Améliorer la résistance des plantes aux bio-agresseurs : de nouvelles voies ouvertes par les biotechnologies

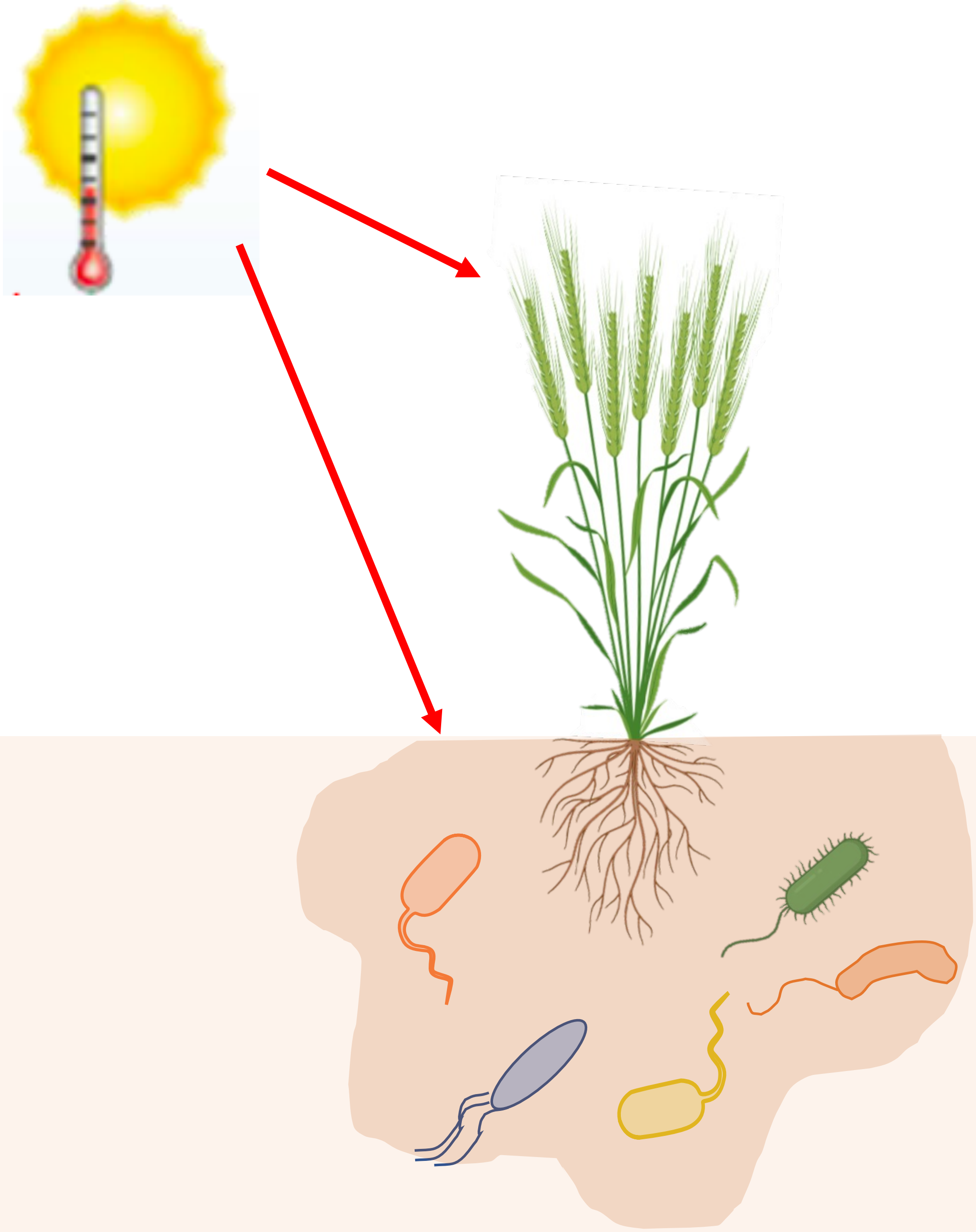
T. Langin

Biotechnologies végétales et Changement climatique

Effets du changement climatique

- Stress hydrique et thermique des cultures
- Perturbation des calendriers culturaux
- Accélération de la phénologie des végétaux (cycles)
- Augmentation de la croissance des végétaux
- Sécheresse du sol
- …

Impact direct du changement climatique sur les résistances aux maladies ou aux bioagresseurs



Effets du changement climatique

- Stress hydrique et thermique des cultures
- Perturbation des calendriers culturaux
- Accélération de la phénologie des végétaux (cycles)
- Augmentation de la croissance des végétaux
- Sécheresse du sol
- Risque accru de maladies et ravageurs
- …

Impact du changement climatique sur les maladies des plantes et l'évolution des bioagresseurs ?

Elévation de la température
Augmentation des épisodes de sécheresse aux latitudes moyennes
Elévation de la concentration en [CO_2]atm
Un impact différent en fonction de la proximité à l'équateur (Europe, Chine particulièrement vulnérable)
…

- Augmentation de la sensibilité des plantes résultant d'un mauvais état physiologique
- Evolution des cortèges parasitaires
- Evolution des populations naturelles des pathogènes et des ravageurs : augmentation fréquences de souches (multi-)résistantes aux traitements, apparition de souches virulentes avec un contournement plus rapide des résistances, apparition de souches plus agressives…
- (ré-)émergence de nouvelles maladies (rouille noire, wheat blast, …)
- Evolution des fréquences d'apparition des maladies

	Culture	Agent pathogène	Evolution
	Orge	oïdium (*Blumeria graminis*) charbon (*Ustilago hordei*)	diminution augmentation
	Maïs	charbon (*Ustilago maydis*)	diminution
	Pomme de terre	mildiou (*Phytophthora infestans*) alternariose (*Alternaria solani*)	augmentation pas de changement
	Riz	rhizoctone (Rhizoctonia *solani*) Pyriculariose (*Magnaporthe oryzae*)	augmentation augmentation
	Soja	mildiou (*Peronospora manshurica*) tache septorienne (*Septoria glycines*)	diminution augmentation
	Blé	rouille jaune (*Puccinia striiformis*) fusariose (*Fusarium sp.*)	augmentation augmentation

Luck et al., 2011

Améliorer la résistance des plantes aux bio-agresseurs

Contribution des biotechnologies

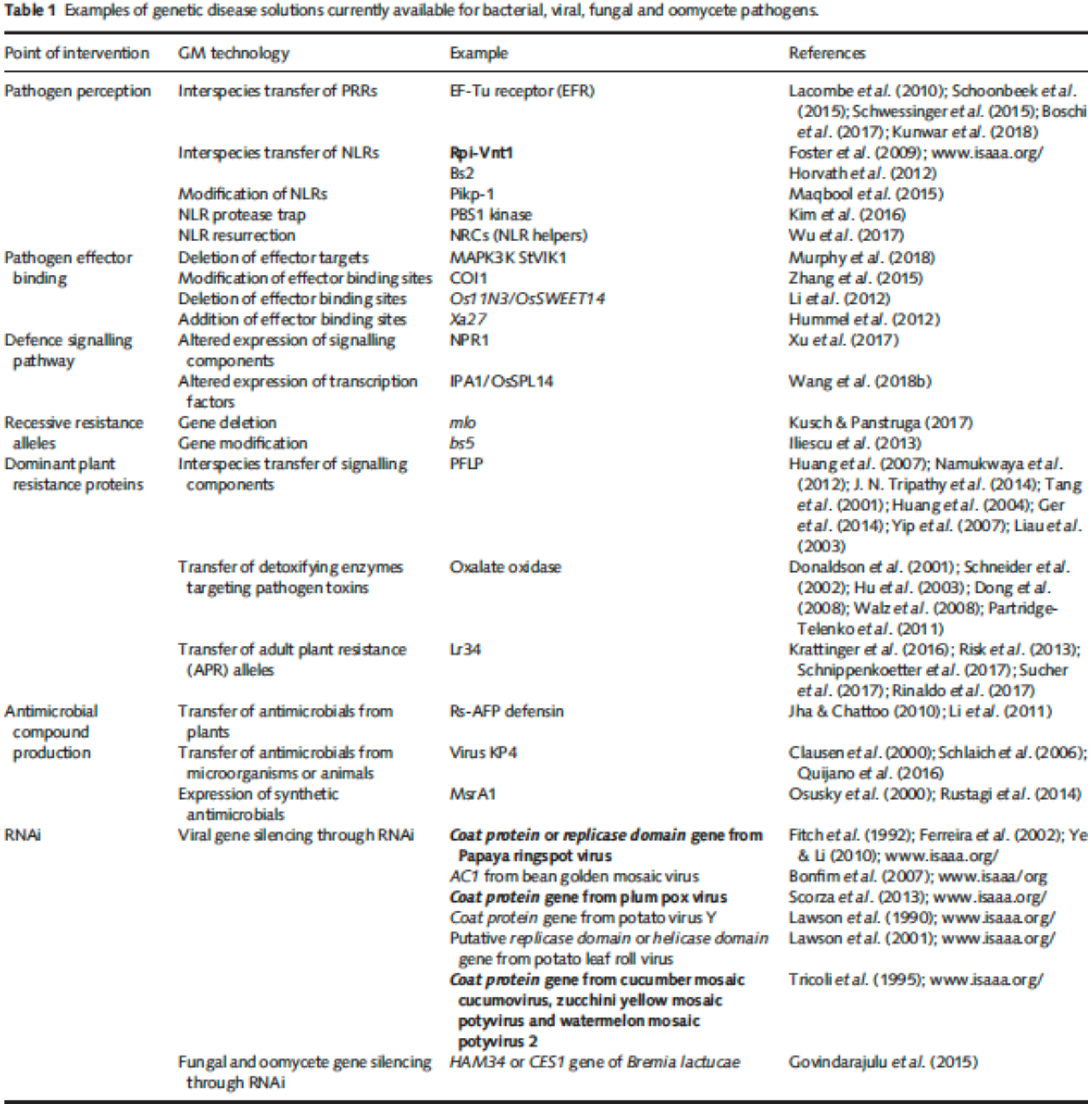


Table 1 Examples of genetic disease solutions currently available for bacterial, viral, fungal and oomycete pathogens.

Point of intervention	GM technology	Example	References
Pathogen perception	Interspecies transfer of PRRs	EF-Tu receptor (EFR)	Lacombe *et al*. (2010); Schoonbeek *et al*. (2015); Schwessinger *et al*. (2015); Boschi *et al*. (2017); Kunwar *et al*. (2018)
	Interspecies transfer of NLRs	**Rpi-Vnt1**	Foster *et al*. (2009); www.isaaa.org/
		Bs2	Horvath *et al*. (2012)
	Modification of NLRs	Pikp-1	Maqbool *et al*. (2015)
	NLR protease trap	PBS1 kinase	Kim *et al*. (2016)
	NLR resurrection	NRCs (NLR helpers)	Wu *et al*. (2017)
Pathogen effector binding	Deletion of effector targets	MAPK3K StVIK1	Murphy *et al*. (2018)
	Modification of effector binding sites	COI1	Zhang *et al*. (2015)
	Deletion of effector binding sites	*Os11N3/OsSWEET14*	Li *et al*. (2012)
	Addition of effector binding sites	*Xa27*	Hummel *et al*. (2012)
Defence signalling pathway	Altered expression of signalling components	NPR1	Xu *et al*. (2017)
	Altered expression of transcription factors	IPA1/OsSPL14	Wang *et al*. (2018b)
Recessive resistance alleles	Gene deletion	*mlo*	Kusch & Panstruga (2017)
	Gene modification	*bs5*	Iliescu *et al*. (2013)
Dominant plant resistance proteins	Interspecies transfer of signalling components	PFLP	Huang *et al*. (2007); Namukwaya *et al*. (2012); J. N. Tripathy *et al*. (2014); Tang *et al*. (2001); Huang *et al*. (2004); Ger *et al*. (2014); Yip *et al*. (2007); Liau *et al*. (2003)
	Transfer of detoxifying enzymes targeting pathogen toxins	Oxalate oxidase	Donaldson *et al*. (2001); Schneider *et al*. (2002); Hu *et al*. (2003); Dong *et al*. (2008); Walz *et al*. (2008); Partridge-Telenko *et al*. (2011)
	Transfer of adult plant resistance (APR) alleles	Lr34	Krattinger *et al*. (2016); Risk *et al*. (2013); Schnippenkoetter *et al*. (2017); Sucher *et al*. (2017); Rinaldo *et al*. (2017)
Antimicrobial compound production	Transfer of antimicrobials from plants	Rs-AFP defensin	Jha & Chattoo (2010); Li *et al*. (2011)
	Transfer of antimicrobials from microorganisms or animals	Virus KP4	Clausen *et al*. (2000); Schlaich *et al*. (2006); Quijano *et al*. (2016)
	Expression of synthetic antimicrobials	MsrA1	Osusky *et al*. (2000); Rustagi *et al*. (2014)
RNAi	Viral gene silencing through RNAi	***Coat protein* or *replicase domain* gene from Papaya ringspot virus**	Fitch *et al*. (1992); Ferreira *et al*. (2002); Ye & Li (2010); www.isaaa.org/
		AC1 from bean golden mosaic virus	Bonfim *et al*. (2007); www.isaaa/org
		***Coat protein* gene from plum pox virus**	Scorza *et al*. (2013); www.isaaa.org/
		Coat protein gene from potato virus Y	Lawson *et al*. (1990); www.isaaa.org/
		Putative *replicase domain* or *helicase domain* gene from potato leaf roll virus	Lawson *et al*. (2001); www.isaaa.org/
		***Coat protein* gene from cucumber mosaic cucumovirus, zucchini yellow mosaic potyvirus and watermelon mosaic potyvirus 2**	Tricoli *et al*. (1995); www.isaaa.org/
	Fungal and oomycete gene silencing through RNAi	*HAM34* or *CES1* gene of *Bremia lactucae*	Govindarajulu *et al*. (2015)

van Esse, Reuber and van der Does, 2020)

Résistances par utilisation de l'ARN interférence (RNAi)

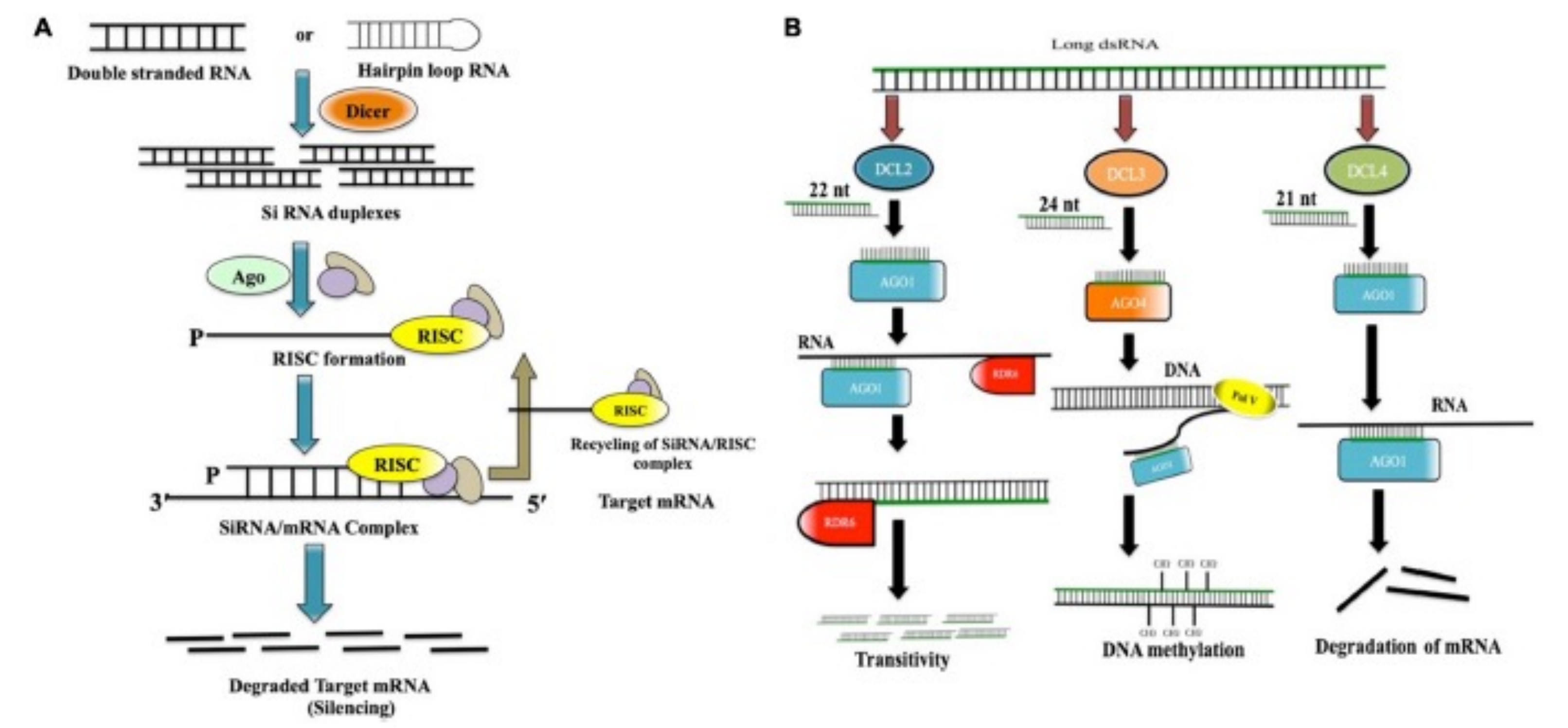


FIGURE 1 | (A) In RNAi-mediated gene silencing, long dsRNA/hpRNA gets chopped off into short (21–23 nucleotides) interfering RNA duplexes (siRNAs). siRNA duplexes unwind and one of the strands (Guide strand) gets incorporated into the RISC complex, which finally degrades the targeted complementary mRNA. RISC complex gets recycled again; **(B)** Dicer-mediated processing of long dsRNA in *Arabidopsis thaliana*. DCL2 generates 22 nucleotide-long siRNAs, which interacts with AGO1 and recruits RDR6 to induce transitive silencing. DCL3 generates 24 nucleotide-long siRNAs, which interacts with AGO4 and induces DNA methylation by recruiting DNA PolV, whereas DCL4 generates 21 nucleotide-long siRNAs, which interacts with AGO1 and directs the cleavage of complementary mRNA.

Halder et al, 2022

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Transgenic strategies to confer resistance against viruses in rice plants

Takahide Sasaya[1]*, *Eiko Nakazono-Nagaoka*[2], *Hiroaki Saika*[3], *Hideyuki Aoki*[4], *Akihiro Hiraguri*[5], *Osamu Netsu*[5], *Tamaki Uehara-Ichiki*[3], *Masatoshi Onuki*[1], *Seichi Toki*[3], *Koji Saito*[4] *and Osamu Yatou*[4]

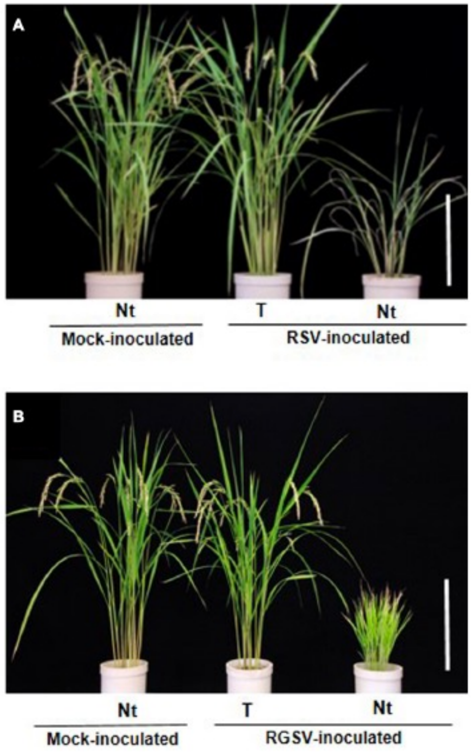

FIGURE 4 | Transgenic rice plants with enhanced resistance against two tenuiviruses. (A) Phenotype of transgenic rice plants (cv. Nipponbare)

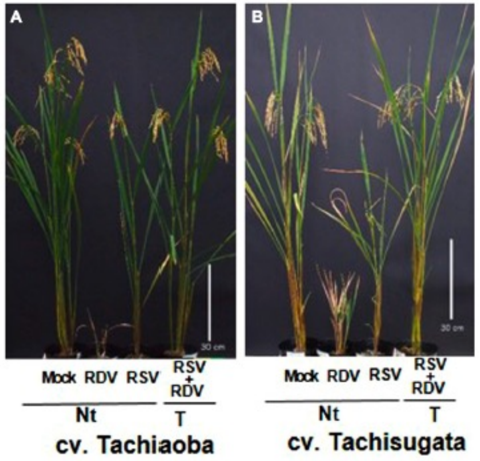

FIGURE 5 | Transgenic forage rice cultivars inoculated with *Rice stripe virus* (RSV) and *Rice dwarf virus* (RDV) (from Sasaya et al., 2013). Phenotypes of transgenic forage rice cultivars Tachiaoba **(A)** and Tachisugata **(B)** that harbored the RNAi trigger sequence targeting the RSV gene for pC3 and the RDV gene for Pns12 at 5 months after RDV and RSV inoculation. Ten-day-old transgenic forage rice seedlings were exposed to approximately 15 RSV-carrying viruliferous small brown hoppers and 10 RDV-carrying leaf hoppers per plant for each 1 day, and evaluate plant response to infection with RSV and RDV at 4 months after virus inoculation. The forage rice cultivars in pots from left to right are: mock-inoculated non-transgenic forage rice cultivars (Nt) exposed to virus-free insect vectors, showing normal growth; RDV-inoculated non-transgenic forage rice cultivars (Nt), showing typical symptoms caused by RDV infection; RSV-inoculated non-transgenic forage rice cultivars (Nt), showing typical symptoms caused by RSV infection; RDV+RSV-inoculated transgenic forage rice cultivars, showing healthy growth and fertility. Bar, 30 cm.

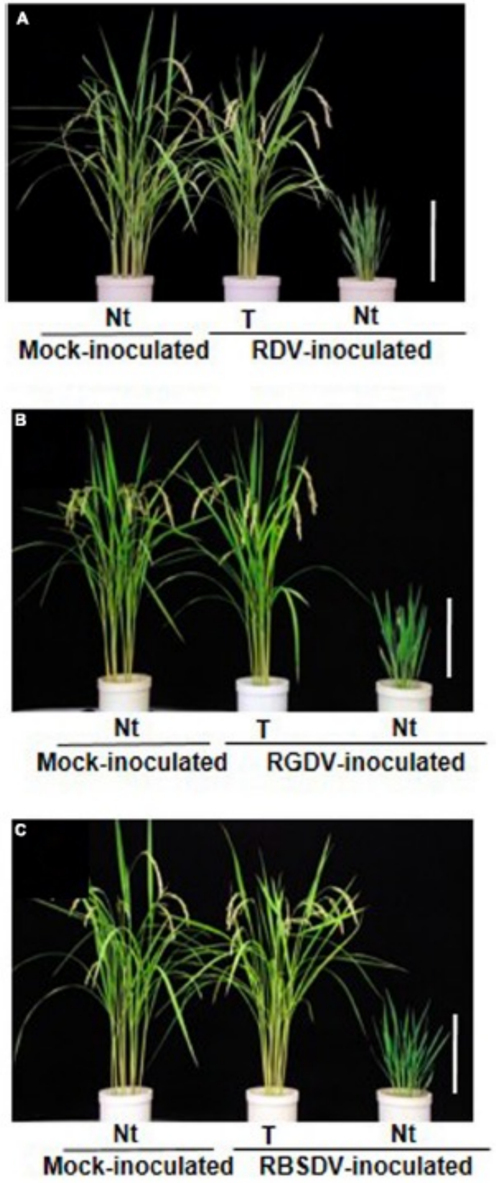

FIGURE 2 | Transgenic rice plants enhanced resistance against three rice-infecting reoviruses. (A) Phenotype of transgenic rice plants (cv.

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Transgenic strategies to confer resistance against viruses in rice plants

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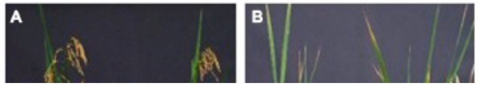


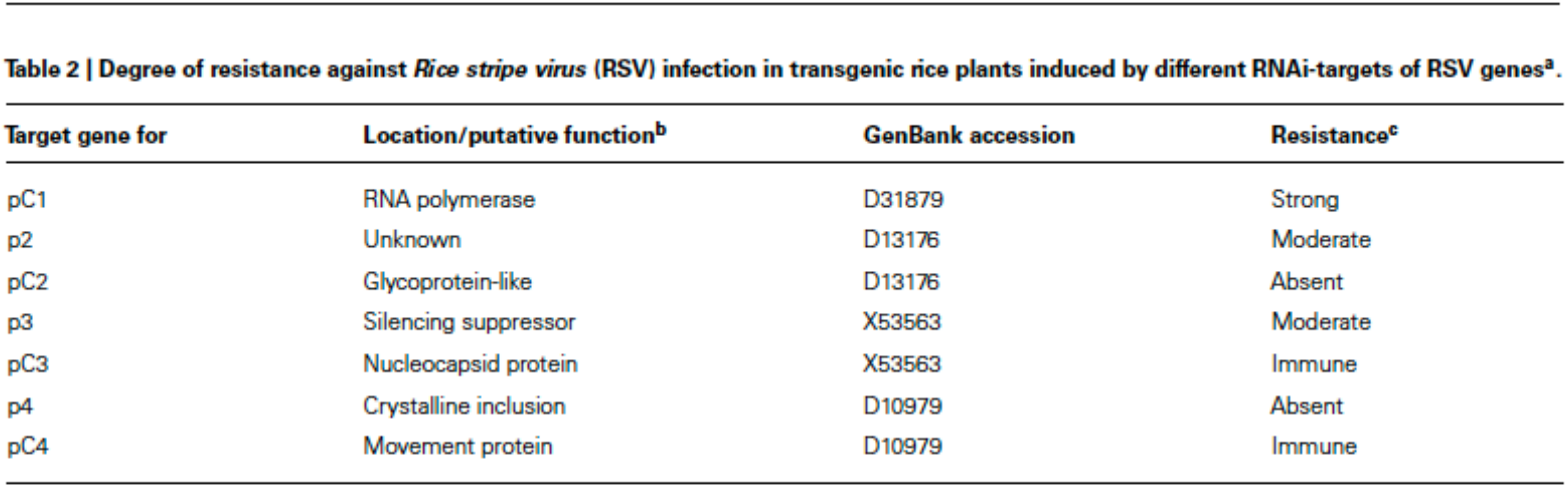


Table 2 | Degree of resistance against *Rice stripe virus* (RSV) infection in transgenic rice plants induced by different RNAi-targets of RSV genes[a].

Target gene for	Location/putative function[b]	GenBank accession	Resistance[c]
pC1	RNA polymerase	D31879	Strong
p2	Unknown	D13176	Moderate
pC2	Glycoprotein-like	D13176	Absent
p3	Silencing suppressor	X53563	Moderate
pC3	Nucleocapsid protein	X53563	Immune
p4	Crystalline inclusion	D10979	Absent
pC4	Movement protein	D10979	Immune

FIGURE 4 | Transgenic rice plants with enhanced resistance against two tenuiviruses. (A) Phenotype of transgenic rice plants (cv. Nipponbare)

forage rice cultivars, showing healthy growth and fertility. Bar, 30 cm.

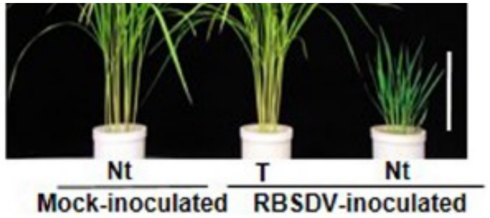
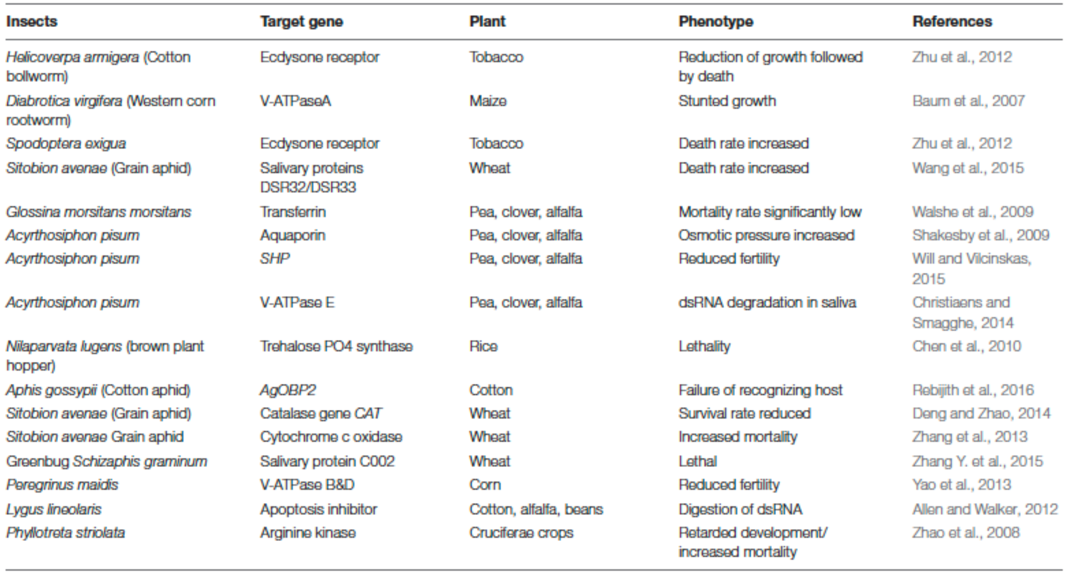


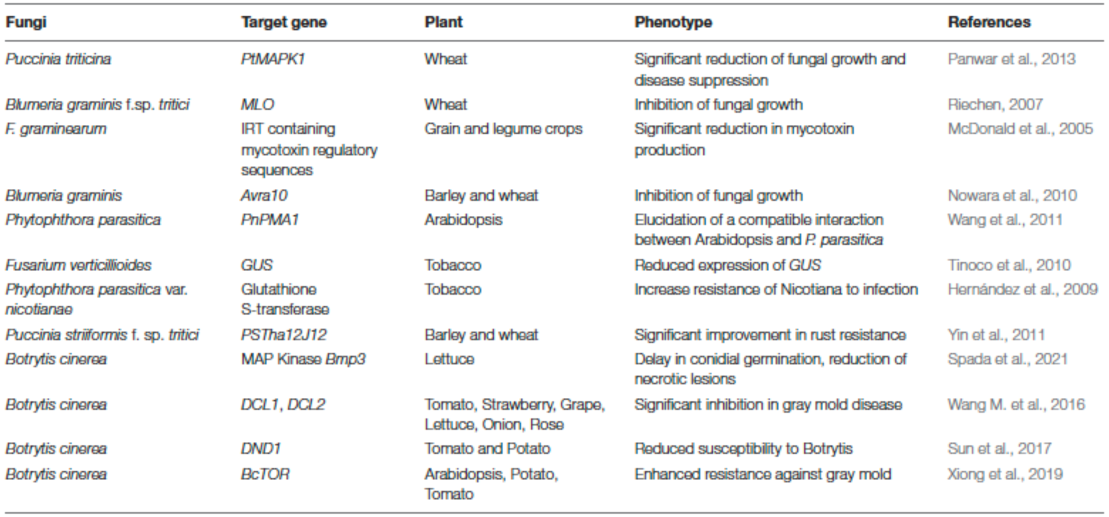
FIGURE 2 | Transgenic rice plants enhanced resistance against three rice-infecting reoviruses. (A) Phenotype of transgenic rice plants (cv.

TABLE 1 | RNAi-targeted editing in plants against insects.



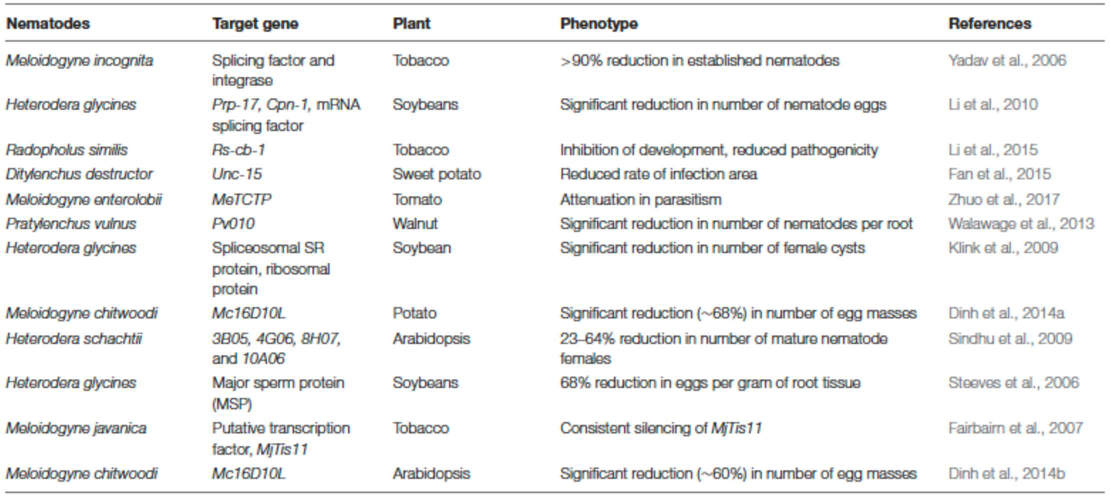
Insects	Target gene	Plant	Phenotype	References
Helicoverpa armigera (Cotton bollworm)	Ecdysone receptor	Tobacco	Reduction of growth followed by death	Zhu et al., 2012
Diabrotica virgifera (Western corn rootworm)	V-ATPaseA	Maize	Stunted growth	Baum et al., 2007
Spodoptera exigua	Ecdysone receptor	Tobacco	Death rate increased	Zhu et al., 2012
Sitobion avenae (Grain aphid)	Salivary proteins DSR32/DSR33	Wheat	Death rate increased	Wang et al., 2015
Glossina morsitans morsitans	Transferrin	Pea, clover, alfalfa	Mortality rate significantly low	Walshe et al., 2009
Acyrthosiphon pisum	Aquaporin	Pea, clover, alfalfa	Osmotic pressure increased	Shakesby et al., 2009
Acyrthosiphon pisum	*SHP*	Pea, clover, alfalfa	Reduced fertility	Will and Vilcinskas, 2015
Acyrthosiphon pisum	V-ATPase E	Pea, clover, alfalfa	dsRNA degradation in saliva	Christiaens and Smagghe, 2014
Nilaparvata lugens (brown plant hopper)	Trehalose PO4 synthase	Rice	Lethality	Chen et al., 2010
Aphis gossypii (Cotton aphid)	*AgOBP2*	Cotton	Failure of recognizing host	Rebijith et al., 2016
Sitobion avenae (Grain aphid)	Catalase gene *CAT*	Wheat	Survival rate reduced	Deng and Zhao, 2014
Sitobion avenae Grain aphid	Cytochrome c oxidase	Wheat	Increased mortality	Zhang et al., 2013
Greenbug *Schizaphis graminum*	Salivary protein C002	Wheat	Lethal	Zhang Y. et al., 2015
Peregrinus maidis	V-ATPase B&D	Corn	Reduced fertility	Yao et al., 2013
Lygus lineolaris	Apoptosis inhibitor	Cotton, alfalfa, beans	Digestion of dsRNA	Allen and Walker, 2012
Phyllotreta striolata	Arginine kinase	Cruciferae crops	Retarded development/ increased mortality	Zhao et al., 2008

TABLE 2 | RNAi-targeted editing in plants against fungi.



Fungi	Target gene	Plant	Phenotype	References
Puccinia triticina	*PtMAPK1*	Wheat	Significant reduction of fungal growth and disease suppression	Panwar et al., 2013
Blumeria graminis f.sp. *tritici*	*MLO*	Wheat	Inhibition of fungal growth	Riechen, 2007
F. graminearum	IRT containing mycotoxin regulatory sequences	Grain and legume crops	Significant reduction in mycotoxin production	McDonald et al., 2005
Blumeria graminis	*Avra10*	Barley and wheat	Inhibition of fungal growth	Nowara et al., 2010
Phytophthora parasitica	*PnPMA1*	Arabidopsis	Elucidation of a compatible interaction between Arabidopsis and *P. parasitica*	Wang et al., 2011
Fusarium verticillioides	*GUS*	Tobacco	Reduced expression of *GUS*	Tinoco et al., 2010
Phytophthora parasitica var. *nicotianae*	Glutathione S-transferase	Tobacco	Increase resistance of Nicotiana to infection	Hernández et al., 2009
Puccinia striiformis f. sp. *tritici*	*PSTha12J12*	Barley and wheat	Significant improvement in rust resistance	Yin et al., 2011
Botrytis cinerea	MAP Kinase *Bmp3*	Lettuce	Delay in conidial germination, reduction of necrotic lesions	Spada et al., 2021
Botrytis cinerea	*DCL1*, *DCL2*	Tomato, Strawberry, Grape, Lettuce, Onion, Rose	Significant inhibition in gray mold disease	Wang M. et al., 2016
Botrytis cinerea	*DND1*	Tomato and Potato	Reduced susceptibility to Botrytis	Sun et al., 2017
Botrytis cinerea	*BcTOR*	Arabidopsis, Potato, Tomato	Enhanced resistance against gray mold	Xiong et al., 2019

TABLE 3 | RNAi-targeted editing in plants against nematodes.



Nematodes	Target gene	Plant	Phenotype	References
Meloidogyne incognita	Splicing factor and integrase	Tobacco	>90% reduction in established nematodes	Yadav et al., 2006
Heterodera glycines	*Prp-17*, *Cpn-1*, mRNA splicing factor	Soybeans	Significant reduction in number of nematode eggs	Li et al., 2010
Radopholus similis	*Rs-cb-1*	Tobacco	Inhibition of development, reduced pathogenicity	Li et al., 2015
Ditylenchus destructor	*Unc-15*	Sweet potato	Reduced rate of infection area	Fan et al., 2015
Meloidogyne enterolobii	*MeTCTP*	Tomato	Attenuation in parasitism	Zhuo et al., 2017
Pratylenchus vulnus	*Pv010*	Walnut	Significant reduction in number of nematodes per root	Walawage et al., 2013
Heterodera glycines	Spliceosomal SR protein, ribosomal protein	Soybean	Significant reduction in number of female cysts	Klink et al., 2009
Meloidogyne chitwoodi	*Mc16D10L*	Potato	Significant reduction (~68%) in number of egg masses	Dinh et al., 2014a
Heterodera schachtii	*3B05*, *4G06*, *8H07*, and *10A06*	Arabidopsis	23–64% reduction in number of mature nematode females	Sindhu et al., 2009
Heterodera glycines	Major sperm protein (MSP)	Soybeans	68% reduction in eggs per gram of root tissue	Steeves et al., 2006
Meloidogyne javanica	Putative transcription factor, *MjTis11*	Tobacco	Consistent silencing of *MjTis11*	Fairbairn et al., 2007
Meloidogyne chitwoodi	*Mc16D10L*	Arabidopsis	Significant reduction (~60%) in number of egg masses	Dinh et al., 2014b

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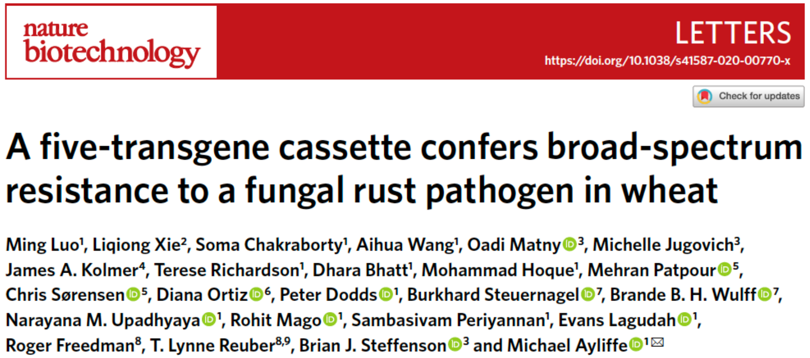

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LETTERS
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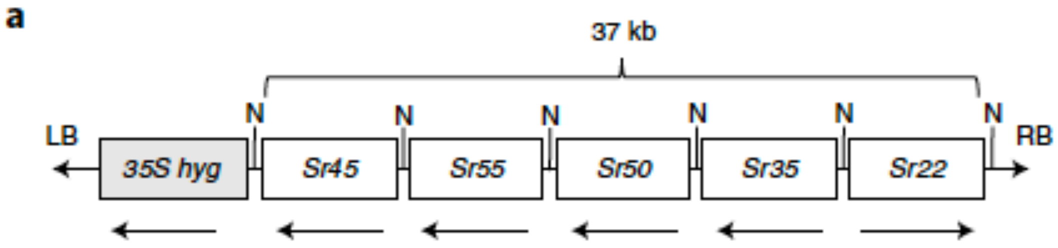
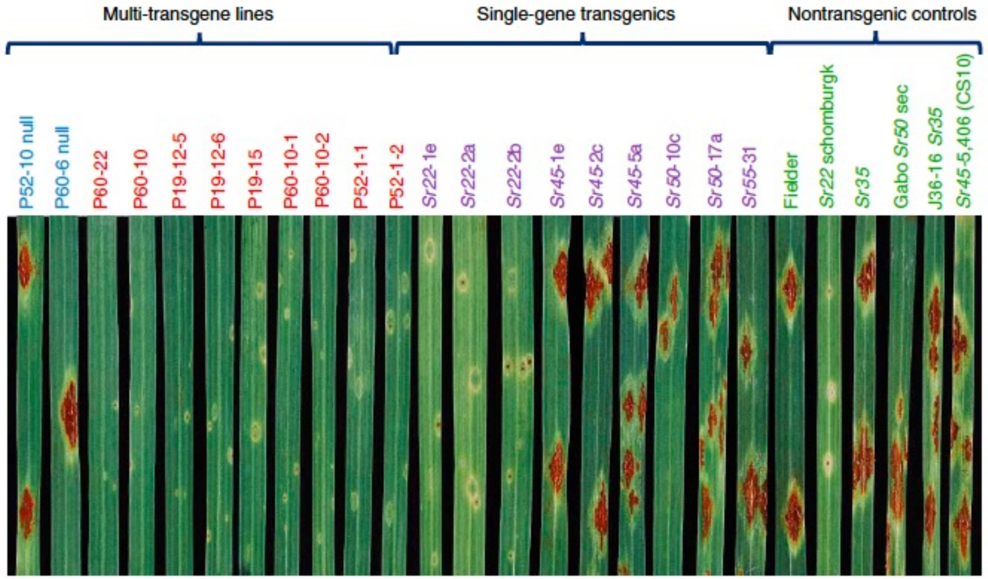
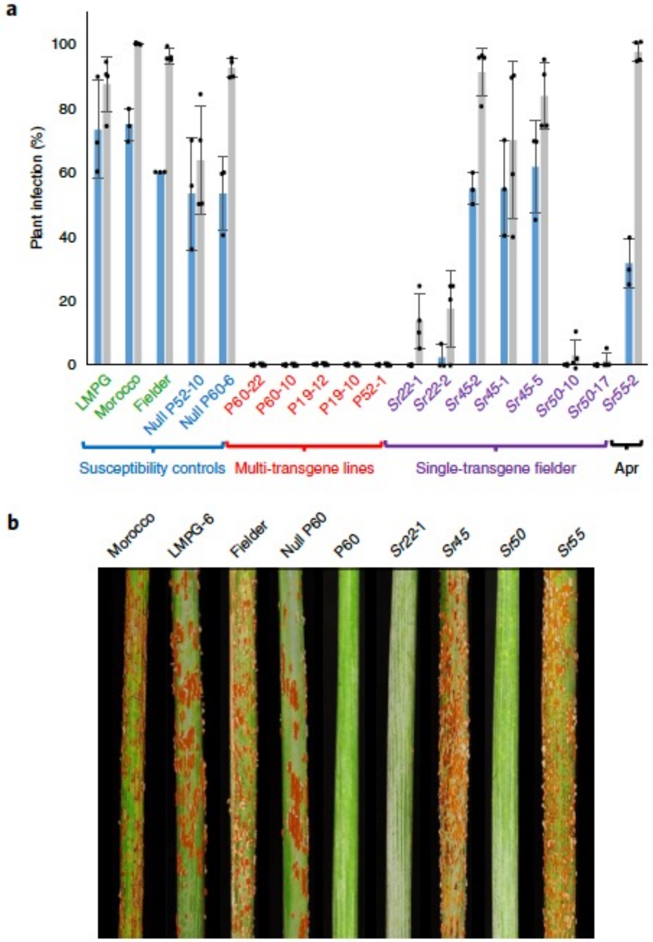
A five-transgene cassette confers broad-spectrum resistance to a fungal rust pathogen in wheat

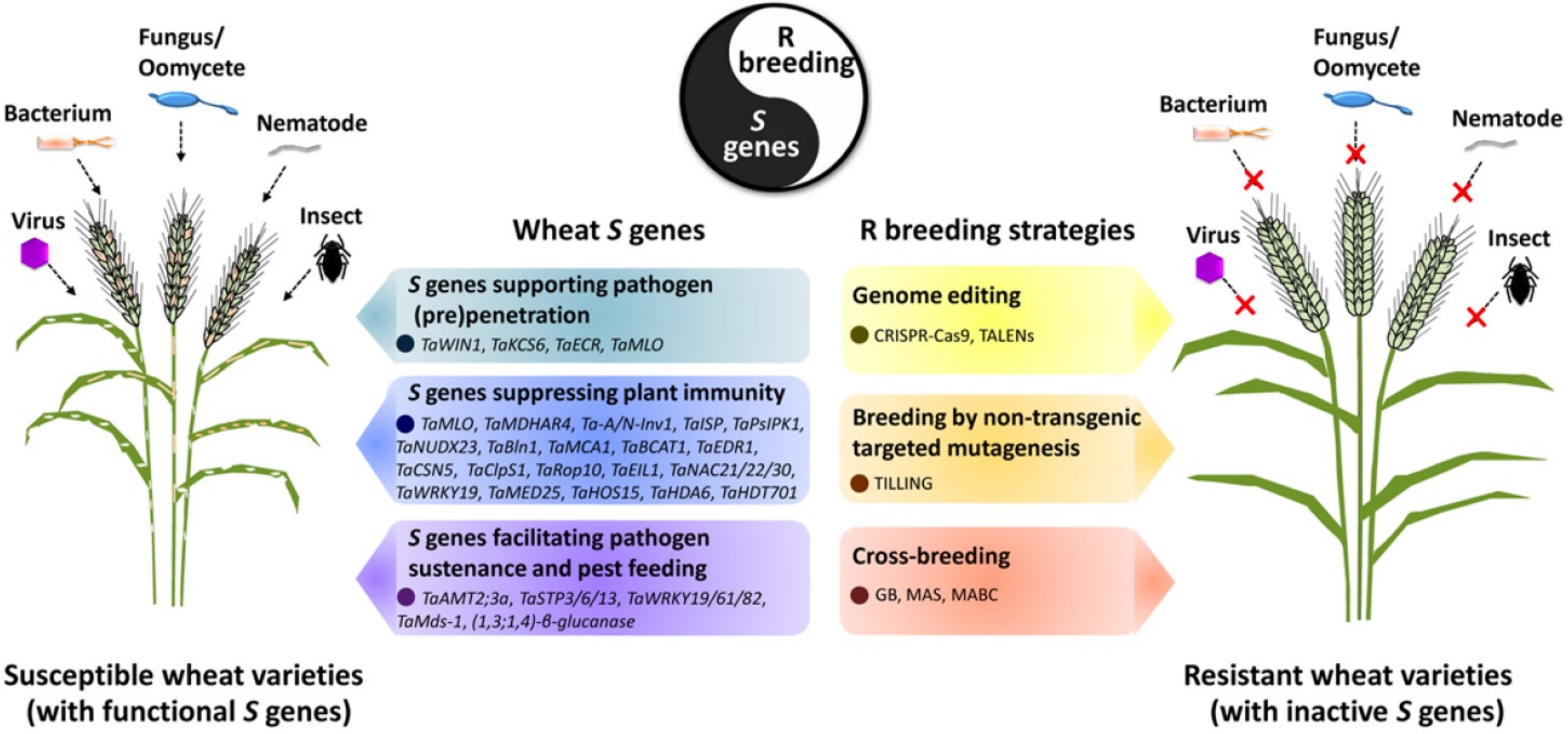
Ming Luo[1], Liqiong Xie[2], Soma Chakraborty[1], Aihua Wang[1], Oadi Matny[3], Michelle Jugovich[3], James A. Kolmer[4], Terese Richardson[1], Dhara Bhatt[1], Mohammad Hoque[1], Mehran Patpour[5], Chris Sørensen[5], Diana Ortiz[6], Peter Dodds[1], Burkhard Steuernagel[7], Brande B. H. Wulff[7], Narayana M. Upadhyaya[1], Rohit Mago[1], Sambasivam Periyannan[1], Evans Lagudah[1], Roger Freedman[8], T. Lynne Reuber[8,9], Brian J. Steffenson[3] and Michael Ayliffe[1]✉



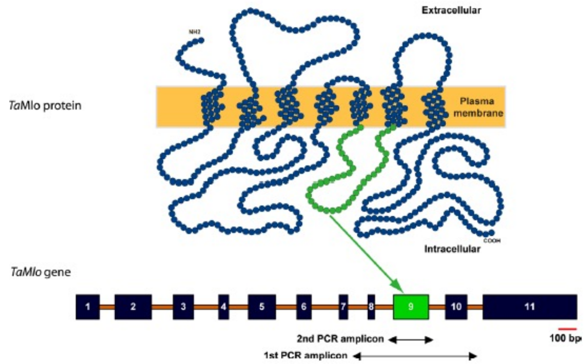




Gènes de sensibilité



Mutagénèse par TILLING



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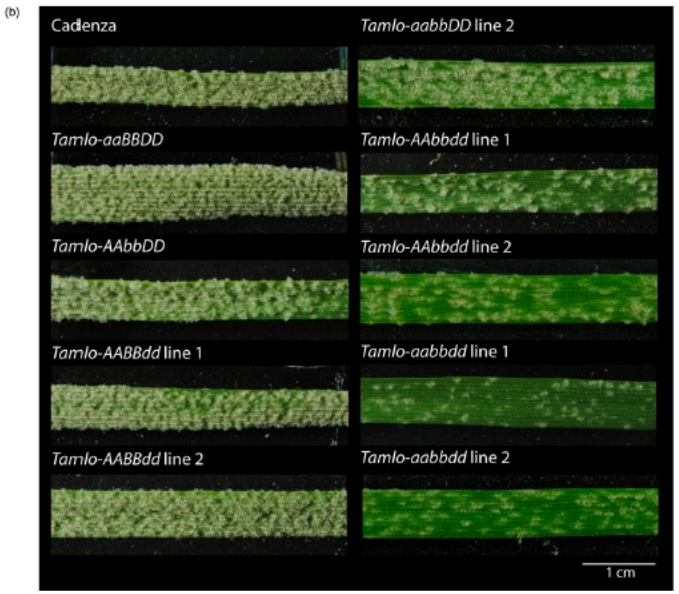
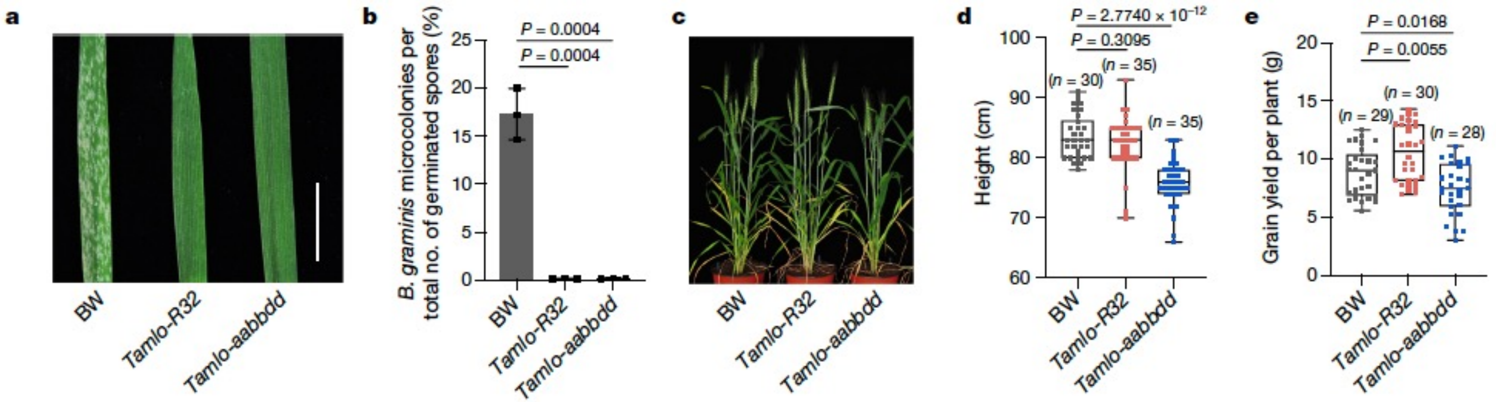
mlo-based powdery mildew resistance in hexaploid bread wheat generated by a non-transgenic TILLING approach

Johanna Acevedo-Garcia[1], David Spencer[1], Hannah Thieron[1], Anja Reinstädler[1], Kim Hammond-Kosack[2], Andrew L. Phillips[2] and Ralph Panstruga[1]*





Mutagénèse ciblée par Genome Editing - CRISPR

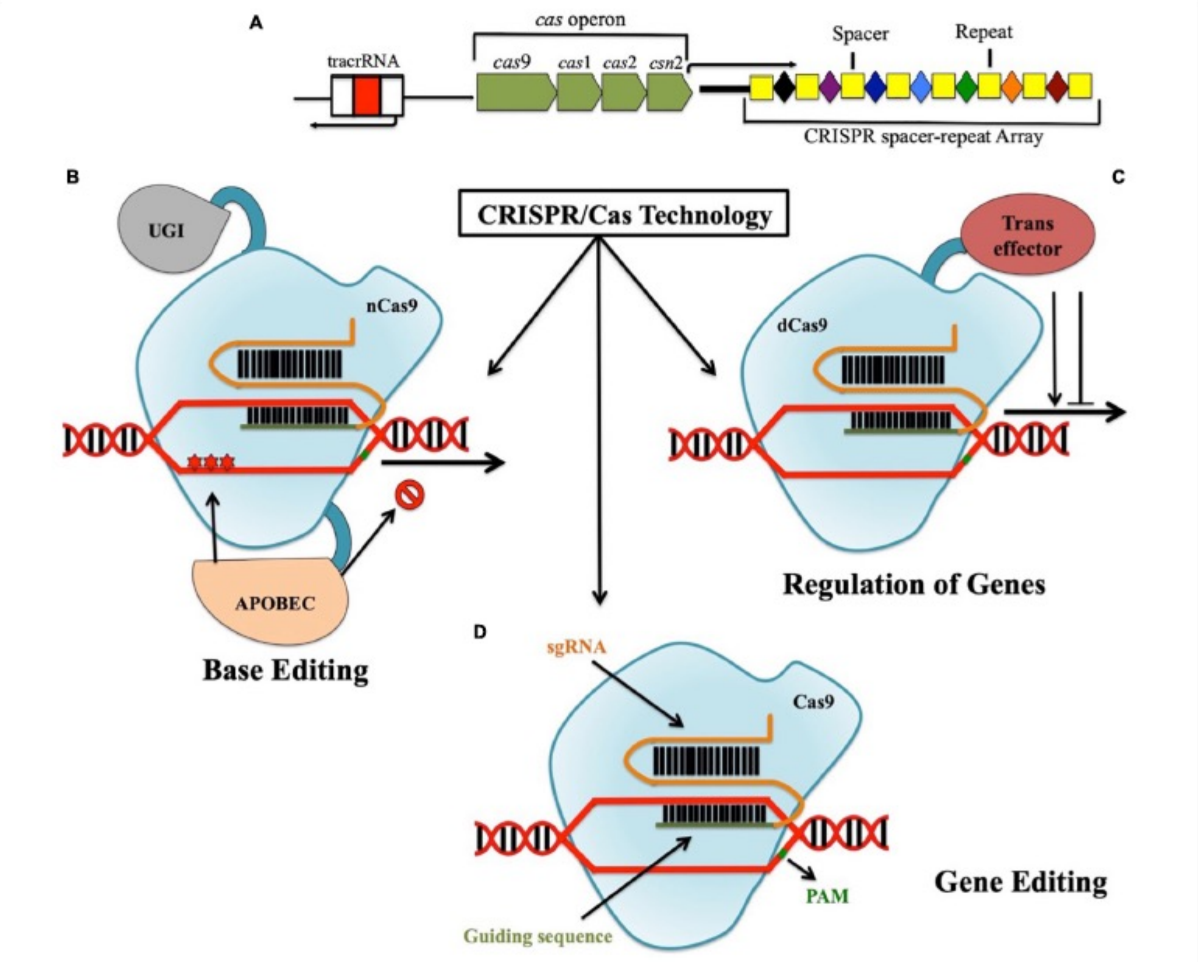
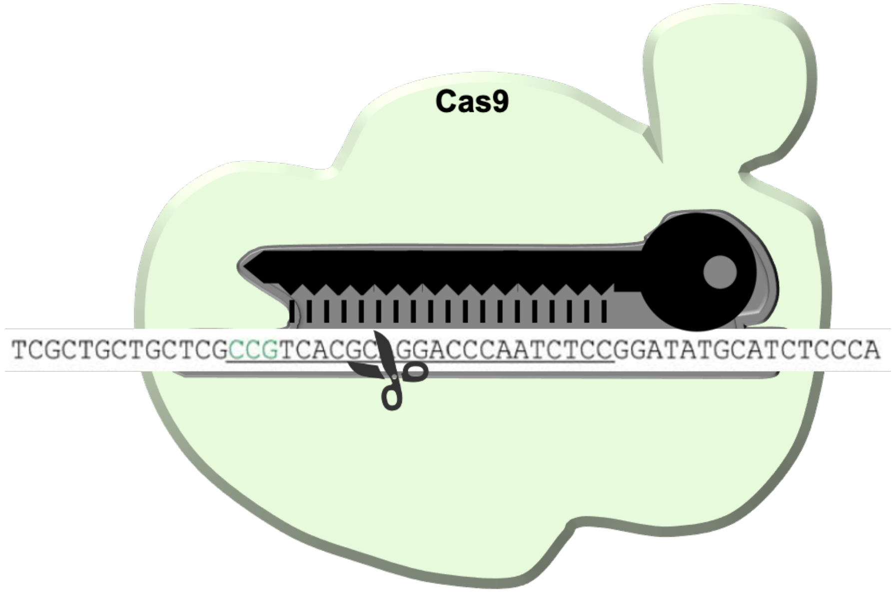
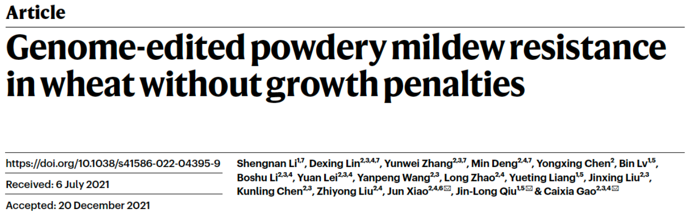


FIGURE 2 | CRISPR locus in genome comprises of CRISPR spacer-repeat array, Cas operon, and tracrRNA. Apart from being able to specifically target nucleotides in the genome (gene editing), using impaired Cas9 enzymes such as dCas9 and nickase Cas9, gene regulation and targeted base editing without double-strand breaks can also be achieved, respectively. **(A)** CRISPR locus in genome; **(B)** CRISPR/Cas9-mediated gene editing; **(C)** CRISPR/dCas9-mediated gene regulation; **(D)** CRISPR/nCas9-mediated base editing.



L’édition d’allèles pour la résistance à l’oïdium



Article

Genome-edited powdery mildew resistance in wheat without growth penalties

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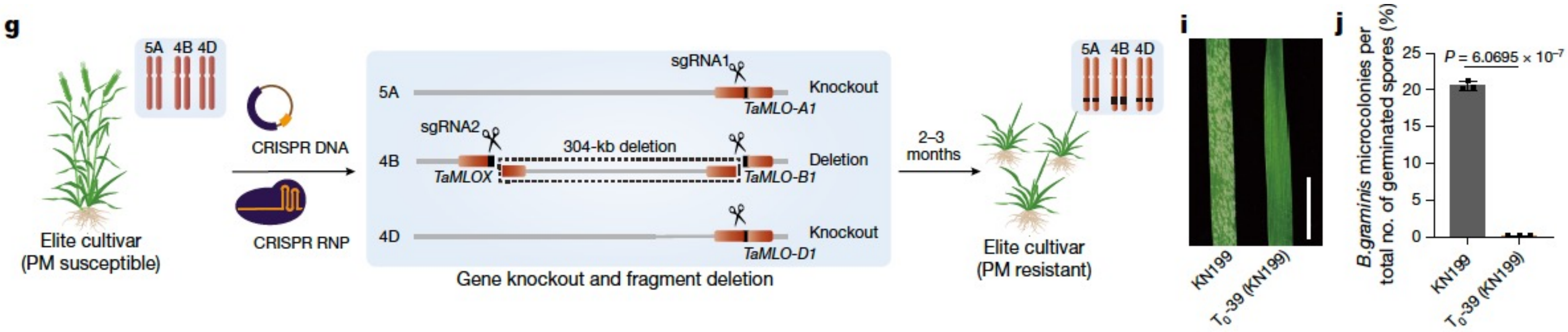
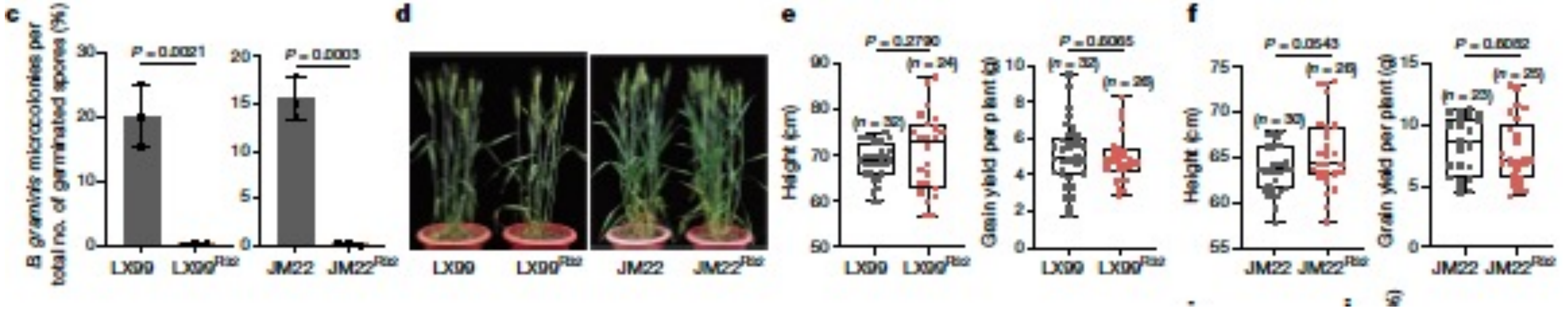
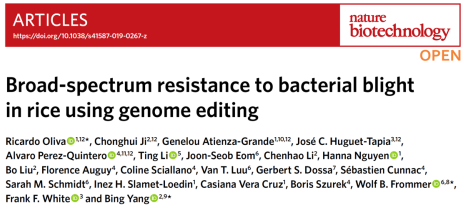
Shengnan Li[1,7], Dexing Lin[2,3,4,7], Yunwei Zhang[2,3,7], Min Deng[2,4,7], Yongxing Chen[2], Bin Lv[1,5], Boshu Li[2,3,4], Yuan Lei[2,3,4], Yanpeng Wang[2,3], Long Zhao[2,4], Yueting Liang[1,5], Jinxing Liu[2,3], Kunling Chen[2,3], Zhiyong Liu[2,4], Jun Xiao[2,4,6] ✉, Jin-Long Qiu[1,5] ✉ & Caixia Gao[2,3,4] ✉





Gènes de sensibilité : exemple du gène *Sweet*



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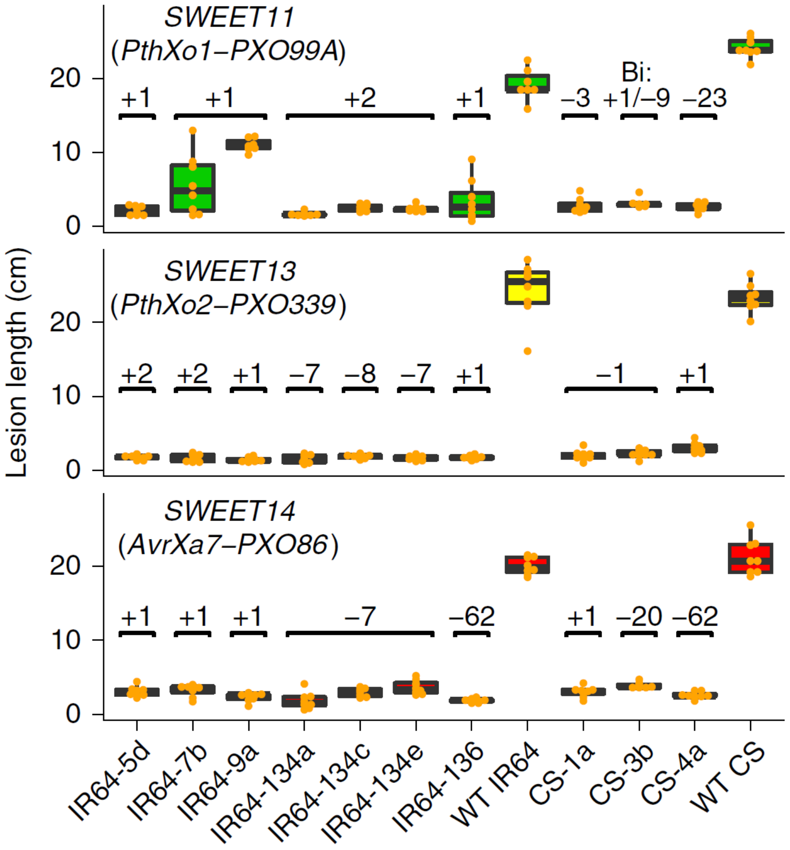
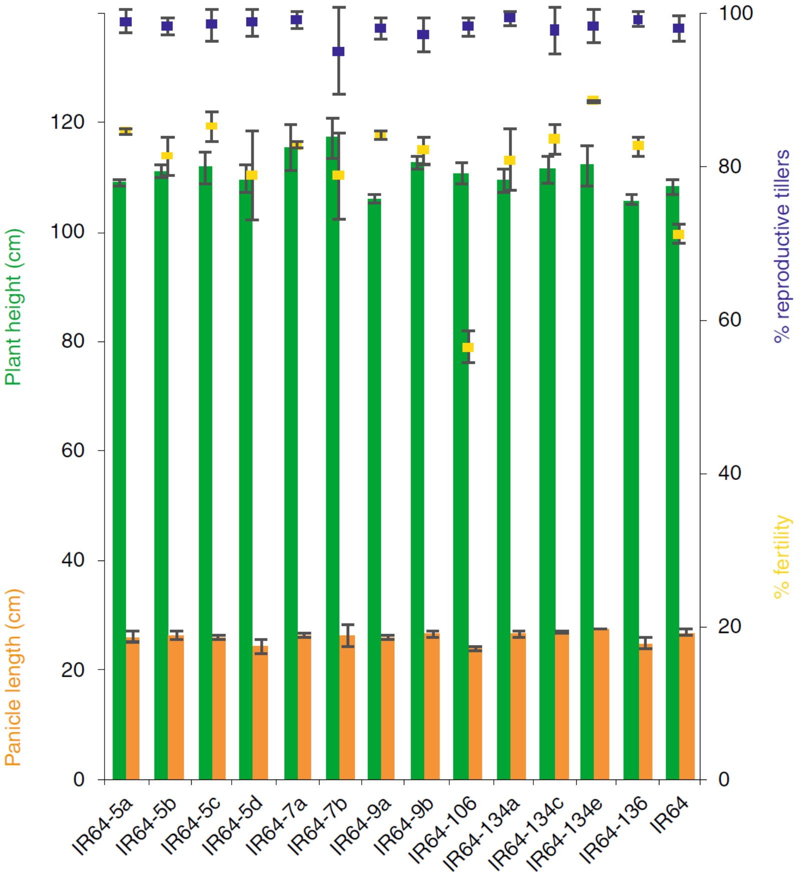
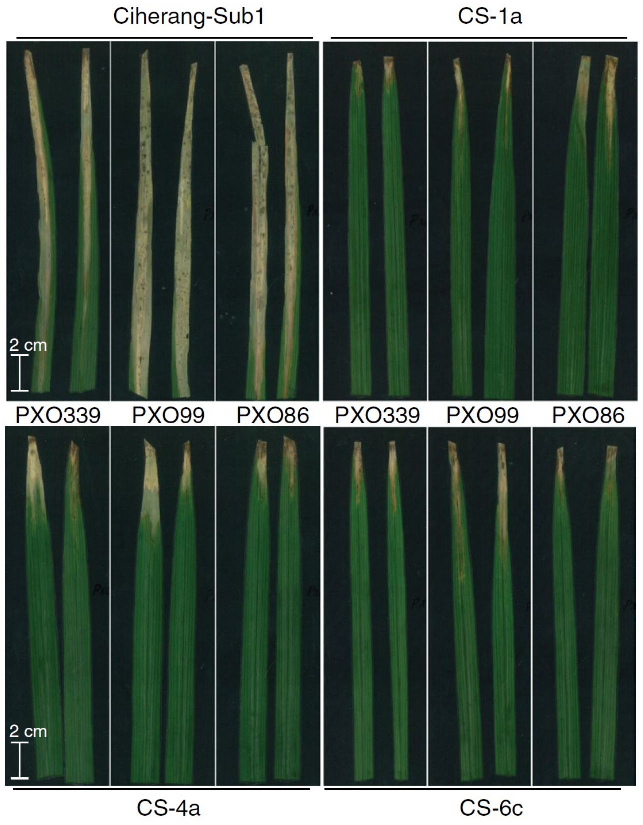
Broad-spectrum resistance to bacterial blight in rice using genome editing

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*]







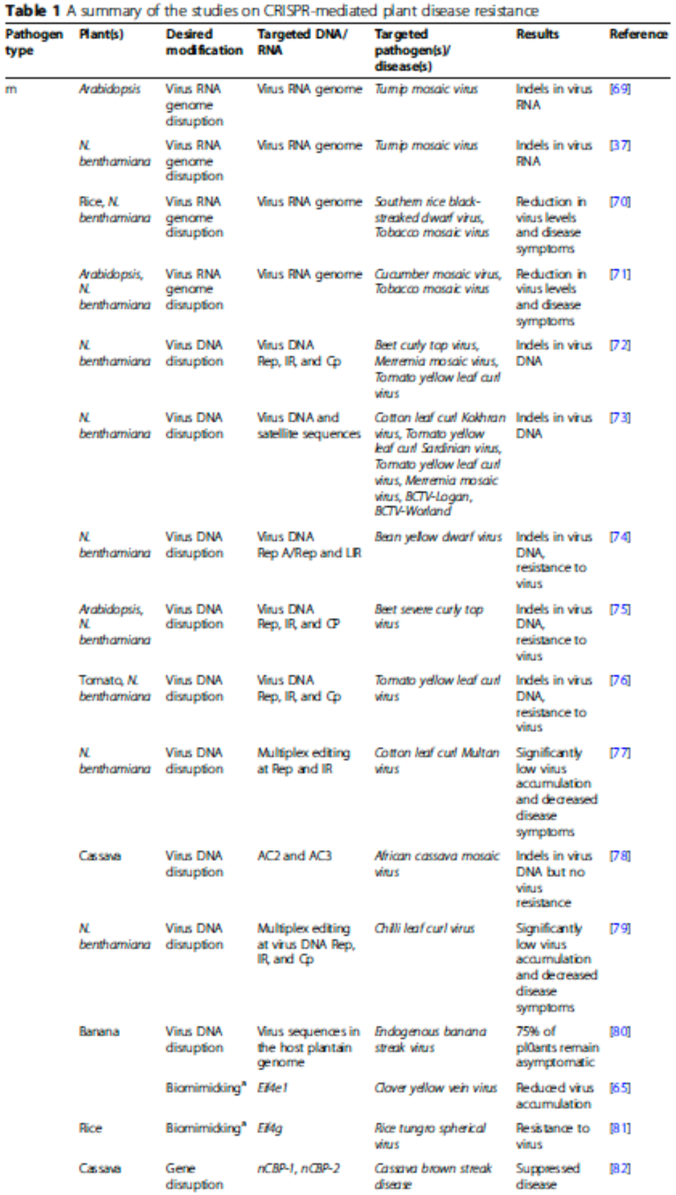


Table 1 A summary of the studies on CRISPR-mediated plant disease resistance

Pathogen type	Plant(s)	Desired modification	Targeted DNA/ RNA	Targeted pathogen(s)/ disease(s)	Results	Reference
m	*Arabidopsis*	Virus RNA genome disruption	Virus RNA genome	*Turnip mosaic virus*	Indels in virus RNA	[69]
	N. benthamiana	Virus RNA genome disruption	Virus RNA genome	*Turnip mosaic virus*	Indels in virus RNA	[37]
	Rice, *N. benthamiana*	Virus RNA genome disruption	Virus RNA genome	*Southern rice black-streaked dwarf virus, Tobacco mosaic virus*	Reduction in virus levels and disease symptoms	[70]
	Arabidopsis, N. benthamiana	Virus RNA genome disruption	Virus RNA genome	*Cucumber mosaic virus, Tobacco mosaic virus*	Reduction in virus levels and disease symptoms	[71]
	N. benthamiana	Virus DNA disruption	Virus DNA Rep, IR, and Cp	*Beet curly top virus, Merremia mosaic virus, Tomato yellow leaf curl virus*	Indels in virus DNA	[72]
	N. benthamiana	Virus DNA disruption	Virus DNA and satellite sequences	*Cotton leaf curl Kokhran virus, Tomato yellow leaf curl Sardinian virus, Tomato yellow leaf curl virus, Merremia mosaic virus, BCTV-Logan, BCTV-Worland*	Indels in virus DNA	[73]
	N. benthamiana	Virus DNA disruption	Virus DNA Rep A/Rep and LIR	*Bean yellow dwarf virus*	Indels in virus DNA, resistance to virus	[74]
	Arabidopsis, N. benthamiana	Virus DNA disruption	Virus DNA Rep, IR, and CP	*Beet severe curly top virus*	Indels in virus DNA, resistance to virus	[75]
	Tomato, *N. benthamiana*	Virus DNA disruption	Virus DNA Rep, IR, and Cp	*Tomato yellow leaf curl virus*	Indels in virus DNA, resistance to virus	[76]
	N. benthamiana	Virus DNA disruption	Multiplex editing at Rep and IR	*Cotton leaf curl Multan virus*	Significantly low virus accumulation and decreased disease symptoms	[77]
	Cassava	Virus DNA disruption	AC2 and AC3	*African cassava mosaic virus*	Indels in virus DNA but no virus resistance	[78]
	N. benthamiana	Virus DNA disruption	Multiplex editing at virus DNA Rep, IR, and Cp	*Chili leaf curl virus*	Significantly low virus accumulation and decreased disease symptoms	[79]
	Banana	Virus DNA disruption	Virus sequences in the host plantain genome	*Endogenous banana streak virus*	75% of pl0ants remain asymptomatic	[80]
		Biomimicking[a]	*Eif4e1*	*Clover yellow vein virus*	Reduced virus accumulation	[65]
	Rice	Biomimicking[a]	*Eif4g*	*Rice tungro spherical virus*	Resistance to virus	[81]
	Cassava	Gene disruption	*nCBP-1, nCBP-2*	*Cassava brown streak disease*	Suppressed disease	[82]

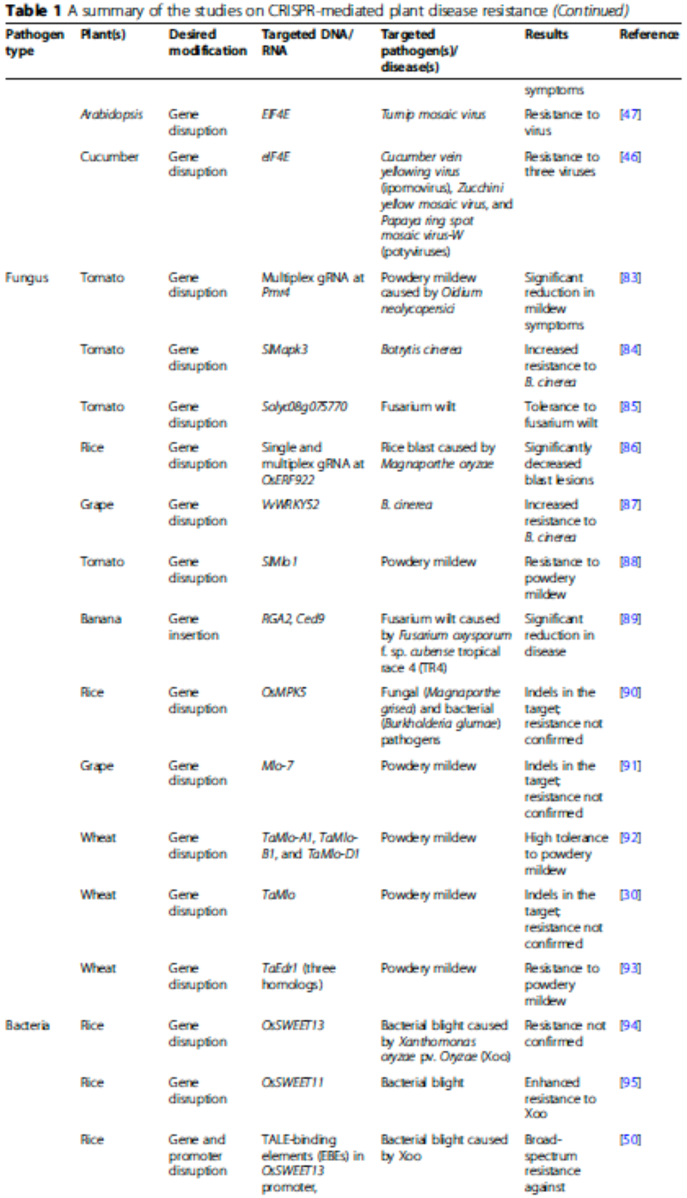


Table 1 A summary of the studies on CRISPR-mediated plant disease resistance *(Continued)*

Pathogen type	Plant(s)	Desired modification	Targeted DNA/ RNA	Targeted pathogen(s)/ disease(s)	Results	Reference
					symptoms	
	Arabidopsis	Gene disruption	*EIF4E*	*Turnip mosaic virus*	Resistance to virus	[47]
	Cucumber	Gene disruption	*eIF4E*	*Cucumber vein yellowing virus* (ipomovirus), *Zucchini yellow mosaic virus*, and *Papaya ring spot mosaic virus-W* (potyviruses)	Resistance to three viruses	[46]
Fungus	Tomato	Gene disruption	Multiplex gRNA at *Pmr4*	Powdery mildew caused by *Oidium neolycopersici*	Significant reduction in mildew symptoms	[83]
	Tomato	Gene disruption	*SlMapk3*	*Botrytis cinerea*	Increased resistance to *B. cinerea*	[84]
	Tomato	Gene disruption	*Solyc08g075770*	Fusarium wilt	Tolerance to fusarium wilt	[85]
	Rice	Gene disruption	Single and multiplex gRNA at *OsERF922*	Rice blast caused by *Magnaporthe oryzae*	Significantly decreased blast lesions	[86]
	Grape	Gene disruption	*VvWRKY52*	*B. cinerea*	Increased resistance to *B. cinerea*	[87]
	Tomato	Gene disruption	*SlMlo1*	Powdery mildew	Resistance to powdery mildew	[88]
	Banana	Gene insertion	*RGA2, Ced9*	Fusarium wilt caused by *Fusarium oxysporum* f. sp. *cubense* tropical race 4 (TR4)	Significant reduction in disease	[89]
	Rice	Gene disruption	*OsMPK5*	Fungal (*Magnaporthe grisea*) and bacterial (*Burkholderia glumae*) pathogens	Indels in the target; resistance not confirmed	[90]
	Grape	Gene disruption	*Mlo-7*	Powdery mildew	Indels in the target; resistance not confirmed	[91]
	Wheat	Gene disruption	*TaMlo-A1, TaMlo-B1*, and *TaMlo-D1*	Powdery mildew	High tolerance to powdery mildew	[92]
	Wheat	Gene disruption	*TaMlo*	Powdery mildew	Indels in the target; resistance not confirmed	[30]
	Wheat	Gene disruption	*TaEdr1* (three homologs)	Powdery mildew	Resistance to powdery mildew	[93]
Bacteria	Rice	Gene disruption	*OsSWEET13*	Bacterial blight caused by *Xanthomonas oryzae* pv. *Oryzae* (Xoo)	Resistance not confirmed	[94]
	Rice	Gene disruption	*OsSWEET11*	Bacterial blight	Enhanced resistance to Xoo	[95]
	Rice	Gene and promoter disruption	TALE-binding elements (EBEs) in *OsSWEET13* promoter,	Bacterial blight caused by Xoo	Broad-spectrum resistance against	[50]

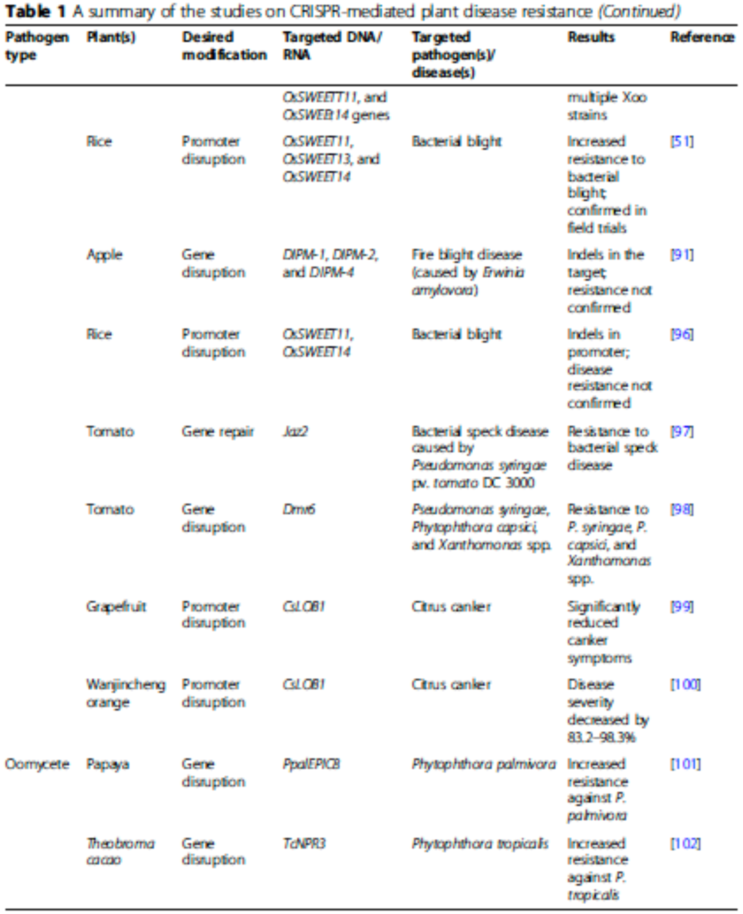


Table 1 A summary of the studies on CRISPR-mediated plant disease resistance *(Continued)*

Pathogen type	Plant(s)	Desired modification	Targeted DNA/ RNA	Targeted pathogen(s)/ disease(s)	Results	Reference
			OsSWEETT11, and *OsSWEEt14* genes		multiple Xoo strains	
	Rice	Promoter disruption	*OsSWEET11, OsSWEET13*, and *OsSWEET14*	Bacterial blight	Increased resistance to bacterial blight; confirmed in field trials	[51]
	Apple	Gene disruption	*DIPM-1, DIPM-2*, and *DIPM-4*	Fire blight disease (caused by *Erwinia amylovora*)	Indels in the target; resistance not confirmed	[91]
	Rice	Promoter disruption	*OsSWEET11, OsSWEET14*	Bacterial blight	Indels in promoter; disease resistance not confirmed	[96]
	Tomato	Gene repair	*Jaz2*	Bacterial speck disease caused by *Pseudomonas syringae* pv. *tomato* DC 3000	Resistance to bacterial speck disease	[97]
	Tomato	Gene disruption	*Dmr6*	*Pseudomonas syringae, Phytophthora capsici*, and *Xanthomonas* spp.	Resistance to *P. syringae, P. capsici*, and *Xanthomonas* spp.	[98]
	Grapefruit	Promoter disruption	*CsLOB1*	Citrus canker	Significantly reduced canker symptoms	[99]
	Wanjincheng orange	Promoter disruption	*CsLOB1*	Citrus canker	Disease severity decreased by 83.2–98.3%	[100]
Oomycete	Papaya	Gene disruption	*PpalEPIC8*	*Phytophthora palmivora*	Increased resistance against *P. palmivora*	[101]
	Theobroma cacao	Gene disruption	*TcNPR3*	*Phytophthora tropicalis*	Increased resistance against *P. tropicalis*	[102]

Zaidi et, Genome Biology 2022

Les facteurs de sensibilité peuvent être partagés par plusieurs agents pathogènes

Ouvre la voie à la construction de résistances multi-pathogènes

Mutant MNR 220 (Campbell et al, TAG 2012)

Alpowa

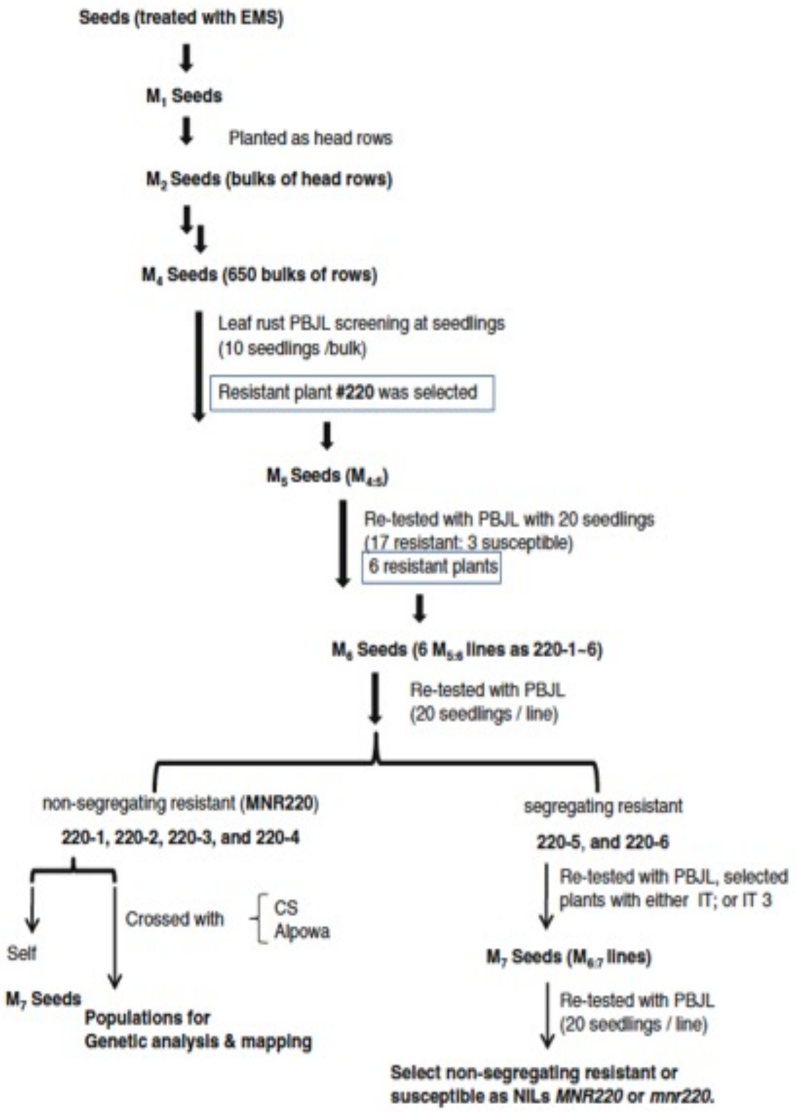
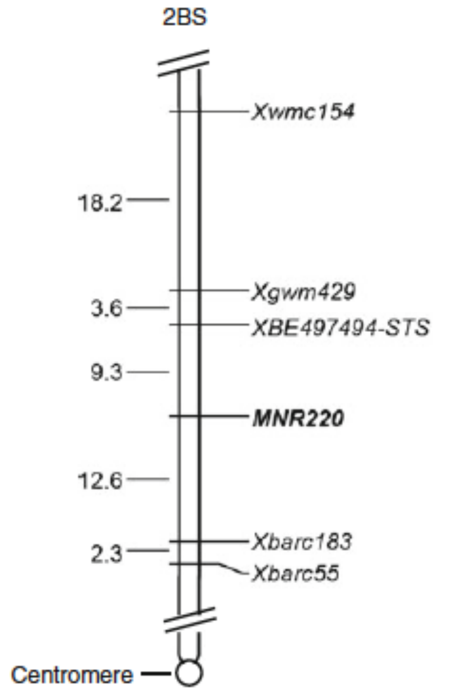


Fig. 1 A scheme showing steps of mutant identification, confirmation and genetic analysis. $M_{n:n+1}$ line is used to describe n_{+1} generation seeds that derived from one selected *n* generation plant



Chinese Spring X MNR220 (95 F_2 individuals)

Genetic map of *MNR220*

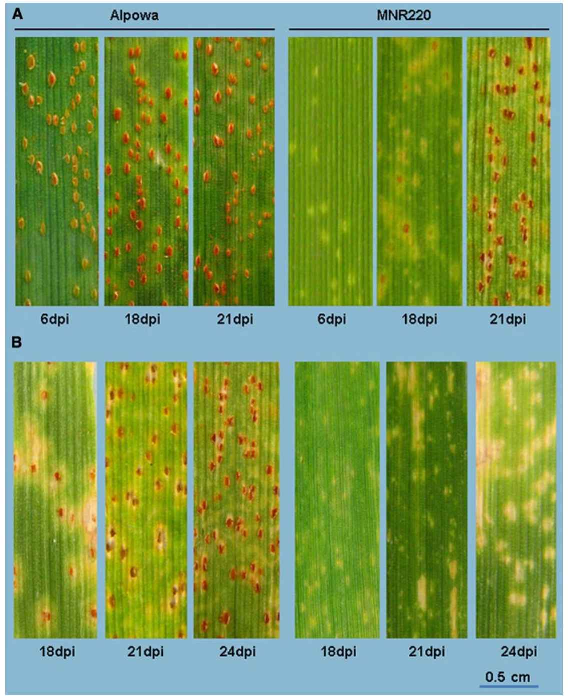
Localisé sur le bras court du chromosome 2B

Mutant MNR 220 (Campbell et al, TAG 2012)

Puccinia triticina (wheat leaf rust)
P. graminis f. sp. tritici **(**stem rust)
P. striiformis f. sp. tritici (stripe rust)
Blumeria graminis f. sp. tritici (powdery mildew)

Biotrophes

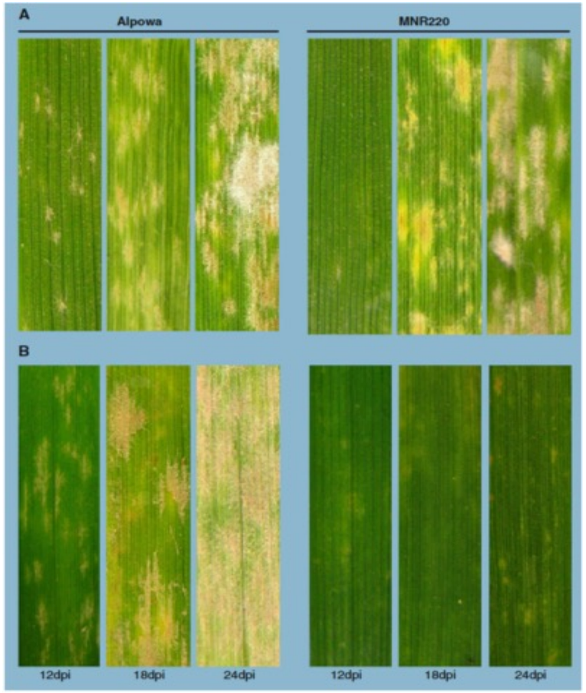
Septoriose
Zymoseptoria tritici



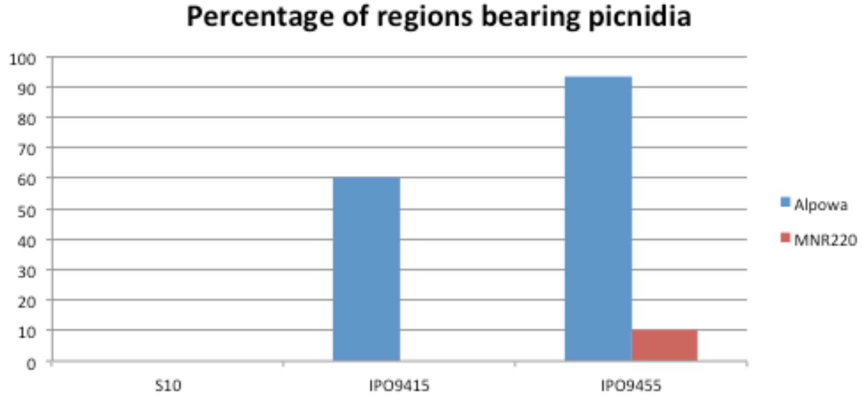
Puccinia triticina

Plantules

Plantes adultes



Blumeria graminis f. sp. tritici



Prime Editing
(Edition primaire ou édition de base)

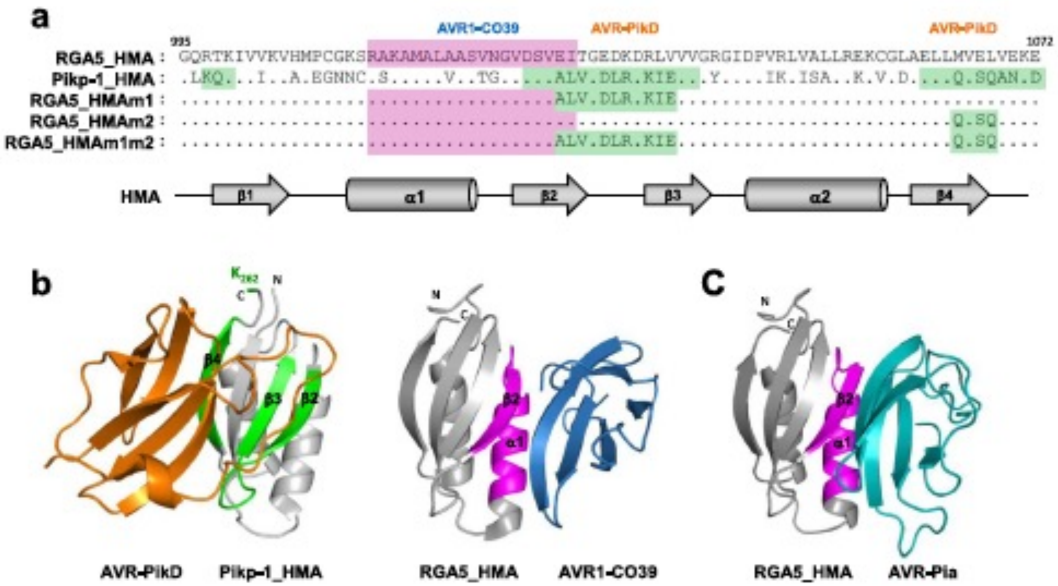
ARTICLE

Check for updates

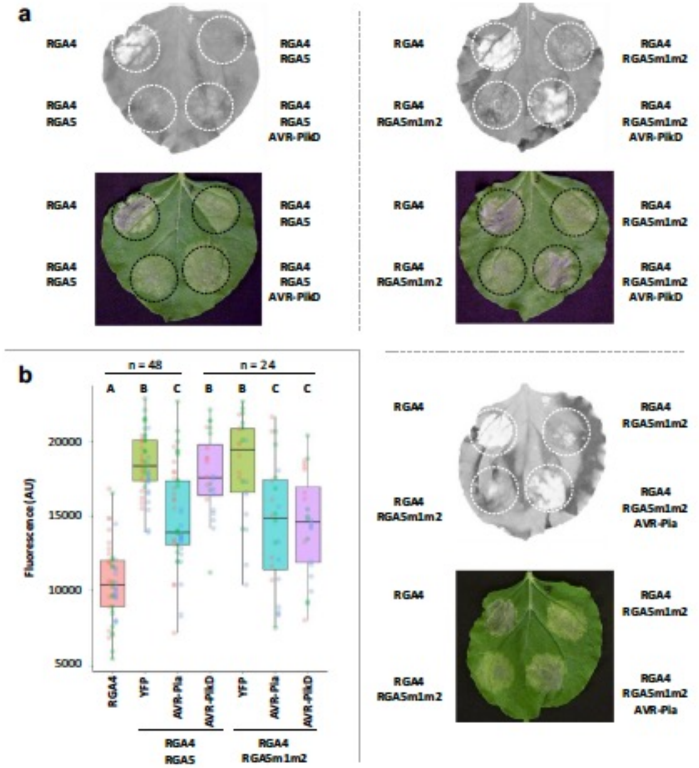
https://doi.org/10.1038/s41467-022-29196-6 OPEN

New recognition specificity in a plant immune receptor by molecular engineering of its integrated domain

Stella Cesari[1✉], Yuxuan Xi[1], Nathalie Declerck[1], Véronique Chalvon[1], Léa Mammri[2], Martine Pugnière[3], Corinne Henriquet[3], Karine de Guillen[2], Vincent Chochois[4], André Padilla[2] & Thomas Kroj[1✉]



Plant nucleotide-binding and leucine-rich repeat domain proteins (NLRs)



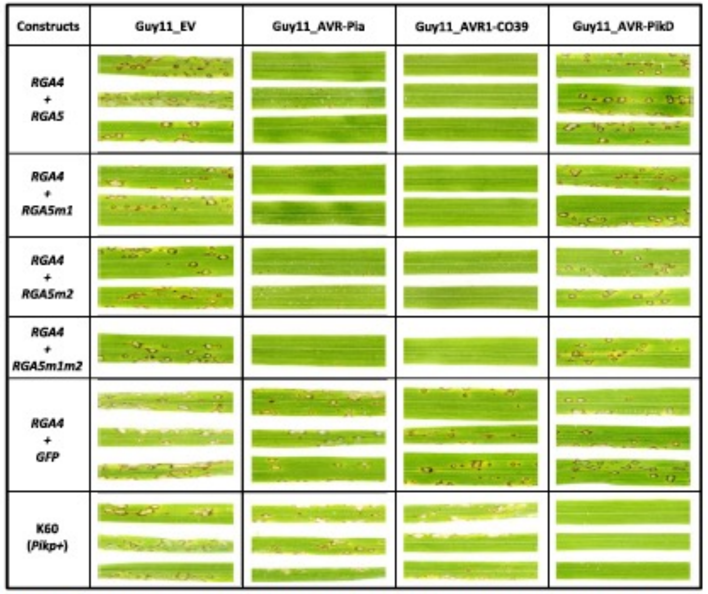
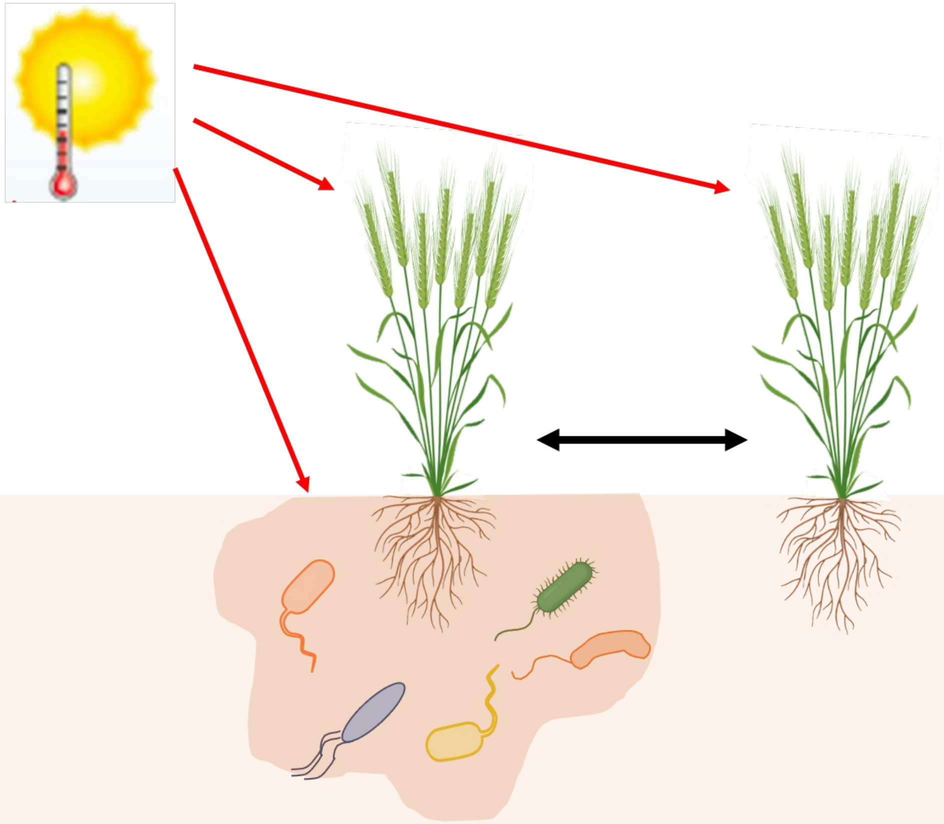


Fig. 8 The RGA5 m1, m2, and m1m2 mutants recognize AVR-Pia but not AVR-PikD in rice. The rice cultivar Nipponbare was co-transformed with a

Possibilités offertes par les biotechnologies

- Création de novo de sources de résistance pour des maladies « orphelines »
- Remplacement d'allèles simple ou multiplex
- Suppression du linkage drive
- Possibilités de créer de nouvelle combinaison d'allèles pour des gènes très étroitement liés
- Transfert rapide d'allèles exotiques vers des variétés « Elites »
- Réactivation des pseudogènes
- Création de séries alléliques originales pour des gènes R clonés
- …

Rendre plus durable les résistances aux pathogènes et bioagresseurs face au changement climatique



Identifier des sources de résistances durables

Bases génétiques et moléculaires

Mécanismes (éco)physiologiques

Interactions plante-pathogène-environnement

Effets des associations plante-plante

Rôle des microbiotes

Solutions agronomiques
Systèmes de culture
Gestion des résistances (parcelles, paysage, territoire)
…

Merci de votre attention