Detlef Weigel

Max Planck Institute for Developmental Biology

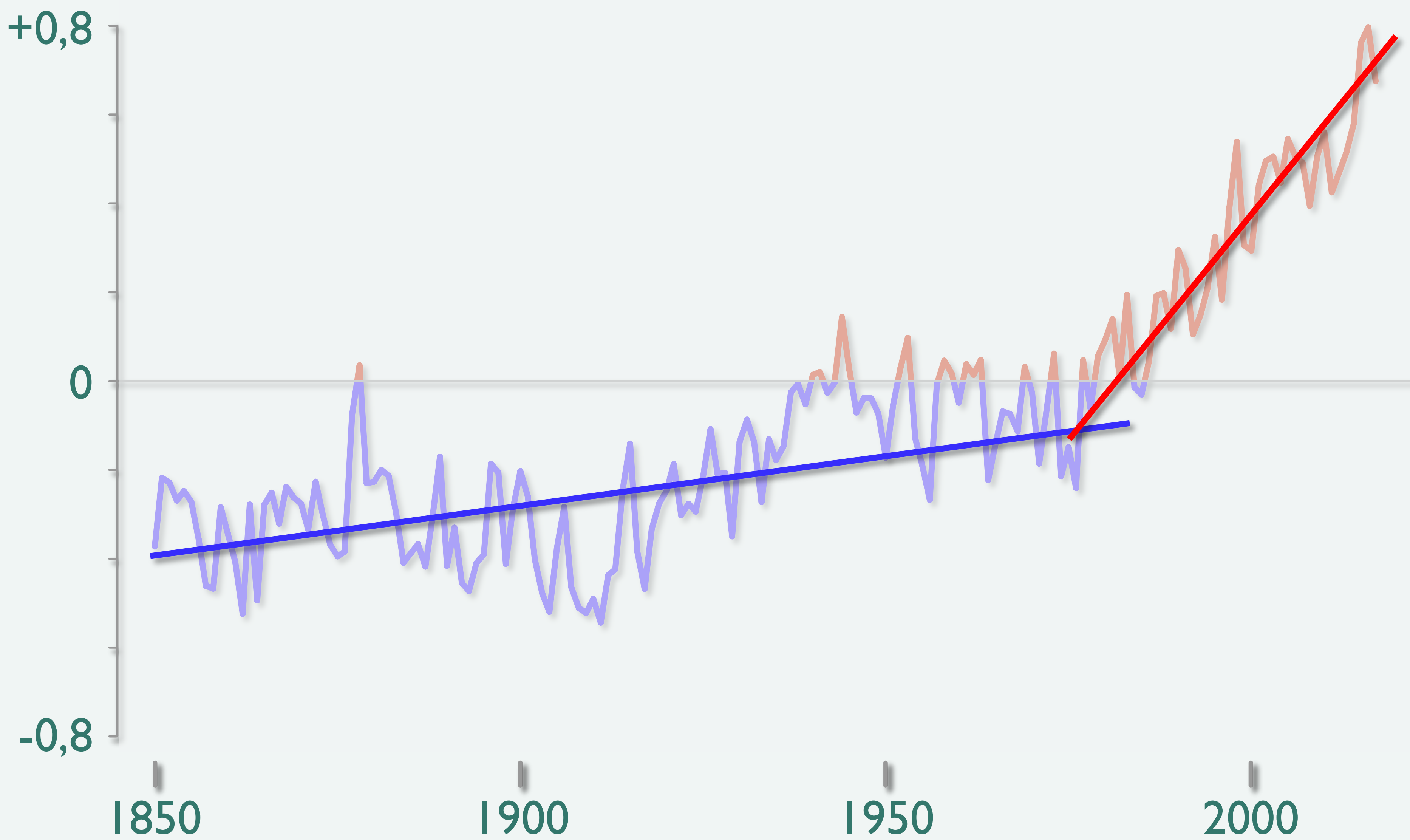
http://weigelworld.org

@PlantEvolution

(I regularly consult for industry)

The World Is Changing

Global deviation from 1961-1990 medium (in °C)



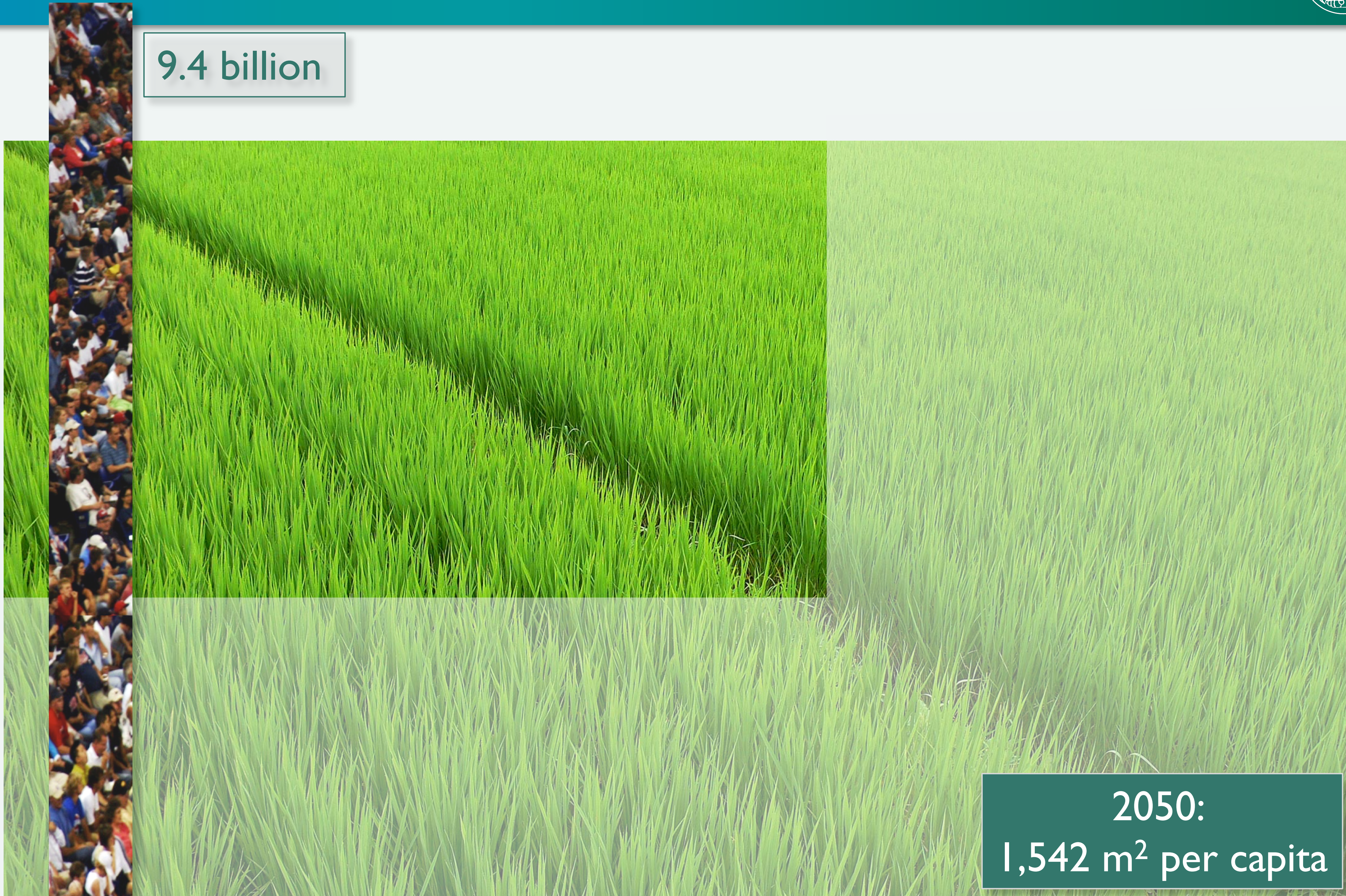
http://www.cru.uea.ac.uk/cru/data/temperature

Agricultural Land Is Shrinking

FAO

Agricultural Land Is Shrinking

9.4 billion

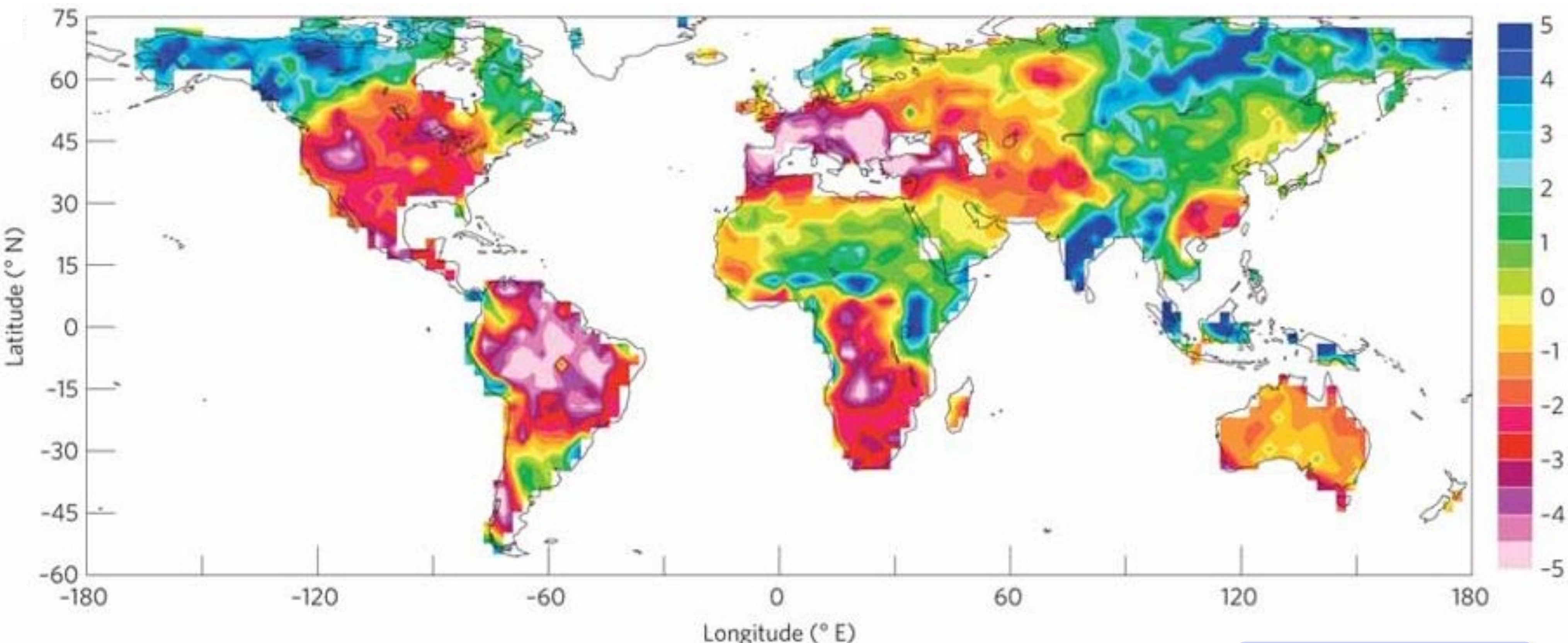


FAO

Fortunately, Yields Have Increased

But we must do better

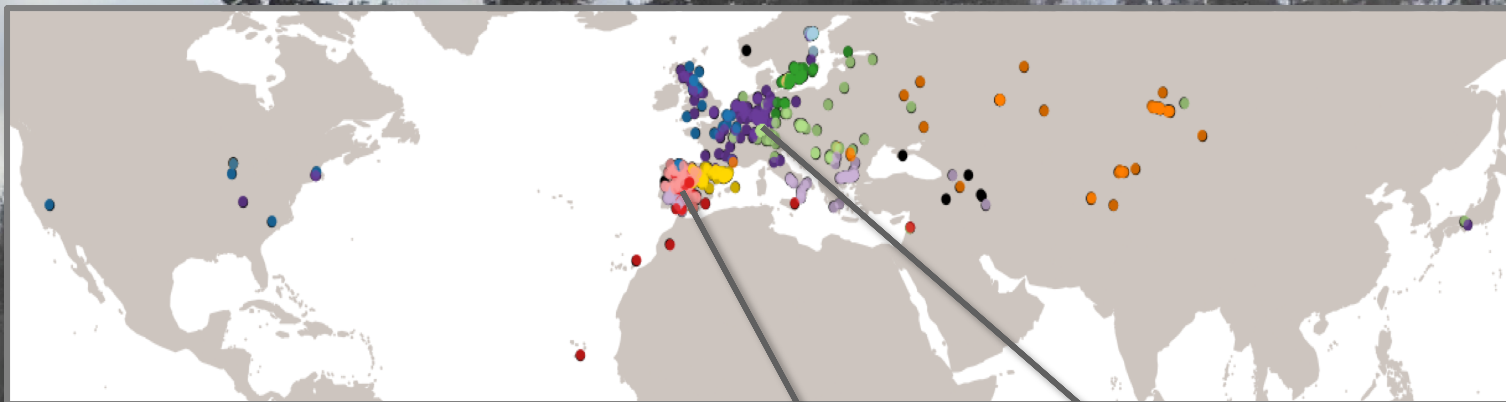
Threat of More Frequent and Extreme Droughts



Dai et al., 2013

self-calibrated Palmer drought severity index (PDSI) 2100 vs. present
”value of −3.0 or below indicates severe to extreme droughts“

Field Experiments in Tübingen und Madrid



Plenty of rain fall: Tübingen

517 *A. thaliana* accession
24,000 pots
October 2015 – May 2016

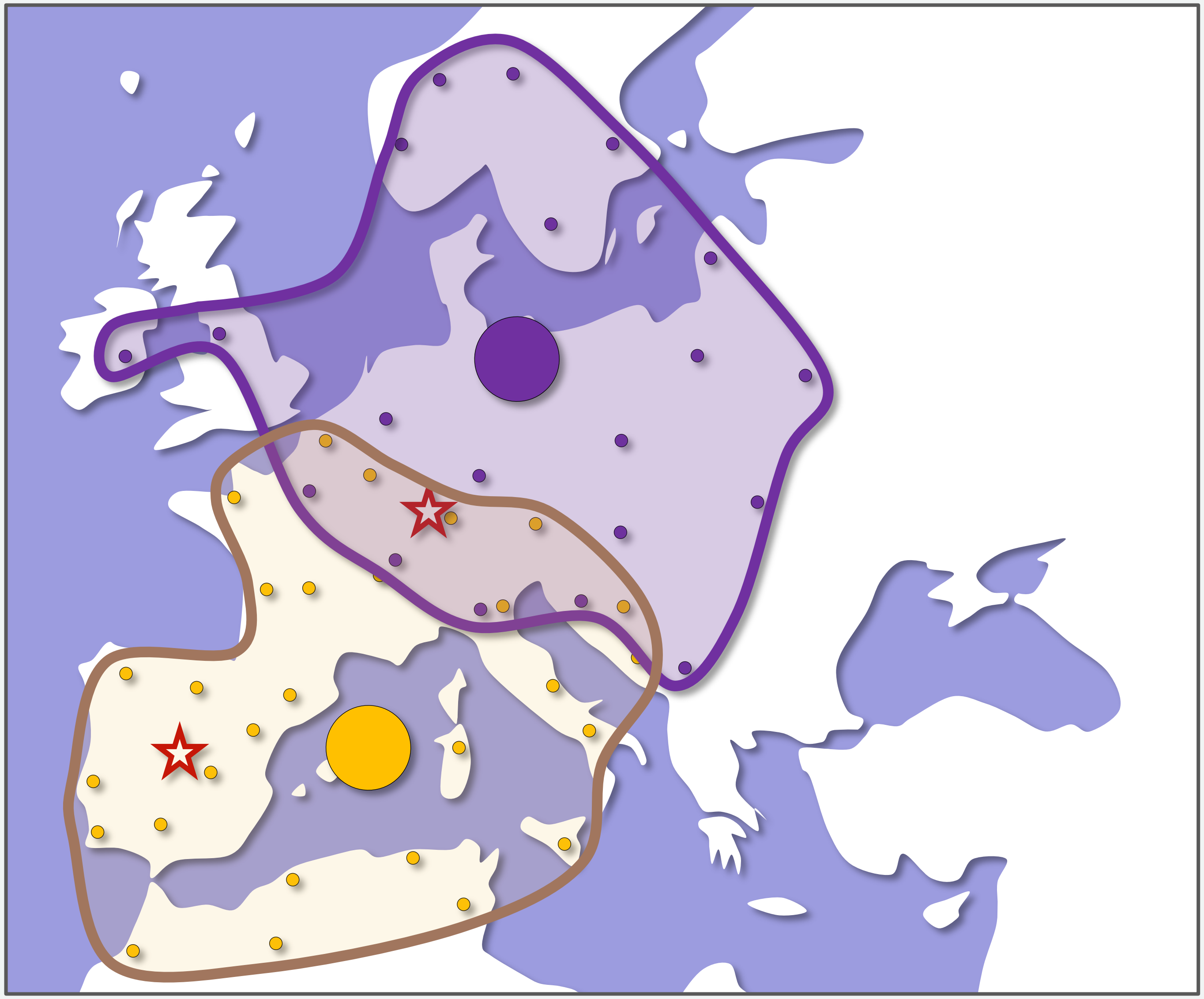
Limited rain fall: Madrid

Survival

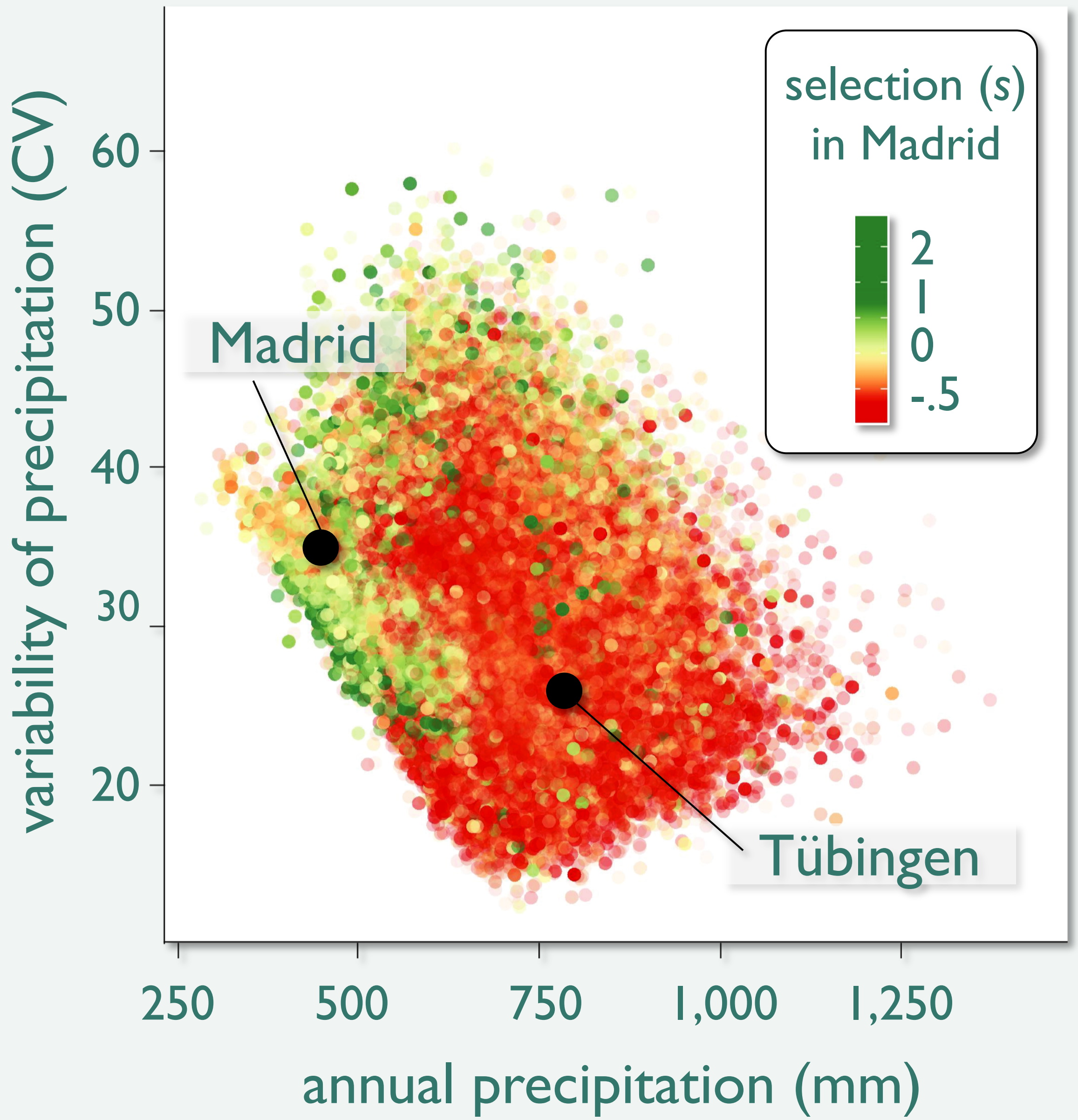
Number of seeds

Survival x progeny = Darwinian fitness

Where Are the Advantageous Variants?



Home Advantage of Genetic Variants



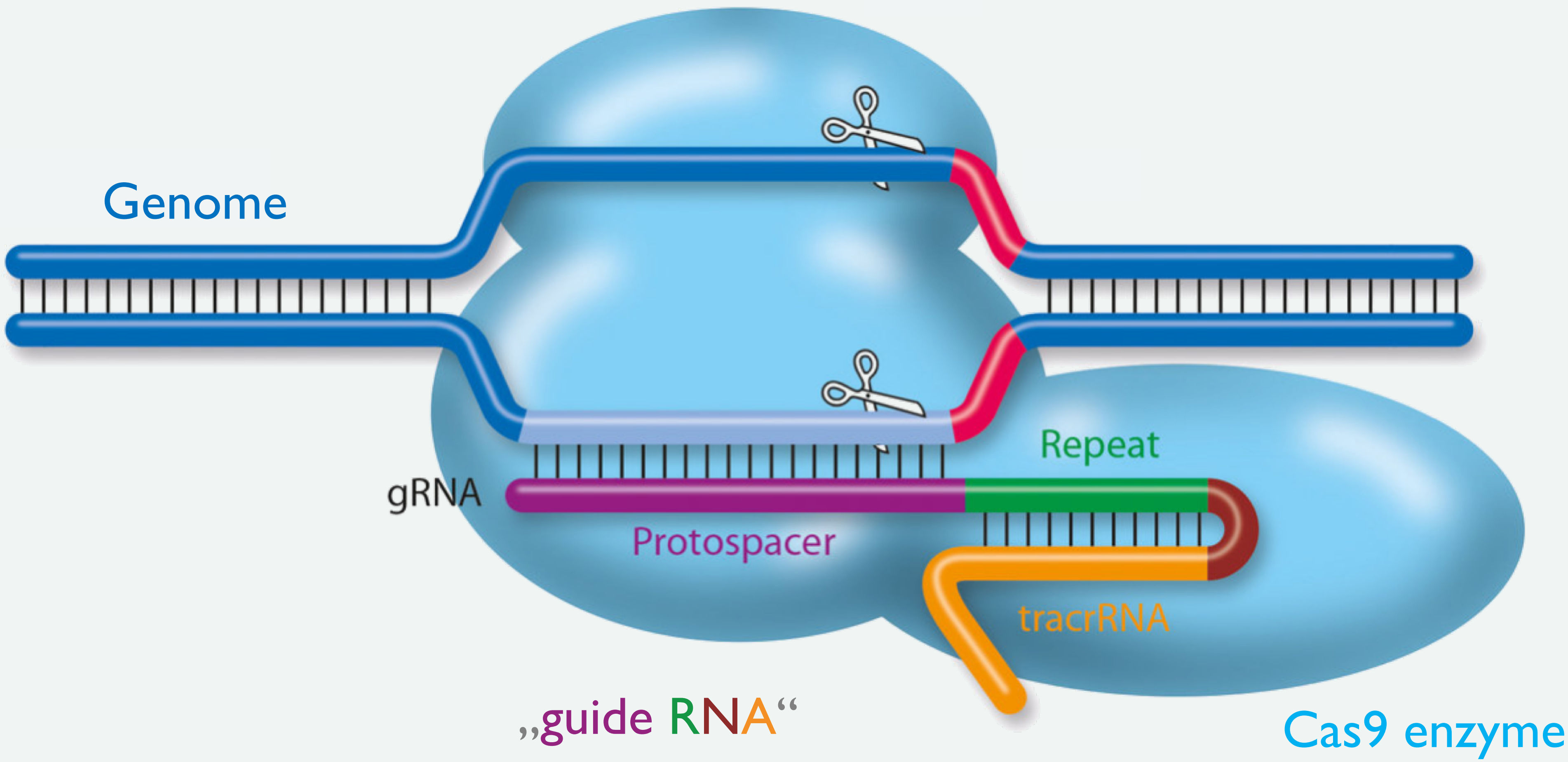
M Expósito
(now Carnegie)

With Burbano, Bossdorf & Nielsen labs

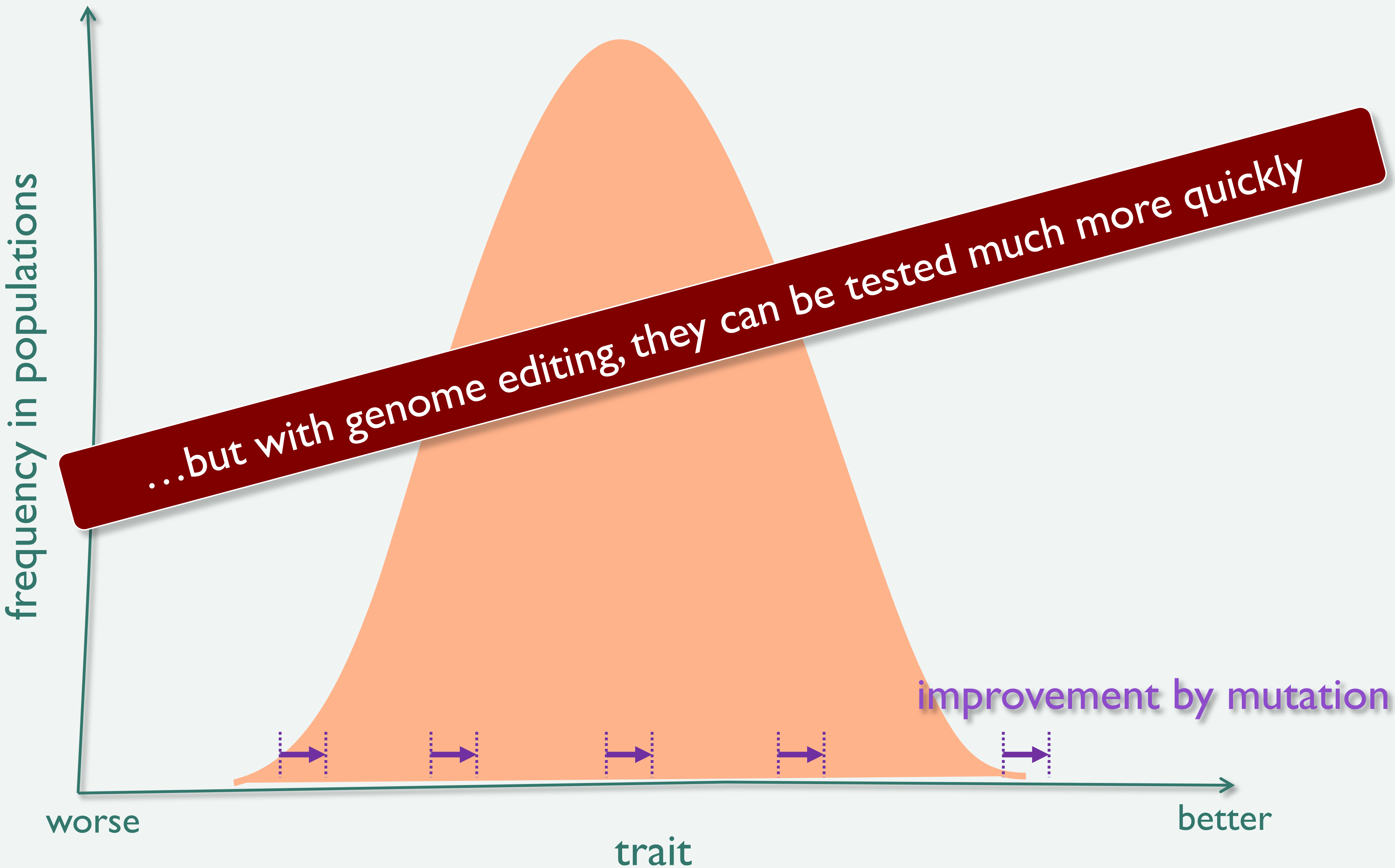
Exposito-Alonso et al. (2019)

How do we get such variants into our crops?

The Promise of Genome Editing



Advantageous Variants Do Not Always Help…



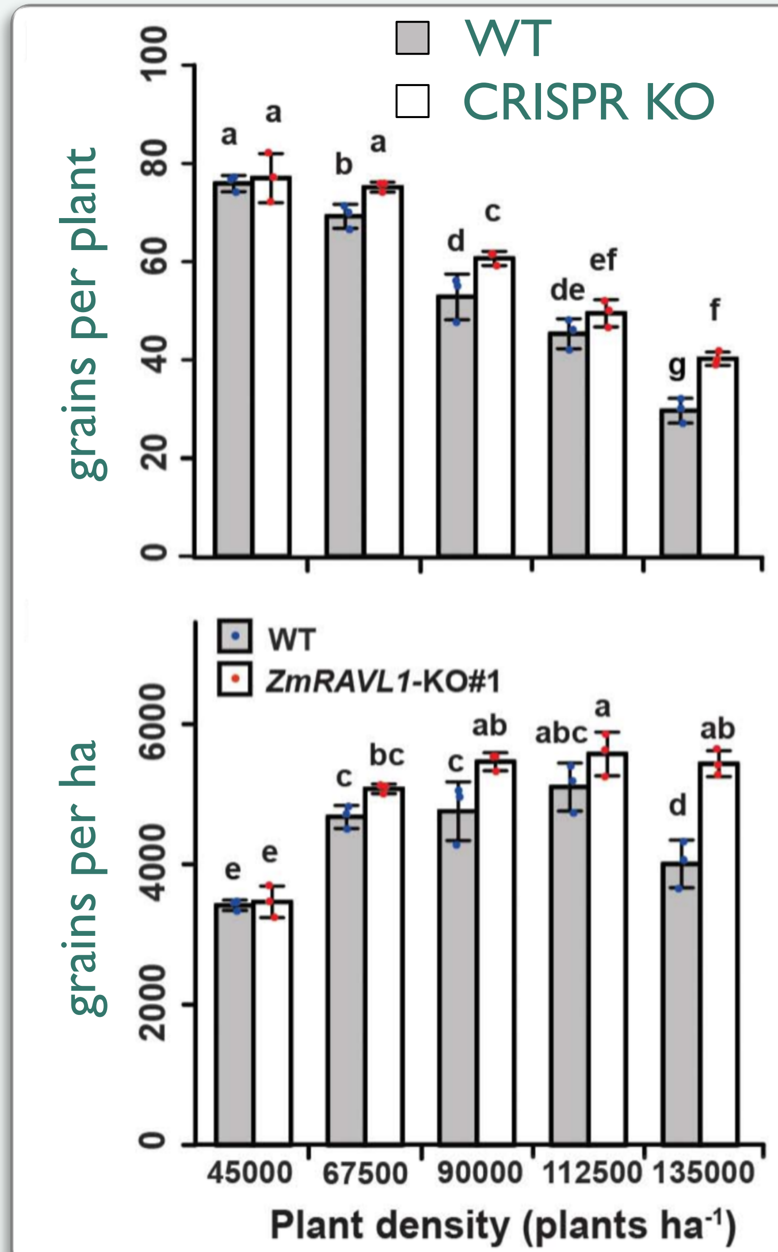
Some recent hits of genome editing

A Genetic Variant Discovered in Teosinte Improves Maize

Teosinte ligule allele narrows plant architecture and enhances high-density maize yields *Science* 2019

Jinge Tian*, Chenglong Wang*, Jinliang Xia, Lishuan Wu, Guanghui Xu, Weihao Wu, Dan Li, Wenchao Qin, Xu Han, Qiuyue Chen, Weiwei Jin, Feng Tian†

teosinte variant (weak) | maize variant (strong)



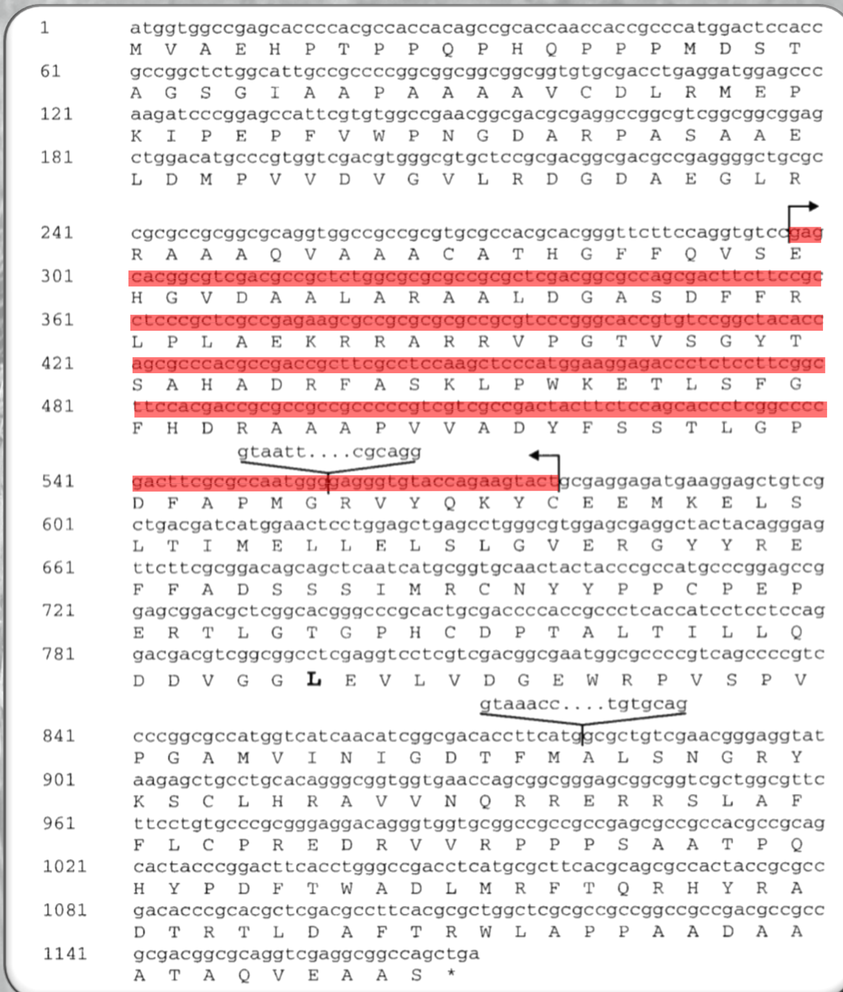
Plenty of Examples of Advantageous Gene Inactivation

Semidwarf (*sd-1*), "green revolution" rice, contains a defective gibberellin 20-oxidase gene

PNAS 2002

Wolfgang Spielmeyer*†, Marc H. Ellis*, and Peter M. Chandler

Division of Plant Industry, Commonwealth Scientific and Industrial Research Organization, GPO Box 1600, Canberra ACT 2601, Australia



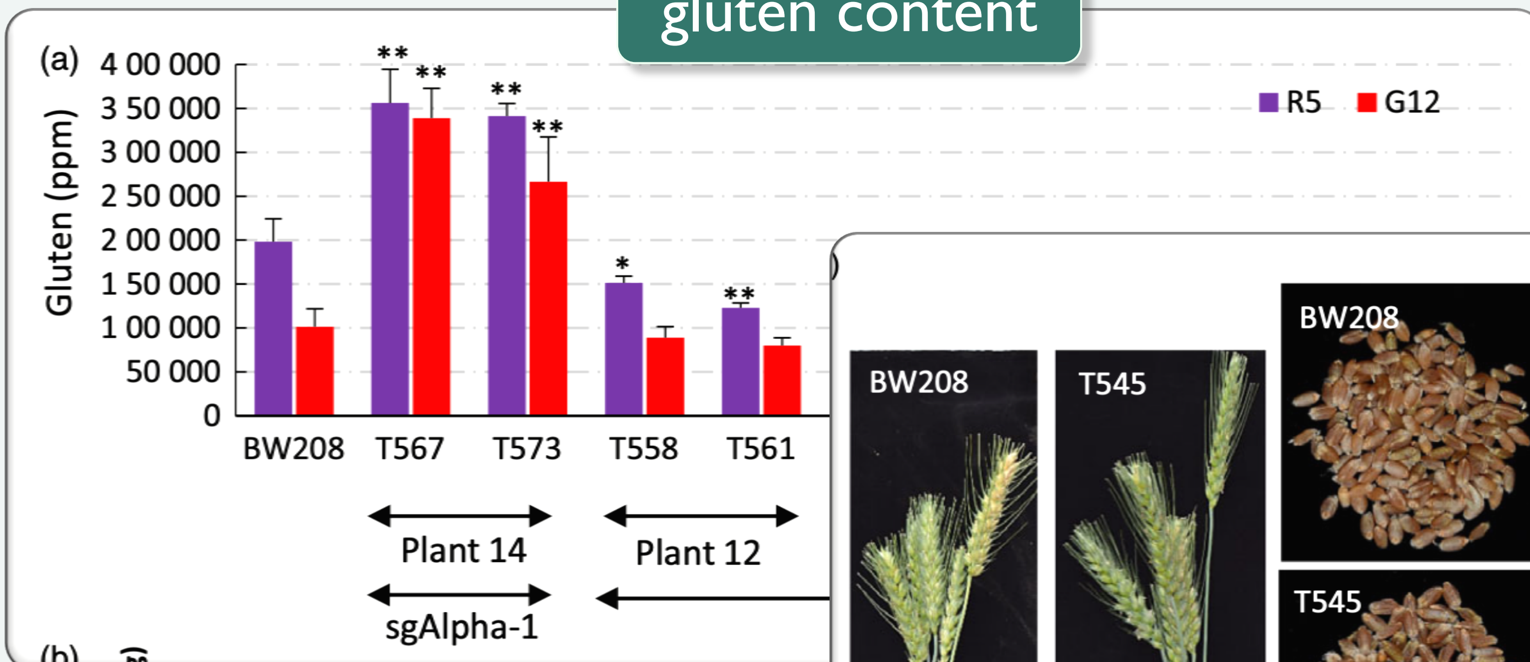
Wheat With Reduced Allergenicity

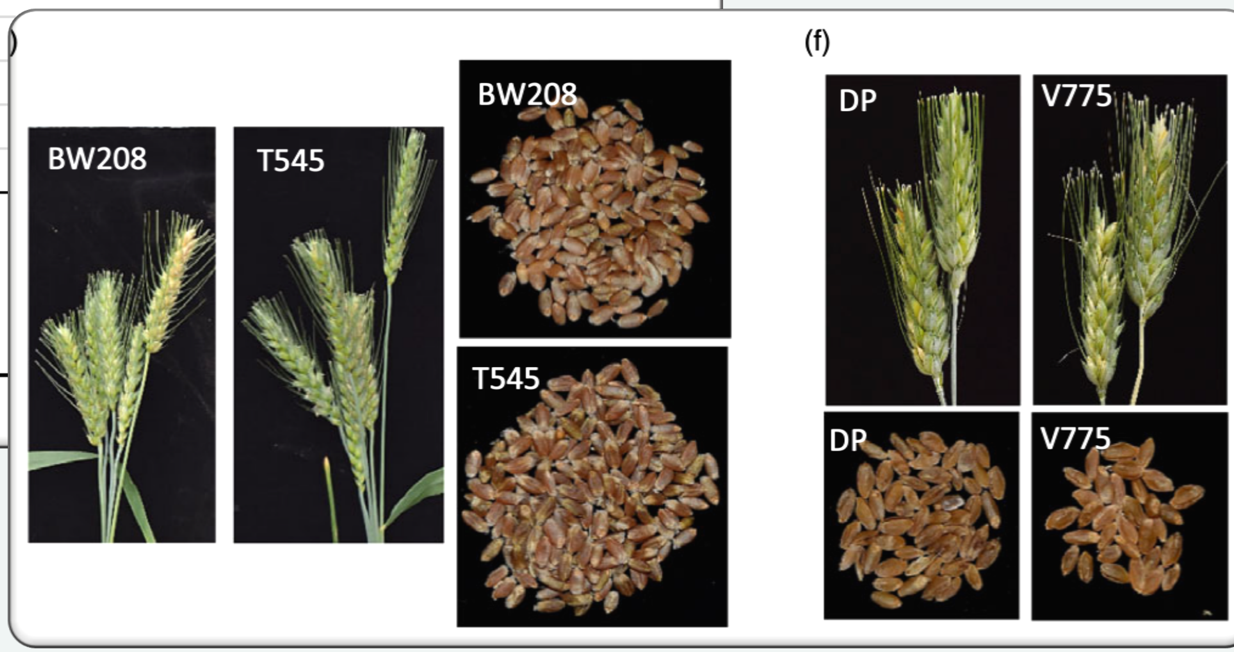
Low-gluten, nontransgenic wheat engineered with CRISPR/Cas9

Plant Biotech. J., 2018

Susana Sánchez-León[1,#], Javier Gil-Humanes[2,*,#], Carmen V. Ozuna[1], María J. Giménez[1], Carolina Sousa[3], Daniel F. Voytas[2] and Francisco Barro[1,*]

gluten content





A Controversial Trait: Herbicide Tolerance

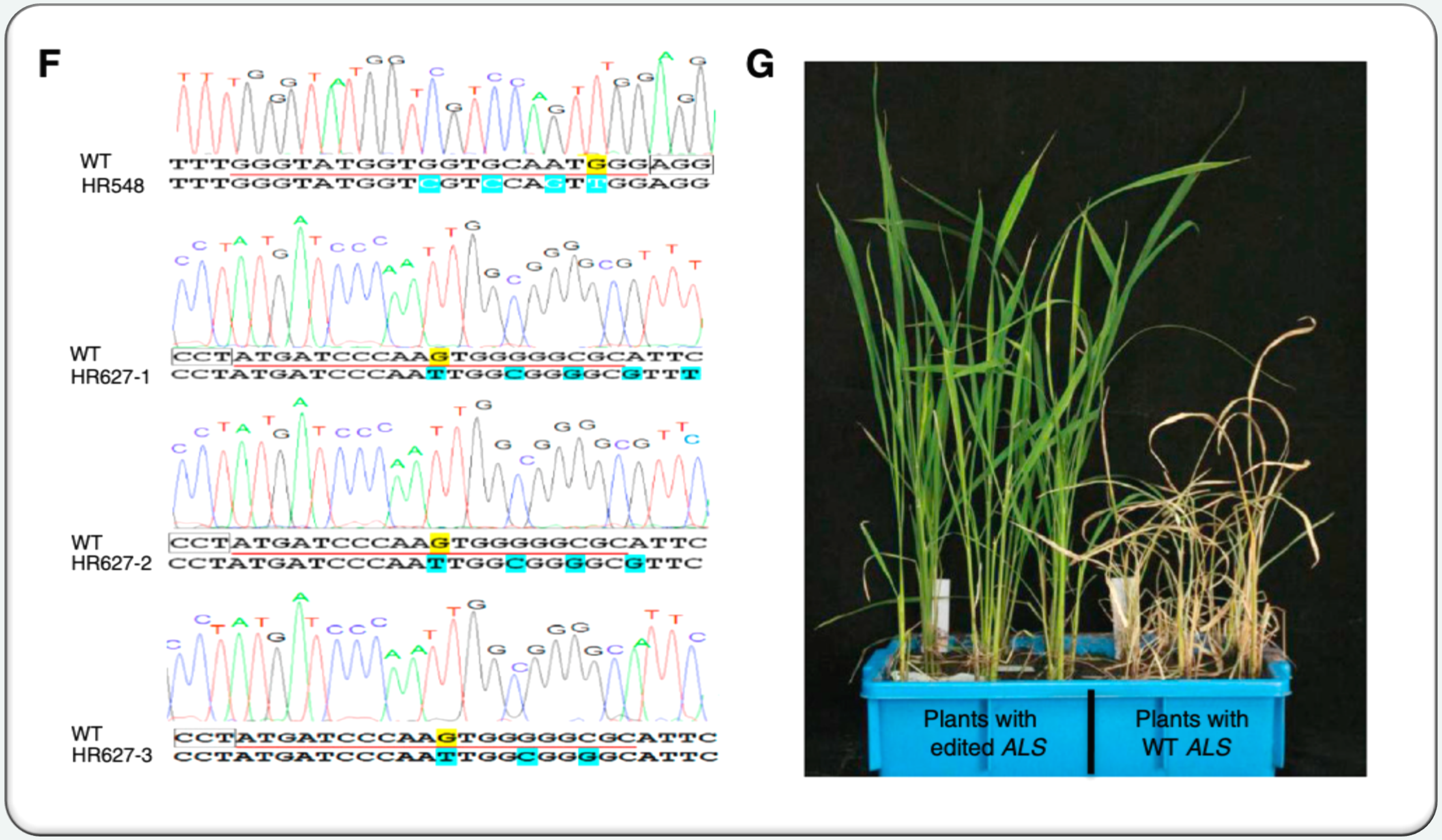
Engineering Herbicide-Resistant Rice Plants through CRISPR/Cas9-Mediated Homologous Recombination of Acetolactate Synthase

Dear Editor,

Genome editing technologies enable precise modifications of DNA sequences *in vivo* and offer great promise for crop improve-

demonstrating that this strategy works much less efficie

Sun et al., *Mol. Plant* 2016



Herbicide Tolerance – Without GMOs or Genome Editing

Have you heard about Clearfield® Canola?

It's the only canola system that delivers control of flushing weeds.

Clearfield canola is giving growers the kind of results they can't stop talking about. It's easy to use and the benefits are exceptional. So, say goodbye to your weeds and hello to your neighbour, because you'll be excited to tell them all about **Clearfield** canola.

The **Clearfield** canola system controls weeds with a single in-crop application, saving time you might ordinarily have to spend in the sprayer. And less weeds means higher yield potential.

Clearfield Production System for Canola

We strive to provide growers with holistic trait and herbicide solution package that support their canola crops. Get to know why our history, benefits and sustainability efforts matter. Discover what **Clearfield** can

Clearfield Products

Find solutions that work for you and your yield goals by applying **Clearfield** products. Ares™ SN is a herbicide designed for the **Clearfield** Production System. It offers growers consistent and reliable control of grassy and broadleaf weeds,

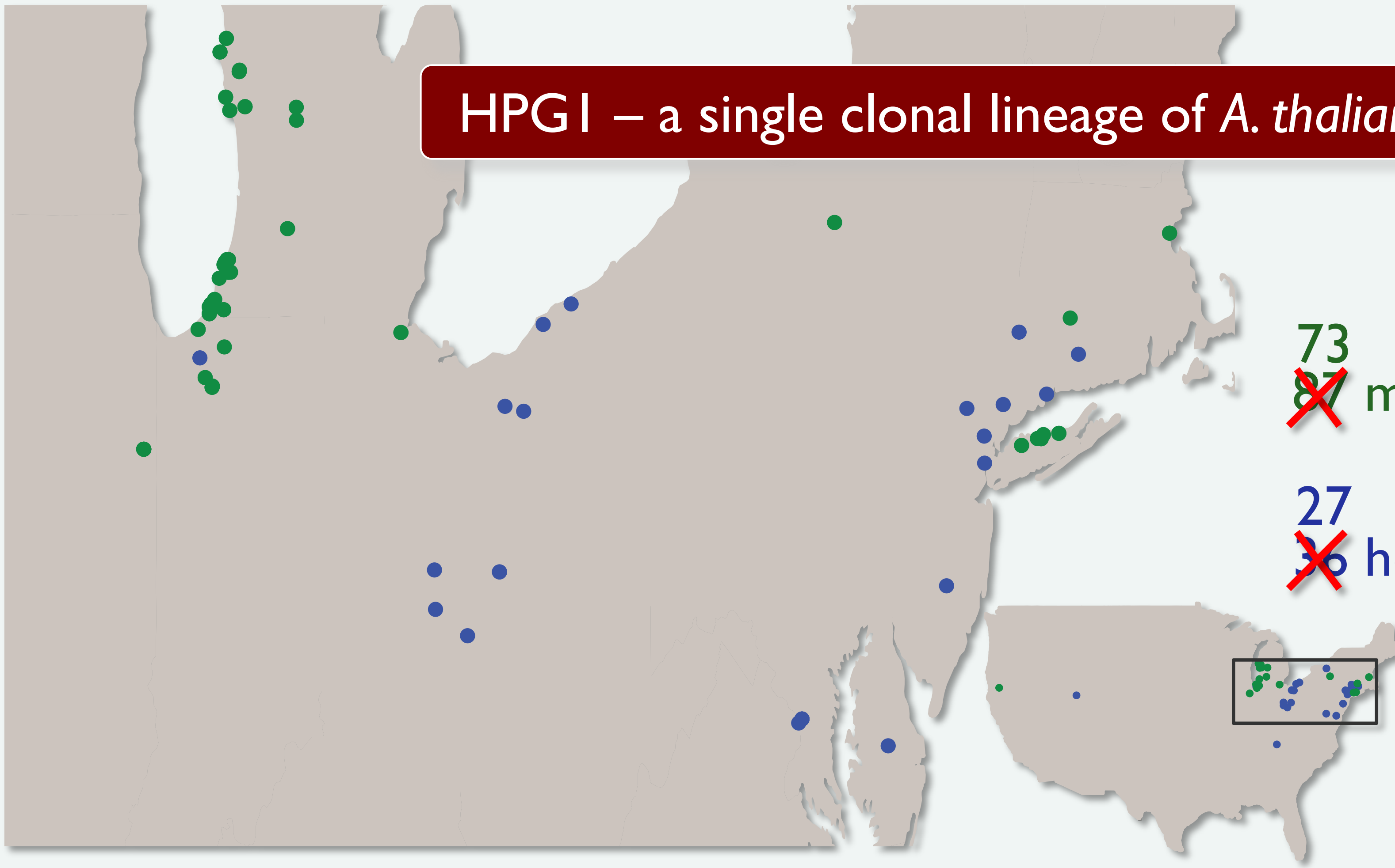
Information about the Clearfield Commitment

The **Clearfield** Commitment for canola is an agreement that allows growers to access the benefits of canola hybrids with the **Clearfield** trait. Uncover more about the **Clearfield** Production System

CORTEVA™ agriscience

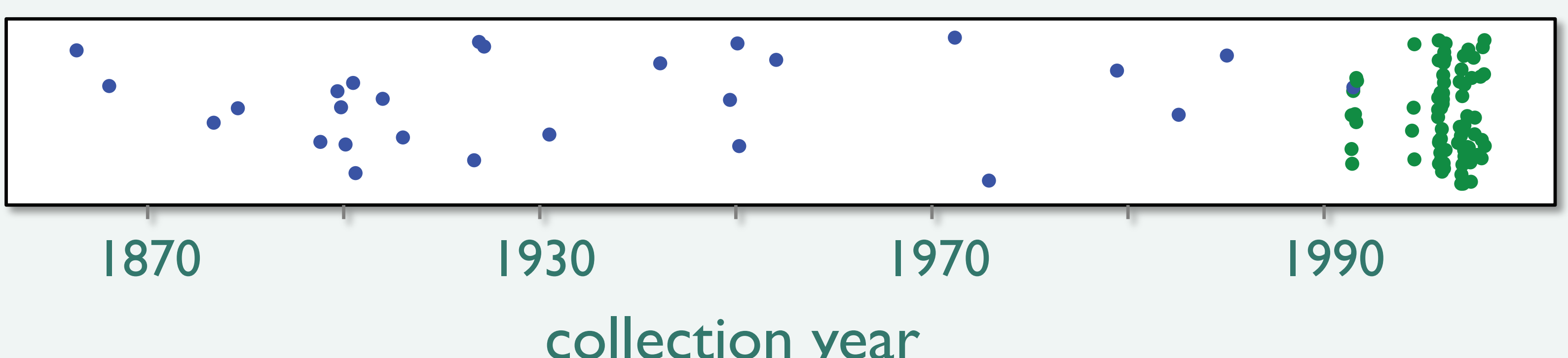
Natural Mutation Rates

HPG1 – a single clonal lineage of *A. thaliana*



73
~~87~~ modern genomes

27
~~36~~ herbarium genomes

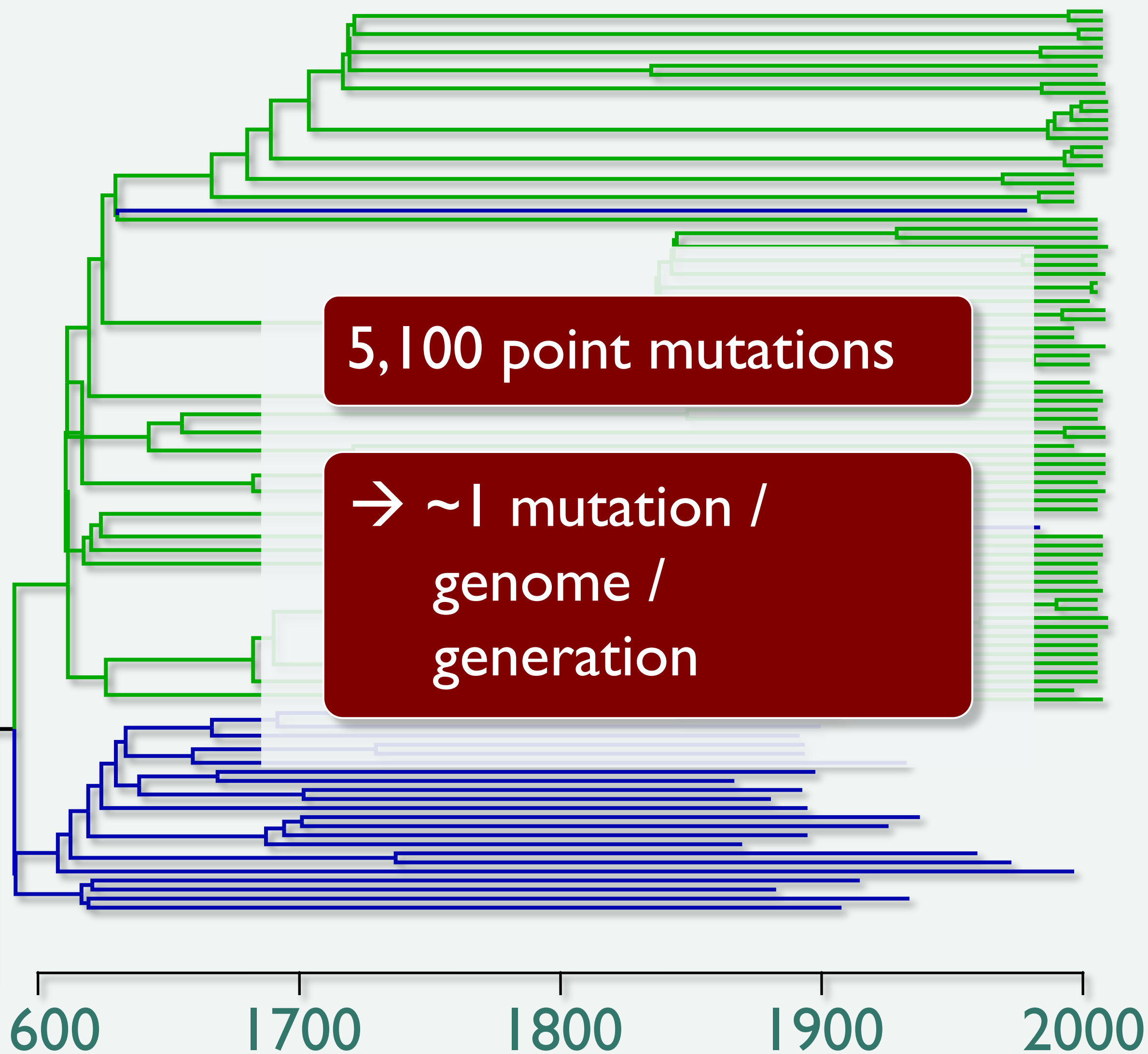


Reconstruction of Phylogeny and Mutation Rates

modern genomes

herbarium genomes

With Burbano lab



5,100 point mutations

→ ~1 mutation / genome / generation

M Expósito (now Carnegie)

C Becker (now GMI/LMU)

Exposito-Alonso, Becker et al. (2018)

What Does This Imply For Crops Such as Wheat?

A. thaliana:	1 mutation/genome (0.1 billion bp)
wheat:	100 mutations/genome (10 billion bp)

1 ha field → 10 t = 10 million g wheat

1 wheat grain = 50 mg → 20 grains/g

200 million grains → 20 billion mutations

How Different Are, For Example, Two Maize Varieties?

Table 2 | Variations within genes between B73 and Mo17 genomes

Variation type	Syntenic genes		Nonsyntenic genes	
	B73 genes	Mo17 genes	B73 genes	Mo17 genes
Structurally conserved genes	28,122	28,186	1,534	1,216
Without amino acid substitutions	12,167	12,674	326	306
No DNA variation in CDS region	9,760	10,231	256	246
No DNA variation in CDS and intron region	6,870	7,344	169	169
No DNA variation in genic region[b]	2,498	2,458	12	10
With amino acid changes	15,955	15,512	1,198	910
With missense mutation in CDS	15,611	15,438	1,130	899
With 3*n* indel in CDS	5,941	5,632	186	221
Genes with large effect mutations	3,947	4,020	1,387	977
Start-codon mutation	240	374	175	109
Stop-codon mutation	268	418	244	236
Splice-donor mutation	170	124	73	37
Splice-acceptor mutation	256	162	175	90
With $3n \pm 1$ indel in CDS	2,044	1,983	547	384
Premature stop codon	2,692	2,635	922	648
Genes with large structural variations	1,612	1,391	2,112	1,765
At least one exon missing	1,025	811	1,725	1,508
PAV genes	-	-	72	50
Total	33,681[a]	33,597[a]	5,105[a]	4,008[a]

[a]Only genes and their best hits in the counterpart genome anchored in ten pseudomolecules were included for the analysis. [b]Genic regions include 2 kb upstream and downstream of the gene body.

	B73	Mo17
total number of genes	38,686	37,605
synonymous substitutions	16,744	16,437
nonsense-mutations	3,614	3,283
≥1 exon missing	2,750	2,319

nature

Forscher über EuG

LE FIGARO PREMIUM

Suivre Recherche

Société Vox International Economie Culture Figaro Live

Actualité > Sciences & Environnement

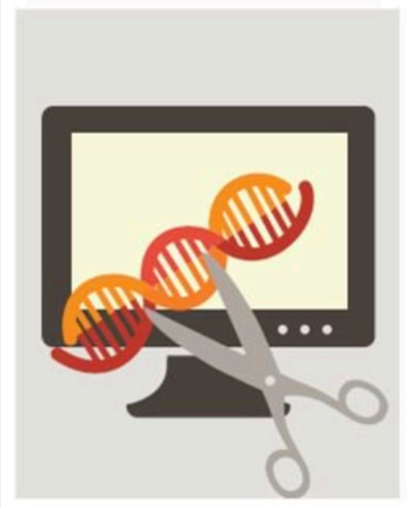
...lification génétique crée un OGM

Martin Häusling @MartinHaeusling

Follow

#EuGH lässt sich von Agrarindustrie nichts vormachen. Das Urteil ist wichtig für Lebensmittelsicherheit und Umweltschutz. Keine Unsicherheiten mehr #CRISPR Die Länder müssen jetzt gesetz... schliessen. Wo Gentechnik... draufstehn. martin-haeuslin... medien/ ...

Translate Tweet



2:23 PM - 25 Jul 2018

GREENPEACE Greenpeace European Unit

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Home > Press centre > 2018 > New GMOs cannot escape testing and labelling under EU law, EU court rules

New GMOs cannot escape testing and labelling under EU law, EU court rules

Press release - July 25, 2018

Brussels – A new brand of genetically modified organisms (GMOs), derived from so-called gene editing techniques, must comply with risk assessment, traceability and labelling requirements under EU GMO law, the European Court of Justice ruled on Wednesday.

The Court said that any organism obtained with new genetic engineering techniques falls within the scope of GMO law. It argued that the risks linked to the use of these techniques are comparable to those associated with conventional genetic engineering.

The ruling confirms warnings by scientists who have argued that gene editing can cause unintended DNA damage with unknown consequences. A recent

to do with field trials already app...
trials. Many researchers say it will...

Phenomics-assisted breeding appears to be a promising tool for deciphering the stress responsiveness of crop and animal species (Papageorgiou 2017; Kole et al. 2015; Lopes et al. 2015; Boettcher et al. 2015). Initially discovered in bacteria and archaea, CRISPR–Cas9 is an adaptive immune system found in prokaryotes and since 2013 has been used as a genome editing tool in plants. The main use of CRISPR systems is to achieve improved yield performance, biofortification, biotic and abiotic stress tolerance, with rice (Oryza sativa) being the most studied crop (Gao 2018; Ricroch et al. 2017).

Intergovernmental Panel on Climate Change
2019 report