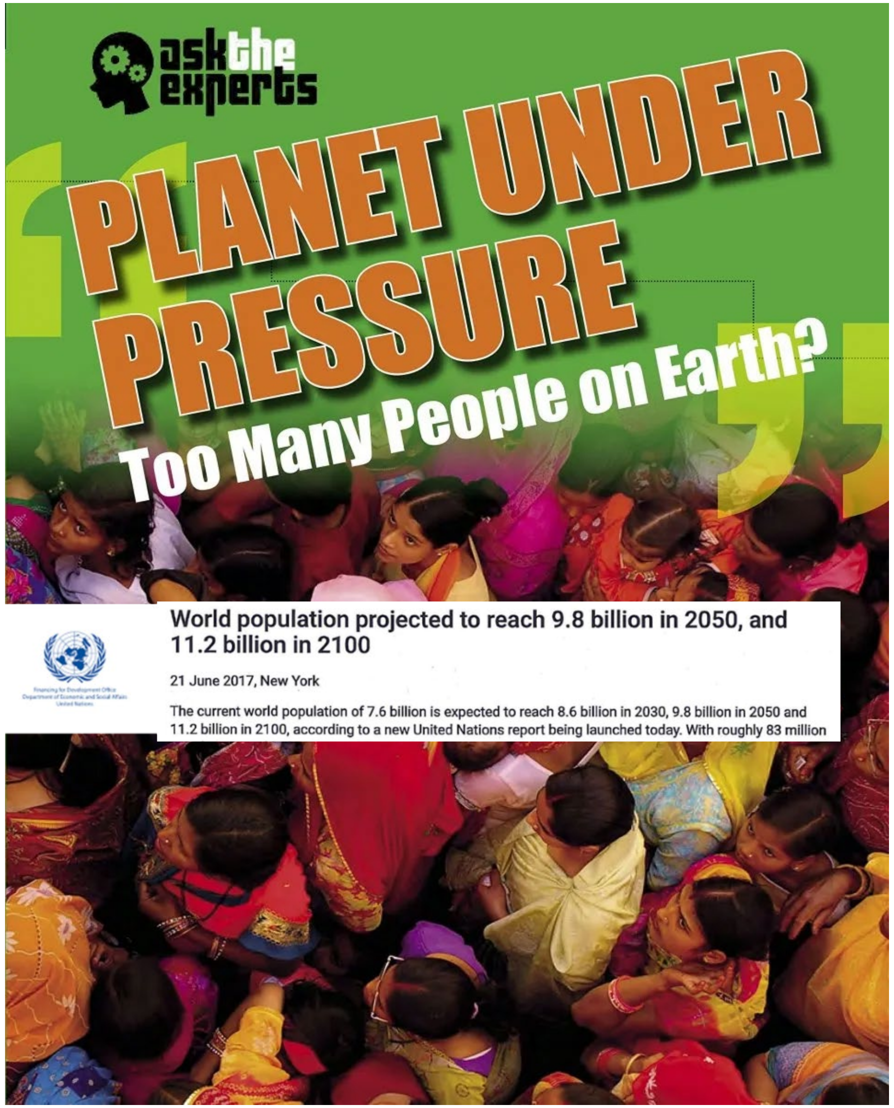
Julius Kühn-Institut
Bundesforschungsinstitut für Kulturpflanzen
Federal Research Centre for Cultivated Plants

Resistance Breeding – cornerstone for meeting future challenges

Frank Ordon

Introduction

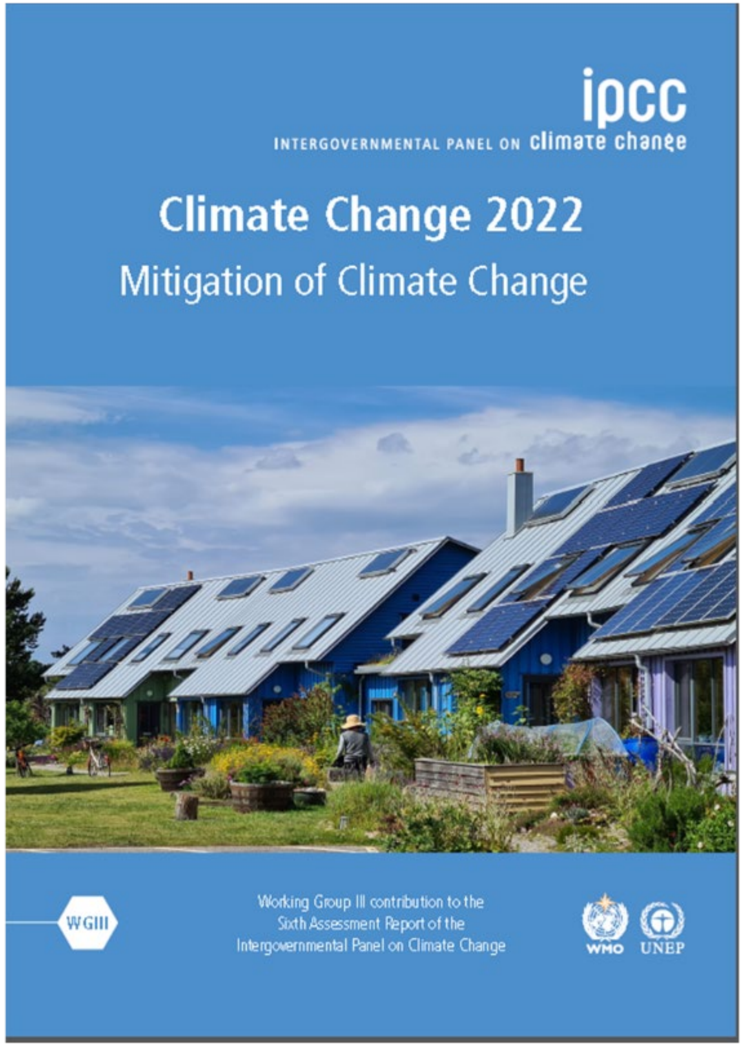


World population projected to reach 9.8 billion in 2050, and 11.2 billion in 2100

21 June 2017, New York

The current world population of 7.6 billion is expected to reach 8.6 billion in 2030, 9.8 billion in 2050 and 11.2 billion in 2100, according to a new United Nations report being launched today. With roughly 83 million

Matt Anniss (Author)
https://books.google.de/books/about/Planet_Under_Pressure.html?id=0wK7oQEACAAJ&redir_esc=y



https://www.wcrp-climate.org/news/wcrp-news/1879-ipcc-wg3-ar6

https://www.wfp.org/publications/food-security-implications-ukraine-conflict

Plant Production Chain

www.fotolia.de

www.fotolia.de

www.fotolia.de

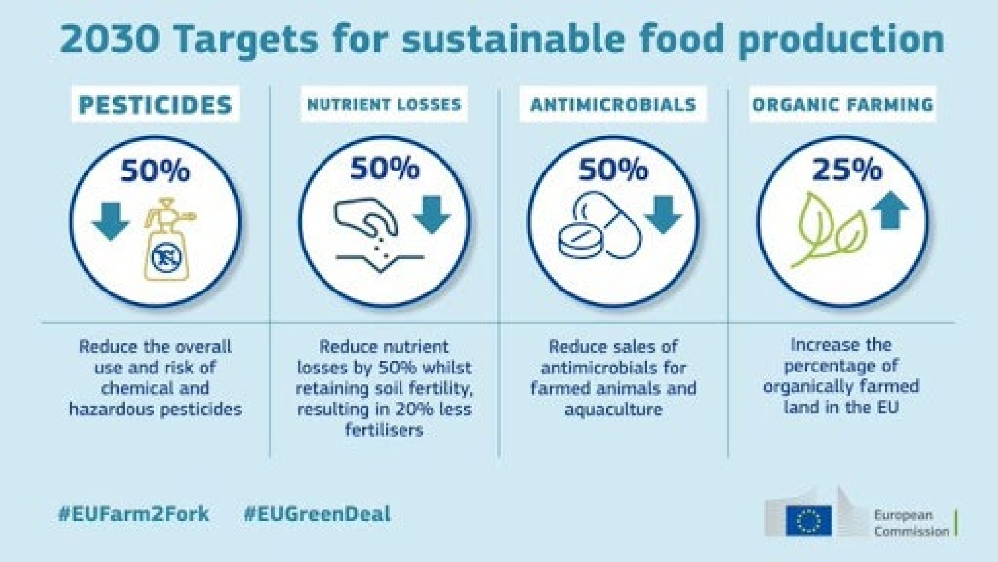
https://www.earlytaste.de/produkt/brotkorb/

$$Y=GxEx\cancel{M}$$

Genotyp
Cultivar

Soil
Weather
……..

Plant Protection
Fertilization
……..



2030 Targets for sustainable food production

PESTICIDES	NUTRIENT LOSSES	ANTIMICROBIALS	ORGANIC FARMING
50%	50%	50%	25%
Reduce the overall use and risk of chemical and hazardous pesticides	Reduce nutrient losses by 50% whilst retaining soil fertility, resulting in 20% less fertilisers	Reduce sales of antimicrobials for farmed animals and aquaculture	Increase the percentage of organically farmed land in the EU

#EUFarm2Fork #EUGreenDeal

European Commission

Yield losses

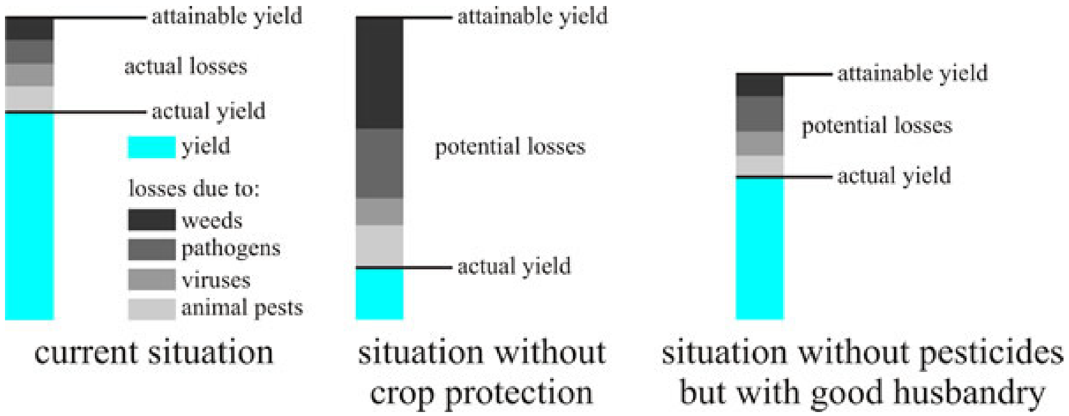
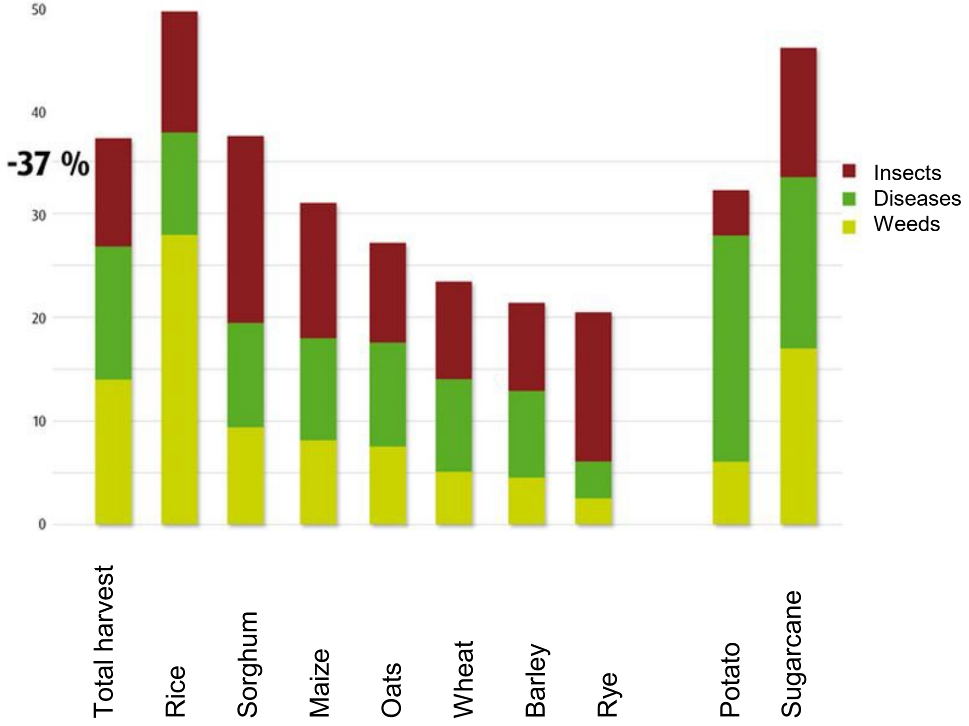


Fig. 2. Typical crop losses and yield levels estimated with and without various protection regimes. The value of crop protection practices (shown at left as 'current situation') can be calculated as the percentage of potential losses prevented by all the crop protection measures that are employed (compare with centre panel). In contrast, the impact of pesticide use on crop productivity (right hand panel) takes into account consequential changes in the agricultural system (for example, **use of alternative varieties of the crop**, modified crop rotation, reduced fertiliser use), which are provoked by the abandonment of pesticides and which are often accompanied by reduced attainable yield. Redrawn after Oerke, 2006.

Moore et al. 2021

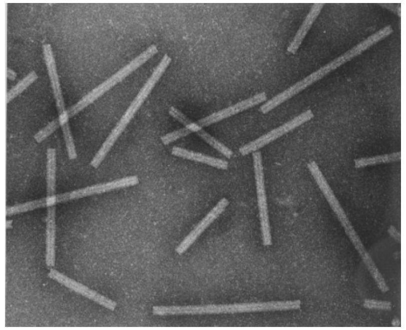


http://www.transgen.de/pflanzenforschung/pflanzengesundheit/

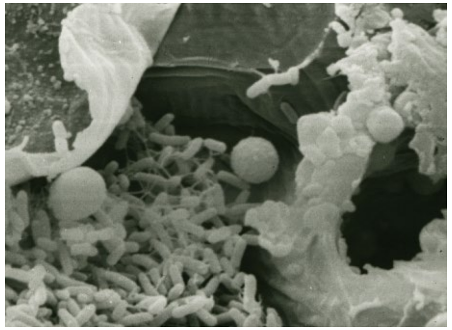
Pests and diseases in the background of climate change

Insects

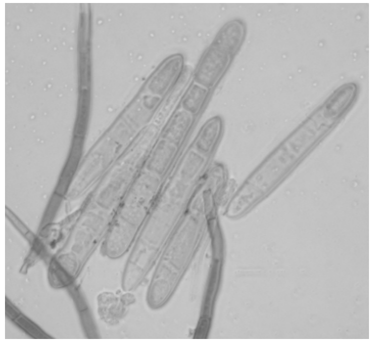
Viruses



Bacteria



Fungi



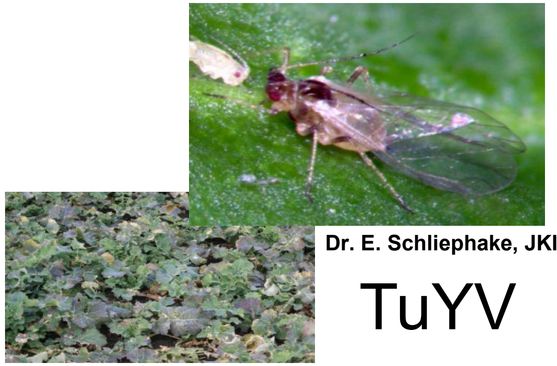
+2°C = 213 Mio t loss in wheat, maize and rice due to insects

Deutsch, C.A.; Tewksbury, J.J.; Tigchelaar, M.; Battisti, D.S.; Merrill, S.C.; Huey, R.B.; Naylor, R. Increase in crop losses to insectpests in a warming climate. Science 2018, 361, 916–919.

Chmielewski, 2007: Rise in average temperature about 3-6°C facilitates moving north of insects of about 1000 km

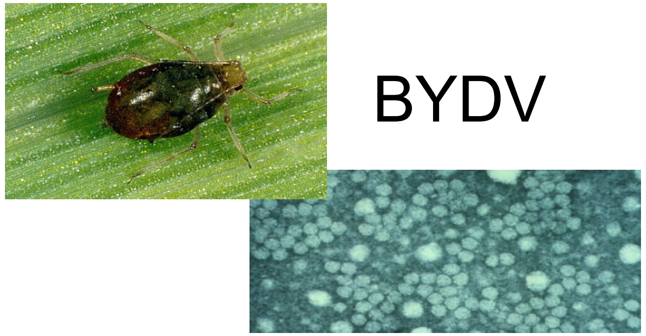
Fungal pathogens adapted to higher temperature like stem rust in wheat or *Cercospora beticola* will gain importance

Commons.wikimedia.org/wiki/File: Suíkerbiet



Dr. E. Schliephake, JKI

TuYV



BYDV

Dr. A. Habekuss, JKI

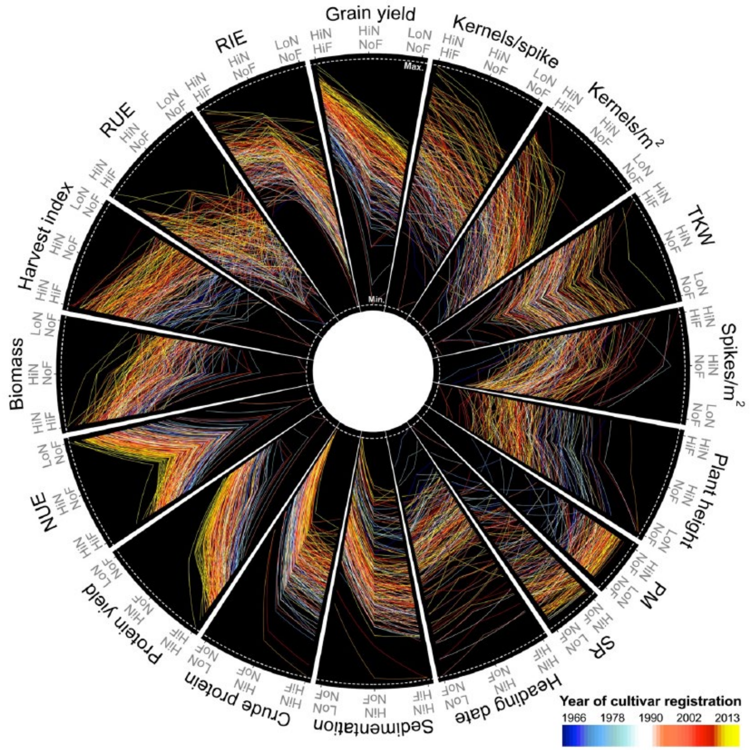
Breeding progress in wheat

Article | Published: 17 June 2019

Breeding improves wheat productivity under contrasting agrochemical input levels

Kai P. Voss-Fels, Andreas Stahl, Benjamin Wittkop, Carolin Lichthardt, Sabrina Nagler, Till Rose, Tsu-Wei Chen, Holger Zetzsche, Sylvia Seddig, Mirza Majid Baig, Agim Ballvora, Matthias Frisch, Elizabeth Ross, Ben J. Hayes, Matthew J. Hayden, Frank Ordon, Jens Leon, Henning Kage, Wolfgang Friedt, Hartmut Stützel & Rod J. Snowdon

Nature Plants (2019)

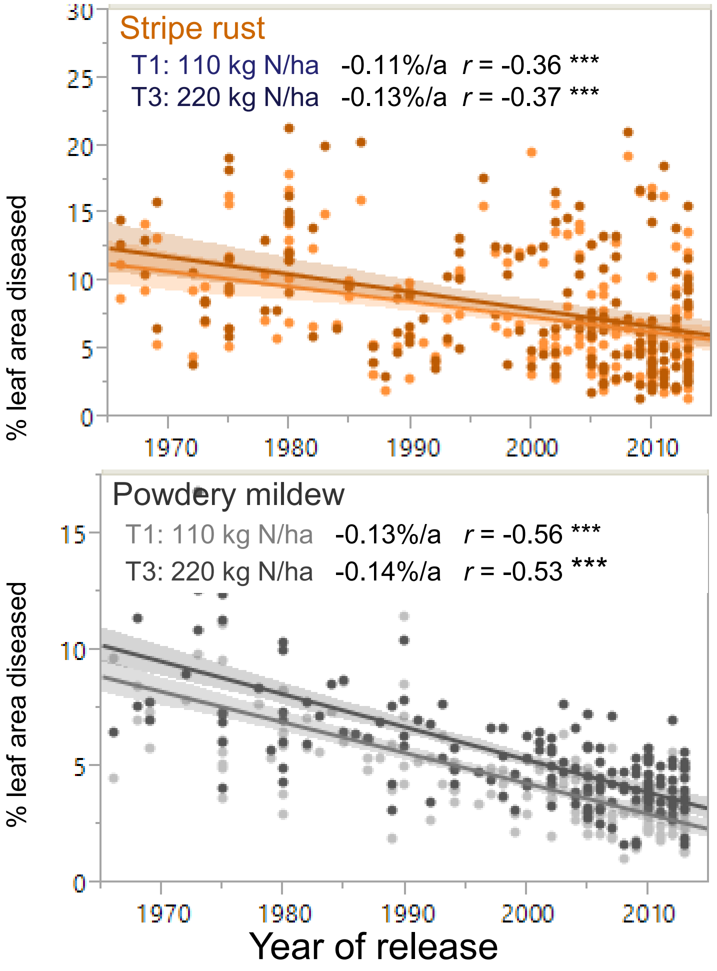


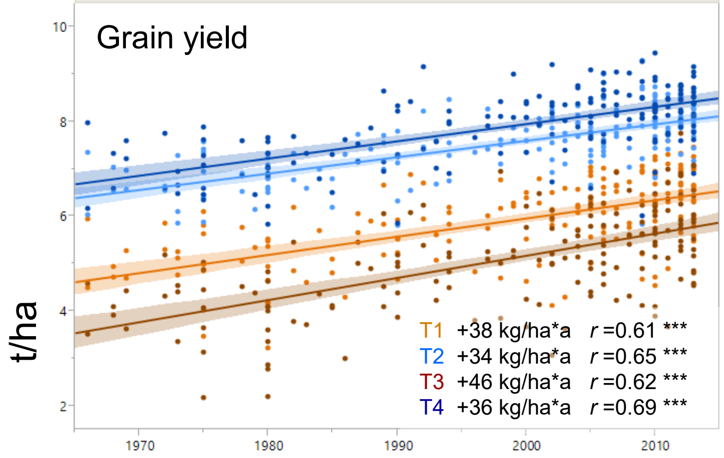
scientific reports

OPEN

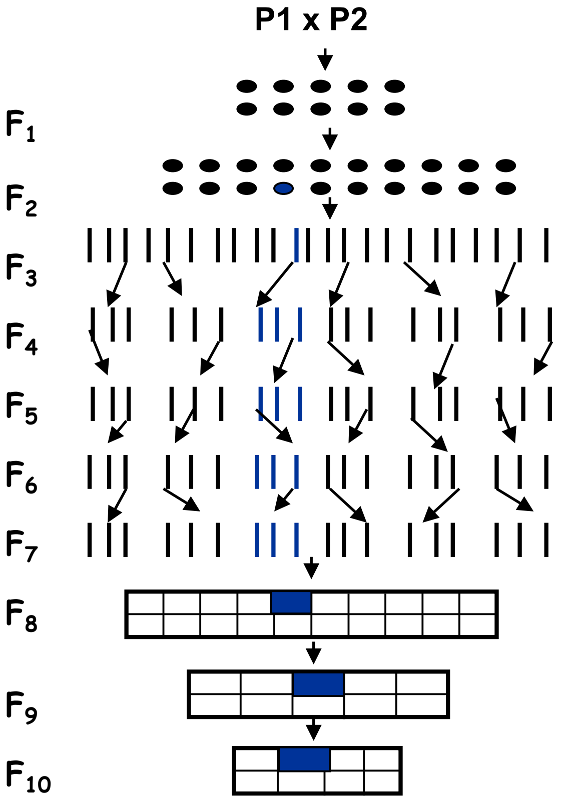
Breeding progress for pathogen resistance is a second major driver for yield increase in German winter wheat at contrasting N levels

Holger Zetzsche, Wolfgang Friedt & Frank Ordon

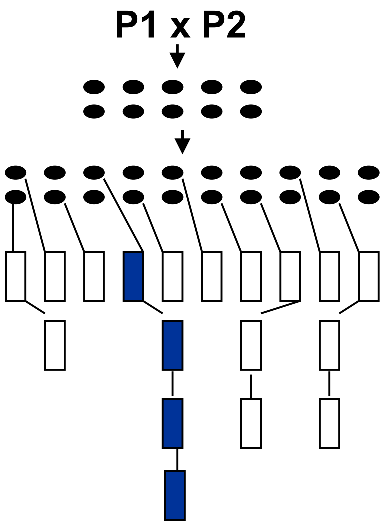




Breeding progress in wheat

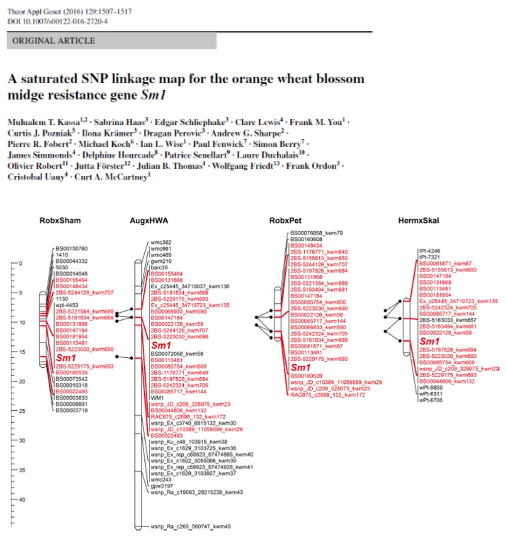


Pedigree Selection



Use of doubled haploids

Marker based selection

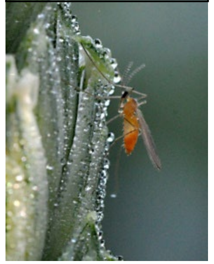


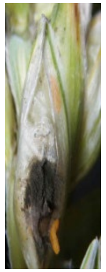
Theor Appl Genet (2016) 129:1507–1517
DOI 10.1007/s00122-016-2720-4

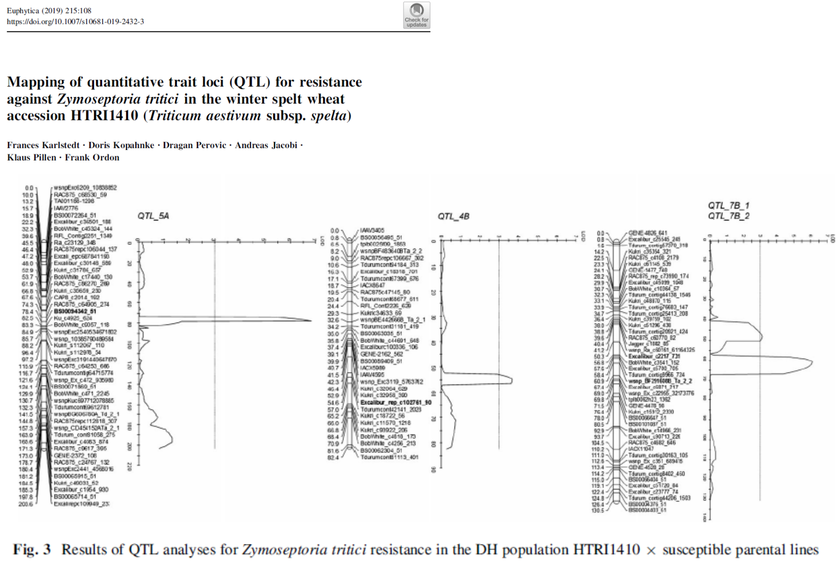
ORIGINAL ARTICLE

A saturated SNP linkage map for the orange wheat blossom midge resistance gene *Sm1*

Mulualem T. Kassa[1,2] · Sabrina Haas[3] · Edgar Schliephake[3] · Clare Lewis[4] · Frank M. You[1] · Curtis J. Pozniak[5] · Ilona Krämer[3] · Dragan Perovic[3] · Andrew G. Sharpe[2] · Pierre R. Fobert[2] · Michael Koch[6] · Ian L. Wise[1] · Paul Fenwick[7] · Simon Berry[7] · James Simmonds[4] · Delphine Hourcade[8] · Patrice Senellart[9] · Laure Duchalais[10] · Olivier Robert[11] · Jutta Förster[12] · Julian B. Thomas[1] · Wolfgang Friedt[13] · Frank Ordon[3] · Cristobal Uauy[4] · Curt A. McCartney[1]







Euphytica (2019) 215:108
https://doi.org/10.1007/s10681-019-2432-3

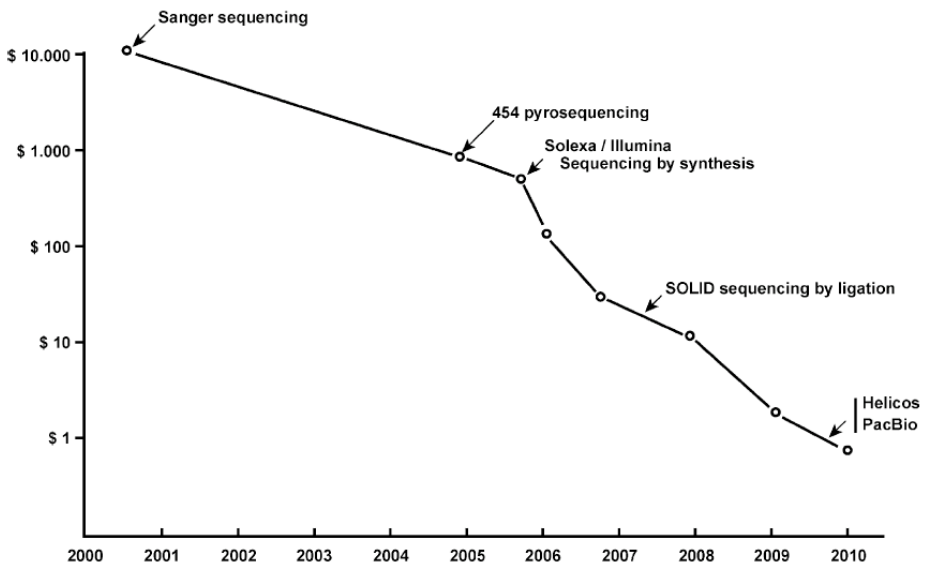
Mapping of quantitative trait loci (QTL) for resistance against *Zymoseptoria tritici* in the winter spelt wheat accession HTRI1410 (*Triticum aestivum* subsp. *spelta*)

Frances Karlstedt · Doris Kopahnke · Dragan Perovic · Andreas Jacobi · Klaus Pillen · Frank Ordon

Fig. 3 Results of QTL analyses for *Zymoseptoria tritici* resistance in the DH population HTRI1410 × susceptible parental lines

Plant breeder‘s toolbox

Marker type	RFLPs	Genomic SSRs	AFLPs	EST SNPs/SSRs	DArTs	BOPAs/OPAs	iSelect		Genotyping by sequencing
Throughput	single marker application	single marker application	few marker application	single marker application	6K	1,5K	9K	50K	
Multiplexing	no mutiplexing	few markers multiplexing	low multiplexing	few markers multiplexing	platform/ simultaneous analysis	platform/ simultaneous analysis	platform/ simultaneous analysis	platform/ simultaneous analysis	simultaneous multiplexing NGS/GBS
Amount of D N A	Large amount	low amount	low amount	low amount	low amount	low amount	low amount	low amount	low amount
Quality of D N A	very good	average	average	average	very good	very good	very good	very good	very good



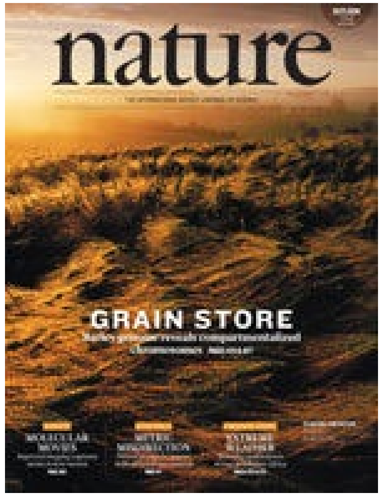
An estimate of the evolution of sequencing costs over the last 10 years.
Costs are given for sequencing a megabase using a logarithmic scale.
M. Delseny et al. (2010) *Plant Sci.* 179: 407-422

ARTICLE

OPEN

doi:10.1038/nature22043

A chromosome conformation capture ordered sequence of the barley genome



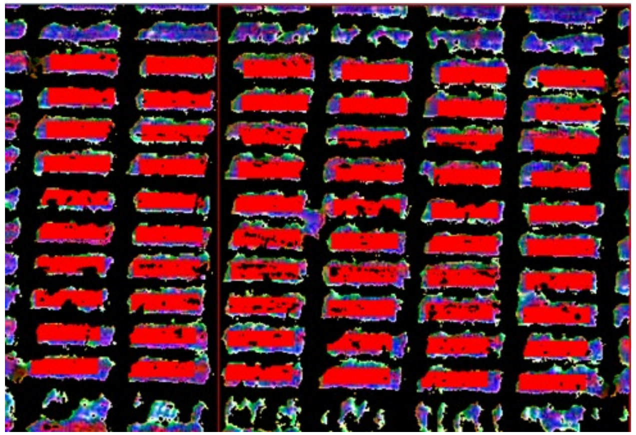
Article

Multiple wheat genomes reveal global variation in modern breeding

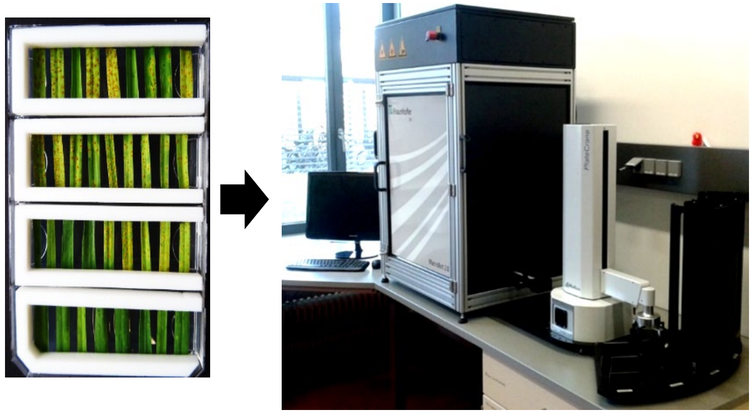
Systematic use of plant genetic resources

Genome wide association studies GWAS

Phenotyping

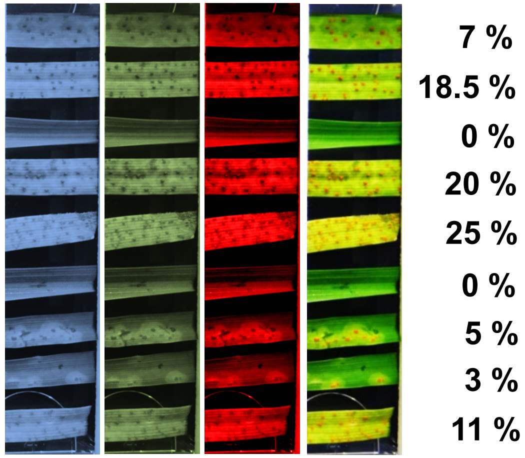


Tattaris M, Reynolds MP, Chapman SC, 2016. A direct comparison of remote sensing approaches for high-throughput phenotyping in plant breeding. Front. Plant Sci. 7: 1131.



High throughput phenotyping

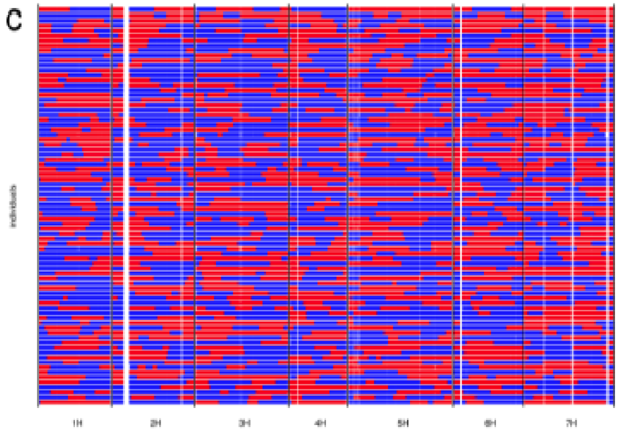
A. Serfling und U. Beukert



Automatic detection of leaf area infected

Genotyping

https://www.illumina.com/systems/sequencing-platforms/hiseq-2500.html

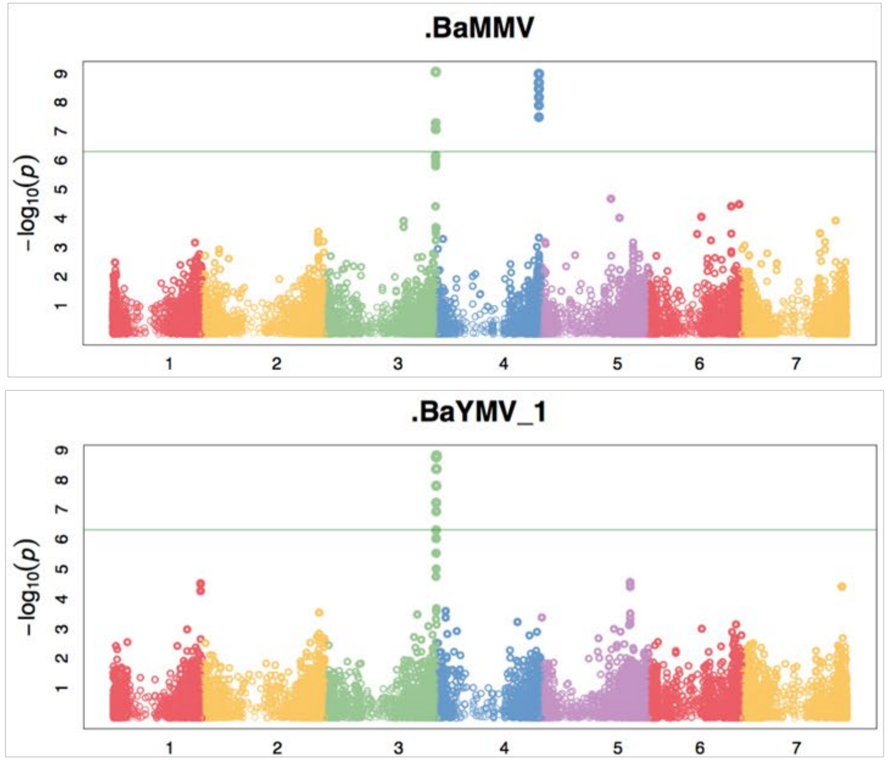


N. Stein

https://www.illumina.com/products/by-type/microarray-kits/infinium-iselect-custom-genotyping.html

Systematic use of genetic resources

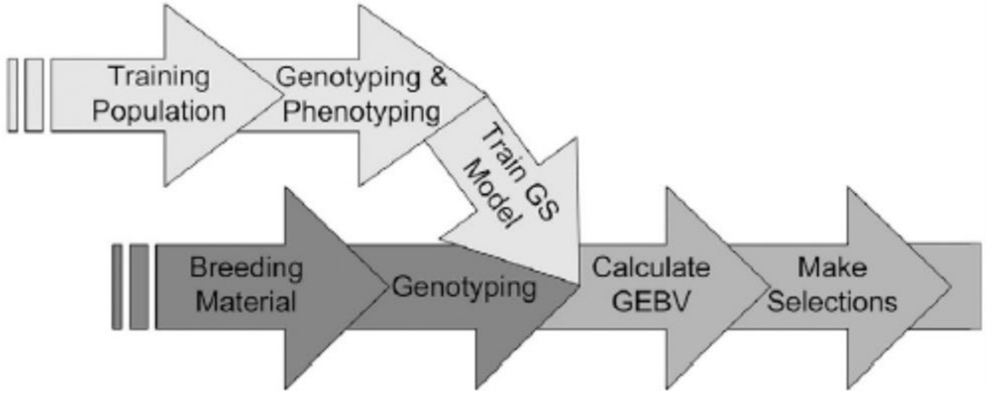
Genomwide association studies (GWAS)

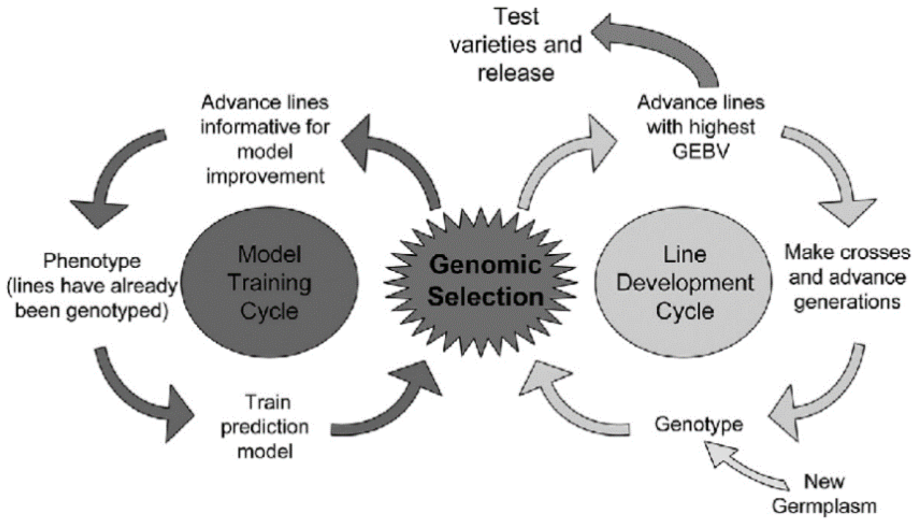


IPK GATERSLEBEN

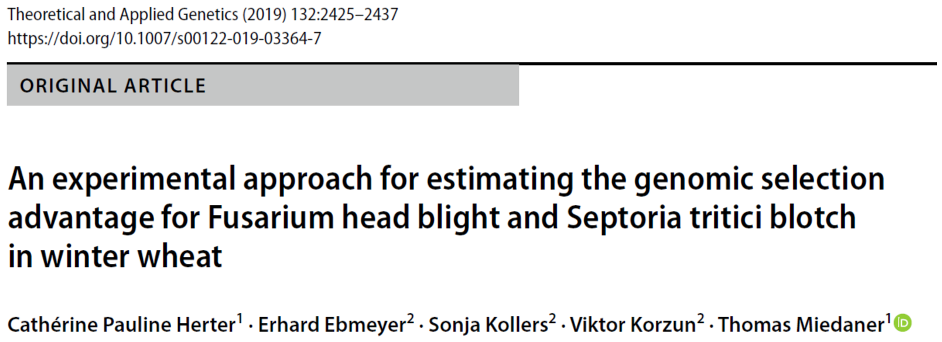
Millner et al. 2018: Nature Genetics

Genomic Selection





Heffner et al. 2009

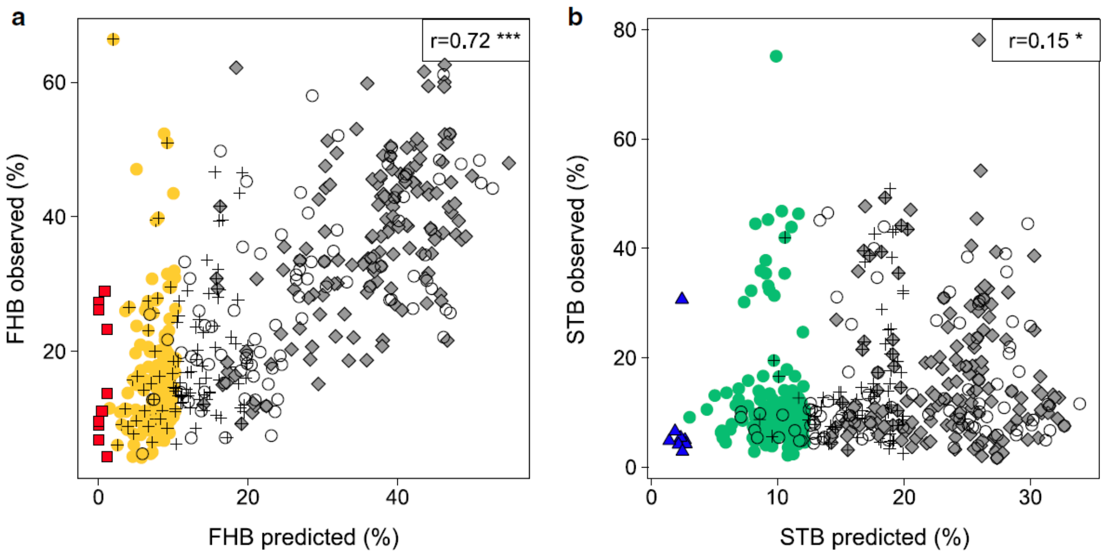


Theoretical and Applied Genetics (2019) 132:2425–2437
https://doi.org/10.1007/s00122-019-03364-7

ORIGINAL ARTICLE

An experimental approach for estimating the genomic selection advantage for Fusarium head blight and Septoria tritici blotch in winter wheat

Cathérine Pauline Herter[1] · Erhard Ebmeyer[2] · Sonja Kollers[2] · Viktor Korzun[2] · Thomas Miedaner[1]



Isolation von resistance genes: map based cloning

1. Mapping of the gene of interest on low to medium resolution

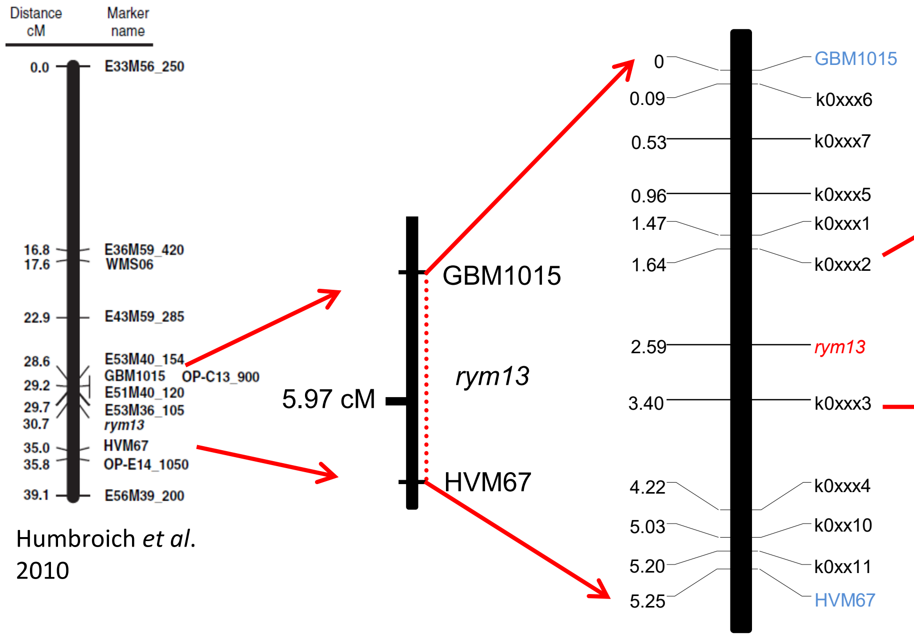
2. Construction of a high resolution mapping population (5191 F_2-plants)

3. Phenotyping of segmental RILs (F_4) and marker saturation using available high density maps

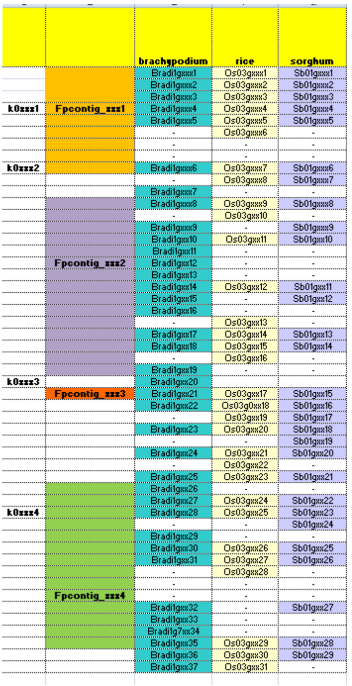
4. Further marker saturation by using sequence information from rice, sorghum brachypodium and NGS data from barley (GenomeZipper)

5. Identification of a BAC contig and candidate genes based on the physical map of barley or re-sequencing of the target interval

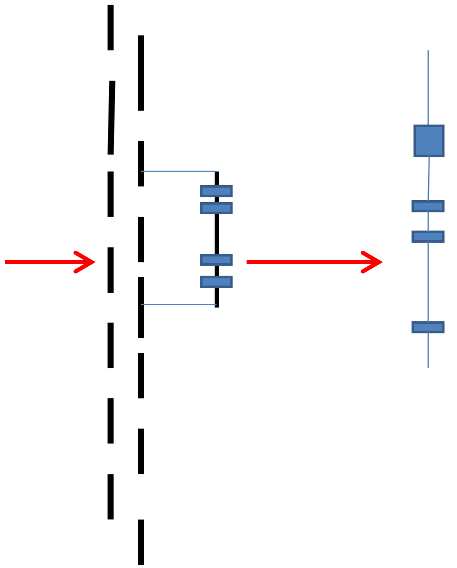
6. Identification of *rym13* by transformation, TILLING, RNAi



Humbroich *et al.* 2010



		brachypodium	rice	sorghum
	Fpcontig_zzz1	Bradi1gxxx1	Os03gxxx1	Sb01gxxx1
		Bradi1gxxx2	Os03gxxx2	Sb01gxxx2
		Bradi1gxxx3	Os03gxxx3	Sb01gxxx3
k0zzz1		Bradi1gxxx4	Os03gxxx4	Sb01gxxx4
		Bradi1gxxx5	Os03gxxx5	Sb01gxxx5
		-	Os03gxxx6	-
		-	-	-
		-	-	-
k0zzz2		Bradi1gxxx6	Os03gxxx7	Sb01gxxx6
		-	Os03gxxx8	Sb01gxxx7
		Bradi1gxxx7	-	-
	Fpcontig_zzz2	Bradi1gxxx8	Os03gxxx9	Sb01gxxx8
		-	Os03gxx10	-
		Bradi1gxxx9	-	Sb01gxxx9
		Bradi1gxx10	Os03gxx11	Sb01gxx10
		Bradi1gxx11	-	-
		Bradi1gxx12	-	-
		Bradi1gxx13	-	-
		Bradi1gxx14	Os03gxx12	Sb01gxx11
		Bradi1gxx15	-	Sb01gxx12
		Bradi1gxx16	-	-
		-	Os03gxx13	-
		Bradi1gxx17	Os03gxx14	Sb01gxx13
		Bradi1gxx18	Os03gxx15	Sb01gxx14
		-	Os03gxx16	-
		Bradi1gxx19	-	-
k0zzz3		Bradi1gxx20		
	Fpcontig_zzz3	Bradi1gxx21	Os03gxx17	Sb01gxx15
		Bradi1gxx22	Os03g0xx18	Sb01gxx16
		-	Os03gxx19	Sb01gxx17
		Bradi1gxx23	Os03gxx20	Sb01gxx18
		-	-	Sb01gxx19
		Bradi1gxx24	Os03gxx21	Sb01gxx20
		-	Os03gxx22	-
		Bradi1gxx25	Os03gxx23	Sb01gxx21
	Fpcontig_zzz4	Bradi1gxx26	-	-
		Bradi1gxx27	Os03gxx24	Sb01gxx22
k0zzz4		Bradi1gxx28	Os03gxx25	Sb01gxx23
		-	-	Sb01gxx24
		Bradi1gxx29	-	-
		Bradi1gxx30	Os03gxx26	Sb01gxx25
		Bradi1gxx31	Os03gxx27	Sb01gxx26
		-	Os03gxx28	-
		-	-	-
		-	-	-
		Bradi1gxx32	-	Sb01gxx27
		Bradi1gxx33	-	-
		Bradi1g7xx34	-	-
		Bradi1gxx35	Os03gxx29	Sb01gxx28
		Bradi1gxx36	Os03gxx30	Sb01gxx29
		Bradi1gxx37	Os03gxx31	-



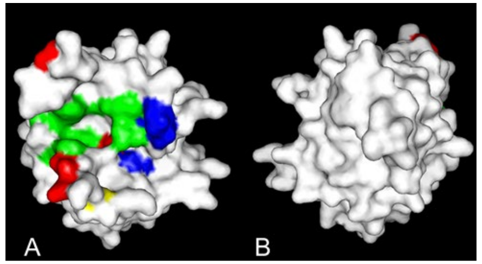
Strategy for marker development and isolation of virus resistance genes in barley using genomic tools examplified for *rym13* being effective against BaMMV/BaYMV (Lehmann et al. unpublished)

Isolation von resistance genes: *rym4* und *rym11*

The Plant Journal (2005) **42**, 912–922 doi: 10.1111/j.1365-313X.2005.02424.x

The eukaryotic translation initiation factor 4E confers multiallelic recessive *Bymovirus* resistance in *Hordeum vulgare* (L.)

Nils Stein[1,†], Dragan Perovic[1,†], Jochen Kumlehn[1], Bettina Pellio[2], Silke Stracke[1], Stefan Streng[1], Frank Ordon[2,3] and Andreas Graner[1,*]



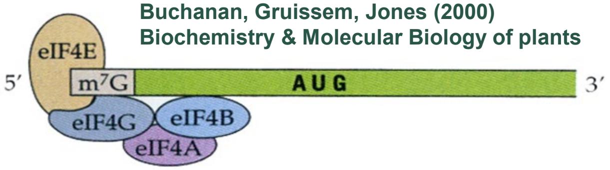
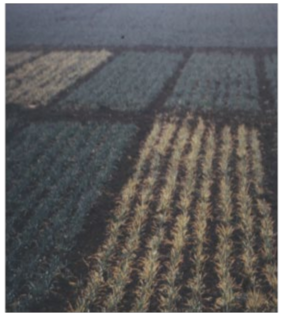
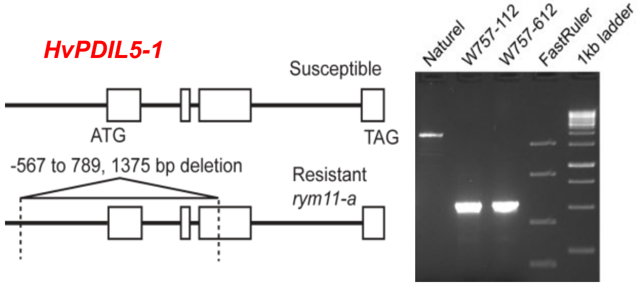


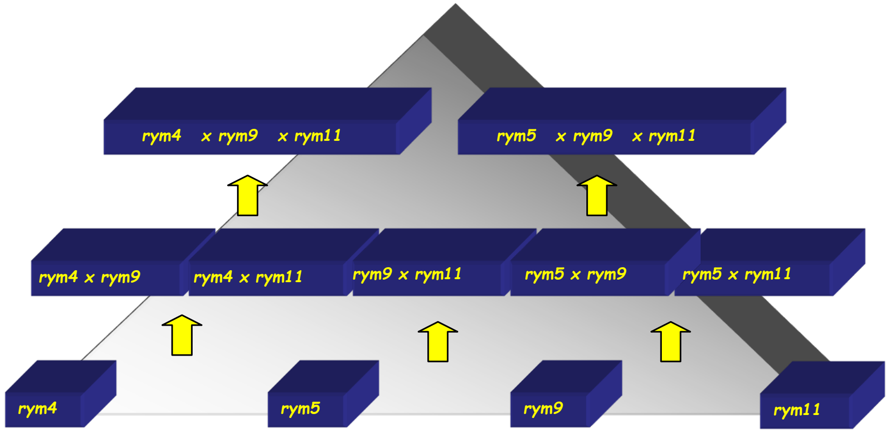
figure taken from:
Buchanan, Gruissem, Jones (2000)
Biochemistry & Molecular Biology of plants



***PROTEIN DISULFIDE ISOMERASE LIKE 5-1* is a susceptibility factor to plant viruses**

Ping Yang[a], Thomas Lüpken[b], Antje Habekuss[b], Goetz Hensel[c], Burkhard Steuernagel[d,1], Benjamin Kilian[a], Ruvini Ariyadasa[a], Axel Himmelbach[a], Jochen Kumlehn[c], Uwe Scholz[d], Frank Ordon[b,2], and Nils Stein[a,2,3]



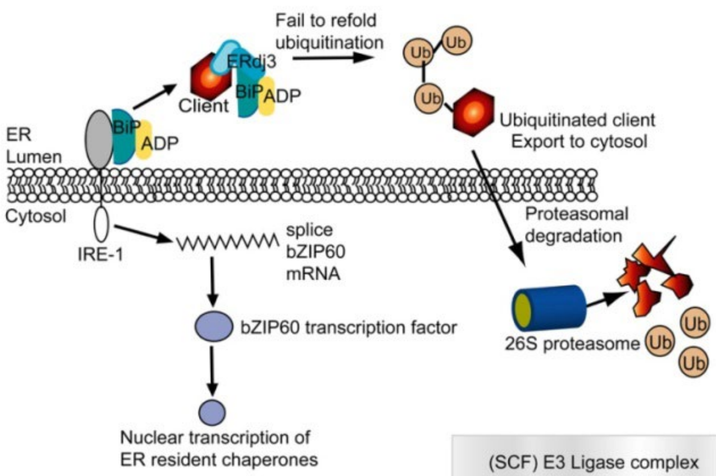


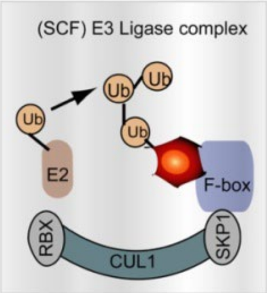
frontiers in PLANT SCIENCE
REVIEW ARTICLE
published: 06 December 2012
doi: 10.3389/fpls.2012.00275

Cellular chaperones and folding enzymes are vital contributors to membrane bound replication and movement complexes during plant RNA virus infection

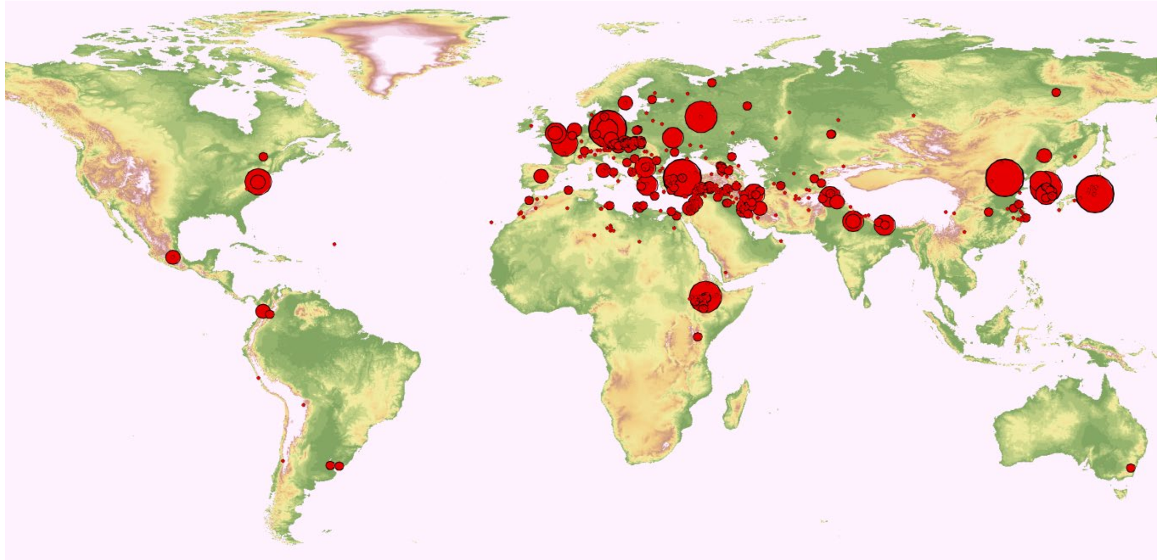
*Jeanmarie Verchot**
Department of Entomology and Plant Pathology, Oklahoma State University, Stillwater, OK, USA

ER Quality Control Machinery





Allele mining: *rym11*



***PROTEIN DISULFIDE ISOMERASE LIKE 5-1* is a susceptibility factor to plant viruses**

Ping Yang[a], Thomas Lüpken[b], Antje Habekuss[b], Goetz Hensel[c], Burkhard Steuernagel[d,1], Benjamin Kilian[a], Ruvini Ariyadasa[a], Axel Himmelbach[a], Jochen Kumlehn[c], Uwe Scholz[d], Frank Ordon[b,2], and Nils Stein[a,2,3]

365 Wild barley (*H. spontaneum*)

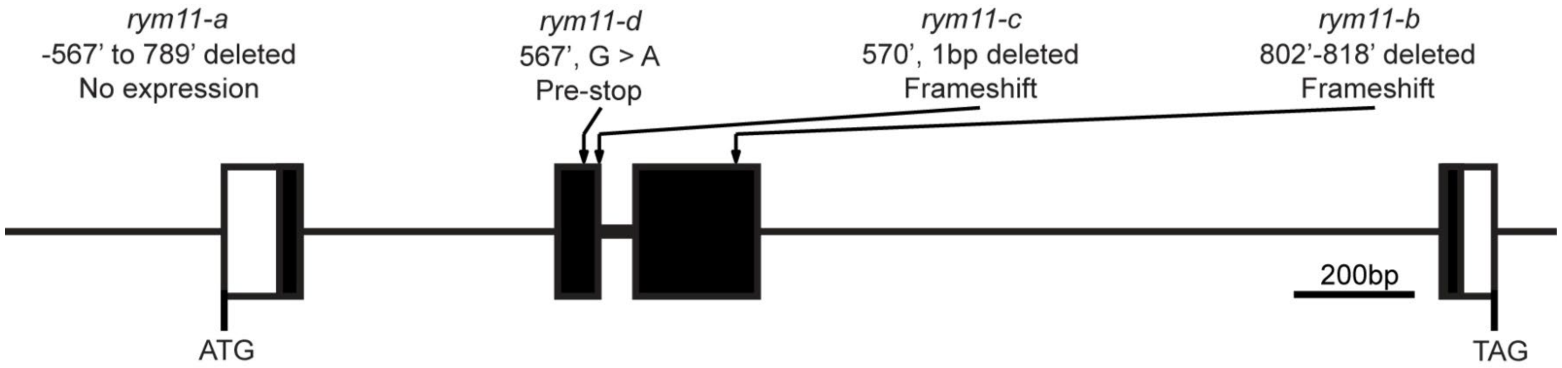
847 Landrace (*H. vulgare*)

559 Cultivar (*H. vulgare*)

5 *H. agriocrithon*

Total = 1.816 accessions

Number of accessions carrying different alleles



1

rym11-a
-567’ to 789’ deleted
No expression

4

rym11-d
567’, G > A
Pre-stop

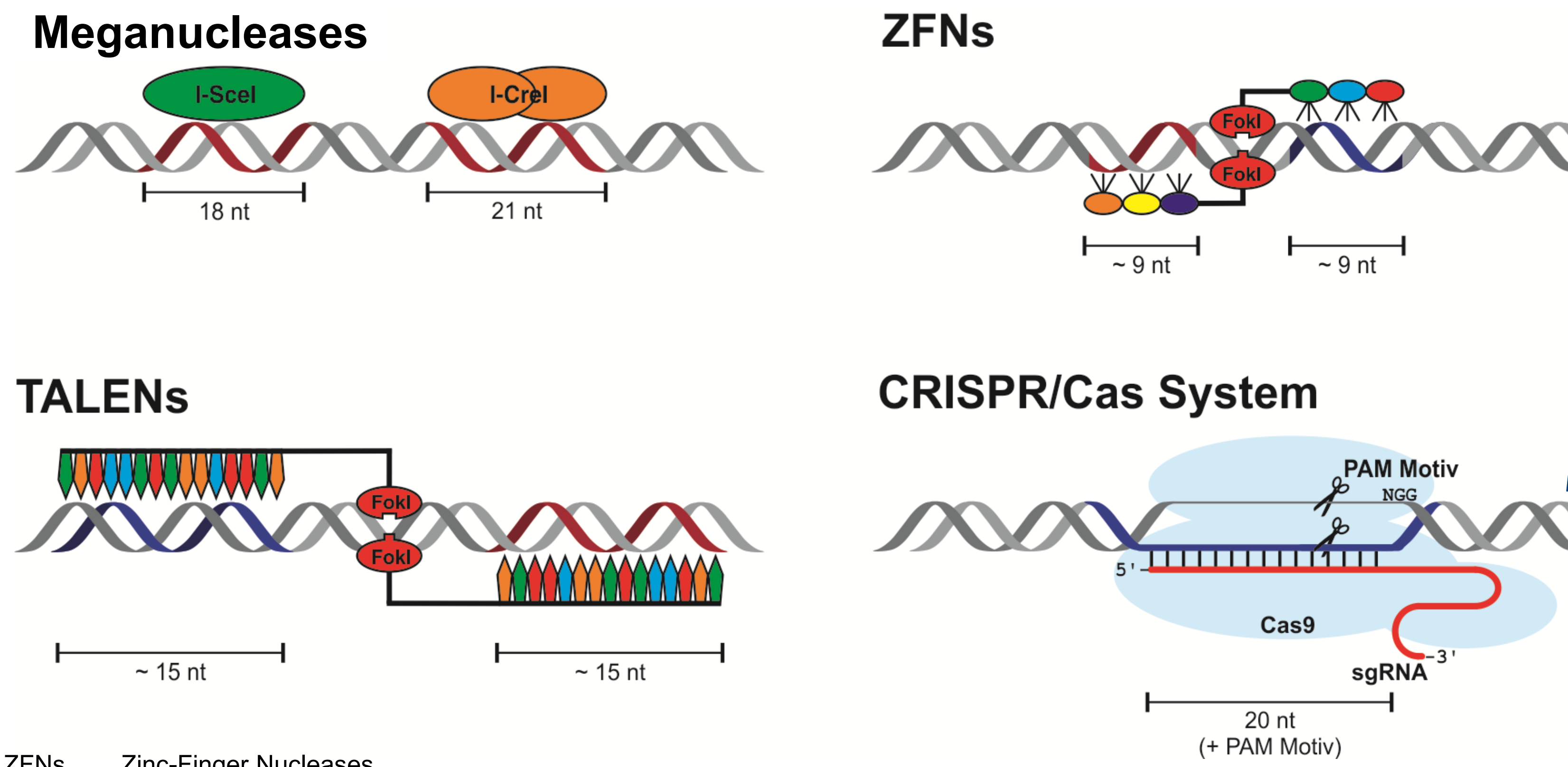
1

rym11-c
570’, 1bp deleted
Frameshift

28

rym11-b
802’-818’ deleted
Frameshift

Plant breeder´s toolbox - Genome editing


Meganucleases

ZFNs

TALENs

CRISPR/Cas System

ZFNs	Zinc-Finger Nucleases
TALENs	Transcription Activator-Like Effector Nucleases
CRISPR	Clustered Regularly Interspaced Short Palindromic Repeats
Cas	CRISPR-associated, RNA-guided endonuclease

Puchta and Fauser (2014) The Plant Journal


NOBELPRISET I KEMI 2020
THE NOBEL PRIZE IN CHEMISTRY 2020

KUNGL. VETENSKAPS-AKADEMIEN
THE ROYAL SWEDISH ACADEMY OF SCIENCES

Emmanuelle Charpentier

Jennifer A. Doudna

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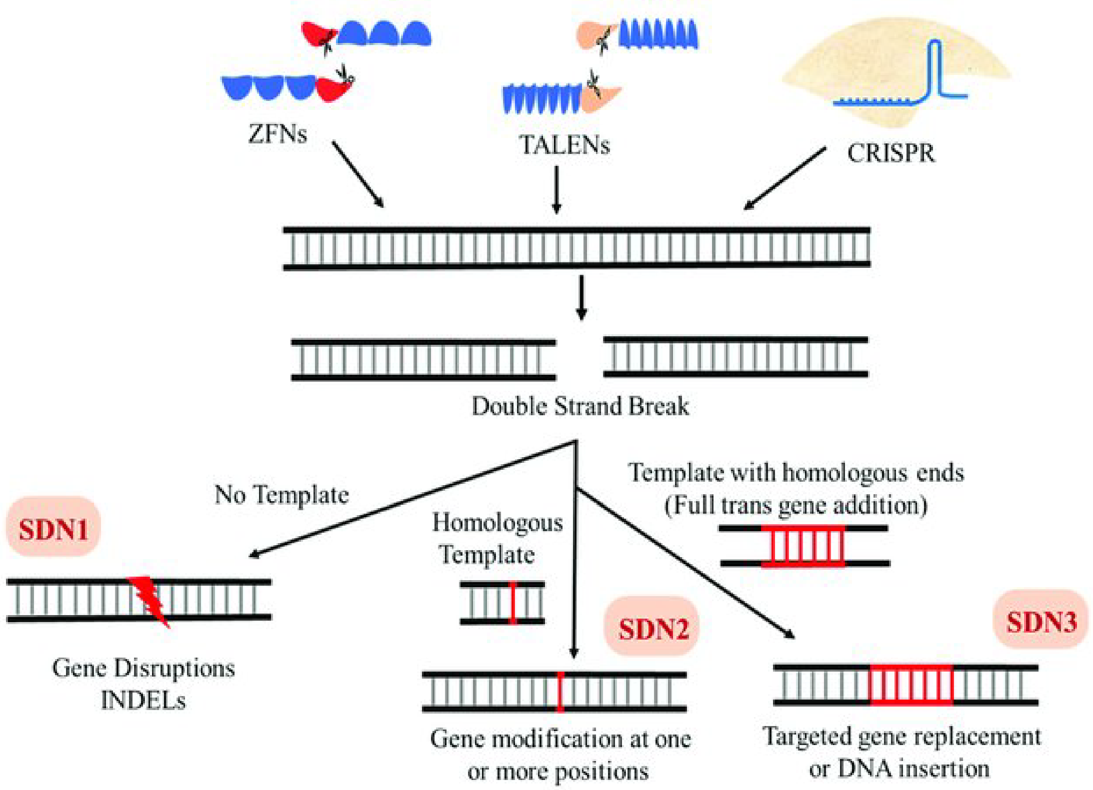
Read more about this year's Nobel Prize in Chemistry: www.kva.se/en

https://www.forschung-und-lehre.de/karriere/charpentier-und-doudna-erhalten-chemie-nobelpreis-3168

Plant breeder´s toolbox - Genome editing



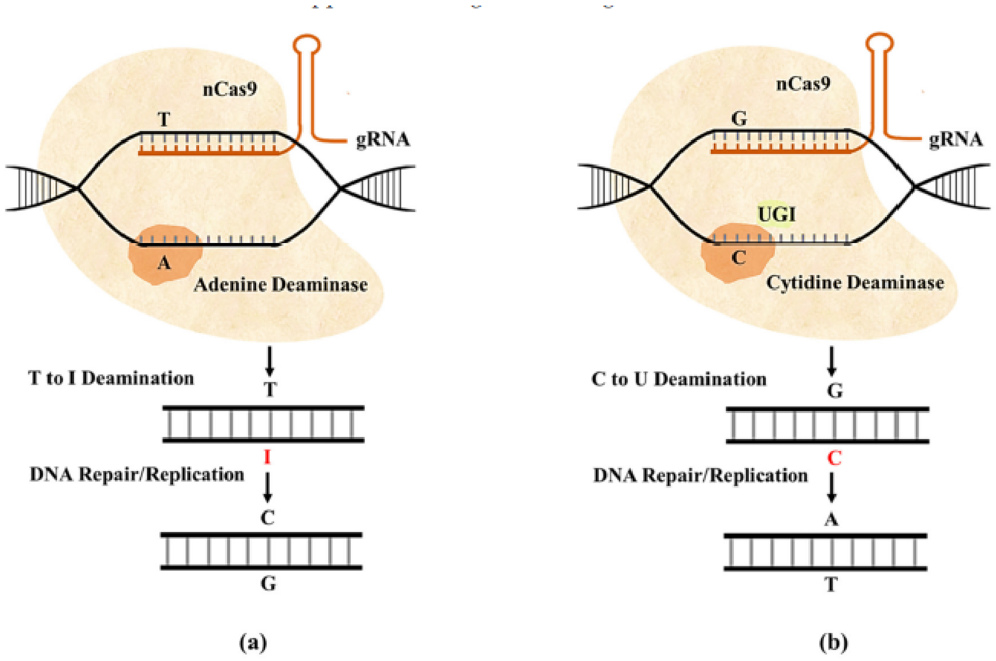
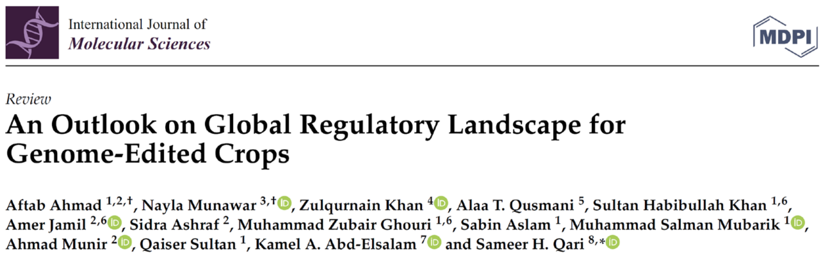


Figure 6. Schematic diagram of base editing with nickase Cas9 (nCas9). (**a**) ABE system uses nCas9 and adenine deaminase to catalyze transformation of adenine into guanine. ABE deaminates adenine to inosine (I), thus converting T-A to T-I. Repair machinery recognizes I as G and repair T-I as C-G; (**b**) CBE system utilizes nCas9 and cytidine deaminase to catalyze transformation of cytosine to uridine. Uracil glycosylase inhibitor (UGI) prevents U:G mismatch from being repaired back to C:G, and U is ultimately transformed into T.



International Journal of *Molecular Sciences*

MDPI

Review

An Outlook on Global Regulatory Landscape for Genome-Edited Crops

Aftab Ahmad [1,2,†], Nayla Munawar [3,†], Zulqurnain Khan [4], Alaa T. Qusmani [5], Sultan Habibullah Khan [1,6], Amer Jamil [2,6], Sidra Ashraf [2], Muhammad Zubair Ghouri [1,6], Sabin Aslam [1], Muhammad Salman Mubarik [1], Ahmad Munir [2], Qaiser Sultan [1], Kamel A. Abd-Elsalam [7] and Sameer H. Qari [8,*]

Genome editing – *rym4*


frontiers
in Genome Editing

ORIGINAL RESEARCH
published: 29 November 2021
doi: 10.3389/fgeed.2021.784233

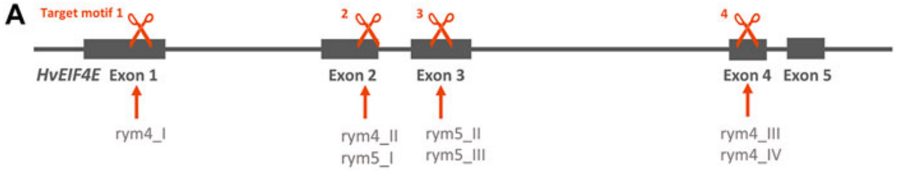
Check for updates

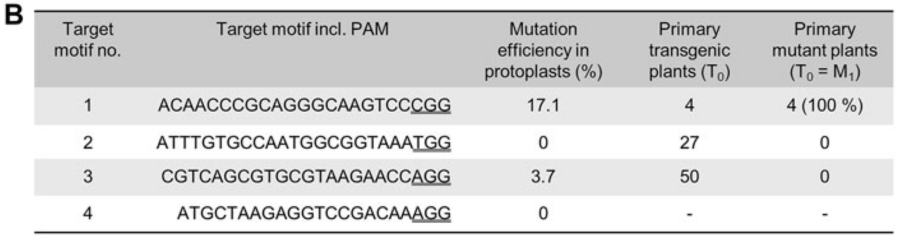
Targeted Knockout of Eukaryotic Translation Initiation Factor 4E Confers Bymovirus Resistance in Winter Barley

OPEN ACCESS

Edited by:

Robert Eric Hoffie[1†], Ingrid Otto[1], Dragan Perovic[2†], Nagaveni Budhagatapalli[1†], Antje Habekuß[2], Frank Ordon[2†] and Jochen Kumlehn[1†]*




B

Target motif no.	Target motif incl. PAM	Mutation efficiency in protoplasts (%)	Primary transgenic plants (T_0)	Primary mutant plants ($T_0 = M_1$)
1	ACAACCCGCAGGGCAAGTCCCGG	17.1	4	4 (100 %)
2	ATTTGTGCCAATGGCGGTAAATGG	0	27	0
3	CGTCAGCGTGCGTAAGAACCAGG	3.7	50	0
4	ATGCTAAGAGGTCCGACAAAGG	0	-	-

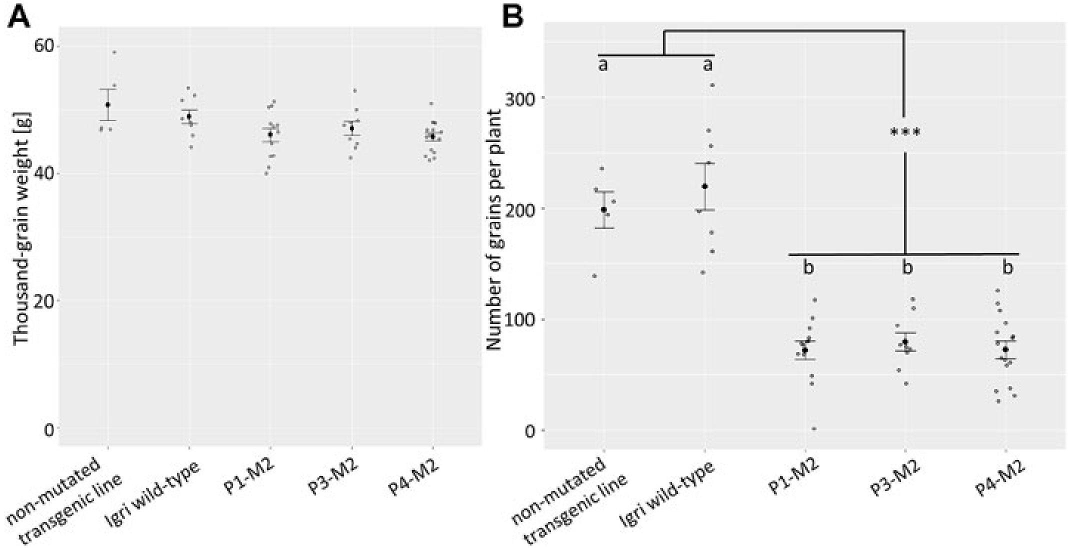
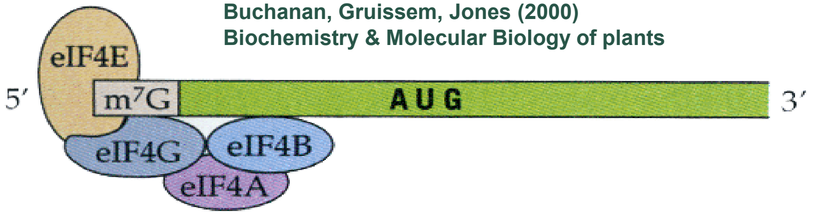
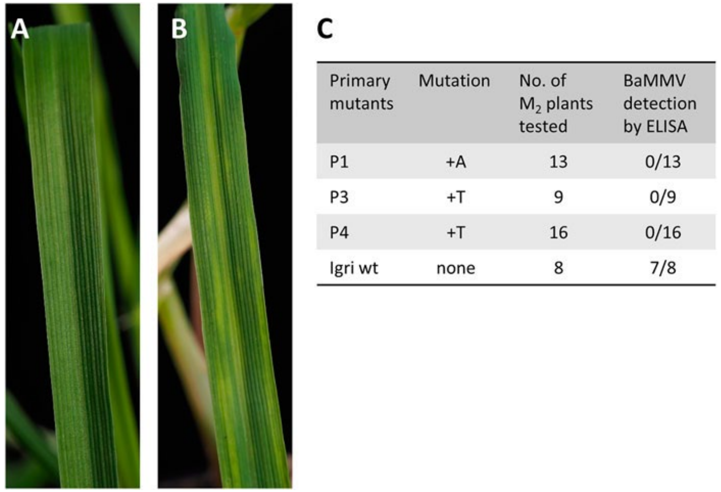


figure taken from:
Buchanan, Gruissem, Jones (2000)
Biochemistry & Molecular Biology of plants



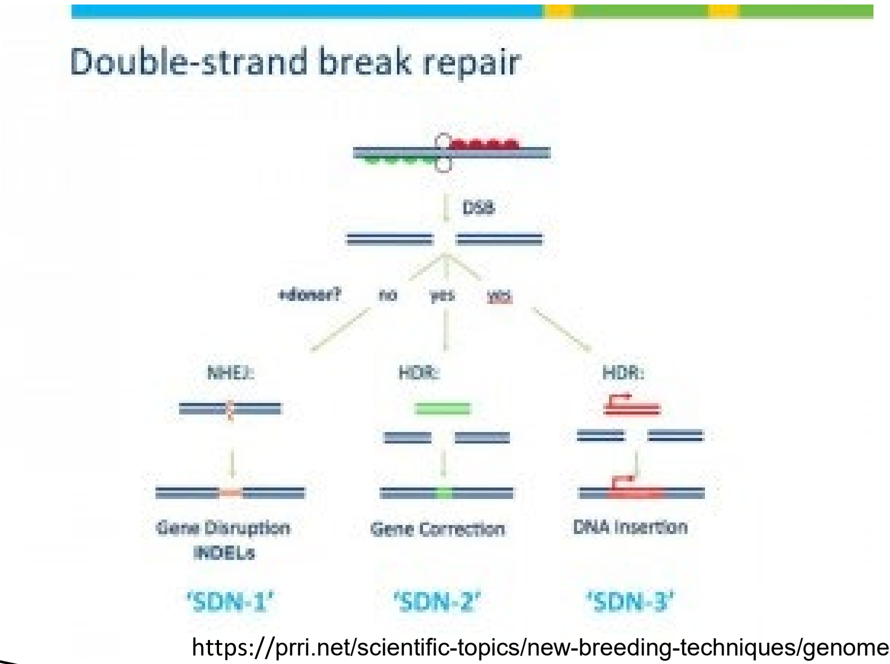


Primary mutants	Mutation	No. of M_2 plants tested	BaMMV detection by ELISA
P1	+A	13	0/13
P3	+T	9	0/9
P4	+T	16	0/16
Igri wt	none	8	7/8

Ruling of the Court of Justice of the EU, 25th July, 2018

Picture: Court of Justice of the European Union

- All organisms generated by mutagenesis are GMO.
- Organisms generated by targeted mutagenesis underly the strict regulations and are not excempted from any obligations.



https://prri.net/scientific-topics/new-breeding-techniques/genome-editing/site-directed-nuclease-sdn-genome-editing

Summary and future prospects

Improvements in plant breeder´s toolbox, e.g. the availability of high throughput marker technologies, genome sequences etc., and the possibilities of genome editing, have transferred plant breeding to a new era.

Knowledge on resistance gene sequences will facilitate efficient allele mining as well as the targeted editing of respective alleles, e.g. by CRISPR/Cas, resulting in a much faster combination of resistance with superior agronomic traits.

↓

Modern breeding for resistance will be the cornerstone for an environmental friendly and productive plant production in the background of climate change and the loss of insectizides and fungizides.

Thank you for your attention