Journal of Life and Social Sciences
eISSN: 3006-2675
www.bbasrjlifess.com
J. Life Soc. Sci, 2024; Volume, **3**: 25

Review Article Open Access

GENETICALLY MODIFIED CROPS GLOBAL REGULATION: IMPLICATIONS FOR FOOD SECURITY AND ENVIRONMENTAL SUSTAINABILITY

ULLAH MA[1], AHMED MA[1], JAVED I[2], SHAFIQ M[3], SHERAZI SHUH[1], WALEED R[1]

[1]*Department of Plant Breeding and Genetics, Faculty of Agricultural Sciences, University of the Punjab P.O.Box.54590, Lahore, Pakistan*
[2]*Department of Plant Breeding and Genetics, Pir Mehr Ali Shah Arid Agriculture University, P.O BOX.46000, Rawalpindi, Pakistan*
[3]*Department of Horticulture, Faculty of Agricultural Sciences, University of the Punjab, P.O BOX. 54590, Lahore, Pakistan*
**Correspondence author email address: asadpbg3@gmail.com*

(Received, 26th February 2023, Revised 14th April 2024, Published 16th April 2024)

Abstract *Genetic engineering and plant transformation play crucial roles in enhancing crops by introducing beneficial foreign genes or suppressing native gene expression. Genetically modified crops offer advantages such as herbicide tolerance, insect resistance, tolerance to abiotic stress, disease resistance, and improved nutrition. Transgenic technology integration has shown significant advantages, such as increased crop yields, less dependence on pesticides and insecticides, decreased CO_2 emissions, and decreased crop production costs. In contrast to transgenic crops, some other techniques can help produce crops without foreign genes, which may gain more consumer acceptance and quicker regulatory approvals. This review provides an extensive overview of various accomplishments in genetic modifications and their present status.*

*[Citation: Ullah, M.A., Ahmed, M.A., Javed, I., Shafiq, M., Sherazi, S.H.U.H., Waleed, R. (2024). Genetically modified crops global regulation: implications for food security and environmental sustainability. J. Life Soc. Sci, **2024**: 25]*

Keywords: *Genetic engineering; herbicide tolerance; insect resistance; abiotic stress; disease resistance*

Introduction

Agriculture plays a critical role in meeting the needs of the global population in the twenty-first century, including clothing, energy, and sustenance. Even with fewer farmers and less arable land available, modern difficulties are addressed by ongoing research and development that expands on previously acquired knowledge. The use of biotechnology in agricultural innovation is crucial to this advancement, as it greatly boosts productivity and accessibility (De Souza and Bonciu, 2022). Adopting new technologies does, however, need extensive awareness of and control over the hazards involved. Legislative organizations have taken on the task of evaluating and reducing possible risks associated with agricultural practices during the last three to four decades (Caradus, 2023). These standards are generally applied to all agricultural products meant for cultivation and consumption; this includes both biotechnology-developed goods and those originating from conventional plant breeding techniques.

Crop plants that have had their genetic makeup changed through genetic manipulation are commonly referred to as genetically modified (GM) crops. These changes are intended to improve upon current characteristics or add new attributes that aren't found in the target crop species naturally. Transgenic plants are those that have had particular foreign nucleotide or gene sequences included in their genome using techniques such as direct gene transfer or Agrobacterium-mediated transformation. A transgenic is an introduced gene that can come from animals, fungi, bacteria, viruses, or other plant species. The traditional constraints of traditional plant breeding, which need sexual compatibility across species as a requirement for crossbreeding, have been bypassed by genetic transformation. Back in 1977, scientists made a discovery. They found out that Agrobacterium tumefaciens can naturally put Ti plasmid DNA (T-DNA) into the genes of plants. These lines unveil a plethora of new opportunities for utilizing the Ti plasmid as a means to introduce foreign genes into plant cells. And that's how they started creating transgenic plants (Somssich, 2022). Later, recombinant DNA and transformation methods were reported to be effective in transferring specific gene sequences to plant cells. In the same year, the first transgenic plants were created, such as petunia and tobacco that are resistant to antibiotics (Sharma et al., 2022). An experiment was conducted where the successful expression of the 'phaseolin' gene from beans was demonstrated in sunflowers. This groundbreaking study showcased the ability to express a plant gene in a taxonomically distinct angiosperm family (Kumar et al., 2020). In 1994, the Food and Drug Administration (FDA) approved the transgenic tomato 'Flavr Savr,' created by Calgene (Monsanto), for sale in the United States due to its prolonged shelf life or delayed ripening (Pradhan et al., 2021). After that breakthrough, several transgenic crops received approval for commercialization. These included Bt cotton, glyphosate-resistant soybeans, Bt potato, Bt maize, and cotton resistant to bromoxynil herbicide. Microbial genes and/or genetic components are the main features of commercialized transgenic crops. 32 crops and 525 transgenic events have been commercialized thus far. The most incidents (238) are found in maize, followed by cotton (61), potatoes (49), soybeans (41), carnation (19), Argentine canola (42), and other crops.

Transgenic technology is still the preferred approach for quickly developing improved crop plants and incorporating many advantageous features, despite environmental and biosafety issues (Ahmar et al., 2021). Over the past 22 years, there has been substantial growth in transgenic crop farming, expanding from 1.7 million hectares in 1996 to 191.7 million hectares in 2018, marking a remarkable increase of 113 times. Specifically, modified soybeans accounted for fifty percent of the hectares covered by transgenic crops (95.9 million), transgenic maize for thirty percent, transgenic cotton for thirteen percent, transgenic canola for ten million hectares (5.3%), and other transgenic crops for one million hectares (<1%) (Kumar et al., 2020). Transgenic technology has emerged as a rapidly adopted crop technology in advanced agriculture practice. Around 17 million farmers across 26 countries cultivated crops during the 2017-18 period, contributing to a global market value estimated at US$18.2 billion. Transgenic crop development and commercialization have primarily targeted traits like herbicide tolerance (HT), insect resistance (IR), disease resistance, abiotic stress tolerance, and nutritional enhancement (Koul 2022a), with other traits accounting for less than 1% of the total cultivated area for transgenic crops. This review's main goal is to present a thorough overview of the state of commercially grown transgenic crops with a variety of features. We'll ensure that we address any public concerns and potential biosafety risks related to the use of transgenic food crops in our review. The paper will also present new developments in plant genetic engineering technologies. The topic of prospects for genetically modified crops created by using genome editing techniques will also be discussed.

Disease resistance via genetic modifications

Pathogens, which comprise viruses, bacteria, spores, and nematodes, are largely responsible for large losses in agricultural output. Agrochemicals are used in the traditional control of plant diseases; however, due to the related environmental risks and the possibility of chemical-resistant pests emerging, alternative approaches must be investigated (Garrigou et al., 2020). Identifying and transferring resistance genes through breeding or biotechnological techniques is necessary to build innate disease resistance in crops to address these difficulties. 29 transgenic events have been commercialized worldwide with the primary focus being on viruses (25 events), to grant resistance to various diseases. Interestingly, potatoes have had the most number of occurrences reported (19), with papaya (four), squash (2), and plum, bean, tomato, and sweet pepper seeing just one event each (Makeshkumar et al., 2021). Most virus-resistant transgenic crops are developed by specifically aiming at viral genes using gene silencing techniques such as co-suppression/RNAi and antisense RNA. Utilizing the gene encoding the viral coat protein to induce resistance via a "pathogen-derived resistance" mechanism is also a successful strategy for combating viruses in transgenic crops (Walsh, 2020). Additionally, resistance is triggered by a gene-silencing mechanism when inadequate viral replicase as well as helicase domains are introduced. Using antisense RNA to efficiently degrade mRNA encoding essential viral proteins is one tactic, while another entails producing antisense and sense RNA strands of viral replication proteins. Promising remedies to plant diseases are provided by the continuous development of transgenic technology (Akbar et al., 2022). To create resilient crops and ensure sustainable agriculture practices, it is imperative to comprehend the genetic basis of resistance and utilize biotechnological technologies.

Abiotic stress tolerance via genetic modifications

There are a lot of abiotic stressors, like heat, cold, flooding, drought, and high salt levels, that can mess with the growth and development of agricultural plants. Unfortunately, these stressors often lead to a decrease in grain yield. The impact of these pressures is thought to be increasing due to the constantly shifting climate. Plants undergo metabolic changes in response to abiotic stressors, which trigger several signalling pathways and regulatory proteins such as heat shock factors and transcription factors (Yoon et al., 2020). To preserve cellular homeostasis, they also alter the antioxidant defense system and produce suitable solutes for osmotic adjustment.

Plants adaptive responses are essential for reducing the negative consequences of abiotic stressors by preserving circumstances that are almost ideal for growth and development. Abiotic stresses harm plants (Muhammad Asad and Zia, 2023), and cause changes in the expression of many different genes at the molecular level. As a result, the complex interactions of several gene networks are necessary for responding to abiotic stress. In contrast to characteristics like herbicide, insect, and disease resistance, the number of events granting abiotic stress tolerance that are commercialized is relatively lower, despite the trait's complexity. Only a few events that confer abiotic stress resistance have been commercialized thus far; three of these events are found in sugarcane, seven in maize, and two in soybean (Manimekalai et al., 2022). This reflects the challenges in developing and commercializing crops with enhanced tolerance to abiotic stresses due to the multifaceted nature of the trait. Ongoing research in this field is essential to unravel the intricacies of plant responses to abiotic stresses and to develop crops that can withstand the challenges posed by environmental fluctuations.

Herbicide tolerance via genetic modifications

Since weeds compete with agricultural plants for vital resources like sunlight, water, nutrients, and space, weeds represent a danger to crop productivity. Herbicide application is one of the most important active management techniques for reducing the amount of agricultural yield reduction caused by weeds (Scavo and Mauromicale, 2020). However getting rid of weeds selectively without harming the crop plant can be difficult, especially since most weeds are herbaceous plants. The discovery of herbicide tolerance characteristics in major crops, which would allow for the flexible application of strong, non-selective, broad-spectrum herbicides, is, therefore, one possible option. There are two main types of herbicides used to manage weeds: selective and non-selective. Both glufosinate and glyphosate are common non-selective herbicides (Pelosi et al., 2022). Several herbicide-tolerant (HT) transgenic plants have been genetically altered to endure glyphosate and glufosinate. Glyphosate functions by inhibiting the enzyme known as 5-enolpyruvyl shikimate-3-phosphate synthase (EPSPS), pivotal in the shikimate pathway, which synthesizes aromatic amino acids. Notably, as the shikimate pathway is absent in the animal realm, glyphosate is generally regarded as safe for humans, birds, insects, and other animals (Ung and Li, 2023).

Glyphosate-resistant transgenic crops are developed using various sources, including a glyphosate-insensitive version of EPSPS obtained from organisms like Agrobacterium tumefaciens strain CP4, a mutated form of maize EPSPS, or a chemically synthesized gene resembling the EPSPS gene (grg23) found in Arthrobacter globiformis. In 1996, the cp4epsps gene-carrying "Roundup Ready" soybean became commercially available as the first herbicide-tolerant transgenic crop. This gene has since been added to numerous glyphosate-resistant crops that are sold commercially (Green and Siehl, 2021). Furthermore, a small number of transgenic crops express enzymes that break down glyphosate, such as Bacillus licheniformis's GAT and Ochrobactrum anthropi's GOX. Glyphosate is detoxified by both enzymes, which also turn it into non-toxic metabolites (Manan et al., 2023). The emergence of herbicide-tolerant transgenic crops, particularly those resistant to glyphosate, has revolutionized weed management in agriculture, allowing for effective weed control without significant harm to the main crop or adverse effects on the environment.

Insect-resistant crops via genetic modification

Significant crop losses are caused by insect pests and diseases; over 67,000 bug species are known to have a detrimental effect on commercially significant crops (Kumar and Omkar, 2018). By either sucking sap or biting on different plant parts like leaves, stems, and roots, these pests harm plants. Insects can also act as carriers of many plant diseases, bringing them to plants while they feed. For insect pest management, farmers have historically turned to costly chemically synthesized insecticides, which is an expensive and environmentally unfriendly approach (Perkins, 2012).

To tackle the downsides linked to insecticide application, newer approaches like genetically modifying crops to enhance their insect resistance have become increasingly popular. At present, ten commercially cultivated transgenic crops exhibit insect resistance. Most of these crops are genetically altered to include insecticidal genes; these genes are often variations of the cry gene and, occasionally, the vip gene (Saeed et al., 2020). These genes are essential for preventing damaging insect attacks on crops. In 2017, transgenic crops resistant to insects became the second largest category in terms of farmed area, covering 23.3 million hectares. Globally, 304 events have been sanctioned for cultivation, with maize being involved in 208 of them (Koul, 2022). These occurrences entail a variety of insect-resistant genes that have been tailored to the predominance of particular insect pests in the areas where farming takes place. This method helps to effectively manage insect pests in agriculture by offering a more environmentally friendly and sustainable substitute for traditional insecticide use.

Cry genes from Bacillus thuringiensis (Bt) soil bacteria have been extensively used in the creation of transgenic crops that are resistant to insects (Li et al., 2020)(Kamatham et al., 2021).

The data from tables 1-4 showed different crop plants and their transgencs which has been developed till now.

Table 1. Major Transgenic Cereals

Crop	Trait	Gene Involved	References
Rice	Folic acid(vitamin B9)	Arabidopsis GTP-cyclohydrolase I	(Storozhenko et al., 2007)

	Golden rice (vitamin A)	PSY, crtI	(Ye et al., 2000)
	Disease resistance (blast)	Xa21	Ye et al., (2000)
	Dehydration Tolerance	HVA1, a LEA gene	(Babu et al., 2004)
	Enhanced tolerance to low iron availability	Iron transporter OsIRT	(Takahashi et al., 2001)
	Iron	nicotianamine synthase and ferritin	(Wirth et al., 2009)
	Tolerance to several herbicides	CYP2B22 CYP2C49, P450CYP	(Jung et al., 2008)
	Zinc	Activation tagging of Osnas2	(Lee et al., 2011)
Maize	Herbicide resistance	PAT	Lee et al., (2011)
	Bt toxin (insect resistance)	cry1Ab	Lee et al., (2011)
	Drought tolerance	DREB1A	Wirth et al., (2009)
	Reduction in seed phytate and increase in Pi contents	fungal phyA2 gene	(Chen et al., 2008)
	Vit-E	HGGT	(Cahoon et al., 2003)
	Vit-C	(DHAR)	(Chen et al., 2003)
Wheat	Provitamin A	PSY and carotene desaturase	(Wang et al., 2014)
	Heat Stress Tolerance	(sHSP26)	(Chauhan et al., 2012)
	Tocochromanol pathway	HGGT and HPT	(Dolde and Wang, 2011)
	Increased yield	GA20ox1	Chen et al., (2003)
	Iron	ferritin gene	(Xiaoyan et al., 2012)
Barley	Frost tolerant	TaCBF14 and TaCBF15	(Soltész et al., 2013)
	Cold tolerant	TaDREB3	(Chen et al. 2003)
	Drought tolerant	Cytokinin dehydrogenase gene	(Pospíšilová et al., 2016)
	enhanced P, nutrition & grain production	TaALMT1	(Wang et al. 2014)
Sorghum	Herbicide resistance	PAT	Cahoon et al., (2003)
	lysine	high lysine protein	(Zhao et al., 2003)
	Sweet sorghum (increased sugar)	SUS	Zhao et al., (2003)
Millet	leaf blast resistance	bar and pin	(Ignacimuthu and Ceasar, 2012)
	Tolerant to low N stress	SiMYB3	(Wang et al. 2014)
	Salt Tolerant	SbVPPase	(Anjaneyulu et al., 2014)
Oats	Salt Tolerant	CBF3	(Oraby and Ahmad, 2012)
	Increased beta-glucan	OatBGlu1	(Chen et al. 2003)
Rye	Herbicide resistance	Bar	Dolde and Wang, 2011
	Disease resistance (ergot)	PER1	Dolde and Wang, 2011
Triticale	Herbicide resistance	Bar	Dolde and Wang, 2011
	Salinity tolerance	HAL1	Dolde and Wang, 2011

Table 2. Major Transgenic Oilseeds

Crop	Trait	Gene Involved	References
Soybean	Increased Oleic Acid	DGAT2 (diacylglycerol acyltransferase 2)	(Clemente and Cahoon, 2009).
	Resistant to Helicoverpa zea	CrylAc and cry1ab	(Stewart et al., 2001)
	Enhanced oleate and protein content	β-carotene	(Schmidt et al., 2015)
	Delated flowring	GmFT2a	(Cai et al., 2018)
	Insect resistant	Cry1Ac	Wang et al. 2019

Canola	Increased oil content	DGAT1	(Wang et al., 2019)
	Insects resistant	Cry1Ac	(Stewart Jr et al., 1996)
	Salt tolerant	1-aminocyclopropane-1-carboxylate (ACC) deaminase gene	(Wang et al. 2019)
	enhanced seed protein methionine	Brazil nut albumin	(Altenbach et al., 1992)
	Metal tolerant	ACC	(Stearns et al., 2005)
	Salt Tolerant	YHem1	(Sun et al., 2015)
Cottonseed	Fungal resistant	D4E1 gene	(Rajasekaran et al., 2005)
	Increased oleic acid content	fad2 gene	(Chapman et al., 2001)
	Salt tolerant	AtNHX1 and TsVP	(Cheng et al., 2018)
	reduction of toxic gossypol	δ-cadinene synthase gene	(Sunilkumar et al., 2006)
Sunflower	Enhanced feduncity	Cry1Ac	(Snow et al., 2003)
	phosphinothricin-resistant	bar	(Neskorodov et al., 2010)
	Enhanced salinity and development	TaNHX2	(Mushke et al., 2019)
Peanut	Gives Higher yield under drought stress	BREB1A	(Bhatnagar-Mathur et al., 2014)
	Lesser corn stalk borer	cryIA (c)	(Singsit et al., 1997)
	Resistant to leaf spot	Rice chitinase gene	(Iqbal et al., 2012)
	Soil moist. Deficiency tolerant	AtBREB1A	(Sarkar et al., 2016)
Flaxseed	High Stearic Acid Content	SCD (stearoyl-CoA desaturase)	(Iqbal et al. 2012)
	Anti inflammatory role	NAP-SsGT1	(Matusiewicz et al., 2014)
Safflower	Increased Acc. of Quinochalcone in Safflower	CtCHS1	(Petal et al. 2015)
	Alternaria leaf spot	Chitenase gene	(Kumar et al., 2009)
	Increased Oleic Acid	DGAT2 (diacylglycerol acyltransferase 2)	
Castor bean	Improved Ricinoleic Acid Content	DGAT1 (diacylglycerol acyltransferase 1)	(Petal et al. 2015)
	Insect resistant	Cry1Aa	(Muddanuru et al., 2019)
	salt tolerant	SbNHX1	(Patel et al., 2015)
Sesame	Tolerenat to many biotic and abiotic stresses	SindOLP	(Chowdhury et al., 2017)
	Reduced oxidative stress	SKN-1	(Ma et al., 2017)
	Enhanced methionine and cysteine	2S albumin	(Lee et al., 2003)
	Improved Oil Stability	FAD2 (fatty acid desaturase 2)	(Lee et a., 2003)

Table 3. Major Transgenic Legumes

Name	Trait	Gene Involved	References
Chickpea	Drought tolerance	RD29A (Arabidopsis), DREB1, HVA1 (Barley)	(Das et al., 2021)
	Salinity tolerance	NHX1 (Barley), SOS1 (Arabidopsis)	(Das et al., 2021)
	resistance to Helicoverpa armigera(Pod borer)	Cry 1Ac	(Kar et al., 1997)
Pigeonpea	Insect resistance	Cry1Ac (Bt), Cry2Aa (Bt), GNA lectin (Snowdrop)	(Kar et al., 1997)

	Wilt resistance	Fusarium resistance genes (Fokkerinia oxysporum)	(Foti and Pavli, 2020)
	resistance to the Helicoverpa armigera	(Tfgd2) and (RsAFP2)	(Nalluri and Karri, 2023)
Lentil	Drought & salinity tolerant	DREB1A gene	(Khatib et al., 2011)
	Embryo apex	MBF1c	(Kamçı, 2011)
	hairy roots induction	rhizogenes	(Foti and Pavli, 2020)
Cowpea	Herbicide resistant	acetohydroxyacid synthase coding gene (Atahas)	(Citadin et al., 2013)
	Maruca vitrata legume pod borer	Cry2Aa	(Kumar et al., 2021)
	Herbicide tolerance	PAT (Glufosinate)	(Kumar et al.2021).
	Cowpea severe mosaic virus (CPSMV) and Cowpea aphid-borne mosaic virus (CABMV)	bla gene	(Cruz and Aragão, 2014)
	resistance to storage pests, bruchid beetles	α-amylase inhibitor 1	(Solleti et al., 2008)
Mungbean	Salt tolerant	(NHX1) gene VrNHX1	(Sahoo et al., 2016) (Mishra et al., 2014)
	Cold tolerant	ICE1 gene	(Rout et al., 2020)
	Salinity, OS & herbicide tolerant	NHX1 and bar	(Kumar et al., 2017)
	Pathogen-resistant	BjNPR1	(Vijayan and Kirti, 2012)
	Drought-tolerant	VrDREB2A	(Chen et al., 2016)
Common bean	Whitefly resistant	Bt-vATPase	(Ferreira et al., 2022)
	Golden mosaic virus resistant	rep gene	(Faria et al., 2006)
Pea	Resistance to Helicoverpa armigera	Proteinase inhibitors	(Anderson et al., 1999)
	Res. to Bruchus pisorum	Bean amylase inhibitor	(Schroeder et al., 1995)

Table 4. Transgenic Vegetables and Fruits

Crop	Trait	Gene Involved	References
Tomato	Delayed ripening	rin or nor	Fraser et al., 2007
	drought resistance	C-5, sterol desaturase (FvC5SD)	(Kamthan et al., 2012)
	lycopene, betacarotene, and lutein	PSY gene (crtB)	(Fraser et al., 2007)
	carotenoid and flavonoid	photomorphogenesis regulatory gene DET1	(Davuluri et al., 2005)
	delayed fruit ripening	ClERF069	(Zhou et al., 2020)
Melon	Virus resistance	Ribozyme Genes	(Huttner et al., 2001)
	Resistant to fungal pathogens	antifungal protein and chitinase	(Bezirganoglu et al., 2013)
Orange	Citrus tristeza virus (CTV) resistance	Replicase gene from CTV	Zhou et al., 2020
	tolerance to Phytophthora citrophthora	pathogenesis related protein PR-5	(Fagoaga et al., 2001)
	Xanthomonas citri	attacin A	(Cardoso et al., 2010)
	resistance to citrus canker	sarcotoxin IA gene	(Kobayashi et al., 2017)
Grape	Fungal disease resistance	Stilbene synthase gene	Kobayashi et al., 2017
	Fungal disease resistance	thaumatin-like protein	(Dhekney et al., 2011)
	Cold stress resistant	DREB)1b	(Jin et al., 2009)
	Cold tolerant	VaSAP15	(Shu et al., 2021)
	Enhanced fecundity	DefH9-iaaM	(Costantini et al., 2007)
Watermelon	Virus resistance	Coat protein gene from watermelon mosaic virus	Shu et al., 2021

	Salt tolerant	HAL1 gene	(Ellul et al., 2003)
	Resistant to (ZYMV) and Papaya ringspot virus type W (PRSV W)	ZYMV coat protein (CP) and PRSV W CP genes	(Yu et al., 2011)
Cassava	Drought tolerance	DREB1 transcription factor gene	(Yu et al. 2011)
	African cassava mosaic virus (ACMV)	AC1 antisense RNA	(Yadav et al., 2011)
Eggplant	Insect resistance	Cry1Ac gene from Bt	Ellul et al., 2003
	Abiotic stress tolerance	mannitol-1-phosphodehydrogenase(mtlD)	(Prabhavathi et al., 2002)
	resistant to Colorado Potato Beetle	CryIIIB toxin	(Arpaia et al., 1997)
	resistance to fungal wilts	glucanase gene	(Singh et al., 2014)
Lettuce	Virus resistance	Coat protein gene from lettuce mosaic virus	Singh et al., 2014
	Calcium	scax1	(Park et al., 2004)
	Enhanced Development and Senescence	PSAG12-IPT	(McCabe et al., 2001)
	tolerance to salt- and Drought	LEA	(Park et al., 2005)
	Cold tolerant	ABF3 gene	(Vanjildorj et al., 2005)
Mango	Fungal disease resistance	Chitinase and glucanase genes	Yadav et al., 2010
Pineapple	Pink flesh coloration	Lycopene biosynthesis genes	Park et al., 2004
	control flowering and ripening	ACC synthase, ACC oxidase	(Botella et al., 1998)
	herbicide tolerance	bar gene	(Sripaoraya et al., 2006)
Carrot	Calcium	scax1	(Park et al., 2004)
	higher interferon activity in young leaves	human interferon alpha-2b	(Luchakivskaya et al., 2011)
Papaya	Papaya ringspot virus (PRSV)	Coat protein gene from papaya ringspot virus	(Ferreira et al., 2002)
Squash (Zucchini)	Zucchini yellow mosaic virus (ZYMV)	Coat protein gene from zucchini yellow mosaic virus	(Fuchs et al., 1998)
Sweet corn (Bt corn)	Corn Earworm and Fall Armyworm resistant	Bacillus thuringiensis (Bt) cry1Ab gene	(Lynch et al., 1999)
Potato	Late blight resistance	R gene from Solanum demissum	Xu et al., 2019
	Enhanced beta-carotene and total carotenoids	*LCY-e*	(Diretto et al., 2006)
	increased triacylglycerol along with other lipids	AGPase & SDP1	(Xu et al., 2019)
	Over-accumulation of vitamin C.	GalUR and GLOase	(Upadhyaya et al., 2009)
	reduction in starch and amylose content	psPPase and NTT	(Anderson et al., 1999)
	Increased Nutritive values	Non-allergenic seed albumin gene	(Chakraborty et al., 2000)
Apple	Non-browning	kanamycin resistant antisense PPO gene	Bolar et al., 2000 (Murata et al., 2001)
	Apple scab resistant	Endochitinase	(Bolar et al., 2000)
	Drought and cold tolerant	Osmyb4	(Pasquali et al., 2008)
	basal thermotolerance	MdATG18a	(Huo et al., 2020)
Strawberry	Enhanced shelf life	ACC oxidase antisense gene	Dolgov et al., 2005
	Resistant to bugs and Weevils	(CpTi) gene	(Qin et al., 2008)
	resistance to Botrytis cinerea	thaumatin II gene	(Schestibratov and Dolgov, 2005)

	frost tolerant	wcor410 protein	(Houde et al., 2004)
	Salt Tolerant	osmotin gene	(Hussain and Abid, 2011)
Banana (Musa spp.)	Tolerant to various Abiotic stresses	MusaPIP1,2	(Sreedharan et al., 2013)
	Resistant to Wilt	Pflp gene	(Yip et al., 2011)
	specific antibody response	HBsAg	(Kumar et al., 2005)
	Fungal resistance	Chit. and glu. genes	Kumar et al., 2005
		(Als) acetolactate synthase gene	(Ganapathi et al., 2001; Sturtevant, 1913)

The Future

Genetic modification promoters see GM as a game-changing technology that can reduce world hunger by improving farming methods, sustainability, food safety, and profitability. They contend that the potential benefits of GM products—better, new ones with desirable traits—outweigh any associated hazards. Concerns about the effects on the environment and public health still exist, notwithstanding the growing global popularity of this practice. To guarantee consumer acceptability and safety, new legislative and technical frameworks are essential. By pointing out the differences and similarities between genetically modified and traditional foods, equivalency assessments help direct future safety analyses. Along with post-market surveillance of foods resulting from genetic alteration, reliable techniques for identifying unintended effects of genetic modification are also crucial. Customer confidence is important because it affects market competitiveness and leads some food companies to avoid using genetically modified foods. To support well-informed decision-making and regulatory actions, review papers should go towards clarifying the advantages and disadvantages of genetically modified agriculture technology, improving detection techniques, and addressing consumer concerns.

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Declarations

Data Availability statement

All data generated or analyzed during the study are included in the manuscript.

Ethics approval and consent to participate

Not applicable

Consent for publication

Not applicable

Funding

Not applicable

Conflict of Interest

Regarding conflicts of interest, the authors state that their research was carried out independently without any affiliations or financial ties that could raise concerns about biases.