Journal of Genetic and Environment Conservation

www.jogec.com

Print ISSN: 3007-4509 Online ISSN: 3007-4517

Genetic elements of GM rice events based on BCH and ISAAA databases: A Review

Shatha Ayed Yousif

Scientific Research Commission, Ministry of Higher Education and Scientific Research, Iraq.

***Correspondence:** yousif.sh@src.edu.iq

ORCID: https://orcid.org/0000-0003-1985-4412

Received: March 16th 2026

Accepted April 26th 2026

Published: May 17th 2026

DOI: https://doi.org/10.63799/jgec.14.1.5

ABSTRACT

The increasing global use of genetically modified (GM) crops has raised significant concerns regarding biosafety, traceability, and regulatory monitoring, particularly for rice as a staple food crop. This study aimed to analyze genetically modified rice events registered in international biosafety databases, including the Biosafety Clearing-House (BCH) and the International Service for the Acquisition of Agri-biotech Applications (ISAAA), in order to identify commonly used genetic elements and evaluate their applicability in molecular detection strategies. The results revealed that several functional genes are consistently used in GM rice development, particularly insect resistance genes (cry1Ab and cry1Ac), herbicide tolerance genes (bar and pat), and selectable marker genes such as Hygromycin B phosphotransferase gene (hpt). In addition, regulatory elements including the Cauliflower mosaic virus (CaMV) 35S promoter and the nopaline synthase (NOS) terminator were frequently identified across multiple events. These elements represent conserved components of transformation constructs and are widely utilized in PCR-based GMO detection. Furthermore, the analysis indicated that only a limited number of GM rice events currently retain valid international regulatory approvals, primarily for food and feed use. The recurrence of specific genetic elements among these events provides a practical basis for developing efficient screening strategies. A stepwise molecular detection approach based on common regulatory elements followed by event-specific confirmation is proposed as an effective framework for GMO identification. This study highlights the importance of integrating biosafety database information with molecular detection tools to enhance the monitoring of genetically modified rice in food systems. The findings provide valuable insights for regulatory authorities and research laboratories in designing reliable and cost-effective GMO detection protocols.

Keywords: Genetically modified rice, BCH, ISAAA, Regulatory approval, Molecular detection, PCR.

Introduction

Rice is the primary food source for more than half of the global population (Magubika et al., 2025). Advances in genetic engineering have enabled the introduction of foreign or modified genes into rice to achieve traits that are difficult or time-consuming to obtain through conventional breeding (Seid and Berhanu, 2021). These traits include resistance to lepidopteran insects, tolerance to herbicides such as glufosinate, enhanced resistance to diseases, improved tolerance to environmental stresses, and biofortification, as exemplified by Golden Rice (Ansari et al., 2015; Tang et al., 2009; Zhao et al., 2015).

Several genetically modified rice events have been recorded in international biosafety and biotechnology databases, including the International

Service for the Acquisition of Agri-biotech Applications - ISAAA. (https://www.isaaa.org/) and the Biosafety Clearing-House - BCH (https://bch.cbd.int/en/registries). These platforms compile information on living modified organisms (LMOs) and genetically modified (GM) crops that have undergone regulatory review and, in some cases, received approvals for cultivation, food, feed, or environmental release in different countries. The recorded entries typically include information on the introduced genetic elements, intended traits, and regulatory status, thereby providing an important reference source for molecular detection strategies, risk assessment and regulatory monitoring.

The DNA that has been engineered into a crop consists of several elements that govern its functioning. They are typically a promoter sequence, structural gene and a stop sequence for the gene (Ahmed, 1995). Detection of foreign DNA segments (such as gene, promoter or terminator regions) or the novel protein itself produced by foreign genetically modified crop samples can be determined (Ari and Çakir, 2008). PCR is the most useful method for detecting GMO compared to protein-based methods, it has a high potential of increased specificity and sensitivity (Zimmermann et al., 1998) and has also been proven to be very accurate when applied to raw ingredients and to processed food/feed samples conditions (Jacchia et al., 2015).

In addition, with the implementation of regulatory specifications for monitoring genetically modified rice in local markets, identifying appropriate genetic targets for detection has become increasingly important. Therefore, reviewing the commonly used genes and regulatory elements in genetically modified rice events can help determine the most suitable molecular markers for screening and detection programs. Such information may support regulatory authorities and laboratories involved in monitoring genetically modified rice in food products available in local markets.

The objective of this review is to provide a critical overview of genetically modified rice events documented in international biosafety registries (ISAAA and BCH), highlighting the diversity of inserted genetic elements, targeted traits, and approval status.

Materials and Methods

This study was conducted as a narrative review focusing on genetically modified rice events and their molecular characteristics. Information was collected from internationally recognized biosafety and biotechnology databases, primarily the BCH of the Convention on Biological Diversity and the ISAAA GM Approval Database.

Data extraction included the event name, introduced gene(s), donor organism, regulatory elements (promoters and terminators), selectable marker genes, and intended application (food, feed, or research). Additional scientific background was obtained from peer-reviewed journal articles related to rice genetic engineering, trait development, and molecular detection strategies.

The collected data were organized into comparative tables to highlight differences between reported events across databases. Particular attention was given to identifying the diversity of genetic constructs used in rice transformation and evaluating their implications for molecular detection. Events developed through mutation breeding were examined separately to avoid misclassification as transgenic organisms.

Results and Discussion

GM Rice Events Registered in the Biosafety Clearing House: According to tables 1–3, a wide range of GM rice events are registered in the BCH database and can be categorized based on their intended use:

GM Rice Approved for Food Use: A total of ten GM rice events has been registered for food use (table 1). Among them, four events carry insect-resistance genes such as Cry1Ab and Cry1Ac (BCH-LMO-SCBD-106014-2, BCH-LMO-SCBD-108926-3, BCH-LMO-SCBD-115916-2, and BCH-LMO-SCBD-260009-1). Three events contain herbicide-resistance genes (BCH-LMO-SCBD-14858-5, BCH-LMO-SCBD-47517-6, and BCH-LMO-SCBD-14859-7). One event (BCH-LMO-SCBD-101097-1) expresses genes encoding osmotin, β-1,3-glucanase, and chitinase, conferring resistance to fungal pathogens. Other events include Golden Rice (BCH-LMO-SCBD-112997-1), which was genetically engineered to enhance nutritional quality through the introduction of carotenoid biosynthesis genes (psy1 and crtI), resulting in increased provitamin A content. Additionally, event BCH-LMO-SCBD-46122-5 contains the 7CRP gene, which encodes an artificial peptide composed of seven-site sequences recognized by human cedar allergen-specific T cells.

GM Rice Approved for Feed Use: Two GM rice events have been approved for feed use (BCH-LMO-SCBD-115915-2 and BCH-LMO-SCBD-115914-3) (table 2). These events generally share genetic elements similar to those present in food-approved GM rice varieties.

Table (1): Genetically modified rice events registered in the Biosafety Clearing-House (BCH) for food use and their main genetic elements and characteristics.

LMO ID	Introduced / Modified Genetic Elements	LMO characteristics
BCH-LMO-SCBD-112997-1	Ubiquitin promoter and intron (*Zea mays* L.); phosphomannose isomerase (*E coli*); glutelin promoter (*Oryza sativa* L.); phytoene synthase (*Zea mays* L.); phytoene desaturase (*Erwinia uredovora*); rbcS transit peptide (*Pisum sativum* L.); NOS terminator	Changes in quality and metabolite content (vitamin enrichment)
BCH-LMO-SCBD-46122-5	7Crp synthetic gene (cedar pollen allergen derived); glutelin promoter, glutelin signal peptide, Glutelin terminator (*Oryza sativa* L); KDEL ER retention signal; CaMV 35S promoter; hygromycin phosphotransferase (*E. coli*)8- Transcript 7 gene 3' untranslated region | *Agrobacterium tumefaciens* (Agrobacterium); Terminator	Modified allergen content; hygromycin resistance
BCH-LMO-SCBD-101097-1	Osmotin, β-1,3-glucanase and chitinase genes	Resistance to fungal diseases
BCH-LMO-SCBD-106014-2	Rice actin promoter and intron (*Oryza sativa* L); Cry1Ab/Ac (*Bacillus thuringiensis*); hygromycin phosphotransferase; β-lactamase; NOS terminator	Insect resistance (Lepidoptera); hygromycin resistance and reporter genes
BCH-LMO-SCBD-108926-3	Cry1Ab (*Bacillus thuringiensis*); hygromycin phosphotransferase (*E coli*); phosphoenolpyruvate carboxylase promoter (*Zea mays* L.)	Insect resistance (Lepidoptera); hygromycin resistance
BCH-LMO-SCBD-115916-2	CaMV Enhanced 35S promoter; CaMV 35S promoter; CaMV 35S terminator Cry1Ac (*Bacillus thuringiensis*); hygromycin phosphotransferase; catalase 1 intron (*Ricinus communis*); β-glucuronidase (*E coli*); NOS terminator	Insect resistance (Lepidoptera); antibiotic resistance
BCH-LMO-SCBD-260009-1	Ubiquitin promoter (*Zea mays* L.); Cry1Ab (*Bacillus thuringiensis*); neomycin phosphotransferase II; hygromycin phosphotransferase; β-glucuronidase; CaMV 35S promoter; NOS promoter/terminator	Insect resistance; antibiotic resistance (kanamycin, hygromycin); reporter genes
BCH-LMO-SCBD-14858-5	Phosphinothricin N-acetyltransferase (*Streptomyces hygroscopicus*); CaMV 35S promoter and terminator	Herbicide resistance (glufosinate)
BCH-LMO-SCBD-47517-6	Phosphinothricin N-acetyltransferase (*Streptomyces hygroscopicus*); CaMV 35S promoter; NOS terminator	Herbicide resistance (glufosinate)
BCH-LMO-SCBD-14859-7	Phosphinothricin N-acetyltransferase (*Streptomyces hygroscopicus*); CaMV 35S promoter and terminator	Herbicide resistance (glufosinate)

Table (2): Rice GMO events registered in the Biosafety Clearing-House (BCH) for feed use and their main genetic elements and characteristics.

LMO ID	Introduced / Modified Genetic Elements	LMO characteristics
BCH-LMO-SCBD-115915-2	CaMV enhanced 35S promoter (Cauliflower mosaic virus); Cry1Ac (*Bacillus thuringiensis*); CaMV 35S terminator; hygromycin B phosphotransferase (*E coli*); CaMV 35S promoter; catalase 1 intron (*Ricinus communis*); β-glucuronidase (GUS) (*E coli*); NOS terminator (*Agrobacterium tumefaciens*)	Insect resistance (Lepidoptera); hygromycin resistance; selectable marker and reporter genes
BCH-LMO-SCBD-115914-3	Ca MV enhanced 35S promoter (*Cauliflower mosaic virus*); Cry1Ac (*Bacillus thuringiensis*); CaMV 35S terminator; hygromycin B phosphotransferase (*Escherichia coli*); CaMV 35S promoter; catalase 1 intron (*Ricinus communis*); β-glucuronidase (GUS) (*E coli*); NOS terminator (*Agrobacterium tumefaciens*)	Insect resistance (Lepidoptera); hygromycin resistance; selectable marker and reporter genes

Such elements include Bt genes conferring insect resistance, as well as the selectable marker gene hpt (hygromycin B phosphotransferase), which provides resistance to hygromycin antibiotic. In addition, they contain commonly used regulatory sequences that drive transgene expression.

GM Rice for Research Purposes: These events encompass a broad range of engineered traits designed to support diverse scientific applications (table 3).

Several events have been developed to confer resistance to bacterial and fungal diseases, either alone or in combination with herbicide-resistance traits (BCH-LMO-SCBD-104880-2, BCH-LMO-SCBD-104879-4, BCH-LMO- SCBD-104881-2, BCH-LMO-SCBD-103735-3, BCH-LMO-SCBD-104874-2, and BCH-LMO-SCBD-104875-2). Other research-designated events include those carrying insect-resistance genes (BCH-LMO-SCBD-101096-2), as well as events engineered for tolerance to abiotic stresses, such as ultraviolet-B radiation sensitivity (BCH-LMO-SCBD-104772-1 and BCH-LMO-SCBD-104771-2). Additionally, certain GM rice events have been developed for pharmaceutical and medical applications, including the production of vaccines and antigenic proteins (BCH-LMO-SCBD-102156-4).

Table (3): Rice GMO events registered in the Biosafety Clearing-House (BCH) for research purposes and their main genetic elements and characteristics.

LMO ID	Introduced / Modified Genetic Elements	LMO characteristics
BCH-LMO-SCBD-101096-2	Cry1Ac (*Bacillus thuringiensis*)	Insect resistance (Lepidoptera)
BCH-LMO-SCBD-104880-2	Acetohydroxy acid synthase promoter, gene and terminator (*Oryza sativa* L); ubiquitin-7 promoter (*Oryza sativa* L); WRKY45 gene (*Oryza sativa* L); NOS terminator (*Agrobacterium tumefaciens*)	Resistance to herbicides (sulfonylurea); resistance to bacterial and fungal diseases
BCH-LMO-SCBD-104879-4	Acetohydroxy acid synthase promoter, gene and terminator (*Oryza sativa* L); glutathione S-transferase promoter (*Oryza sativa* L); alcohol dehydrogenase 5'UTR, Leader (*Oryza sativa* L); WRKY45 gene (*Oryza sativa* L); NOS terminator; CaMV 35S terminator	Resistance to herbicides (sulfonylurea); resistance to bacterial and fungal diseases
BCH-LMO-SCBD-104881-2	Acetohydroxy acid synthase promoter, gene and terminator (*Oryza sativa* L); ubiquitin promoter (*Zea mays* L.); WRKY45 gene (*Oryza sativa* L); NOS terminator	Resistance to herbicides (sulfonylurea); resistance to bacterial and fungal diseases
BCH-LMO-SCBD-103735-3	WRKY45 gene (*Oryza sativa* L); CaMV 35S promoter; hygromycin phosphotransferase (*E coli*); glutathione S-transferase promoter; alcohol dehydrogenase 5'UTR; CaMV 35S terminator; NOS terminator	Resistance to bacterial and fungal diseases; hygromycin resistance; selectable marker genes
BCH-LMO-SCBD-104874-2	CaMV 35S promoter; hygromycin phosphotransferase (*E coli*); ubiquitin-7 promoter (*Oryza sativa* L); WRKY45 gene (*Oryza sativa* L); NOS terminator	Resistance to bacterial and fungal diseases; hygromycin resistance
BCH-LMO-SCBD-104875-2	CaMV 35S promoter; hygromycin phosphotransferase (*E coli*); ubiquitin promoter (*Zea mays* L.); WRKY45 gene (*Oryza sativa* L); NOS terminator	Resistance to bacterial and fungal diseases; hygromycin resistance
BCH-LMO-SCBD-104772-1	CaMV 35S promoter; cyclobutylpyrimidine dimer photolyase gene (*Oryza sativa* L); hygromycin phosphotransferase (*E coli*); NOS terminator	Tolerance to abiotic stress (UV-B radiation)
BCH-LMO-SCBD-104771-2	CaMV 35S promoter; cyclobutylpyrimidine dimer photolyase gene (*Oryza sativa* L); hygromycin phosphotransferase (*E coli*); NOS terminator	Tolerance to abiotic stress (UV-B radiation)
BCH-LMO-SCBD-102156-4	Cryj gene (*Cryptomeria japonica*); glutelin promoter and terminator (*Oryza sativa* L); CaMV 35S promoter; hygromycin phosphotransferase (*E coli*); transcript 7 gene 3'UTR (*Agrobacterium tumefaciens*)	Production of pharmaceutical compounds (vaccines and antigens); hygromycin resistance

Analysis of the genetic constructs used in the 22 GM rice events revealed the presence of several commonly used regulatory elements, including promoters, terminators, and selectable marker or reporter genes. The promoters identified include the Ubiquitin gene promoter, Glutelin gene promoter, CaMV 35S promoter, CaMV enhanced 35S promoter, Rice actin 1 gene promoter, Phosphoenolpyruvate carboxylase gene promoter, Acetohydroxy acid synthase gene promoter, Glutathione S-transferase gene promoter, and Ubiquitin-7 gene promoter. The terminator sequences detected in these events include the Nopaline synthase (NOS) gene terminator, CaMV 35S terminator, Glutelin terminator, and Acetohydroxy acid synthase gene terminator. In addition, several selectable marker and reporter genes were identified, such as the Hygromycin B phosphotransferase gene (conferring resistance to hygromycin), Beta-lactamase gene (ampicillin resistance), Neomycin phosphotransferase II (kanamycin resistance), Beta-glucuronidase (GUS) reporter gene, and Phosphomannose isomerase (PMI) gene, which enables.

GM Rice Events Registered in ISAAA: As shown in table 4, several GM rice events listed in ISAAA database correspond directly to events registered in the BCH database. The identification codes recorded in the BCH database differ from those listed in the ISAAA database, when referring to the same genetically modified crop event. This variation occurs because each database uses its own registration and coding system for cataloguing GMO events. The table summarizes event names, identification codes, introduced genes, expressed products, and their biological functions. The listed events include insect-resistant rice carrying cry1Ab and/or cry1Ac genes (Huahui-1/TT51-1 and Tarom molaii + cry1Ab), herbicide-tolerant Liberty Link™ rice events containing the bar gene conferring tolerance to glufosinate herbicides (LLRICE06, LLRICE601, and LLRICE62), nutritionally enhanced Golden Rice (GR2E) harboring psy1 and crtI genes, and specialized events such as 7Crp#10 designed for allergen-related immunological applications. The cross-database verification indicates that all GM rice events listed in the ISAAA database are likewise registered in the BCH, reflecting consistency in international reporting mechanisms and regulatory transparency.

This alignment is particularly significant in the context of global biosafety governance, as the BCH functions under the Cartagena Protocol on Biosafety to facilitate information exchange regarding living modified organisms (LMOs). Notably, the only exception identified in this comparative assessment is GM Shanyou 63, which appears in the ISAAA database but does not have a corresponding entry in the BCH records based on the current dataset. This discrepancy underscores the importance of consulting multiple regulatory databases when assessing the approval and notification status of GM crops, as variations may arise due to differences in reporting scope, update timelines, or jurisdictional submission requirements.

The analysis of genetically modified rice events registered in (BCH) and (ISAAA) databases revealed that several genetic elements are commonly used in the development of transgenic rice. Among the most frequently identified genes were cry genes, such as cry1Ab and cry1Ac, which originate from Bacillus thuringiensis and are widely used to confer resistance against lepidopteran insect pests (Xu et al., 2018). These genes produce delta-endotoxins that disrupt the midgut epithelial cells of susceptible insects, leading to insect mortality and improved crop protection (Karim and Dean, 2000). The widespread use of Bt genes in genetically modified crops reflects their effectiveness in reducing crop losses and decreasing reliance on chemical insecticides (Gatehouse et al., 2011).

In addition to insect resistance genes, herbicide tolerance genes such as bar and pat, derived from Streptomyces species (Christ et al., 2017), were also frequently identified among the registered rice events. These genes encode the enzyme phosphinothricin N-acetyltransferase (PAT), which detoxifies the herbicide glufosinate and enables transgenic plants to survive herbicide application (Hérouet et al., 2005). The incorporation of herbicide tolerance traits is an important strategy in modern crop improvement programs because it facilitates weed management and improves agricultural productivity.

Table (4): Rice GMO Registered in ISAAA.

ISAAA Event ID	BCH Event ID	Introduced Gene	Expressed Product	Biological Function
7Crp#10	BCH-LMO-SCBD-46122-5	7crp, aph4 (hpt) Selection Marker	Modified cedar pollen allergen proteins, hygromycin-B phosphotransferase (hph) enzyme	Induces mucosal immune tolerance to cedar pollen allergens, Selection marker allowing resistance to hygromycin B
GM Shanyou 63	-	cry1Ab, cry1Ac	Cry1Ab delta-endotoxin, Cry1Ac delta-endotoxin	confers resistance to lepidopteran insects by damaging their midgut lining
GR2E (Trade Name: Golden Rice)	BCH-LMO-SCBD-112997-1	crt1, psy1, pmi Selection Marker/Reporter	phytoene desaturase enzyme (CRTI), phytoene synthase (ZmPSY1), Phosphomannose Isomerase (PMI) enzyme	Converts phytoene to lycopene in carotenoid biosynthesis, Catalyzes the formation of phytoene from geranylgeranyl diphosphate, Positive selection marker enabling transformed plant recovery
Huahui-1/TT51-1 (Trade Name: Huahui-1)	BCH-LMO-SCBD-106014-2	cry1Ab, cry1Ac	Cry1Ab delta-endotoxin, Cry1Ac delta-endotoxin	Provides resistance to lepidopteran pests
Tarom molaii + cry1Ab	BCH-LMO-SCBD-108926-3	aph4 (hpt) Selection Marker/Reporter, cry1Ab (truncated)	hygromycin-B phosphotransferase (hph) enzyme, Cry1Ab delta-endotoxin	Selection marker for hygromycin resistance, confers resistance to lepidopteran insects
LLRICE06 (Trade Name: Liberty Link™ rice)	BCH-LMO-SCBD-14858-5	bar	phosphinothricin N-acetyltransferase (PAT) enzyme	Confers tolerance to glufosinate herbicide
LLRICE601 (Trade Name: Liberty Link™ rice)	BCH-LMO-SCBD-47517-6	bar	phosphinothricin N-acetyltransferase (PAT) enzyme	Confers tolerance to glufosinate herbicide
LLRICE62 (Trade Name: Liberty Link™ rice)	BCH-LMO-SCBD-14859-7	bar	phosphinothricin N-acetyltransferase (PAT) enzyme	Confers tolerance to glufosinate herbicide

The review also indicated that some rice events contain genes associated with disease resistance, abiotic stress tolerance, and the production of pharmaceutical compounds. For example, the introduction of transcription factors such as WRKY45 has been associated with enhanced resistance to bacterial and fungal pathogens in rice (Shimono et al., 2012). Similarly, genes involved in stress tolerance, such as photolyase genes related to ultraviolet radiation response, illustrate the use of genetic engineering to improve plant resilience under adverse environmental conditions (Mmbando, 2024). In addition, Golden Rice represents a well-known example of nutritional biofortification through the introduction of genes involved in carotenoid biosynthesis (Glover et al., 2020).

The analysis also highlighted the frequent use of selectable marker genes, particularly nptII and hpt which provides resistance to kanamycin and hygromycin antibiotics respectively and are commonly used during plant transformation processes to identify successfully transformed cells (Miki and McHugh, 2004; Rao et al., 1983). Although selectable markers are essential in genetic

engineering, their presence in genetically modified crops has been widely evaluated in biosafety assessments, and many studies have concluded that these genes do not pose significant risks to human health or the environment (EFSA, 2007).

In addition to coding genes, regulatory elements such as the CaMV 35S promoter and the NOS terminator were among the most commonly detected components in the analyzed rice events. The CaMV 35S promoter, derived from Cauliflower mosaic virus, is widely used in plant biotechnology because it drives strong and constitutive expression of transgenes in many plant tissues (Odell et al., 1985). Similarly, the NOS terminator from Agrobacterium tumefaciens is frequently used to ensure proper transcription termination and stability of transgene expression (Depicker et al., 1982). Because of their widespread occurrence in genetically modified crops, these regulatory elements are commonly used as target sequences in PCR-based GMO detection methods (Saltykova et al., 2022).

Regulatory Approval Status: According to the European Union Reference Laboratory for GM Food and Feed (EU-JRC), the globally authorized GM rice events are summarized in table 5. Among these events, Golden Rice (BCH-LMO-SCBD-112997-1) represents the only nutritionally enhanced event, developed through the introduction of carotenoid biosynthetic genes to enable provitamin A accumulation in rice grains. In contrast, the other three approved events BCH-LMO-SCBD-47517-6 (LLRICE601), BCH-LMO-SCBD-14859-7 (LLRICE62) and BCH-LMO-SCBD-14858-5 (LLRICE06) were developed primarily for herbicide tolerance through the incorporation of the phosphinothricin N-acetyltransferase (pat/bar) gene derived from Streptomyces hygroscopicus, which confers resistance to glufosinate herbicides.

Table (5): Regulatory approvals, country and type of approval.

Event ID	Country-authorized events	Type of Approval
BCH-LMO-SCBD-112997-1	New Zealand	Food
	Philippines	Food, feed, cultivation
BCH-LMO-SCBD-47517-6	Colombia	Food
	USA	Food, cultivation
BCH-LMO-SCBD-14859-7	Canada, Colombia, Honduras, Mexico, New Zealand, Philippines, South Africa	Food
	USA	Food, feed, cultivation
BCH-LMO-SCBD-14858-5	USA	Food, feed, cultivation

Molecular Detection of GM Rice Based on Registered Genetic Elements: According to the data summarized in table 5, the number of genetically modified (GM) rice events that currently retain valid international regulatory approvals for commercial use is very limited, comprising only four events. This confirms that the GM rice events recognized at the international level are limited in number and are authorized primarily for food and feed purposes, with cultivation approvals granted in specific jurisdictions. A clear pattern observed in the registered transformation constructs is the repeated occurrence of common regulatory sequences, particularly the 35S promoter, 35S terminator, and NOS terminator derived from *Agrobacterium tumefaciens*. The recurrence of these elements across multiple events supports their suitability as primary molecular targets for preliminary GMO screening. These elements are therefore suitable targets for initial PCR-based screening assays aimed at detecting the potential presence of genetically modified rice material.

The positive amplification of both CaMV 35S promoter and CaMV 35S terminator strongly suggests the presence of the rice events BCH-LMO-SCBD-14858-5 and BCH-LMO-SCBD-14859-7, since both contain similar transformation cassettes carrying the bar gene under the control of CaMV 35S regulatory sequences. In contrast, detection of CaMV 35S promoter together with NOS terminator is indicative of BCH-LMO-SCBD-47517-6, which contains the bar selectable marker gene associated with these two regulatory elements. On the other hand, the detection of NOS terminator alone, in the absence of CaMV 35S promoter and terminator, indicate the presence of BCH-LMO-SCBD-112997-1, which carries the NOS terminator linked to other genetic elements including the maize ubiquitin promoter, pmi selectable marker, and carotenoid biosynthesis genes (psy1 and crtI). Therefore, the use of these regulatory elements in screening assays provides an efficient first step for narrowing down potential GMO rice events prior to applying event-specific molecular confirmation methods.

The recurrence of specific genes and regulatory elements in genetically modified rice provides a useful basis for developing reliable screening strategies for GMO detection. In particular, the CaMV 35S promoter and NOS terminator are widely used as universal screening targets in PCR assays due to their presence in a large number of genetically modified crops (Gidi, 2023). Identifying these common elements can therefore support the development of efficient molecular detection protocols for monitoring genetically modified rice in food products and agricultural markets.

Furthermore, recent studies analyzing rice samples from food markets have shown that PCR-based screening using CaMV 35S promoter and NOS terminator can successfully detect genetically modified rice materials (Gidi, 2023; Saltykova *et al*., 2022), highlighting the importance of reliable molecular detection strategies in food safety monitoring programs. The information presented in this study may assist regulatory laboratories and biosafety authorities in selecting suitable molecular markers for routine screening and verification of genetically modified rice in commercial products. These findings indicate that screening based on shared regulatory elements offers an efficient first-level detection strategy for genetically modified rice, particularly in routine PCR-based analyses. Such an approach reduces analytical cost and processing time while maintaining adequate sensitivity for preliminary detection. The limited number of authorized GM rice events, combined with the recurrence of common regulatory elements, provides a practical framework for designing stepwise molecular detection strategies that begin with general screening markers such as NOS terminator and CaMV 35S, followed by event-specific confirmation. The EU-JRC database serves as a reference point for validated detection methods and officially notified GM events, thereby reinforcing regulatory traceability and harmonization in global GMO monitoring systems. This regulatory variability highlights the importance of continuous monitoring and accurate identification of GM rice events in international trade and food safety control systems.

Conclusion

This review highlights the diversity of genetically modified rice events registered in international biosafety databases and emphasizes the importance of regulatory elements such as the CaMV 35S promoter and NOS terminator in GMO detection strategies. The limited number of commercially authorized GM rice events, together with the recurrence of common genetic elements, provides a practical framework for developing efficient PCR-based screening approaches for monitoring genetically modified rice in food and agricultural systems.

References

Ansari, M., Shaheen, T., Bukhari, S., & Husnain, T. (2015). Genetic improvement of rice for biotic and abiotic stress tolerance. Turkish Journal of Botany, 39 911-919. https://doi.org/10.3906/bot-1503-47

Christ, B., Hochstrasser, R., Guyer, L., Francisco, R., Aubry, S., Hörtensteiner, S., & Weng, J. (2017). Non-specific activities of the major herbicide-resistance gene BAR. Nature Plants, 3, 937-945. https://doi.org/10.1038/s41477-017-0061-1

Depicker, A., Stachel, S., Dhaese, P., Zambryski, P., & Goodman, H. (1982). Nopaline synthase: transcript mapping and DNA sequence. Journal of Molecular and Applied Genetics, 1, 561-573.

EFSA, (2007). Statement on the safe use of the nptII antibiotic resistance marker gene in genetically modified plants by the Scientific Panel on genetically modified organisms (GMO). EFSA Journal, 5, 742. https://doi.org/10.2903/j.efsa.2007.742

Gatehouse, A., Ferry, N., Edwards, M., & Bell, H. (2011). Insect-resistant biotech crops and their impacts on beneficial arthropods. Philosophical Transactions of the Royal Society Lond B Biol Sci, 366, 1438-1452. https://doi.org/10.1098/rstb.2010.0330

Gidi, M. (2023). Detection methods of genetically modified organisms (GMOS). J Microbiol Biotechnol, 8, 000265. https://doi.org/10.23880/oajmb-16000265

Glover, D., Kim, S., & Stone, G. (2020). Golden Rice and technology adoption theory: a study of seed choice dynamics among rice growers in the Philippines. Technology in Society, 60, 101227. https://doi.org/10.1016/j.techsoc.2019.101227

Hérouet, C., Esdaile, D., Mallyon, B., Debruyne, E., Schulz, A., Currier, T., Hendrickx, K., van der Klis, R., & Rouan, D. (2005). Safety evaluation of the phosphinothricin acetyltransferase proteins encoded by the pat and bar sequences that confer tolerance to glufosinate-ammonium herbicide in transgenic plants. Regulatory Toxicology and Pharmacology, 41, 134-149. https://doi.org/10.1016/j.yrtph.2004.11.002

Karim, S., & Dean, D. (2000). Toxicity and receptor binding properties of Bacillus thuringiensis delta-endotoxins to the midgut brush border

membrane vesicles of the rice leaf folders, Cnaphalocrocis medinalis and Marasmia patnalis. Current Microbiology, 41, 276-283. https://doi.org/10.1007/s002840010134

Magubika, A. J., Fukah, F., Nassary, E., & Tryphone, G. (2025). Analysing rice (*Oryza sativa* L.) production trends—area harvested, quantity and yield stability in Tanzania. Discover Agriculture 3, 52 https://doi.org/10.1007/s44279-025-00204-9

Miki, B., & McHugh, S. (2004). Selectable marker genes in transgenic plants: applications, alternatives and biosafety. Journal of Biotechnology, 107, 193-232. https://doi.org/10.1016/j.jbiotec.2003.10.011

Mmbando, G. (2024). The recent possible strategies for breeding ultraviolet-B-resistant crops, Heliyon, 10, e27806. https://doi.org/10.1016/j.heliyon.2024.e27806

Odell, J., Nagy, F., & Chua, N. (1985). Identification of DNA sequences required for activity of the cauliflower mosaic virus 35S promoter. Nature, 313, 810-812. https://doi.org/10.1038/313810a0

Rao, R., Allen, N., Hobbs, J., Alborn, W., Kirst, H., & Paschal, J. (1983). Genetic and enzymatic basis of hygromycin B resistance in Escherichia coli. Antimicrob Agents Chemother, 24, 689-695. https://doi.org/10.1128/AAC.24.5.689

Saltykova, A., Van Braekel, J., Papazova, N., Fraiture, M., Deforce, D., Vanneste, K., De Keersmaecker, S., & Roosens, N. (2022). Detection and identification of authorized and unauthorized GMOs using high-throughput sequencing with the support of a sequence-based GMO database. Food Chemistry: Molecular Sciences, 4, 100096. https://doi.org/10.1016/j.fochms.2022.100096

Seid, A., & Berhanu, A. (2021). The role of green biotechnology through genetic engineering for climate change mitigation and adaptation, and for food security: current challenges and future perspectives. Journal of Advances in Biology & Biotechnology, 24 1-11. https://doi.org/10.9734/jabb/2021/v24i130192

Shimono, M., Koga, H., Akagi, A., Hayashi, N., Goto, S., Sawada, M., Kurihara, T., Matsushita, A., Sugano, S., Jiang, C., Kaku, H., Inoue, H., & Takatsuji, H. (2012). Rice WRKY45 plays important roles in fungal and bacterial disease resistance. Molecular Plant Pathology, 13, 83-94. https://doi.org/10.1111/j.1364-3703.2011.00732.x

Tang, G., Qin, J., Dolnikowski, G., Russell, R., & Grusak, M. (2009). Golden Rice is an effective source of vitamin A. The American Journal of Clinical Nutrition, 89, 1776-1783. https://doi.org/10.3945/ajcn.2008.27119

Zhao, Q., Liu, M., Zhang, X., Lin, C., Zhang, Q., & Shen, Z. (2015). Generation of insect-resistant and glyphosate-tolerant rice by introduction of a T-DNA containing two Bt insecticidal genes and an EPSPS gene. Journal of Zhejiang University-SCIENCE B, 16, 824-831. https://doi.org/10.1631/jzus.B1500056