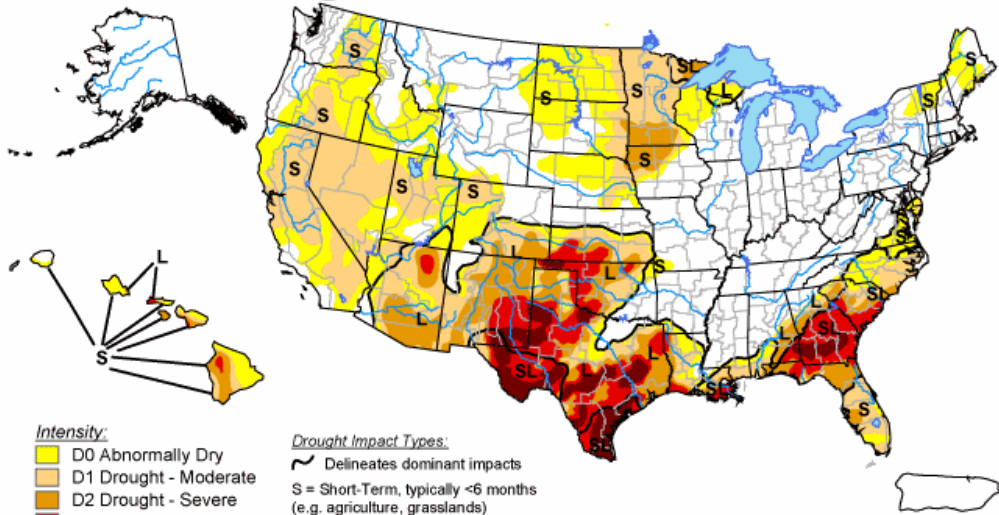
- As mudanças climáticas globais ameaçam a produção mundial de alimentos, com impactos futuros severos nas regiões tropicais e subtropicais.
- A compreensão da dinâmica das respostas moleculares a estresses pode ser utilizada para o desenvolvimento de novos genótipos resistentes a estresses.
- A produção comercial de plantas obtidas pela biotecnologia avançada está concentrada em poucas gigantes da biotecnologia agrícola. Atualmente, 3-4 empresas controlarem 80% da produção de sementes em escala global.
- As gigantes da biotecnologia operam a genética em escala industrial, com *pipelines* de melhoramento genético/biotecnologia e expertise para ultrapassar as barreiras regulatórias.
- Mas, as modernas tecnologias de edição genômica, não susceptíveis a barreiras regulatórias abrem enorme oportunidade para a diversificação e fragmentação do setor de produção de sementes.
- **Será que o Brasil está preparado para organizar atividades de P&D para explorar essas oportunidades e assim se posicionar estrategicamente frente aos desafios das mudanças climáticas?**



Importância da tolerância a seca e ao calor

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

Impacto de seca e calor na produção de milho na safra 2012/13 nos USA:

- Perda de 40 Mt, equivalente a média anual brasileira da produção de milho entre 2005-2010 (49 Mt)
- Perdas estimadas em US\$ 12 bilhões



Tolerância a seca e ao calor é prioridade das gigantes da biotecnologia agrícola



Optimum AQUAmax™

- Seleção assistida por marcadores
- Lançamento em 2011
- Aumento de 9% na produtividade em condições de seca severa sem efeitos adversos em condições normais



Genuity DroughtGard™

- GMO – Chaperona de RNA (*CspB*)
- Lançamento pre-comercial em 2012
- Aumento de 10% na produtividade em condições de seca severa sem efeitos adversos em condições normais

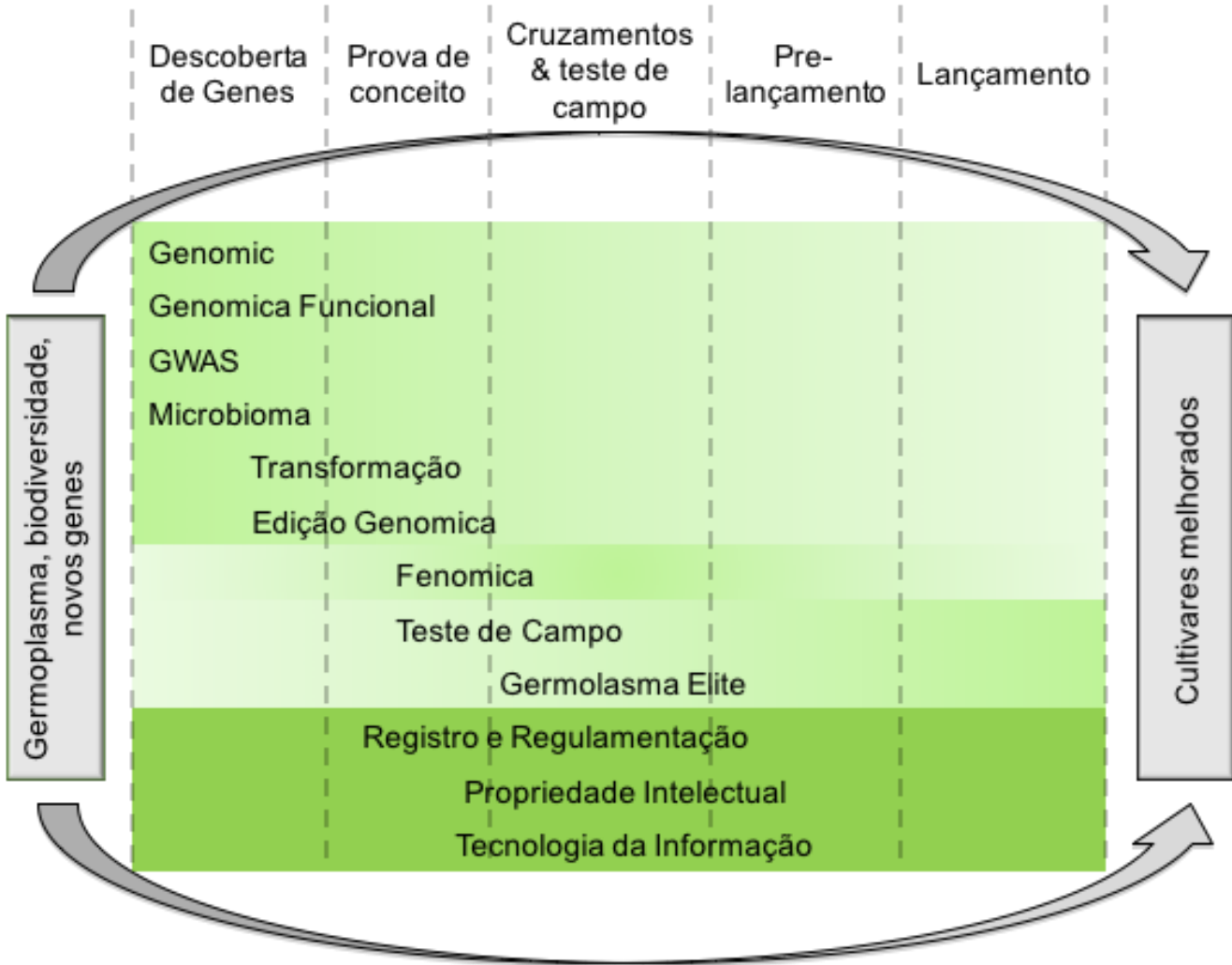


Agrisure Artesian™

- Seleção assistida por marcadores
- lançamento em 2011
- Aumento de 17% na produtividade em condições de seca severa sem efeitos adversos em condições normais



As gigantes da biotecnologia agrícola avançada operam a genética em escala industrial



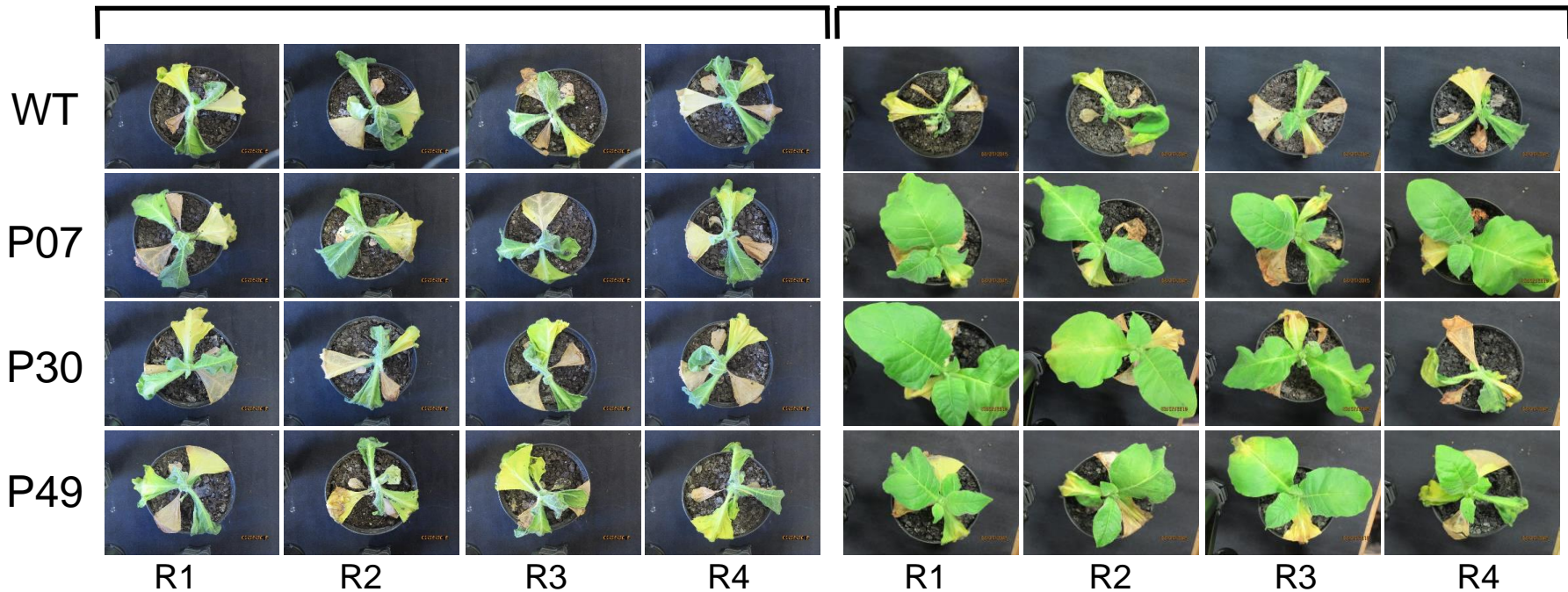
O papel do metabolismo energético na resposta à seca

WT – wild type

P07, P30, P49 – independent events of constitutive *AtUCP1* overexpression

11 days without irrigation

2 days recovery irrigation



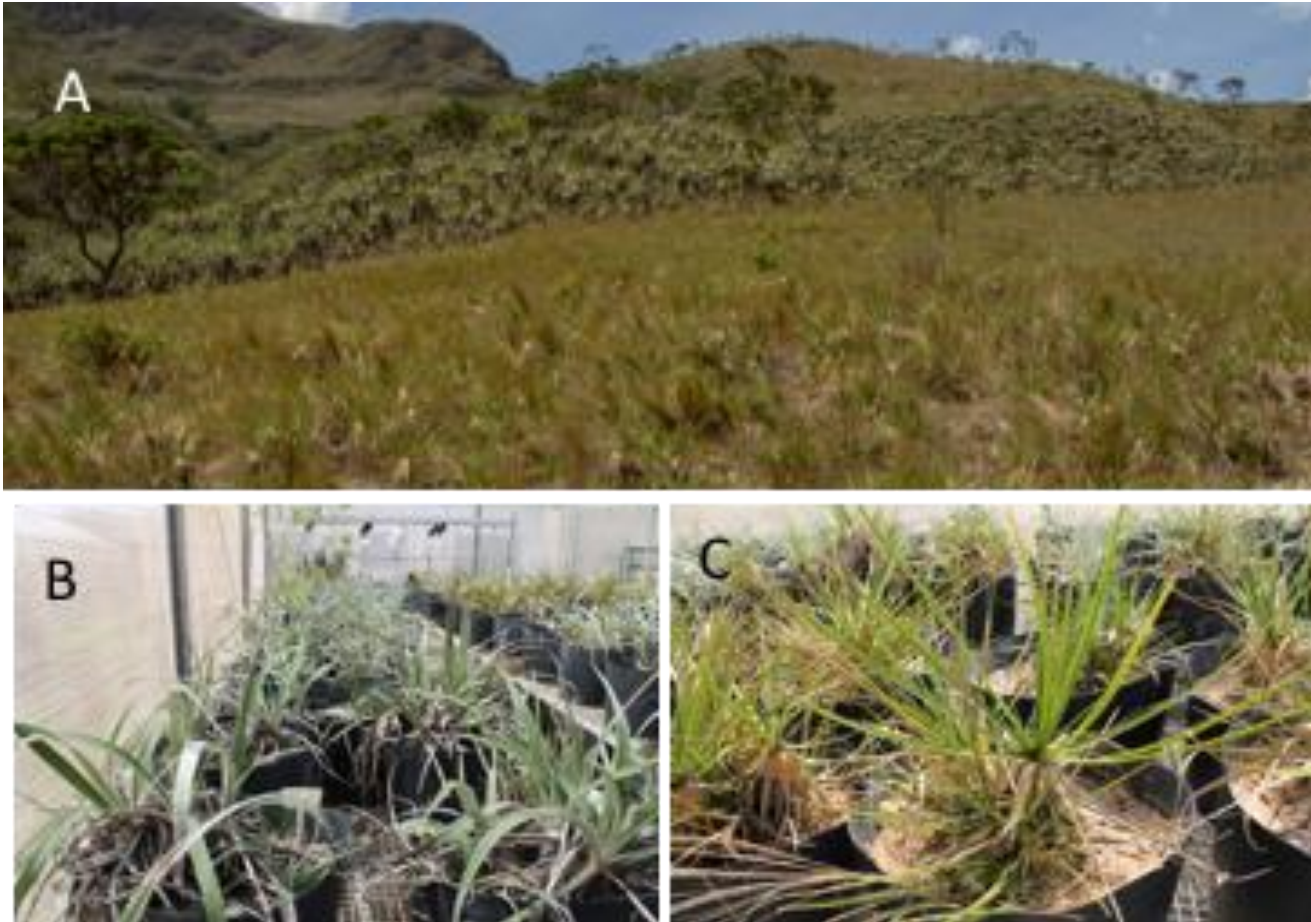
Barreto et al. BMC Plant Biology 2014, 14:144

Barreto et al. J. Exp. Bot. (2016) 67 (1): 301-313



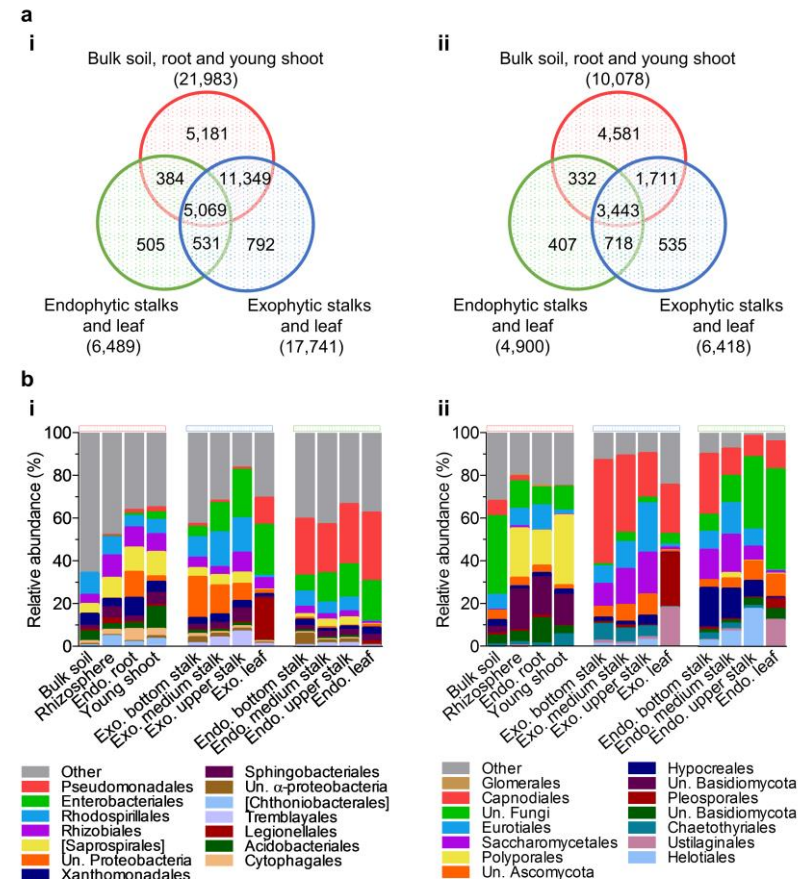
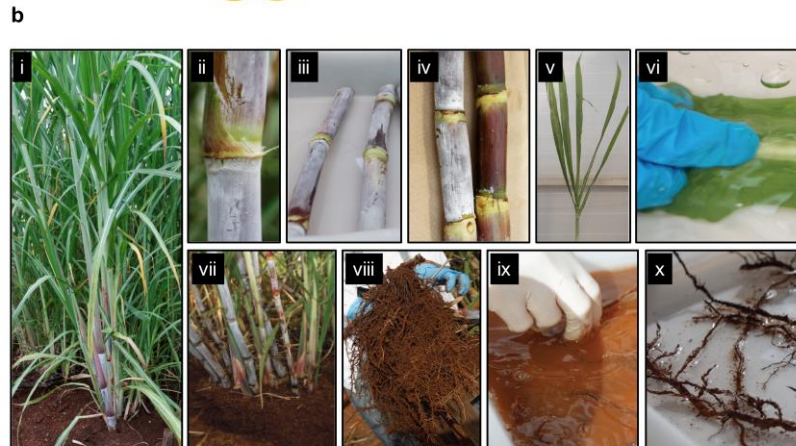
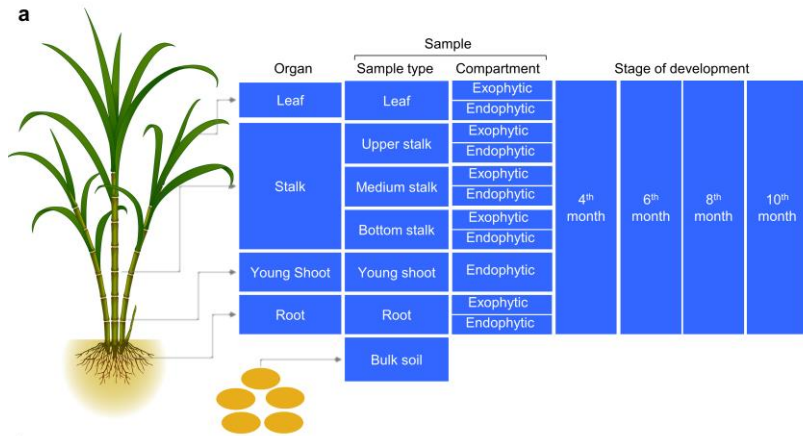
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Um olhar para a biodiversidade: genômica comparativa de espécies selvagens



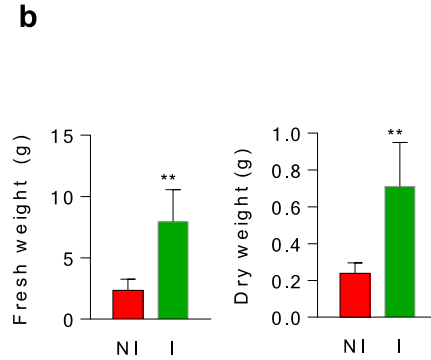
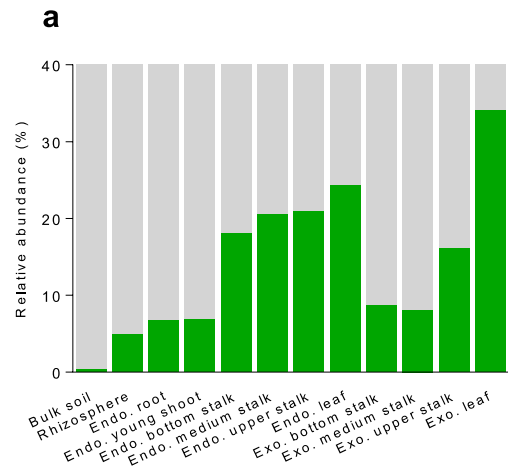
Campos rupestres e espécies de *Vellozia*. (A) Plantas de *Vellozia intermedia* em campo rupestre na Serra da Canastra. (B) *V. nivea* e (C) *V. intermedia* cultivadas em estufa na Universidade Estadual de Campinas.

O microbioma das plantas: uma nova biologia a ser explorada para mecanismos de tolerancia a estresses



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



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

Edição genômica: Uma ferramenta revolucionária na biotecnologia vegetal

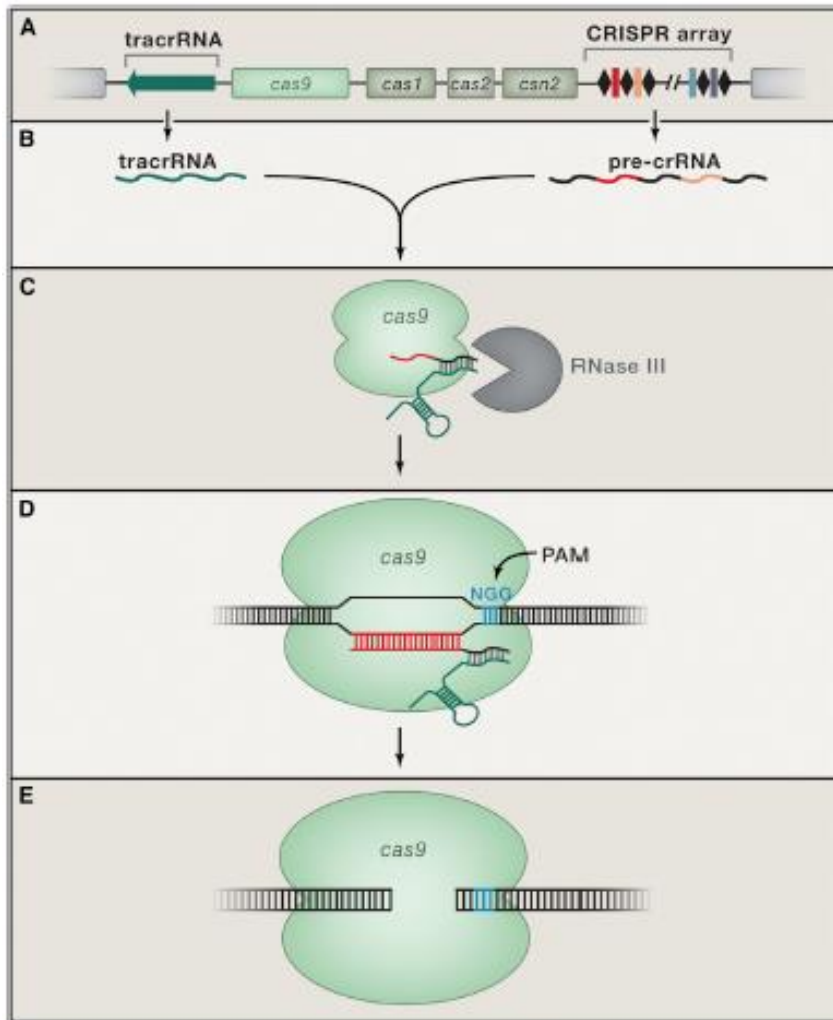


Figure 1. Class 2, Type II CRISPR-Cas9 System from *Streptococcus thermophilus*

(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 desenvolve milho tolerante a seca por edição genômica

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

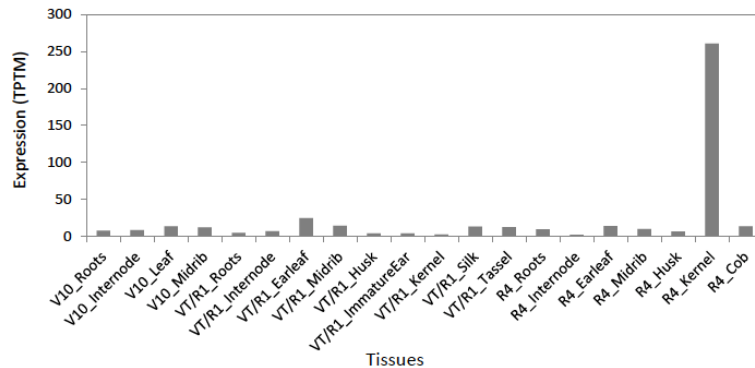


Figure S1. Maize *ARGOS8* gene expression. The transcript abundance of *ARGOS8* in various tissues of maize inbred PH184C was measured by RNA sequencing. Samples were taken from the plants at the developmental stage of V10, VT/R1 and R4. TPTM, transcript per ten million.

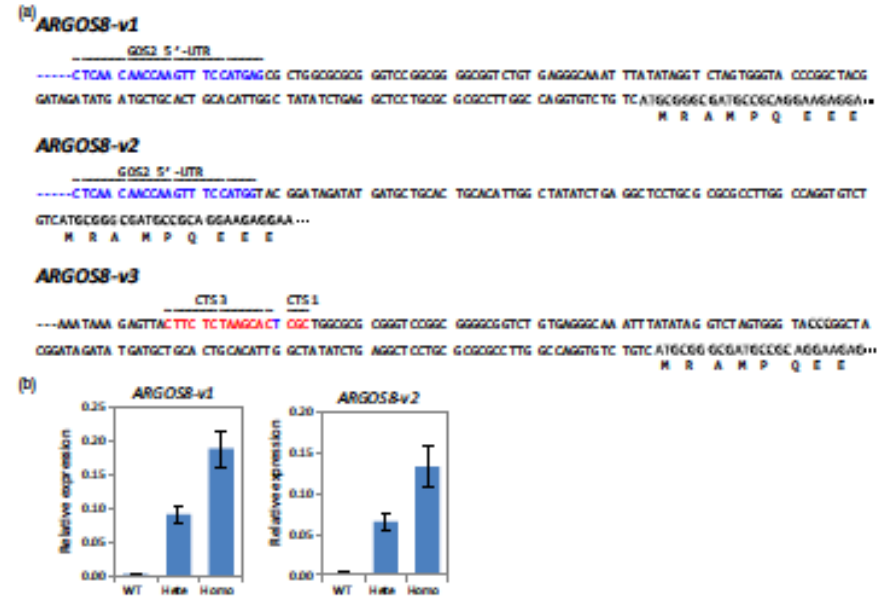


Figure 3 Maize genome-edited *ARGOS8* variants. (a) Genomic sequences upstream of the *ARGOS8* coding region in three genome-edited variants. The entire modification region in homozygous F2 plants was amplified using long PCR, and the PCR products were sequenced. Part of the GOS2 5'-LTR sequence (blue font) and the remaining 5'-LTR 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 AgrEvol with output of the model presented as best linear unbiased predictions (see Experimental procedures).

*Predicted difference significant at $P < 0.1$.

UMiP GenClima team



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