Le TEA per migliorare le varietà di riso italiane

Ente Risi
Casello d’Agogna (PV)
30 agosto 2023

UNIVERSITÀ DEGLI STUDI DI MILANO

VITTORIA BRAMBILLA

DiSAA
DIPARTIMENTO
di SCIENZE
AGRARIE e
AMBIENTALI

E’ necessario continuare a migliorare le nostre piante per rispondere a:

-i cambiamenti climatici
-la siccità
-i parassiti
-la necessità di ridurre gli input
-la richiesta di una maggiore sostenibilità dell’agricoltura

Come miglioriamo le nostre piante?

Varietà poco produttiva ma resistente a siccità

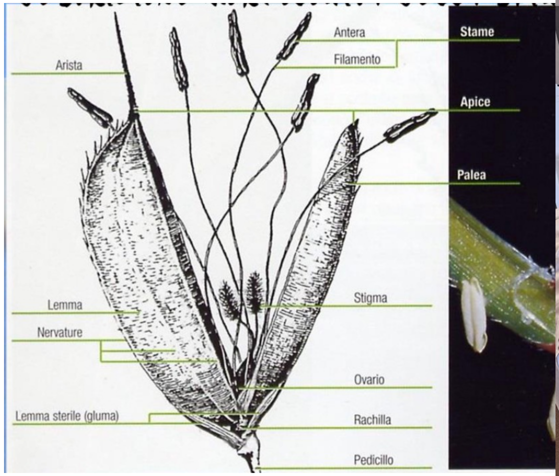
Varietà d’elitè ma poco tollerante alla siccità

combiniamo le caratteristiche migliori

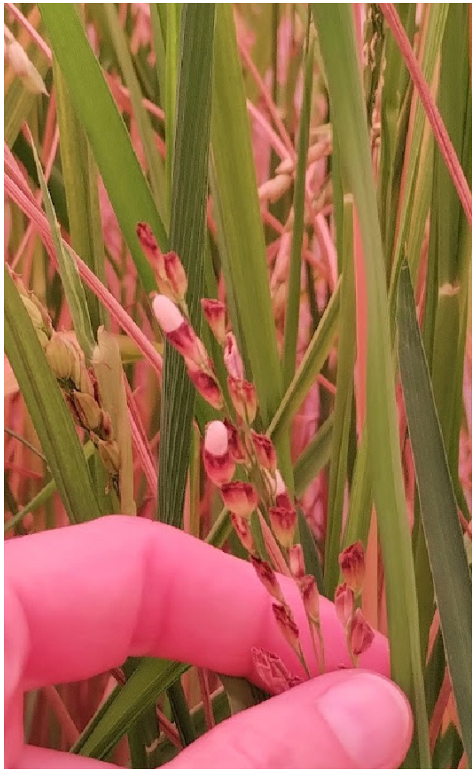
Varietà poco produttiva ma resistente a siccità

Varietà d’elitè ma poco tollerante alla siccità

possiamo incrociare le piante




Federico Mirone

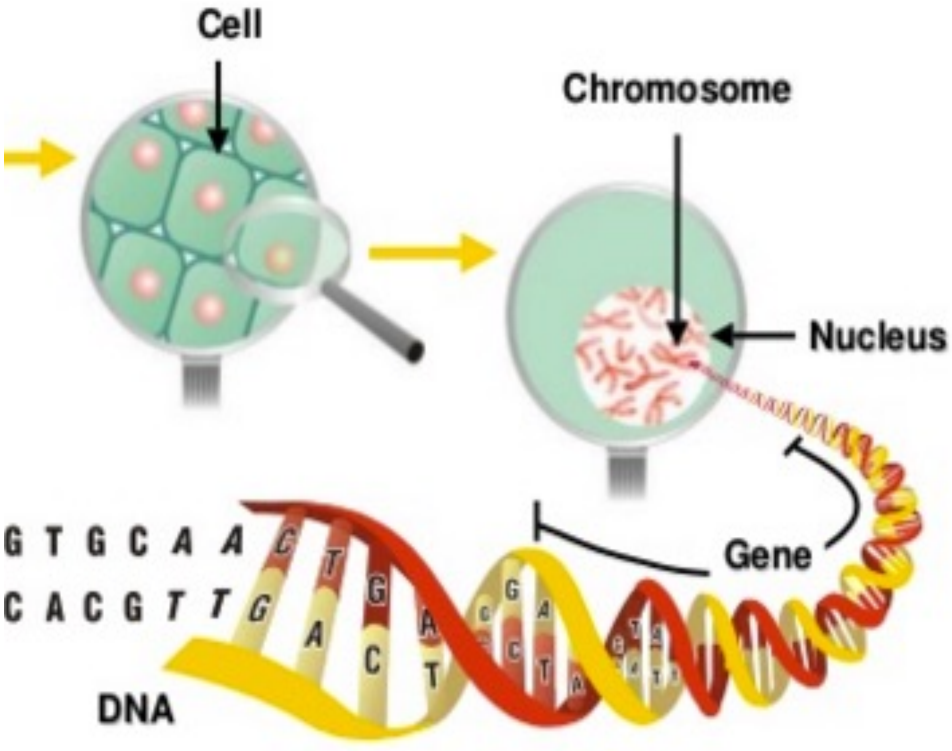


in riso: ci vogliono circa 8 anni per ottenere una nuova varietà per incrocio

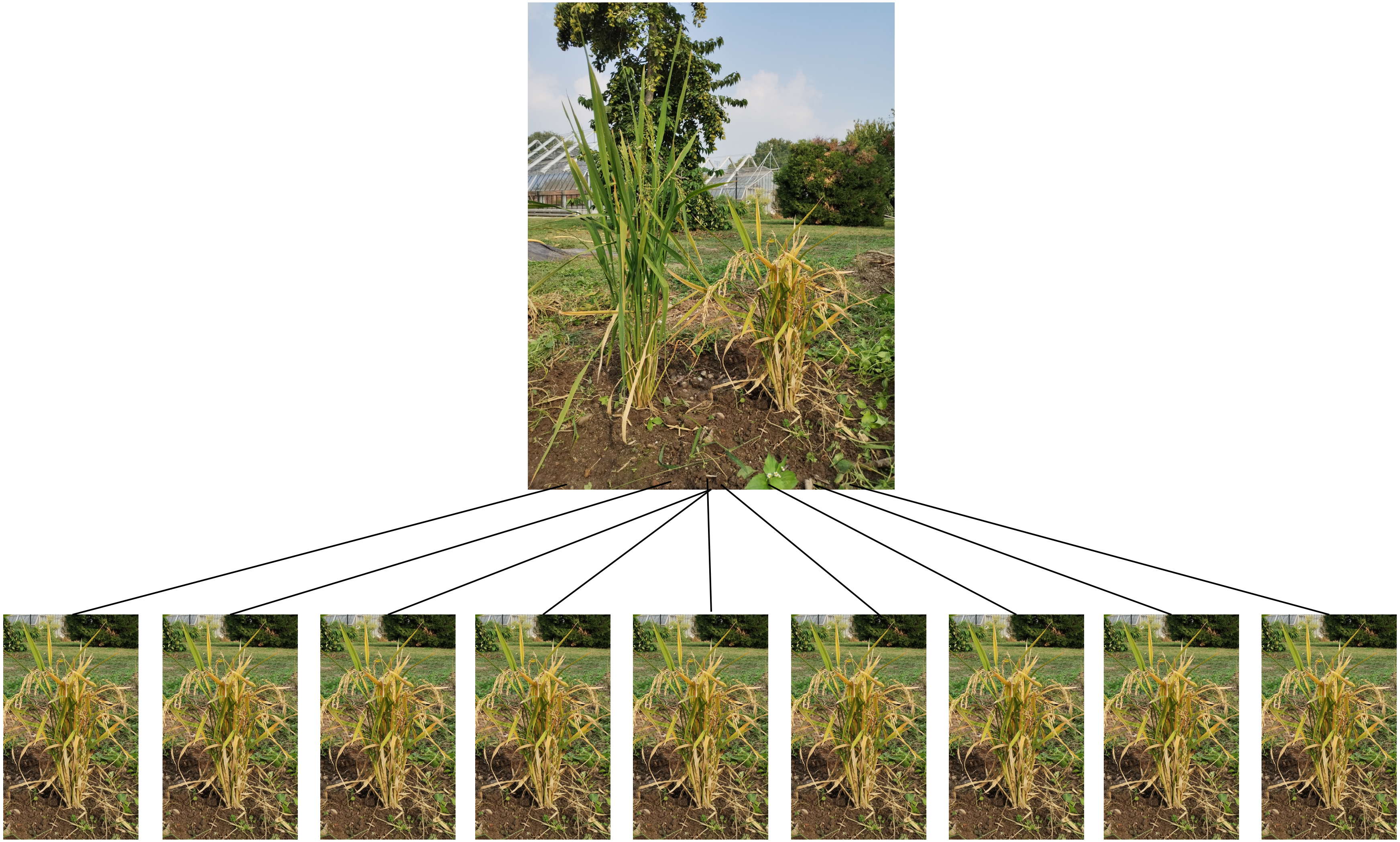
ma differenze nell’aspetto delle piante…

ma differenze nell’aspetto delle piante…

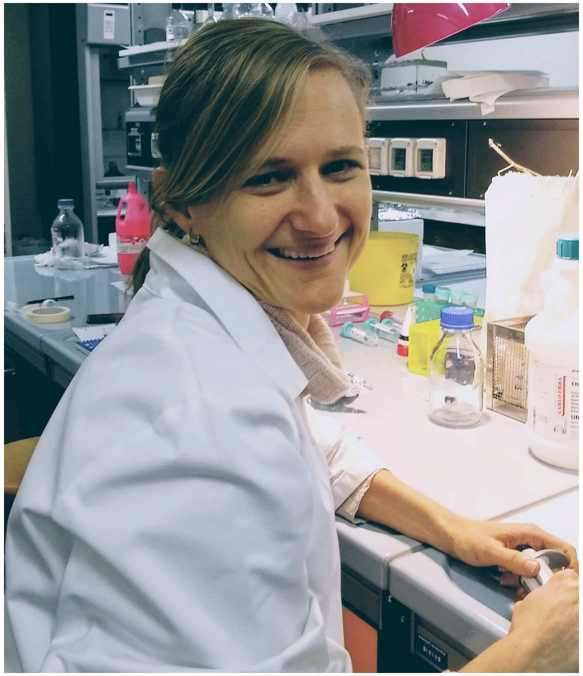
…corrispondono a differenze nei loro DNA

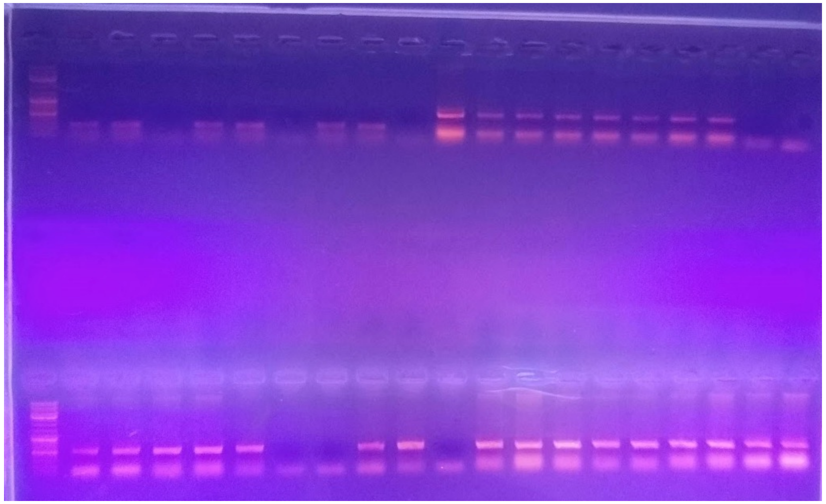


infatti possiamo selezionare le figlie delle piante incrociate



perché possiamo selezionare il DNA delle piante figlie



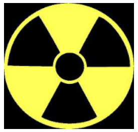


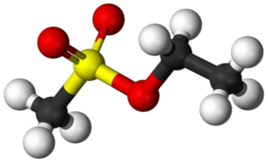
grazie ai marcatori molecolari
(Marker Assisted Selection)

per creare nuovi caratteri si possono anche usare la mutagenesi chimica o fisica

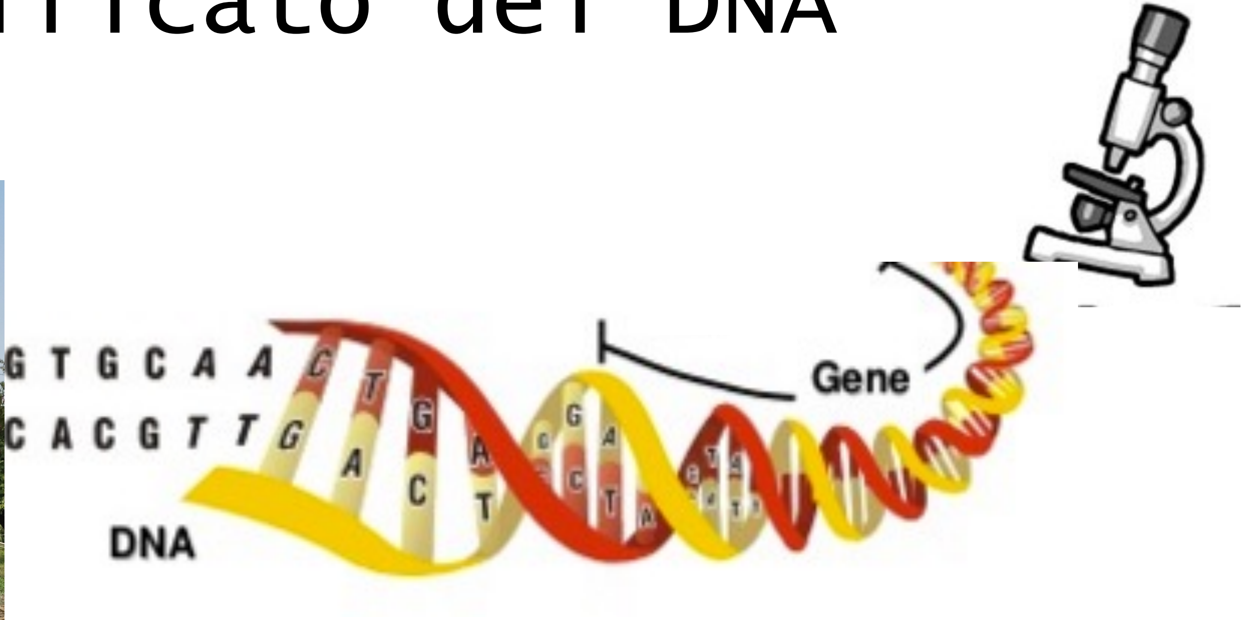
mutare
il DNA
«a caso»

TEMPI
LUNGHI,
risultati
inattesi





in tutto il mondo si studia il significato del DNA



conosciamo la funzione di molti GENI

conosciamo quali varianti nel DNA (o mutazioni nei geni) sono alla base del carattere che ci interessa

grazie a:

1) la conoscenza dei geni

2) le TEA -
- Tecniche di Evoluzione Assistita-

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1) la conoscenza dei geni

2) le TEA -
- Tecniche di Evoluzione Assistita-

possiamo riprodurre i risultati degli incroci o della mutazione casuale in una sola generazione le TEA hanno avuto crescente importanza negli ultimi anni.

Per TEA intendiamo:

1) Genome Editing

2) CISGENESI

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aggiunta di un tratto di DNA da una specie sessualmente compatibile

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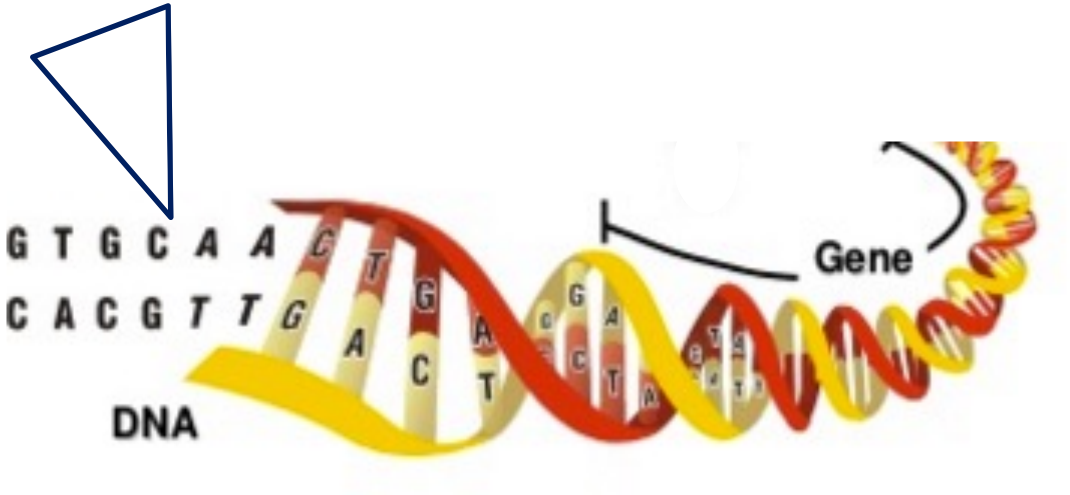
aggiunta di un tratto di DNA da una specie sessualmente compatibile



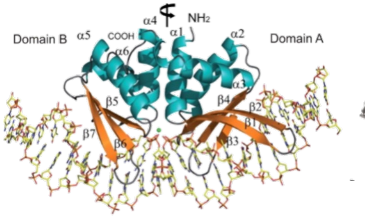
può avere applicazioni utili in riso

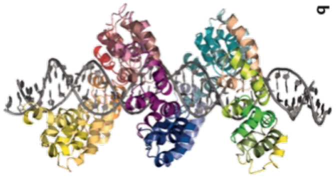
è particolarmente utile nelle specie arboree, difficilmente incrociabili

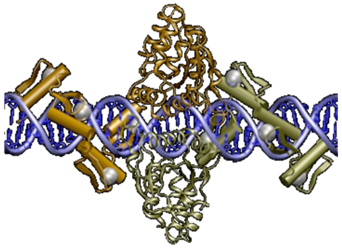
1) Genome Editing

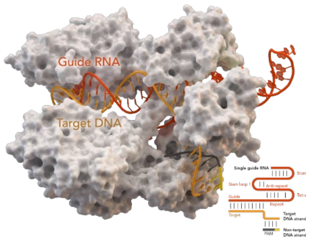
- Oligonucleotide Directed Mutagenesis
- Meganucleases
- Zinc Finger Nucleases
- Transcription Activator Like Effector Nucleases (TALEN)
- CRISPR/Cas9

NUCLEASI









1) Genome Editing

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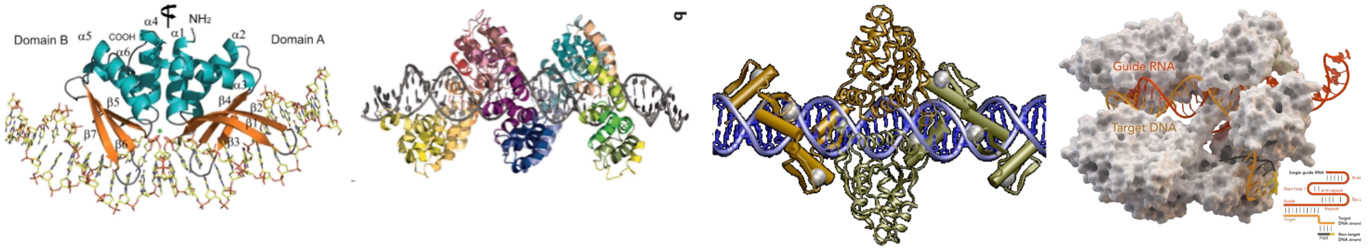
NUCLEASI

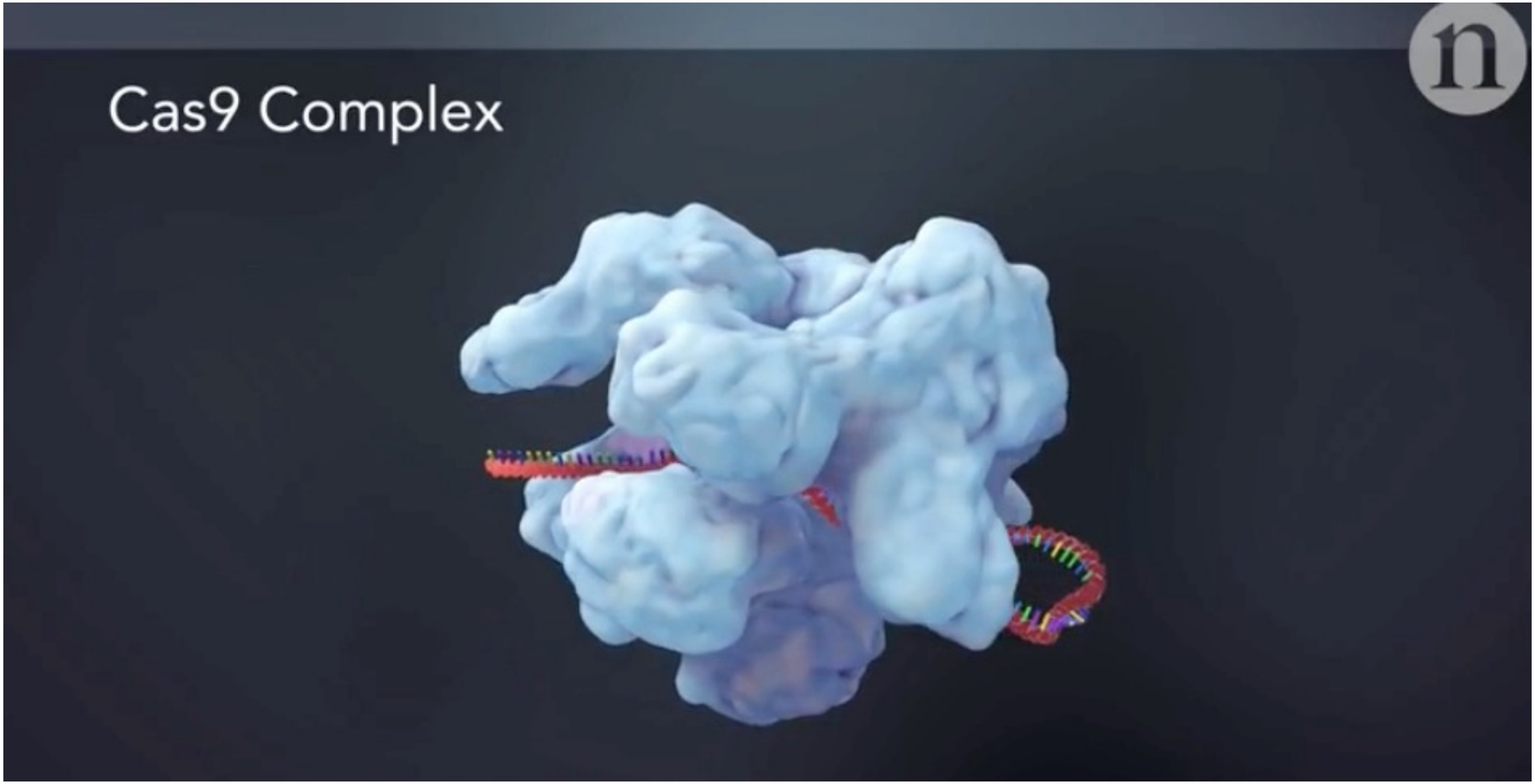


Premio Nobel per la Chimica 2020

CRISPR/Cas9

Emmanuelle Charpentier

Jennifer Doudna


Cas9 Complex

Jennifer Doudna

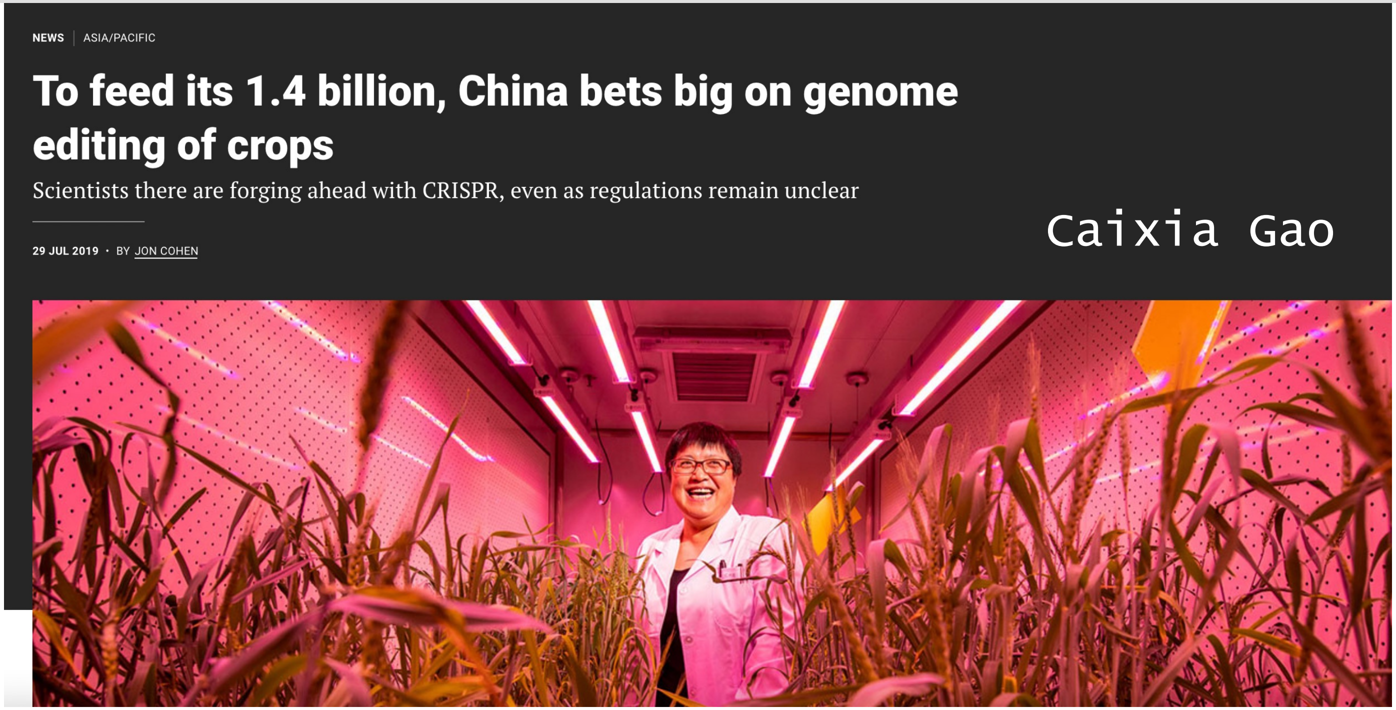
«CRISPR può aiutare l'umanità soprattutto contribuendo a migliorare l'AGRICOLTURA»


Jennifer Doudna

«CRISPR può aiutare l'umanità soprattutto contribuendo a migliorare l'AGRICOLTURA»

State Key Laboratory of Plant Cell and Chromosome Engineering

Institute of Genetics and Developmental Biology , Chinese Academy of Sciences


NEWS | ASIA/PACIFIC

To feed its 1.4 billion, China bets big on genome editing of crops

Scientists there are forging ahead with CRISPR, even as regulations remain unclear

29 JUL 2019 · BY JON COHEN

Caixia Gao

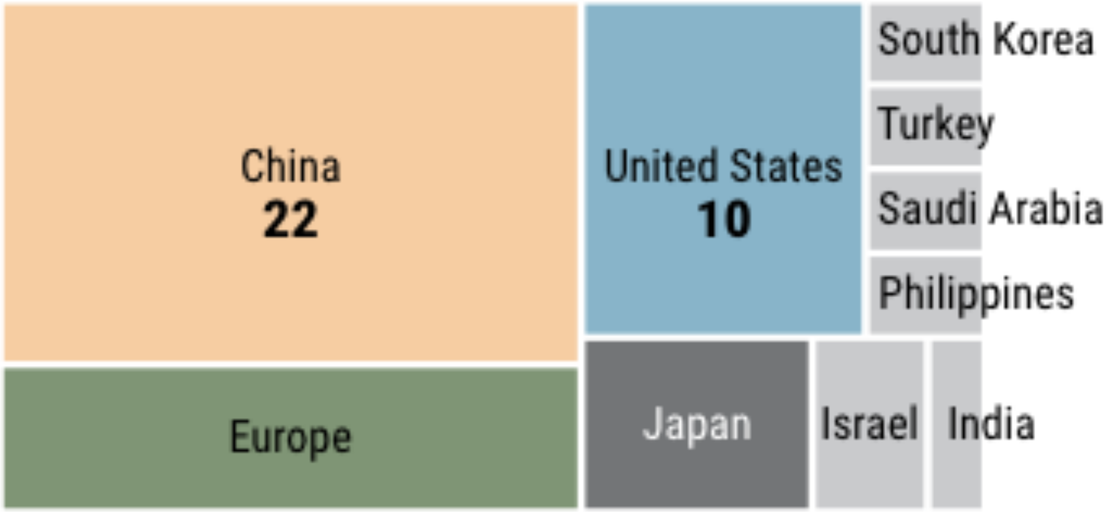
SHARE

With its CRISPR revolution, China becomes a world leader in genome editing

By **Jon Cohen, Nirja Desai** | Aug. 2, 2019 , 8:00 AM

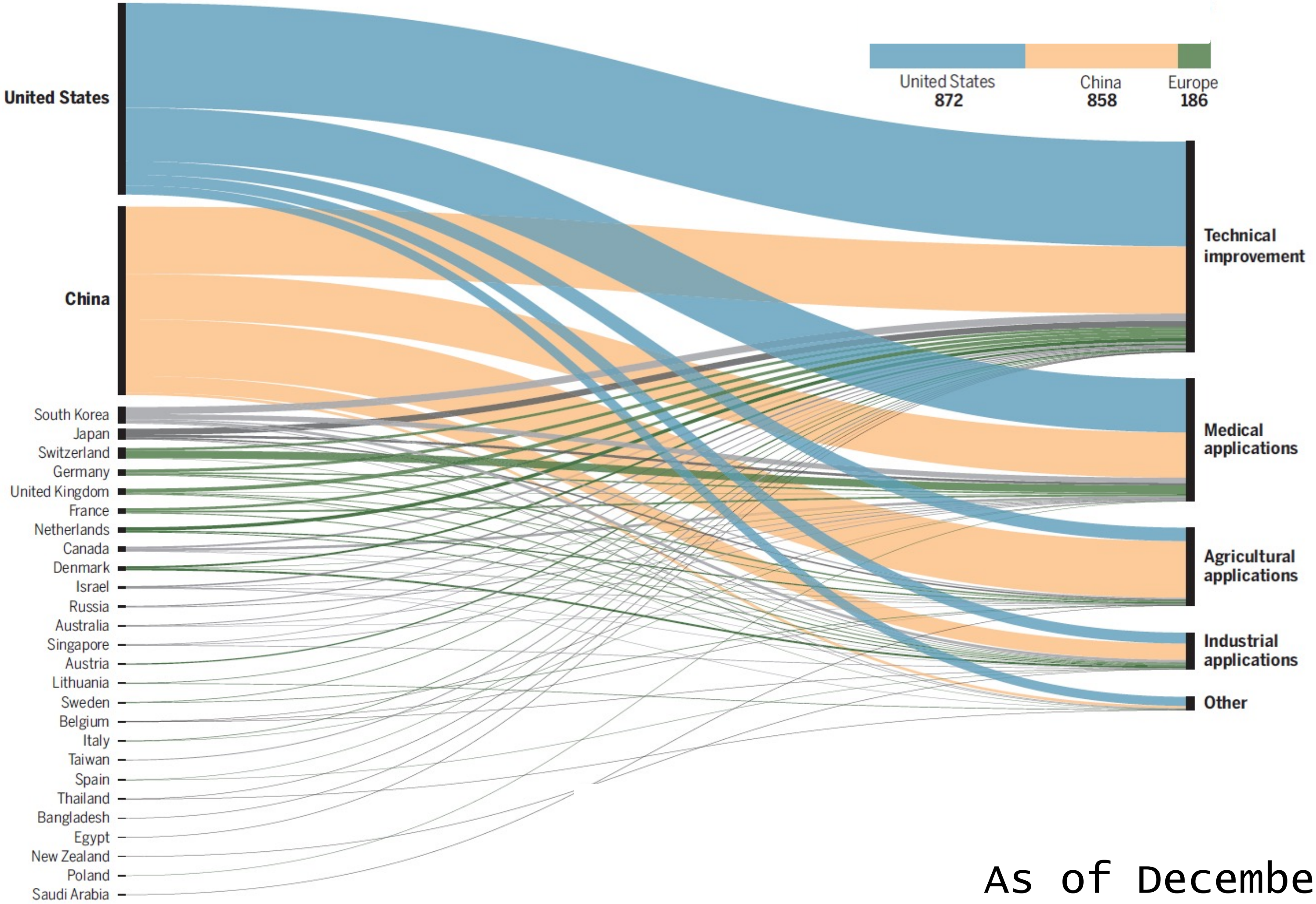
Planting a flag

Among 52 CRISPR publications on improving traits in agricultural crops, published between 2014 and 2017, China accounted for 42% of them.



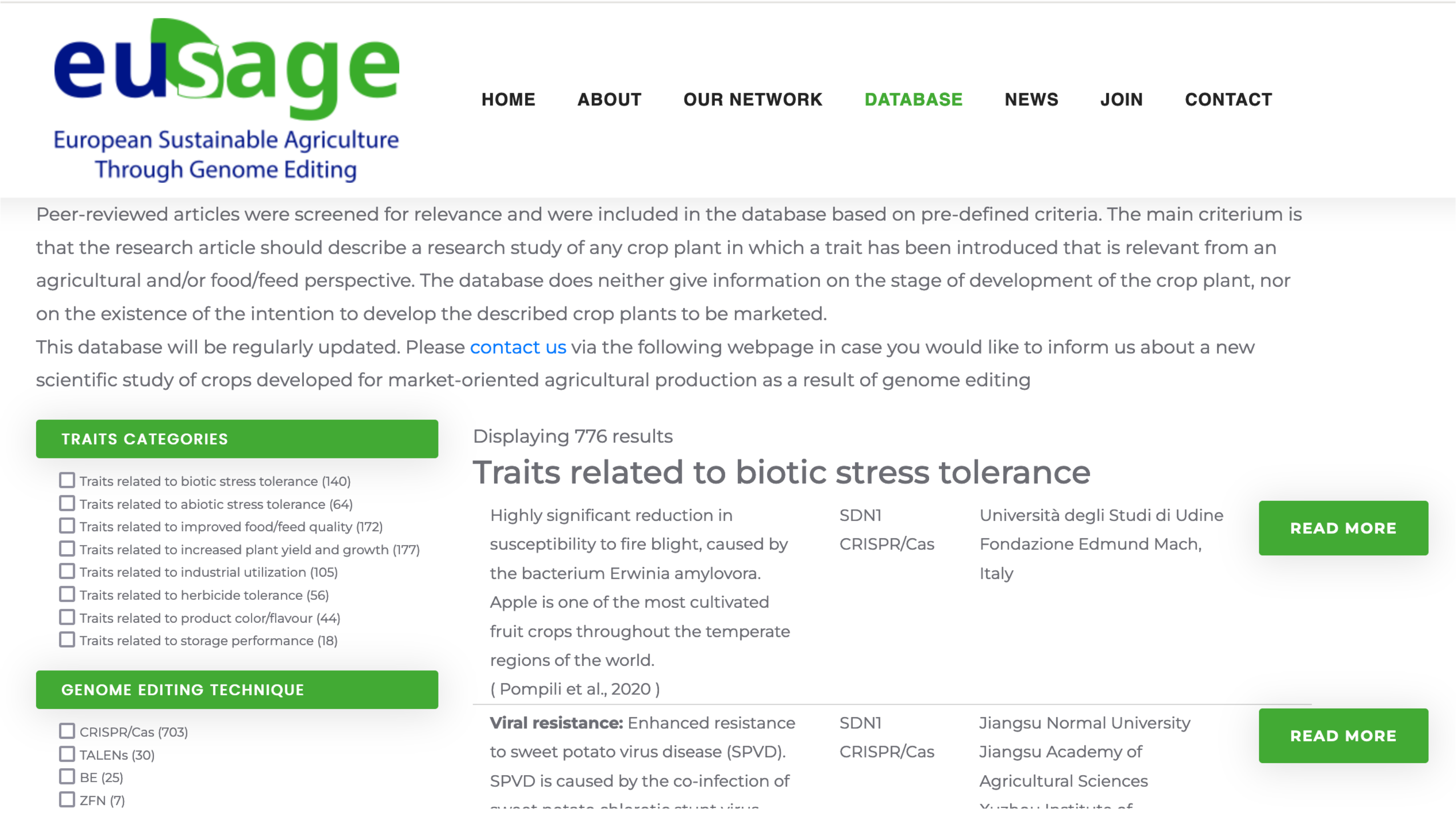
la maggior parte dei brevetti pubblici basati su CRISPR sono stati depositati in Cina

la maggior parte dei brevetti pubblici basati su CRISPR depositati in Cina hanno applicazioni in agricoltura



As of December 2018

database di piante migliorate con TEA



Peer-reviewed articles were screened for relevance and were included in the database based on pre-defined criteria. The main criterium is that the research article should describe a research study of any crop plant in which a trait has been introduced that is relevant from an agricultural and/or food/feed perspective. The database does neither give information on the stage of development of the crop plant, nor on the existence of the intention to develop the described crop plants to be marketed.

This database will be regularly updated. Please contact us via the following webpage in case you would like to inform us about a new scientific study of crops developed for market-oriented agricultural production as a result of genome editing

TRAITS CATEGORIES

- ☐ Traits related to biotic stress tolerance (140)
- ☐ Traits related to abiotic stress tolerance (64)
- ☐ Traits related to improved food/feed quality (172)
- ☐ Traits related to increased plant yield and growth (177)
- ☐ Traits related to industrial utilization (105)
- ☐ Traits related to herbicide tolerance (56)
- ☐ Traits related to product color/flavour (44)
- ☐ Traits related to storage performance (18)

GENOME EDITING TECHNIQUE

- ☐ CRISPR/Cas (703)
- ☐ TALENs (30)
- ☐ BE (25)
- ☐ ZFN (7)

Displaying 776 results

Traits related to biotic stress tolerance

Highly significant reduction in susceptibility to fire blight, caused by the bacterium Erwinia amylovora. Apple is one of the most cultivated fruit crops throughout the temperate regions of the world. (Pompili et al., 2020)	SDN1 CRISPR/Cas	Università degli Studi di Udine Fondazione Edmund Mach, Italy
Viral resistance: Enhanced resistance to sweet potato virus disease (SPVD). SPVD is caused by the co-infection of	SDN1 CRISPR/Cas	Jiangsu Normal University Jiangsu Academy of Agricultural Sciences

https://www.eu-sage.eu/genome-search

con le TEA possiamo cambiare SOLO il carattere che ci interessa

TEMPI BREVISSIMI, grande precisione

Nel 2013 studiavamo la fioritura in riso e abbiamo mutato due geni

mutanti CRISPR
nei geni *hfb1 hbf2*

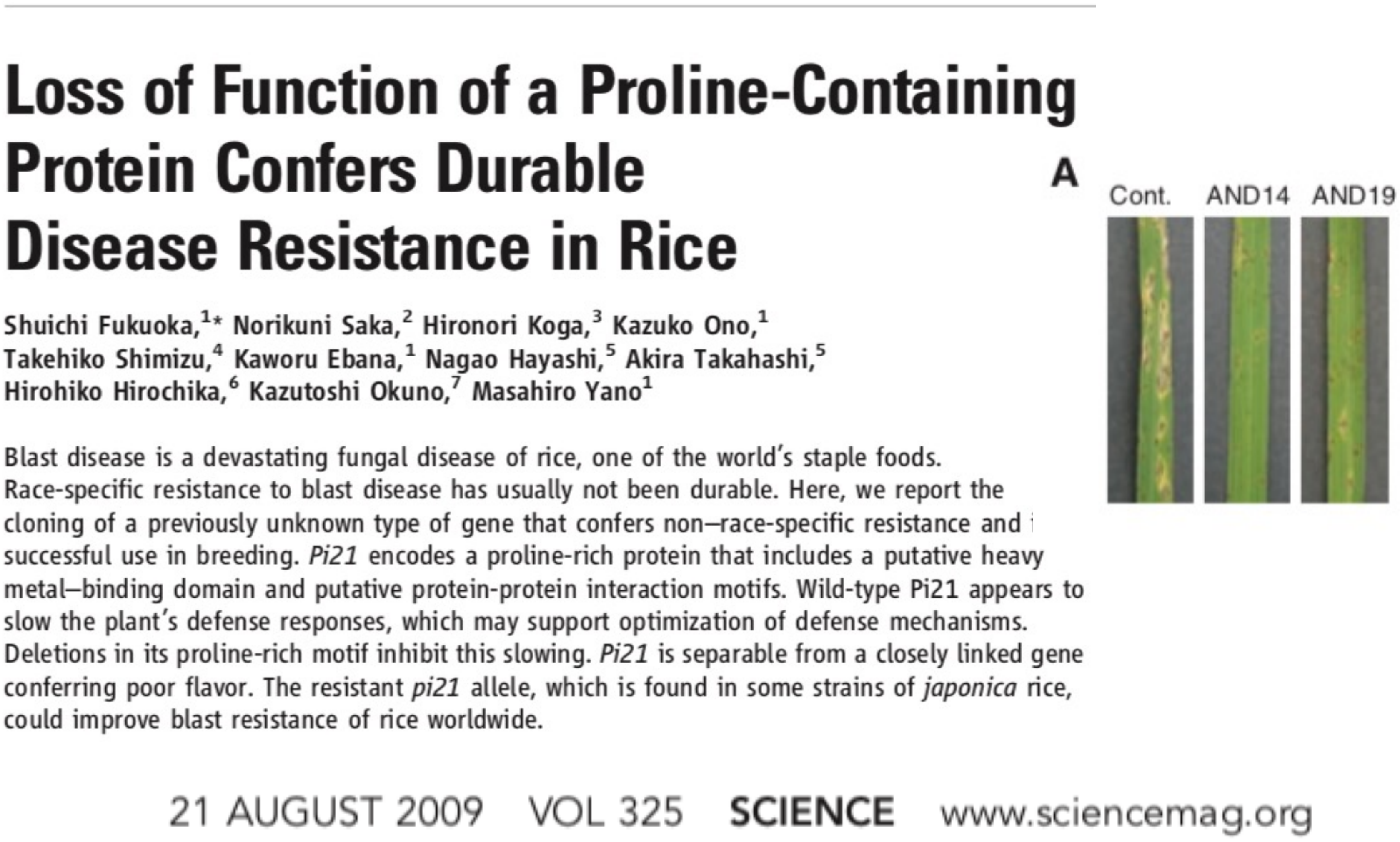
controllo

Ciclo piu’ breve

Brambilla et al., the Plant Cell 2017

piante suscettibili a brusone (causata dal patogeno Pyricularia oryzae) possono essere gravemente colpite da questa malattia

da molti anni è nota una variante del gene Pi21 che conferisce resistenza durevole a brusone



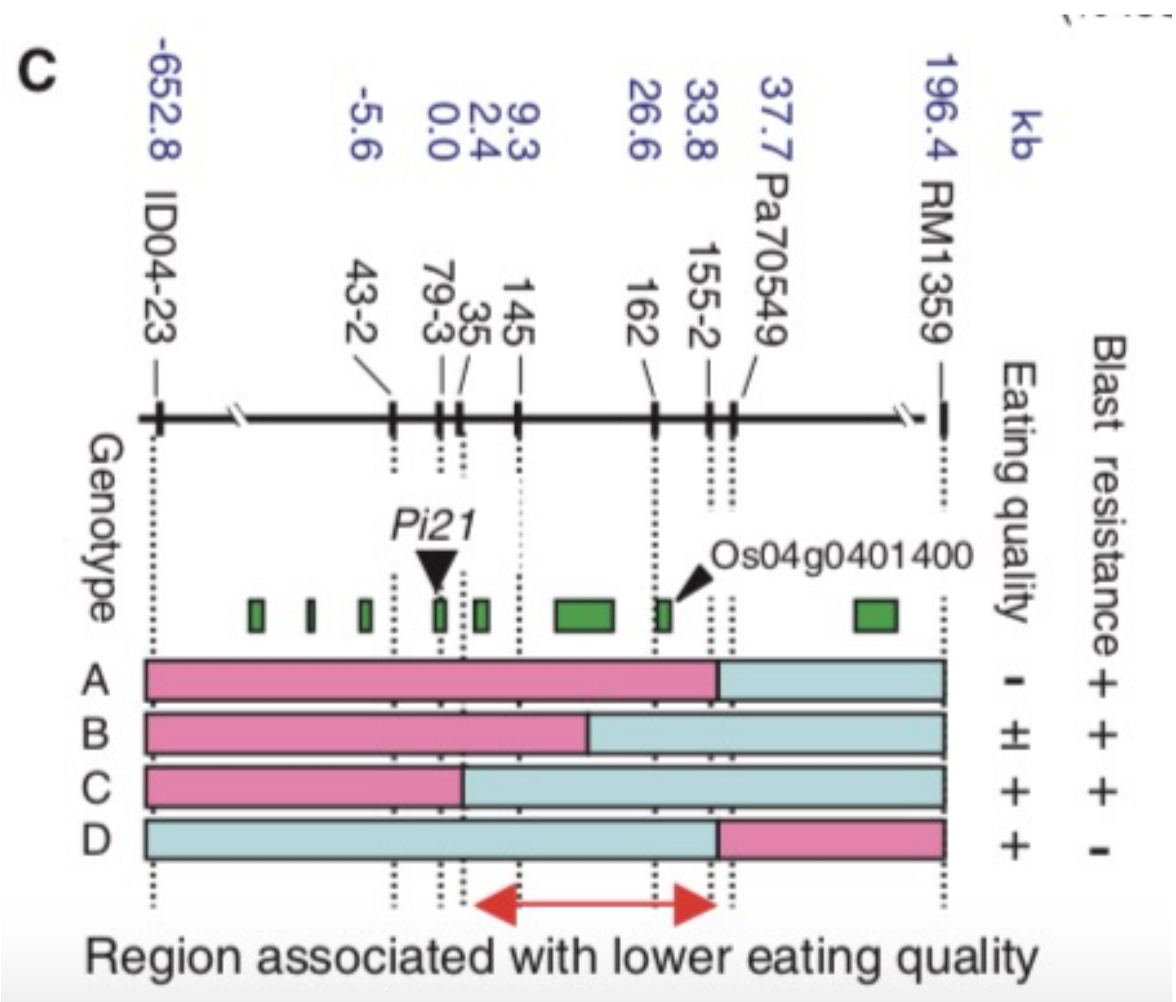
Loss of Function of a Proline-Containing Protein Confers Durable Disease Resistance in Rice

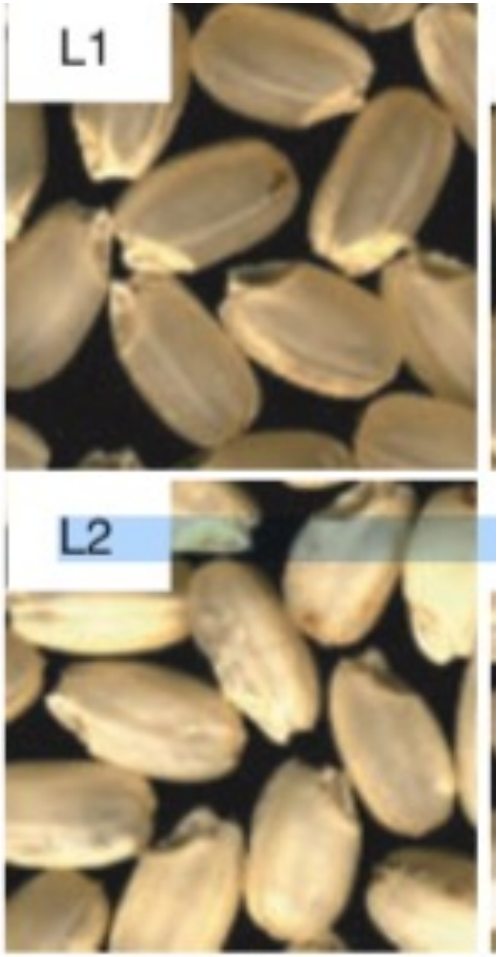
Shuichi Fukuoka,[1]* Norikuni Saka,[2] Hironori Koga,[3] Kazuko Ono,[1] Takehiko Shimizu,[4] Kaworu Ebana,[1] Nagao Hayashi,[5] Akira Takahashi,[5] Hirohiko Hirochika,[6] Kazutoshi Okuno,[7] Masahiro Yano[1]

Blast disease is a devastating fungal disease of rice, one of the world's staple foods. Race-specific resistance to blast disease has usually not been durable. Here, we report the cloning of a previously unknown type of gene that confers non–race-specific resistance and successful use in breeding. *Pi21* encodes a proline-rich protein that includes a putative heavy metal–binding domain and putative protein-protein interaction motifs. Wild-type Pi21 appears to slow the plant's defense responses, which may support optimization of defense mechanisms. Deletions in its proline-rich motif inhibit this slowing. *Pi21* is separable from a closely linked gene conferring poor flavor. The resistant *pi21* allele, which is found in some strains of *japonica* rice, could improve blast resistance of rice worldwide.

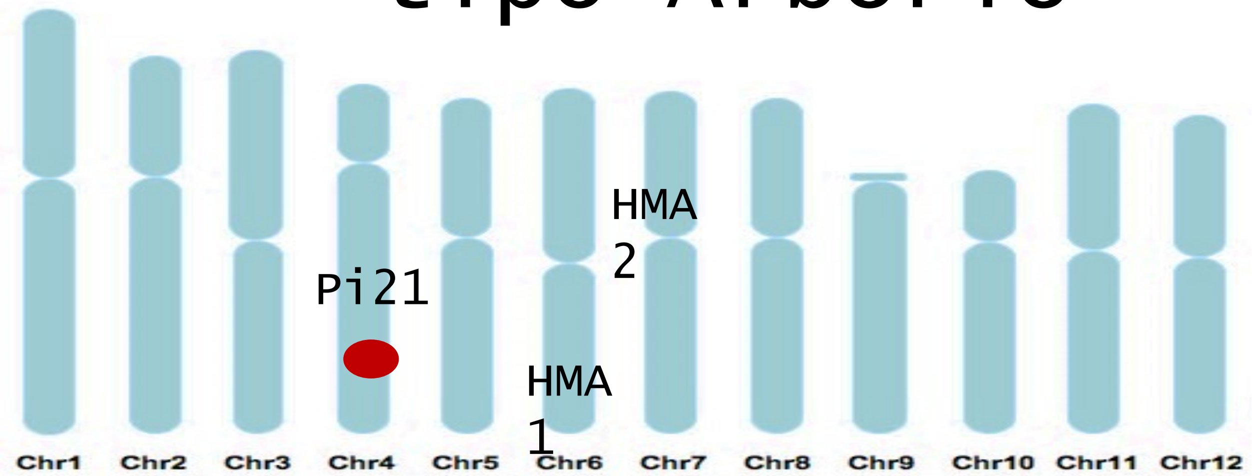
21 AUGUST 2009 VOL 325 **SCIENCE** www.sciencemag.org

questa resistenza non è stata usata dai breeder perché associata ad una granella di cattiva qualità





nel 2017 abbiamo inserito con CRISPR la mutazione in Pi21 e altri due geni in una varietà tipo Arborio

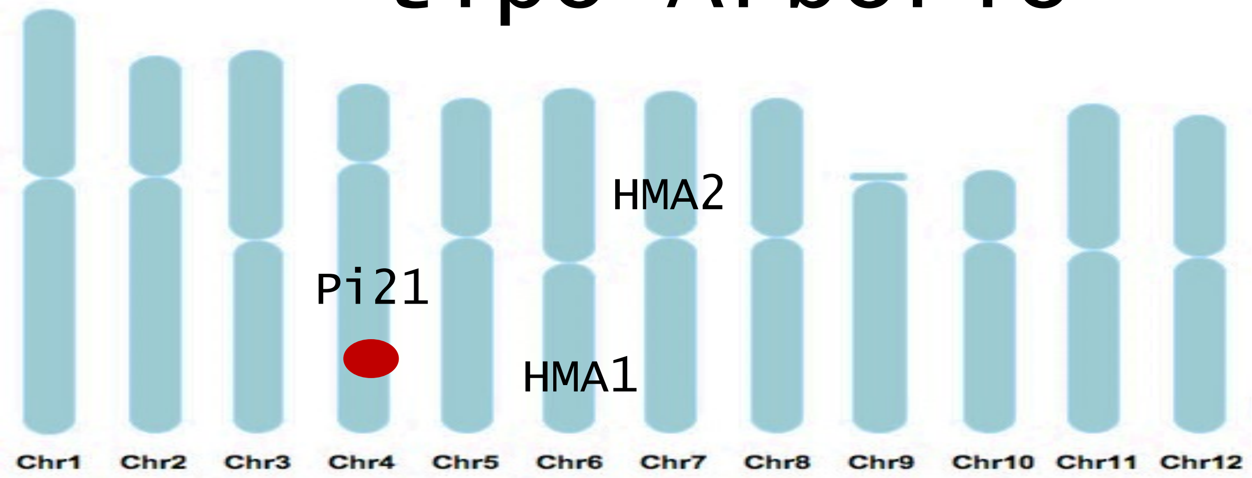


- influisce negativamente sulla qualità della granella

UNIVERSITAS STUDIORUM MEDIOLANENSIS

TheSainsburyLaboratory
TSL

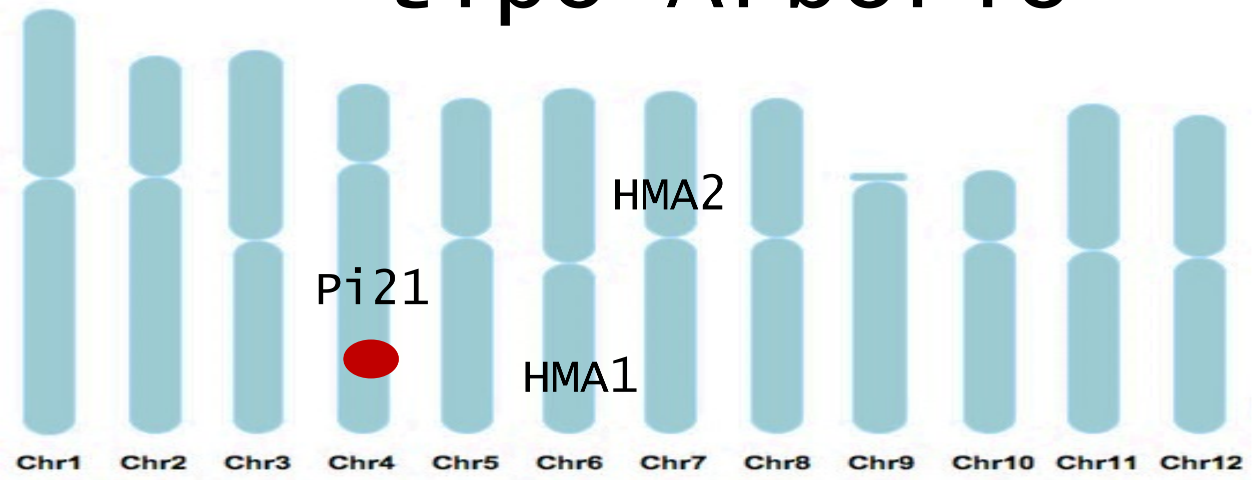
nel 2017 abbiamo inserito con CRISPR la mutazione in Pi21 e altri due geni in una varietà tipo Arborio



● influisce negativamente sulla qualità della granella

SENZA ALTERARE LA QUALITA’ DELLA GRANELLA

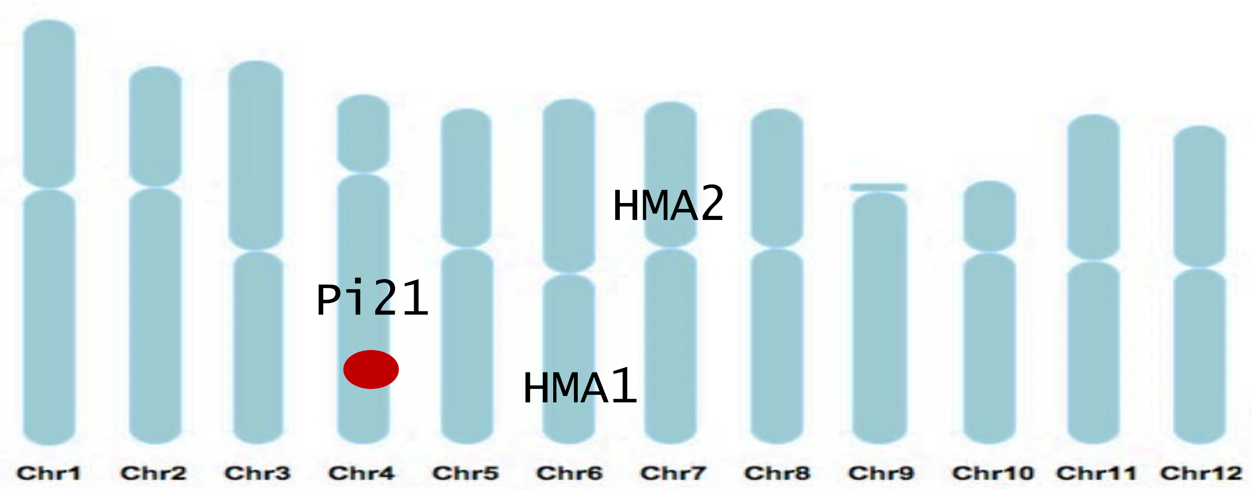
nel 2017 abbiamo inserito con CRISPR la mutazione in Pi21 e altri due geni in una varietà tipo Arborio



● influisce negativamente sulla qualità della granella

I SEMI SONO IN FRIGORIFERO DA 5 ANNI

confidiamo di fare le prime sperimentazioni in campo nel 2024



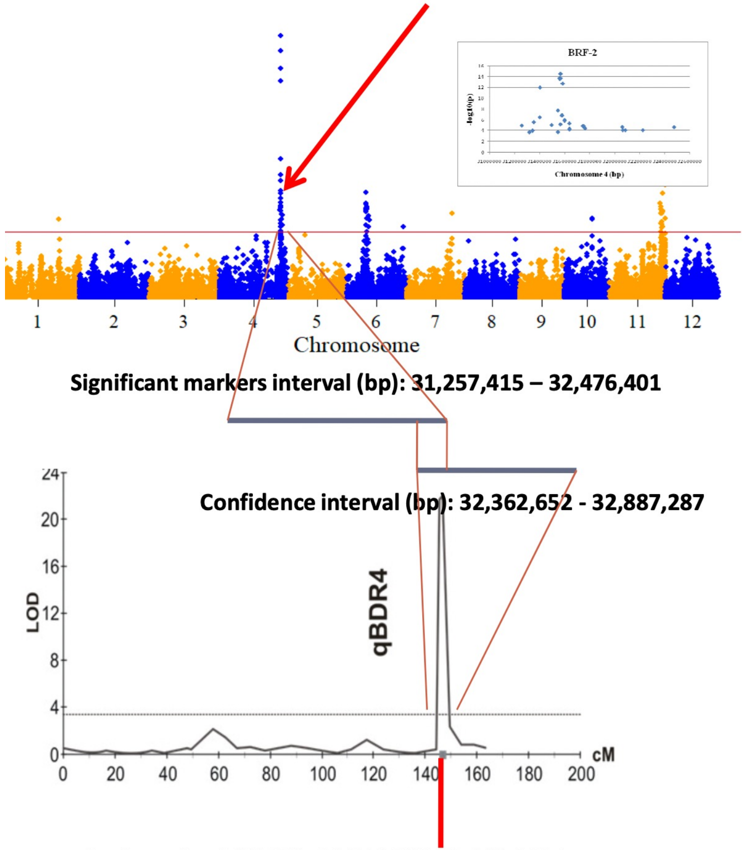
● influisce negativamente sulla qualità della granella

FONDAZIONE BUSSOLERA BRANCA

Un altro gene probabilmente coinvolto nella resistenza a brusone

identificato da:

- **Giampiero Valè** Università del Piemonte Orientale, Vercelli
- -**Blanca San Segundo** CRAG, Bacellona, Spagna


Peak marker position: bp 31,566,281 (marker S4_31566281)

Significant markers interval (bp): 31,257,415 – 32,476,401

Confidence interval (bp): 32,362,652 - 32,887,287

Peak marker RM3335: 32,841,259-32,841,499 bp

Un altro gene probabilmente coinvolto nella resistenza a brusone

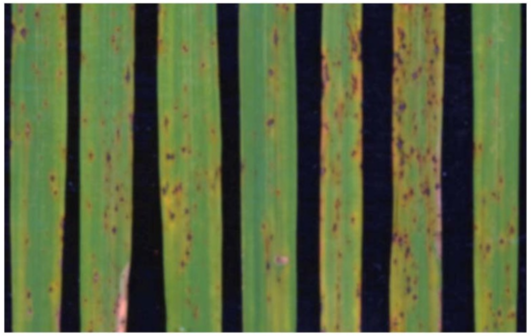
identificato da:

- **Giampiero Valè** Università del Piemonte Orientale, Vercelli

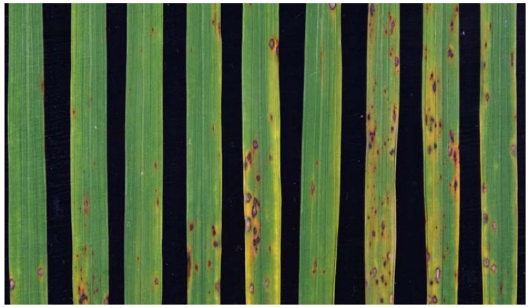
- -**Blanca San Segundo** CRAG, Bacellona, Spagna

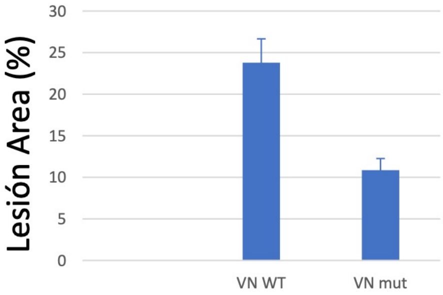
LINEE CRISPR FATTE DA **Giulia Ave Bono** sembrano essere più resistenti

VN
(Azy)

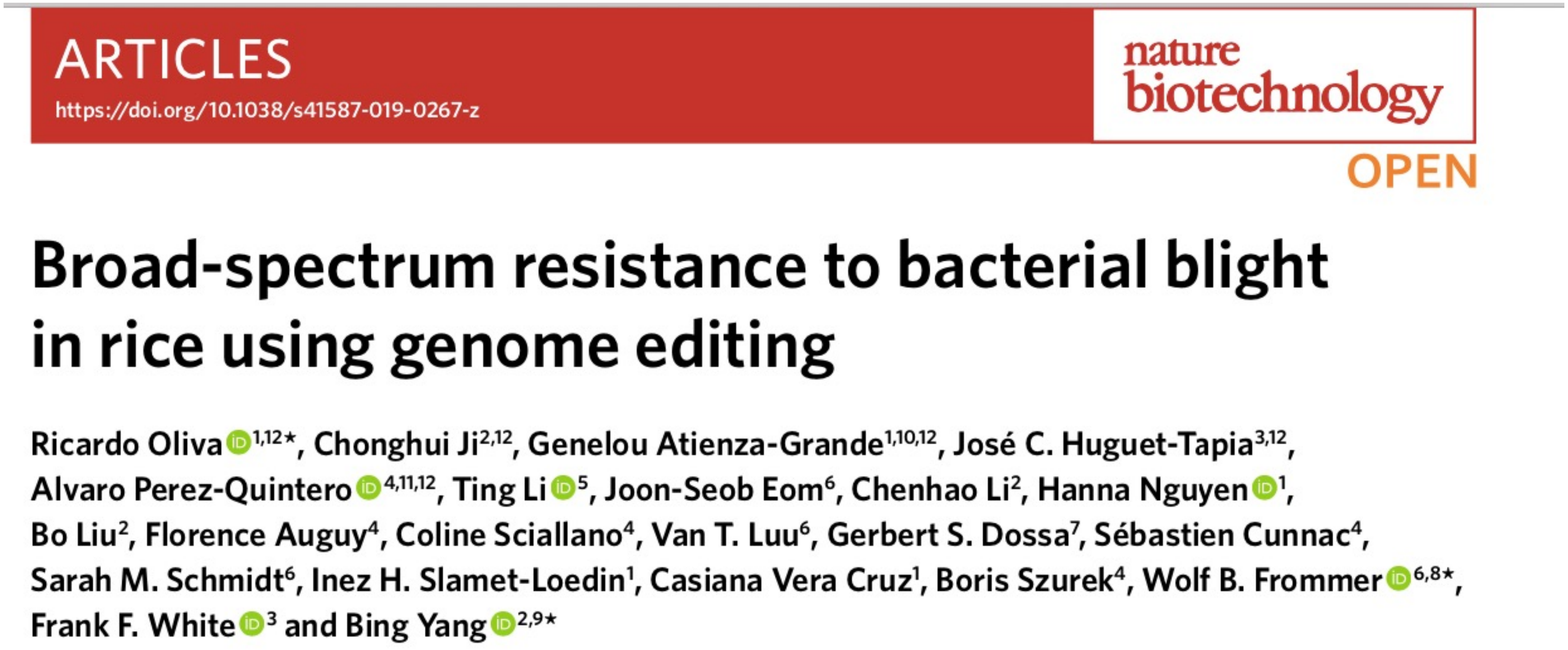


CRISPR





Resistenza a *Xantomonas oryzae*



ARTICLES
https://doi.org/10.1038/s41587-019-0267-z

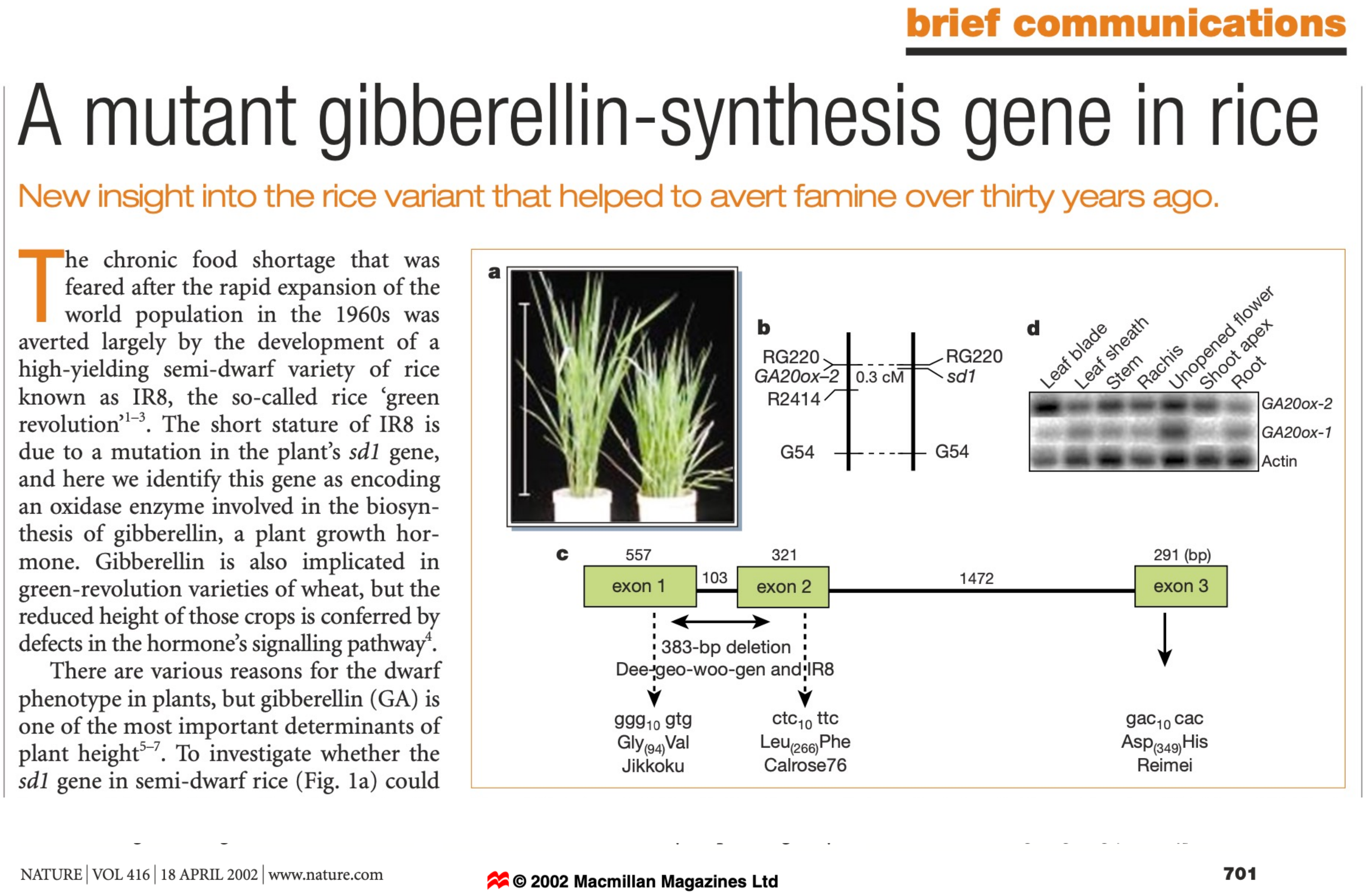
nature biotechnology

OPEN

Broad-spectrum resistance to bacterial blight in rice using genome editing

Ricardo Oliva[1,12]*, Chonghui Ji[2,12], Genelou Atienza-Grande[1,10,12], José C. Huguet-Tapia[3,12], Alvaro Perez-Quintero[4,11,12], Ting Li[5], Joon-Seob Eom[6], Chenhao Li[2], Hanna Nguyen[1], Bo Liu[2], Florence Auguy[4], Coline Sciallano[4], Van T. Luu[6], Gerbert S. Dossa[7], Sébastien Cunnac[4], Sarah M. Schmidt[6], Inez H. Slamet-Loedin[1], Casiana Vera Cruz[1], Boris Szurek[4], Wolf B. Frommer[6,8]*, Frank F. White[3] and Bing Yang[2,9]*

La taglia delle piante è controllata da un gene che serve a produrre gli ormoni della crescita gibberelline



brief communications

A mutant gibberellin-synthesis gene in rice

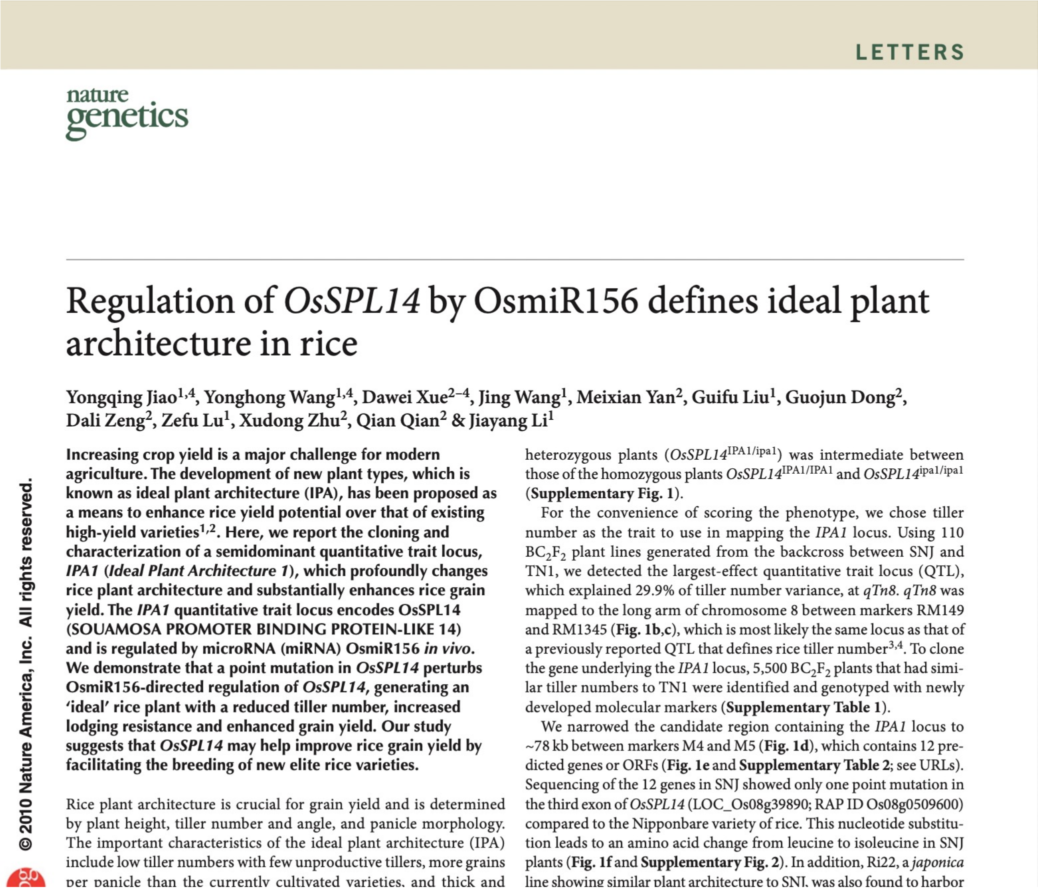
New insight into the rice variant that helped to avert famine over thirty years ago.

The chronic food shortage that was feared after the rapid expansion of the world population in the 1960s was averted largely by the development of a high-yielding semi-dwarf variety of rice known as IR8, the so-called rice 'green revolution'[1–3]. The short stature of IR8 is due to a mutation in the plant's *sd1* gene, and here we identify this gene as encoding an oxidase enzyme involved in the biosynthesis of gibberellin, a plant growth hormone. Gibberellin is also implicated in green-revolution varieties of wheat, but the reduced height of those crops is conferred by defects in the hormone's signalling pathway[4].

There are various reasons for the dwarf phenotype in plants, but gibberellin (GA) is one of the most important determinants of plant height[5–7]. To investigate whether the *sd1* gene in semi-dwarf rice (Fig. 1a) could

si può facilmente ridurre la taglia di varietà troppo alte

una singola mutazione nel gene *SPL14* origina piante con meno culmi, culmi più spessi e pannocchie con più semi



LETTERS

nature genetics

Regulation of *OsSPL14* by OsmiR156 defines ideal plant architecture in rice

Yongqing Jiao[1,4], Yonghong Wang[1,4], Dawei Xue[2–4], Jing Wang[1], Meixian Yan[2], Guifu Liu[1], Guojun Dong[2], Dali Zeng[2], Zefu Lu[1], Xudong Zhu[2], Qian Qian[2] & Jiayang Li[1]

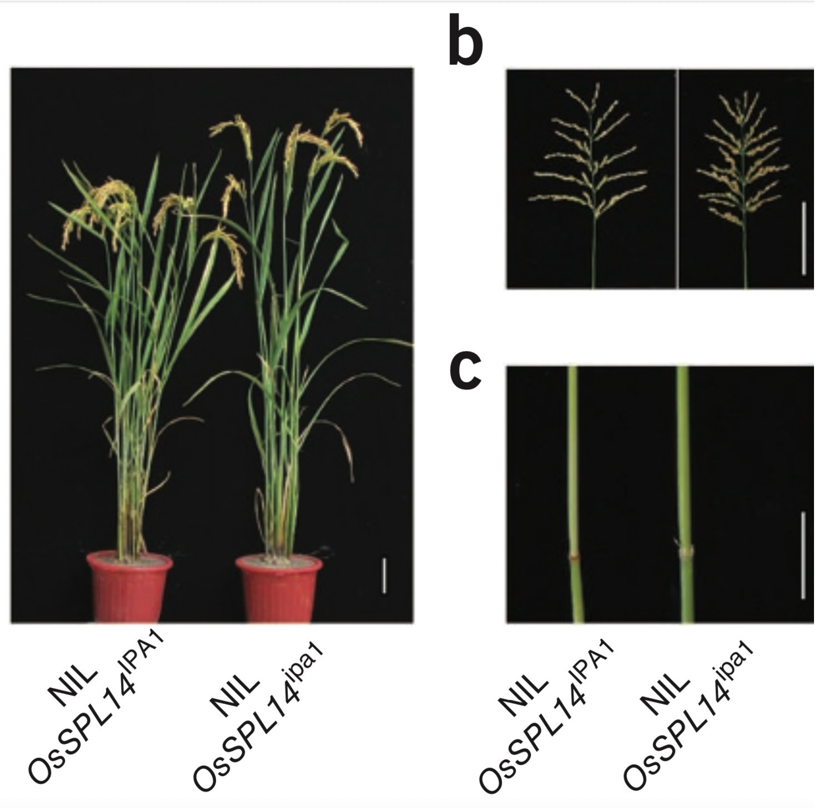
Increasing crop yield is a major challenge for modern agriculture. The development of new plant types, which is known as ideal plant architecture (IPA), has been proposed as a means to enhance rice yield potential over that of existing high-yield varieties[1,2]. Here, we report the cloning and characterization of a semidominant quantitative trait locus, *IPA1* (*Ideal Plant Architecture 1*), which profoundly changes rice plant architecture and substantially enhances rice grain yield. The *IPA1* quantitative trait locus encodes OsSPL14 (SOUAMOSA PROMOTER BINDING PROTEIN-LIKE 14) and is regulated by microRNA (miRNA) OsmiR156 *in vivo*. We demonstrate that a point mutation in *OsSPL14* perturbs OsmiR156-directed regulation of *OsSPL14*, generating an 'ideal' rice plant with a reduced tiller number, increased lodging resistance and enhanced grain yield. Our study suggests that *OsSPL14* may help improve rice grain yield by facilitating the breeding of new elite rice varieties.

Rice plant architecture is crucial for grain yield and is determined by plant height, tiller number and angle, and panicle morphology. The important characteristics of the ideal plant architecture (IPA) include low tiller numbers with few unproductive tillers, more grains per panicle than the currently cultivated varieties, and thick and

heterozygous plants (*OsSPL14*$^{\mathrm{IPA1/ipa1}}$) was intermediate between those of the homozygous plants *OsSPL14*$^{\mathrm{IPA1/IPA1}}$ and *OsSPL14*$^{\mathrm{ipa1/ipa1}}$ (**Supplementary Fig. 1**).

For the convenience of scoring the phenotype, we chose tiller number as the trait to use in mapping the *IPA1* locus. Using 110 BC_2F_2 plant lines generated from the backcross between SNJ and TN1, we detected the largest-effect quantitative trait locus (QTL), which explained 29.9% of tiller number variance, at *qTn8*. *qTn8* was mapped to the long arm of chromosome 8 between markers RM149 and RM1345 (**Fig. 1b**,**c**), which is most likely the same locus as that of a previously reported QTL that defines rice tiller number[3,4]. To clone the gene underlying the *IPA1* locus, 5,500 BC_2F_2 plants that had similar tiller numbers to TN1 were identified and genotyped with newly developed molecular markers (**Supplementary Table 1**).

We narrowed the candidate region containing the *IPA1* locus to ~78 kb between markers M4 and M5 (**Fig. 1d**), which contains 12 predicted genes or ORFs (**Fig. 1e** and **Supplementary Table 2**; see URLs). Sequencing of the 12 genes in SNJ showed only one point mutation in the third exon of *OsSPL14* (LOC_Os08g39890; RAP ID Os08g0509600) compared to the Nipponbare variety of rice. This nucleotide substitution leads to an amino acid change from leucine to isoleucine in SNJ plants (**Fig. 1f** and **Supplementary Fig. 2**). In addition, Ri22, a *japonica* line showing similar plant architecture to SNJ, was also found to harbor



piante con il GS5 più funzionale hanno granella più grande e una maggiore resa

nature genetics

Natural variation in *GS5* plays an important role in regulating grain size and yield in rice

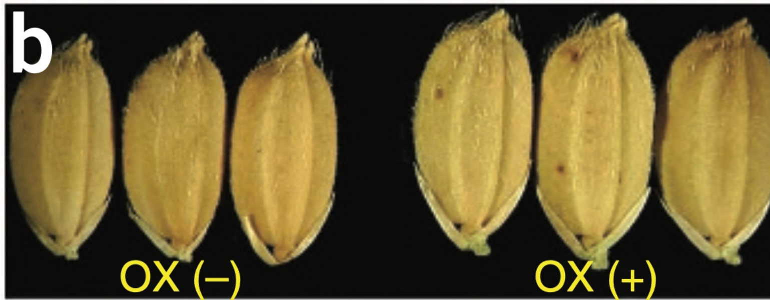
Yibo Li, Chuchuan Fan, Yongzhong Xing, Yunhe Jiang, Lijun Luo, Liang Sun, Di Shao, Chunjue Xu, Xianghu
Jinghua Xiao, Yuqing He & Qifa Zhang

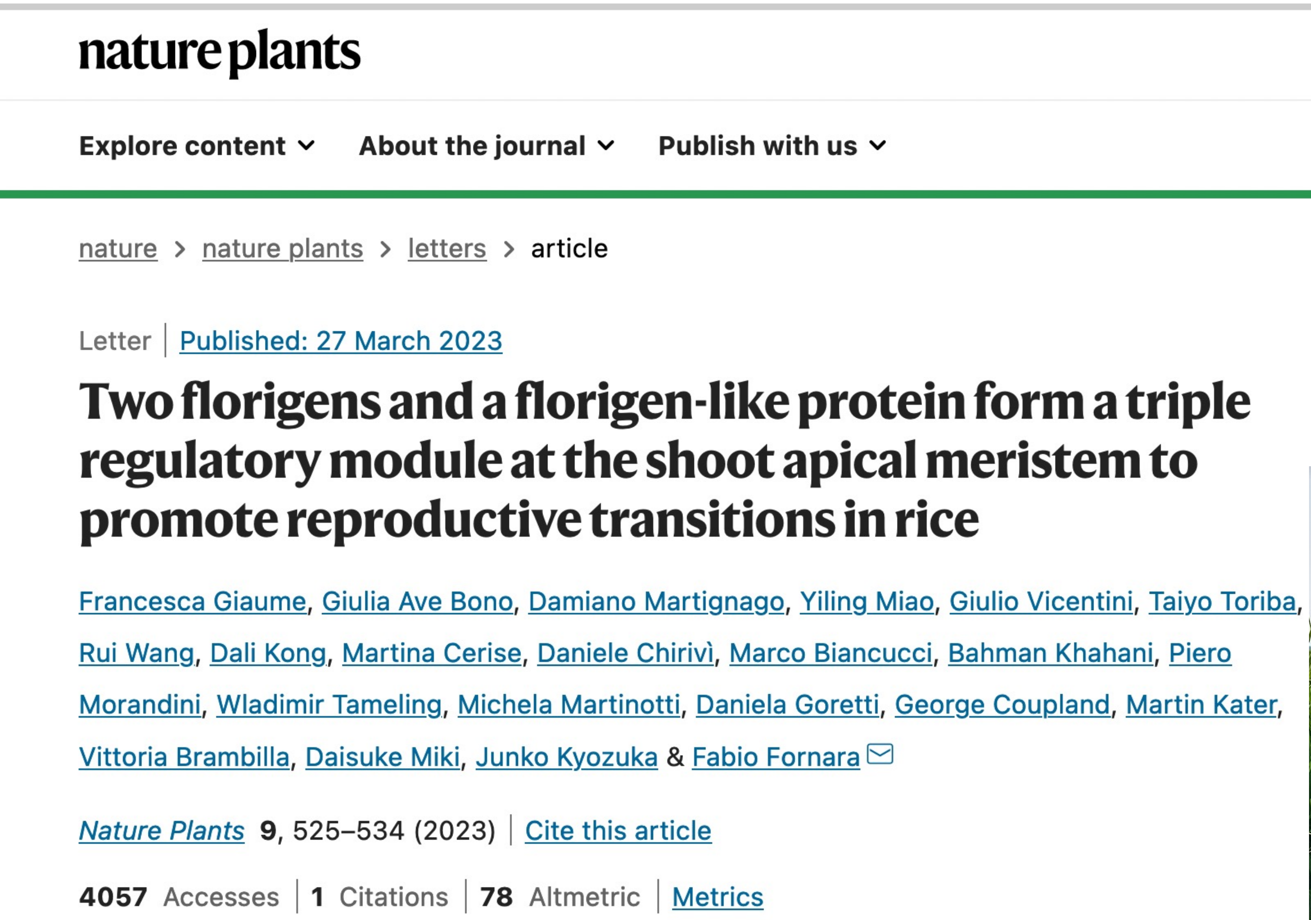
Increasing crop yield is one of the most important goals of plant science research. Grain size is a major determinant of grain yield in cereals and is a target trait for both domestication and artificial breeding[1]. We showed that the quantitative trait locus (QTL) *GS5* in rice controls grain size by regulating grain width, filling and weight. *GS5* encodes a putative serine carboxypeptidase and functions as a positive regulator of grain size, such that higher expression of *GS5* is correlated with larger grain size. Sequencing of the promoter region in 51 rice accessions from a wide geographic range identified three haplotypes that seem to be associated with grain width. The results suggest that natural variation in *GS5* contributes to grain size diversity in rice and may be useful in improving yield in rice and, potentially, other crops[2].

In recent years, a number of genes (or QTLs) for yield traits in rice, including tillering[3,4], number of grains per panicle[5–11] and grain weight[12–19], have been isolated using a map-based cloning approach. These genes regulate yield traits and developmental processes by functioning at various stages, in different pathways and through diverse mechanisms[1]. Molecular characterization of genes affecting grain size (such as *GS3*, *GW2* and q*SW5*/*GW5*) indicate that many are negative

in the summer of 2006 in Wuhan (for example, see **Supplementary Table 2**). Using this data, *GS5* was mapped between C35 and RM574 (**Fig. 1b**). Analysis of population 2 detected 15 recombinants between C35 and RM574 (**Fig. 1c**). In total, 10 recombinant plants were found in the two populations in the interval between S2 and RM574. However, progeny testing revealed an inconsistency for three individuals between the marker genotypes determined using C62, which is located in the middle of the *GS5* region, and the genotype deduced by progeny testing (nos. 30, 8396 and 57-5 in **Fig. 1d** and **Supplementary Table 2**). By referencing the previously cloned *qSW5*/*GW5* locus[16,17], located approximately 2 Mb away on the RM574 side, we found that this inconsistency could be explained by the genotype of *qSW5*/*GW5*, which also affects grain size. We discarded these plants from further analysis. Using information from the remaining seven plants, we resolved *GS5* to an 11.6-kb region between RM574 and S2 (**Fig. 1c**).

We next investigated the effects of *GS5* on grain size and filling (see **Fig. 2**). We isolated two near-isogenic lines (NILs) from BC_3F_2 by fixing *qSW5*/*GW5* for the small-grain allele (**Fig. 2a**). Compared to NIL(H94), the grains of NIL(ZS97) were 8.7% wider and 7.0% heavier, leading to a 7.4% increase in grain yield per plant (**Table 1**). No significant differences were detected in other agronomic traits (**Supplementary Table 3**). An analysis of a BC_3F_2 subpopulation showed that the grain





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nature > nature plants > letters > article

Letter | Published: 27 March 2023

Two florigens and a florigen-like protein form a triple regulatory module at the shoot apical meristem to promote reproductive transitions in rice

Francesca Giaume, Giulia Ave Bono, Damiano Martignago, Yiling Miao, Giulio Vicentini, Taiyo Toriba, Rui Wang, Dali Kong, Martina Cerise, Daniele Chirivì, Marco Biancucci, Bahman Khahani, Piero Morandini, Wladimir Tameling, Michela Martinotti, Daniela Goretti, George Coupland, Martin Kater, Vittoria Brambilla, Daisuke Miki, Junko Kyozuka & Fabio Fornara

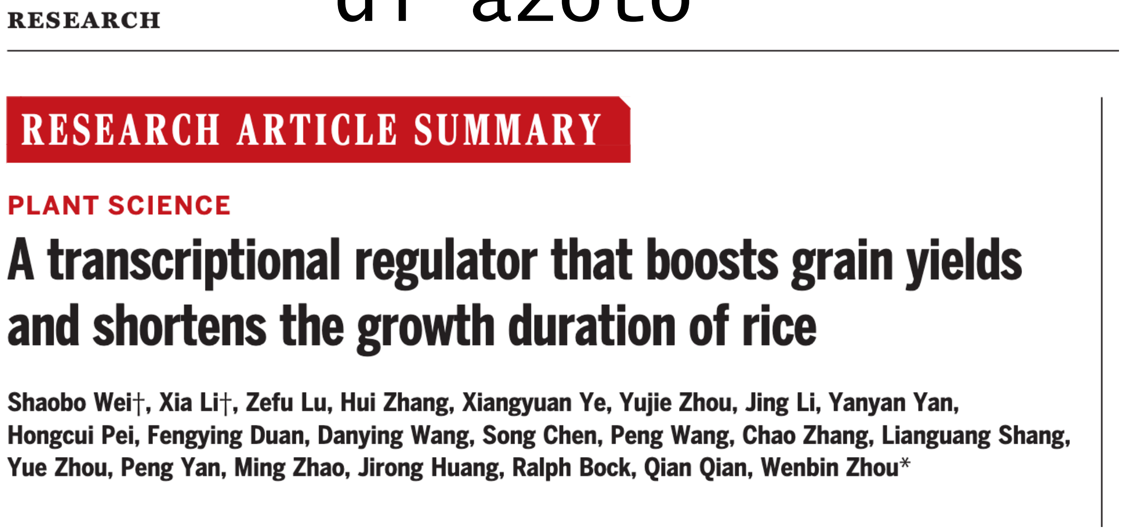
Nature Plants **9**, 525–534 (2023) | Cite this article

4057 Accesses | **1** Citations | **78** Altmetric | Metrics

Francesca Giaume & Giulia Ave Bono

mutazioni nel gene *FT-L1* aumentano le ramificazioni della pannocchia

una mutazione nel gene *OsDREB1C* migliora la fotosintesi e l’efficienza dell’uso di azoto



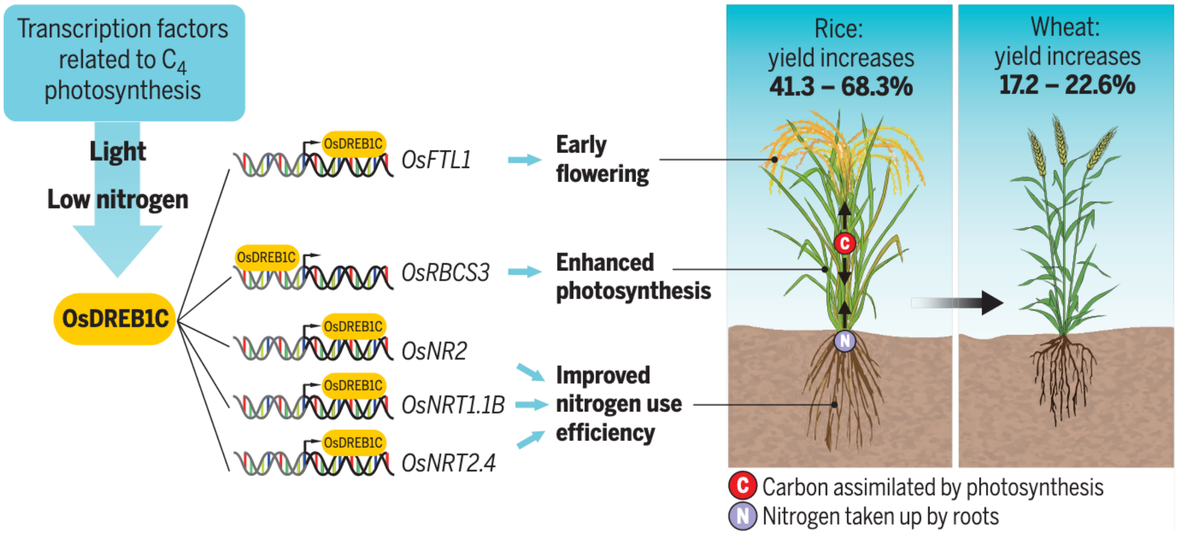
RESEARCH

RESEARCH ARTICLE SUMMARY

PLANT SCIENCE

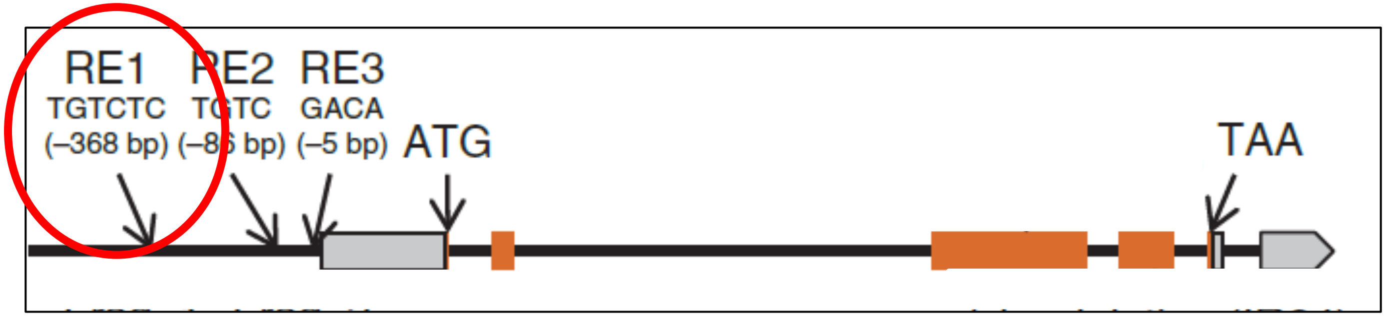
A transcriptional regulator that boosts grain yields and shortens the growth duration of rice

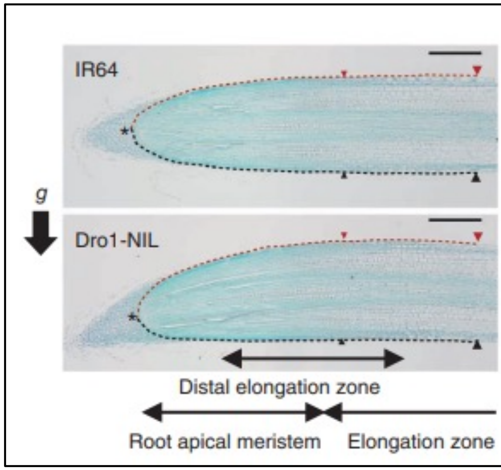
Shaobo Wei†, Xia Li†, Zefu Lu, Hui Zhang, Xiangyuan Ye, Yujie Zhou, Jing Li, Yanyan Yan, Hongcui Pei, Fengying Duan, Danying Wang, Song Chen, Peng Wang, Chao Zhang, Lianguang Shang, Yue Zhou, Peng Yan, Ming Zhao, Jirong Huang, Ralph Bock, Qian Qian, Wenbin Zhou*

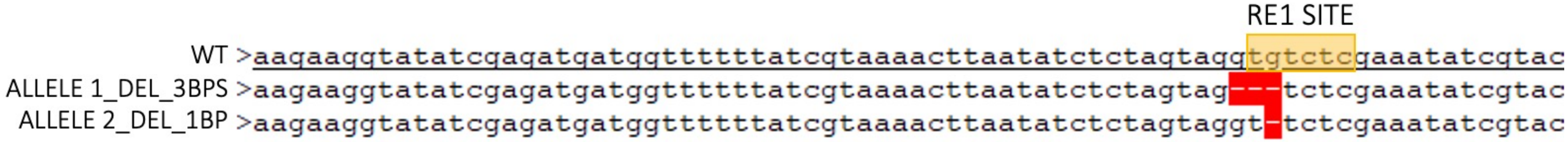


una mutazione nel gene *DRO1* migliora la resistenza alla siccità

Giulia Ave Bono

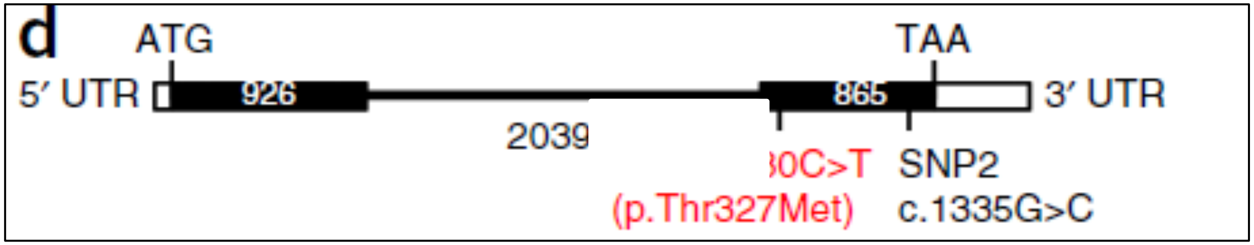




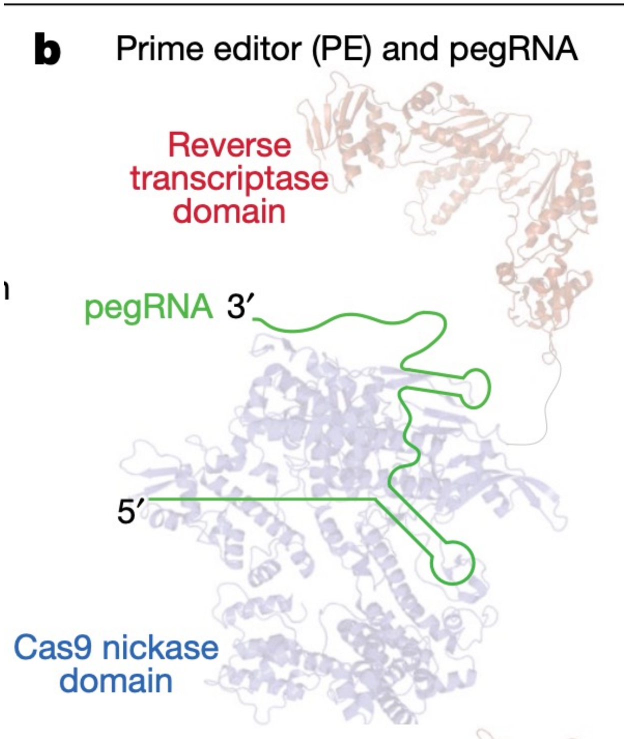


```
                                                                                                  RE1 SITE
           WT >aagaaggtatatcgagatgatggttttttatcgtaaaacttaatatctctagtaggtgtctcgaaatatcgtac
ALLELE 1_DEL_3BPS >aagaaggtatatcgagatgatggttttttatcgtaaaacttaatatctctagtag---tctcgaaatatcgtac
 ALLELE 2_DEL_1BP >aagaaggtatatcgagatgatggttttttatcgtaaaacttaatatctctagtaggt-tctcgaaatatcgtac
```

una mutazione nel gene NRT1.1b migliora l'efficienza dell'uso di azoto



Hu et al. 2015



Giulia Ave Bono

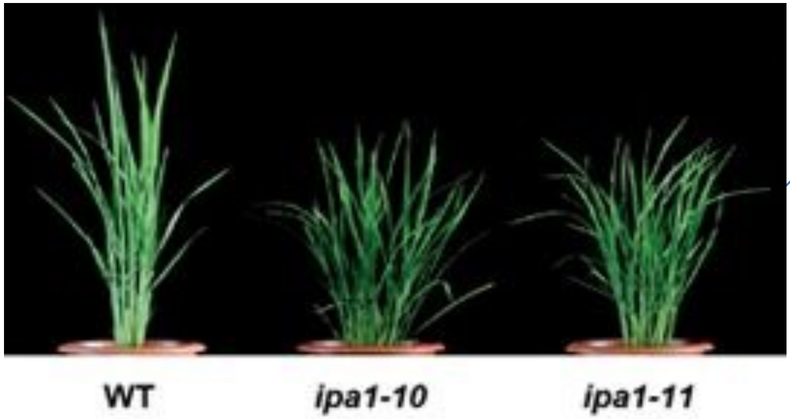
Le mutazioni si possono combinare

peso e dimensioni del seme (*GS3*, *GW2*, *GS5*)

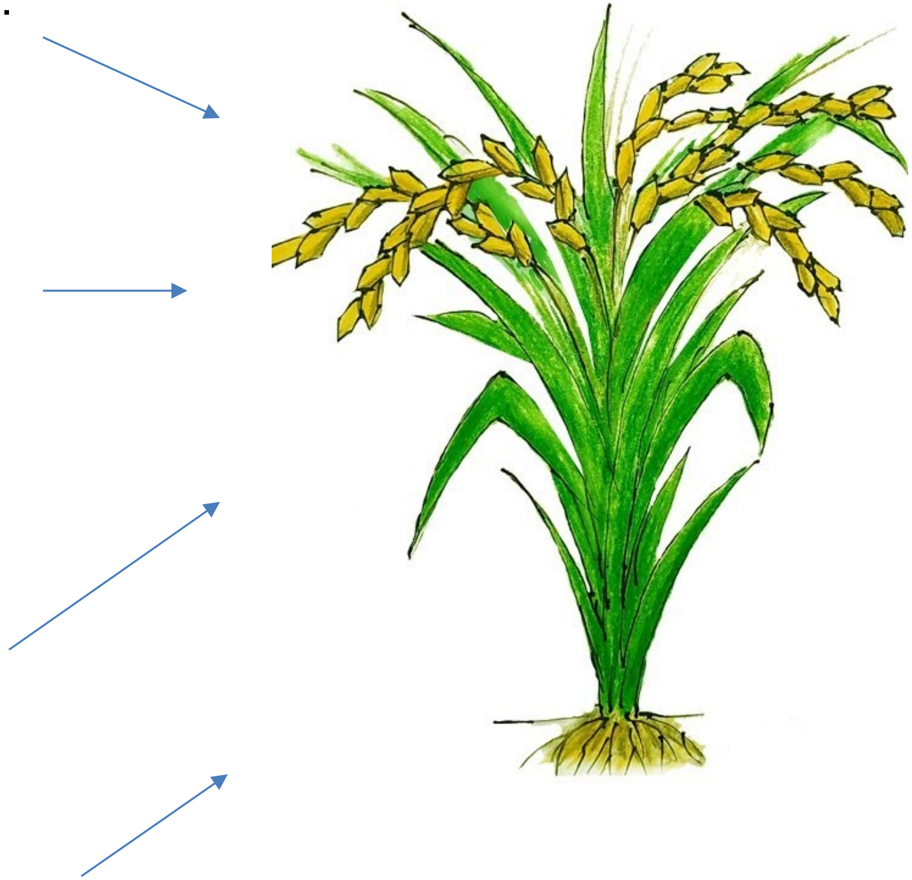
ramificazioni e di semi per pannocchia (*Gn1a*, *DEP1*)

wild dep1

culmi di accestimento (*IPA1*)



Le mutazioni si possono combinare



Resistenza a brusone

Pi21, PiK…

X

Tempo di fioritura

HBF1/2

X

Resistenza a siccità

DRO1

X

Efficienza uso azoto

Nrt1.1b

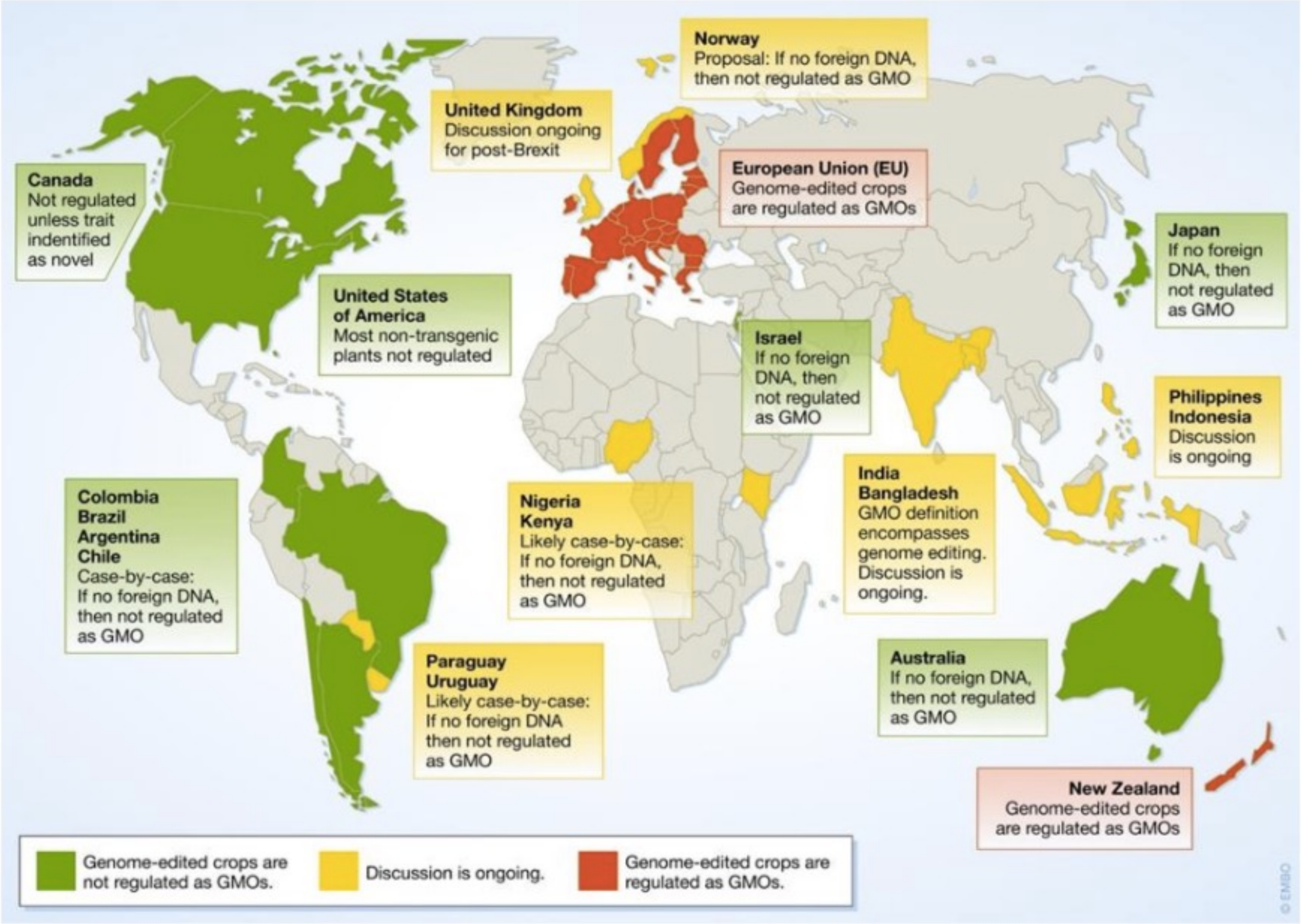
…..

Speciale DNA, editing del genoma: CRISPR, CRISPR/Cas9, evoCAS9...

Innovazione Il Giappone mette in tavola i primi pomodori modificati con la CRISPR

Pomodori «Sicilian Rouge High GABA» contengono cinque volte la normale quantità di acido gamma-amminobutirrico (GABA), che aiuta ad abbassare la pressione sanguigna

LEGISLAZIONE CRISPR IN AGRICOLTURA NEL MONDO



Canada
Not regulated unless trait indentified as novel

United States of America
Most non-transgenic plants not regulated

United Kingdom
Discussion ongoing for post-Brexit

Norway
Proposal: If no foreign DNA, then not regulated as GMO

European Union (EU)
Genome-edited crops are regulated as GMOs

Japan
If no foreign DNA, then not regulated as GMO

Israel
If no foreign DNA, then not regulated as GMO

Philippines
Indonesia
Discussion is ongoing

Colombia
Brazil
Argentina
Chile
Case-by-case: If no foreign DNA, then not regulated as GMO

Nigeria
Kenya
Likely case-by-case: If no foreign DNA, then not regulated as GMO

India
Bangladesh
GMO definition encompasses genome editing. Discussion is ongoing.

Paraguay
Uruguay
Likely case-by-case: If no foreign DNA then not regulated as GMO

Australia
If no foreign DNA, then not regulated as GMO

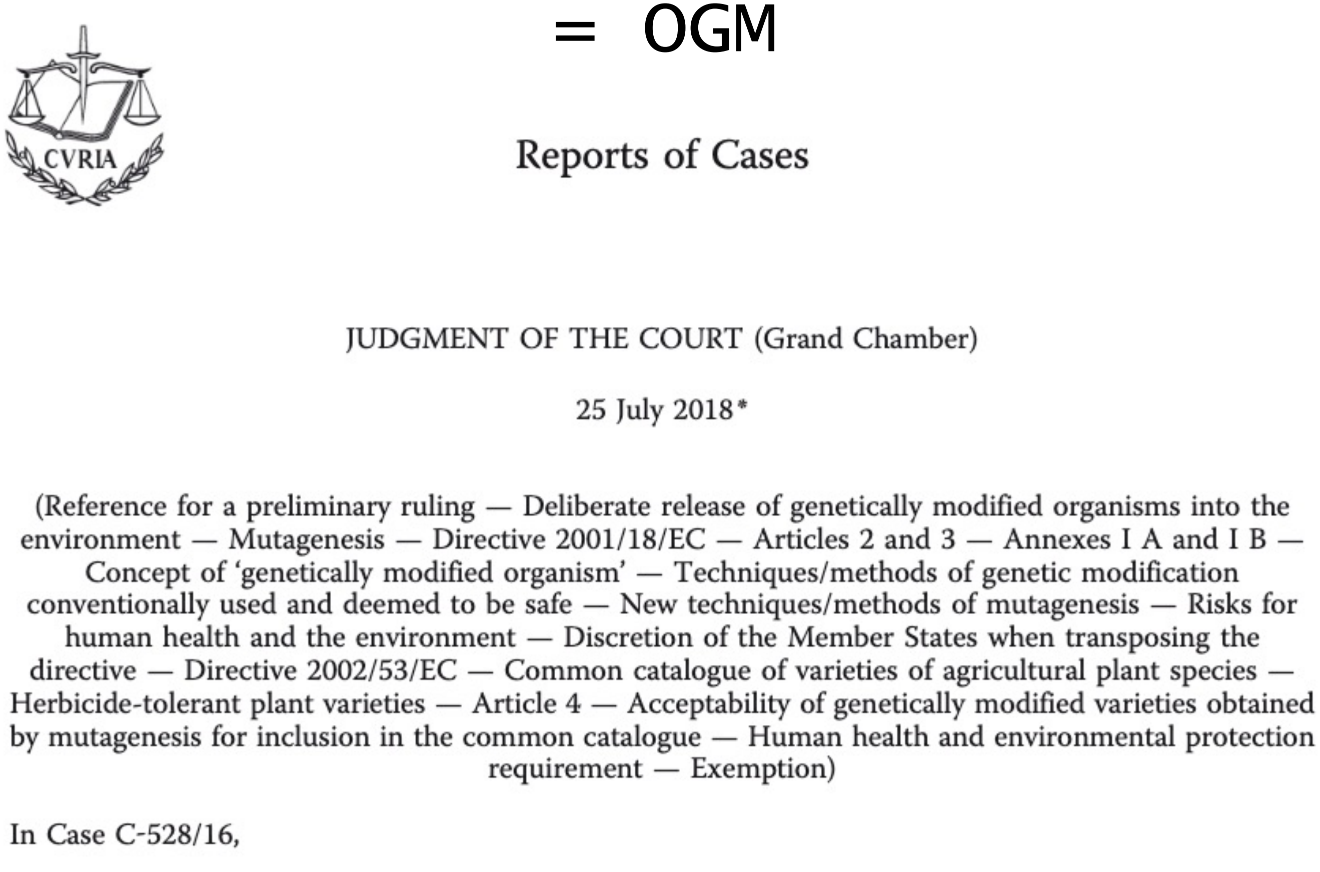
New Zealand
Genome-edited crops are regulated as GMOs

🟩 Genome-edited crops are not regulated as GMOs.
🟨 Discussion is ongoing.
🟥 Genome-edited crops are regulated as GMOs.

© EMBO

Situazione legislativa in Europa

SENTENZA della Corte di Giustizia del 25 luglio 2018: PIANTE CRISPR = OGM



CVRIA

Reports of Cases

JUDGMENT OF THE COURT (Grand Chamber)

25 July 2018*

(Reference for a preliminary ruling — Deliberate release of genetically modified organisms into the environment — Mutagenesis — Directive 2001/18/EC — Articles 2 and 3 — Annexes I A and I B — Concept of 'genetically modified organism' — Techniques/methods of genetic modification conventionally used and deemed to be safe — New techniques/methods of mutagenesis — Risks for human health and the environment — Discretion of the Member States when transposing the directive — Directive 2002/53/EC — Common catalogue of varieties of agricultural plant species — Herbicide-tolerant plant varieties — Article 4 — Acceptability of genetically modified varieties obtained by mutagenesis for inclusion in the common catalogue — Human health and environmental protection requirement — Exemption)

In Case C-528/16,

RegioneLombardia

LA GIUNTA

DELIBERAZIONE N° XI / 7526 Seduta del 15/12/2022

Presidente **ATTILIO FONTANA**

Assessori regionali
FABRIZIO SALA *Vicepresidente*
GUIDO BERTOLASO
STEFANO BOLOGNINI
DAVIDE CARLO CAPARINI
RAFFAELE CATTANEO
MELANIA DE NICHILO RIZZOLI
PIETRO FORONI
STEFANO BRUNO GALLI
GUIDO GUIDESI
ROMANO MARIA LA RUSSA
ELENA LUCCHINI
LARA MAGONI
ALAN CHRISTIAN RIZZI
FABIO ROLFI
MASSIMO SERTORI
CLAUDIA MARIA TERZI

Con l'assistenza del Segretario Enrico Gasparini

Su proposta dell'Assessore Fabio Rolfi

Oggetto

DETERMINAZIONI IN ORDINE ALLA SPERIMENTAZIONE IN CAMPO APERTO DI NUOVE VARIETA' VEGETALI D'NTERESSE AGRARIO OTTENUTE CON NUOVE TECNICHE GENETICHE (NGT)

LEGGI ED ALTRI ATTI NORMATIVI

DECRETO-LEGGE 14 aprile 2023, n. **39**.

Disposizioni urgenti per il contrasto della scarsità idrica e per il potenziamento e l'adeguamento delle infrastrutture idriche.

Testo in vigore dal: 14-6-2023

aggiornamenti all'articolo

Art. 9-bis

(((Disposizioni urgenti in materia di genetica agraria).))

((1. Per consentire lo svolgimento delle attivita' di ricerca presso siti sperimentali autorizzati, a sostegno di produzioni vegetali in grado di rispondere in maniera adeguata a condizioni di scarsita' idrica e in presenza di stress ambientali e biotici di particolare intensita', nelle more dell'adozione, da parte dell'Unione europea, di una disciplina organica in materia, l'autorizzazione all'emissione deliberata nell'ambiente di organismi prodotti con tecniche di editing genomico mediante mutagenesi sito-diretta o di cisgenesi a fini sperimentali e scientifici e' soggetta, fino al 31 dicembre 2024, alle disposizioni di cui al presente articolo.

Proposta della Commissione Europea per una normativa TEA differente da OGM

EUROPEAN
COMMISSION

Brussels, 5.7.2023
COM(2023) 411 final

2023/0226 (COD)

Proposal for a

REGULATION OF THE EUROPEAN PARLIAMENT AND OF THE COUNCIL

on plants obtained by certain new genomic techniques and their food and feed, and amending Regulation (EU) 2017/625

(Text with EEA relevance)

{SEC(2023) 411 final} - {SWD(2023) 411 final} - {SWD(2023) 412 final} -
{SWD(2023) 413 final}

Grazie per l’attenzione!

vittoria.brambilla@unimi.it