Genome editing for crop improvement: A perspective from India

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Abstract

Human population is expected to reach to about 10 billion by 2050. Climate change affects crop production, thus posing food security challenges. Conventional breeding alone will not bridge the gap between current level of crop production and expected levels in the decades to come in the food production systems. Rate of genetic gain with time has remained narrow considerably. Biotechnology-enabled crops developed through genome editing will have a part to play in improving crop productivity, meeting food, nutrition security besides catering to regional preferences and fetching valuable foreign exchange. Political, social, economical proposition, scientific will, retailer and consumer acceptance are a must for genome editing (GE) to succeed and add value in the food value chain. This will also help to make agriculture a lucrative profession and attract youth. Therefore, the present review looks into existing regulations governing crops developed using biotechnology in India, institutes involved in genome editing, prospects of new tools developed in this sphere such as DNA-free editing systems, nanotechnology, their applicability in crop improvement efforts, social and future prospects taking cue from recent global developments. This will make GE more appealing to stakeholders and defray any safety concerns.

Keywords CRISPR/Cas9 · Nanotechnology · Regulation · Acts · Rules

Introduction

Crop improvement is an ongoing process for several thousands of years (Voss-Fels et al. 2019). Much of the effort in the early years focussed on natural variations, selection from related species and some spontaneous mutations (Huang et al. 2016). Later on, artificial hybridisation came into the picture by Fairchild in 1716 (Goulet et al. 2017). Then, in 1930, Stadler used X-rays to induce mutation and assisting in a new era of mutagenesis breeding including chemical means (Uaauy et al. 2017). Thus, plant breeding has evolved over time accompanying new innovations including precision breeding (Hartung and Schiemann 2014). Molecular breeding includes gene editing and marker-assisted selection (see NAAS 2020). Recently, the term new plant technology (NBTs) is used to include all recent developments in the biotechnology field to improve crops (Lusser et al. 2011; Limera et al. 2017). Since, ushering the first green revolution was in fact an orchestrated efforts by various stakeholder in the late 1960s (see Swaminathan 2006). Further, our country has achieved self-sufficiency in food and passed legislation for the Right to Food Act, 2013 (Website 2 n.d.), which means greater efforts need to be invested in local food ecosystems and strengthen them in face of biotic and abiotic challenges. To persistently sustain and further increase food production will need additional incorporation of all developed relevant tools using genomics, genome editing (GE), artificial intelligence and deep learning among others (Mahood et al. 2020). Parkhi et al. (2018) presented early success of GE in India. Genome editing in its elementary form involves allelic variants which are identical to their naturally occurring counterparts (Schmidt et al. 2020). For more details on CRISPR/Cas, see excellent reviews recently published by Barman et al. (2020) and Wada et al. (2020). From economic point of view, genome-edited crops could be far less expensive to develop and more acceptable to the general public than genetically modified GM crops (Lassoued et al. 2019a, 2019b). GE results in editing endogenous genes. These results in developing allelic diversity alter endogenous gene activity (Gaj et al. 2016). This is similar to random mutagenesis and thus could be a robust alternative to crops developed by mutagenesis
GE (Abdallah et al. 2015). GE composes of related types of advanced molecular technique which is used for precise modification of target sequence (Gaj et al. 2013). The CRISPR/Cas system was initially discovered in 1987 from prokaryotic organism and is fairly common in bacterial and archaeal genomes (Barrangou and Marraffini 2014). Even since, the practical application of the GE technology to edit any gene was deciphered in 2012 by Charpentier and Doudna in prokaryotic organism (Ding et al. 2016) and later by Zhang and Church group in 2013 for eukaryotic cells. There has been tremendous spout of interest in this field (see Lander 2016). Basically, GE takes place by the error prone (non-homologous end joining, NHEJ) or precise (homology directed repair, HDR) both involving DNA break and repair. Later, David Lui found base editor system which is a significant improvement over the NHEJ and HDR repair caused by CRISPR/Cas system, with causing DNA break and no off-target risks. For details in base editing, see Mishra et al. (2020). Several other implementations of CRISPR/Cas system are the use of dead Cas9 fusions which can help in activating (VP64, SunTag, implementations of CRISPR/Cas system are the use of dead Cas9 fusions which can help in activating (VP64, SunTag, etc.) and later by Zhang and Church group in 2013 for eukaryotic cells. There has been tremendous spout of interest in this field (see Lander 2016). Basically, GE takes place by the error prone (non-homologous end joining, NHEJ) or precise (homology directed repair, HDR) both involving DNA break and repair. Later, David Lui found base editor system which is a significant improvement over the NHEJ and HDR repair caused by CRISPR/Cas system, with causing DNA break and no off-target risks. For details in base editing, see Mishra et al. (2020). Several other implementations of CRISPR/Cas system are the use of dead Cas9 fusions which can help in activating (VP64, SunTag, etc.) and later by Zhang and Church group in 2013 for eukaryotic cells. There has been tremendous spout of interest in this field (see Lander 2016). Basically, GE takes place by the error prone (non-homologous end joining, NHEJ) or precise (homology directed repair, HDR) both involving DNA break and repair. Later, David Lui found base editor system which is a significant improvement over the NHEJ and HDR repair caused by CRISPR/Cas system, with causing DNA break and no off-target risks. For details in base editing, see Mishra et al. (2020). Several other implementations of CRISPR/Cas system are the use of dead Cas9 fusions which can help in activating (VP64, SunTag, SAM associated box; Rees and Liu 2018) or interference (KRAB—Kruppel associated box) and suppression of any genes (Gilbert et al. 2013). Mainly two classes of CRISPR/Cas are available for DNA and RNA editing, among which class II-types II and V induces double-stranded breaks (DSB) (see Moon et al. 2019). These breaks are repaired by NHEJ (random) or HDR (precise) (Liu et al. 2018). For other details of genome editing and their applications, please refer to the Bhattacharya et al. (2020).

Many other applications of gene editing technology are being discovered nowadays (Website 1 n.d.).

Current Status and Regulation of Genome-Edited Crops A recent report by NAAS (National Academy of Agricultural Sciences, India, July 2020) estimated that genome editing market is a billion dollar industry now. Therefore, there needs to be a clear policy in this field to gain from such advances. DNA edits are classified into three types. SDN-1 is one or few base pair (bp) changes (similar incurred by using base editors; see Mishra et al. 2019), SDN-2 is few bp changes (the definition of a few varies greatly, for example, Gao 2018, restricts changes to 20 bp) and SDN-3 is typically long indels or gene replacements (Gao 2018, Draft document on GE, India). Table 1 shows list of institutes in India working on genome editing. The list is not exhaustive but representative. The NAAS 2020 report further noted that mutation falling under SDN-1 and SDN-2 is indistinguishable from those obtained from mutation breeding and should be made available to the farming community in the shortest possible time. In January of 2020, the Department of Biotechnology under Ministry of Science and Technology, Government of India, came up with draft guidelines for public consultation. The “Draft document on Genome Edited Organisms: Regulatory Framework and Guidelines for Risk Assessment” was released (available at ibkp.dbtindia.gov.in). The consultation period ended on 8 Feb 2020, and various stakeholders were invited to submit their comments by then. The basic risk assessment associated with genome-edited crops is in line with “Risk Assessment Framework and Guidelines for the Environmental Risk Assessment of Genetically Engineered Plants 2016” which is available online at geacindia.gov.in. There is a fundamentally distinct difference between genome-edited crops and genetically modified crops in that GE deals with precise editing of endogenous genes similar to what could have been achieved by random mutation causing gene edits by chemical or physical mutagenised crops. GM crops on the other hand contain foreign DNA sequences from related or other organisms which gives distinct phenotype. The GE draft document advocated that risk assessment would be according to the complexity of edits with single base edits and a few base edits falling under group I, deletions in group II and DNA replacement (foreign or synthetic) in group III. The regulatory approval road map differs from group to group. Exception can occur, like singly base pair change conferring herbicide tolerance or weediness related traits will require additional biosafety studies. Data on comprehensive biosafety assessment needs to be submitted to the approval committee including biology, delivery method, molecular basis of edits, group to which edits belong, molecular characterisation, integration pattern of donor DNA or cassette, off-target study, phenotype and biosafety among others (for more information, please refer to the draft guidelines document, 2020). The final guidelines pertaining to genome-edited crops are awaited at the time of writing of this review. Earlier, the definition of biotechnology and genetically modified organisms (GMO) is considered wide and is covered under Rules, 1989, under the provision of EPA, Environment Protection Act of 1986. Broadly, there are six agencies which oversee the development of genetically modified crops. Initially, regulation of genome engineering technologies in India covering the entire spectrum of genetically modified organisms is in accordance with EPA rules 1989 (Rules for manufacture, use of genetically engineered organisms or cells, 1989 (refer to geacindia.gov.in)). The Ministry of Environment, Forest and Climate change is the final authority in close collaboration with State Governments and DBT (Department of Biotechnology). The competent agency composes of (1) RDAC: rDNA Advisory Committee; (2) IBSC: Institutional Biosafety Committee; (3) RCGM: Review Committee on Genetic Manipulation; (4) GEAC: Genetic Engineering Appraisal Committee; (5) SBCC: State Biotechnology Coordination Committee; and (6) DLC: District Level Committee. India is also a signatory to convention on biological diversity including Cartagena and Nagoya.
| Sr. no. | Institutions | Specific areas of interest | Source (website) | Publications (if any) |
|--------|--------------|----------------------------|------------------|----------------------|
| 1      | NIPGR (National Institute of Plant and Animal Sciences) | Nutritional improvement of Indian oilseed mustard using CRISPR-Cas9-mediated genome editing | http://www.nipgr.ac.in/home/home.php | Not available |
| 2      | Bose Institute, Kolkata | “Developing an optimized toolkit for inducible genome editing and regulation of gene expression in tomato plant: implications in adjusting complex traits via synthetic biology approach” | DBT sponsored project | Not available |
| 3      | Junagadh Agricultural University | (1) Groundnut GE—high oleic acid and low linoleic acid (2) Gene editing in major field crops of Saurashtra—use of CRISPR-CAS9 technology in breeding programme | (1) https://geneticliteracyproject.org/2018/08/03/low-cholesterol-oil-indian-scientists-developing-crispr-gene-edited-groundnut/ (2) http://www.jau.in/attachments/vision2050.pdf | Not available |
| 4      | ICAR-National Institute for Plant Biotechnology | Targeted editing of potato genome to develop variety-specific true potato seed | CRISPR-Cas9-based genome editing of multiple negative regulators for blast resistance in rice | Kumar et al. (2019) |
| 5      | IARI—New Delhi (cooperating centres ICGEB, New Delhi NRCPB, New Delhi NRR, Cuttack IRRI, Hyderabad TNAU, Coimbatore) | Genetic improvement of rice for yield, NUE, WUE, abiotic and biotic stress tolerance through RNA guided Genome editing (CRISPR/Cpf1) Genome edited rice lines of elite mega rice varieties with known/novel alleles of DEP1, CKX2, TB1, SPL14, PP2Cs, DST, mR169a, OesN3 and e4f4g genes which will be useful for direct commercial cultivation or donors in breeding programmes. | GE: rice; wheat, soybean | Kumar et al. (2020), Gouda et al. (2020), Thakare et al. (2020) |
| 6      | ICGEB—New Delhi (International Centre for Genetic Engineering and Biotechnology) | Redesigning rice crop for improved grain micronutrient quality using CRISPR-cas9/Cpf1 genome editing | (1) https://www.icar.gov.in/nasf/documents/Ongoingproject_VII.pdf | Chib et al. (2020) |
| 7      | NRCPB (National Research Centre on Plant Biotechnology) | Development of haploid inducer line and enhancement of seed meal quality in Brassica juncea through CRISPR-Cas mediated genome editing | http://www.indiscienceandtechnology.gov.in/research/development-haploid-inducer-line-and-enhancement-seedmeal-quality-brassica-juncea-through-crisprcas?field_area_id=2356 | Bish et al. (2019) |
| 8      | Rama Devi Women’s University | Anthracnose resistance in chilli pepper: CRISPR/Cas9-fused cytidine base editing (CBE) targeting NAC72 | http://www.nrcpb.res.in/content/germplasm-conservation-crispr-cas9-based-genome-editing-multiple-negative-regulators-blast-resistance-rice | Mishra et al. (2019) |
| Sr. no. | Institutions | Specific areas of interest | Source (website) | Publications (if any) |
|---|---|---|---|---|
| 9 | TNAU | Genome editing for enhancing disease resistance and nutritional properties in rice Coordination with ICAR-NASF | https://www.imedpub.com/conference-abstracts-files/genome-editing-in-chili-pepper-using-a-crisprcas9.pdf | Not available |
| | | CRISPR-mediated genome engineering for developing “Thermo-sensitive genic male sterile lines (TGMS)” in rice (Oryza sativa): Tms5 locus | https://tnau.ac.in/cpmb/research-projects/ | Nagaraj et al. (2019) |
| 10 | National Agri-Food Biotechnology Institute, Mohali | GE-β-carotene rich banana—LCYε | CRISPR-mediated genome engineering for developing “Thermo-sensitive genic male sterile lines (TGMS)” in rice (Oryza sativa): Tms5 locus | Kaur et al. (2020) |
| 11 | IGIB (CSIR-Institute of Genomics and Integrative Biology—New Delhi) | Mammalian cell research. Generation of inheritable, transgene-free abiotic stress (salinity and drought) tolerant and semi-dwarf indica rice cultivars using new plant breeding approach | https://www.igib.res.in | Achrya et al. (2019) |
| | | Cancer research-Ayurvedic herb/Covid 19/Bioinformatics-GE | https://www.igib.res.in/?q=projects | Not available |
| 12 | IIT Delhi | Development of seedless Bhimkol (Musa balbisiana, BB genome) through CRISPR/Cas9 and mutational approaches. (Bhimkol- Banana) DBT funded project-2018 | http://beh.iiitd.ac.in/ | Not available |
| | | GE—tomato, cotton, chickpea, rice and Brassica Enhanced post-harvest life and nutrition quality in tomato Tomato root architecture modification for enhanced yield Development of determinate/semi-determinate sympodial cotton varieties for synchronized fibre yield and quality Development of rice varieties with low arsenic accumulation in grain Development of high yielding and short duration mustard/raya variety Genome-editing of miRNAs and associated miRNA peptides for improving drought stress tolerance in chickpea | https://nbri.res.in/genome-editing-of-plants/ https://nbri.res.in/molecular-scientists/dr-praveen-c-verma/ https://nbri.res.in/media/4.5.4-underway.pdf https://www.biotecnika.org/2019/05/csir-nbri-msc-bsc-phd-life-sciences-research-jobs/ | Not available |
| 13 | ILS Bhubaneswar (Institute of Life Sciences) | Development of seedless Bhimkol (Musa balbisiana, BB genome) through CRISPR/Cas9 and mutational approaches. (Bhimkol- Banana) DBT funded project-2018 | Not available | Shrestha et al. (2019) |
| 14 | NBRI (National Botanical Research Institute) (CSIR-NBRI-NCP) | Development of seedless Bhimkol (Musa balbisiana, BB genome) through CRISPR/Cas9 and mutational approaches. (Bhimkol- Banana) DBT funded project-2018 | Not available | Shrestha et al. (2019) |
| 15 | CSIR-North East Institute of Science & Technology, Assam | Establishing multiplex CRISPR-Cas9 and CRISPR-Cpf1 genome editing systems for abiotic and biotic stress tolerance in tomato (S. lycopersicum L.) and rice (Oryza sativa) | http://www.rrlforhat.res.in/1261.php | Saikia et al. 2020 and Debbarma et al. (2019), Jyoti et al. (2019) |
| 16 | Amity Science Technology and Innovation Foundation | Details not available | https://www.amity.edu/astif/ | }
protocols and is committed towards biosafety of gene edited crops as well (see, cbt.int, Randhawa et al. 2007). This resulted in the introduction of Biotechnology Regulatory Authority of India bill in 2013 but lapsed later on (Ahuja, 2018), which was supposed to provide a single window approval instead of duplication of efforts by various Government Agencies, Department and Ministries.

Prospects of Genome Editing Technology: the Evolving Landscape The common form of genome editing involves DNA vectors expressing both Cas9 and Sg RNAs. Crop transformation is another challenge. Here, we present newly developed tools being used in genome editing. Lowe et al. (2016) showed that by manipulating morphogenetic regulators like BABYBOOM, WUSCHEL helps in overcoming recalcitrance. Kelliher et al. (2019) discovered a one-step haploid editing technology for editing inbred lines. The authors validated CENH3-based HI system, also known as CRISPR pollen method, by editing VRS-1 LIKE HOMEOBOX PROTEIN and GRAIN WEIGHT 2 gene. Usually, CENH3 works in dicots, whereas MATL and MATRILINEAL (also known as NOT LIKE DAD, PHOPHOLIPASE 1) work in monocots. However, clean technologies, i.e. non-vector systems are available today to introduce two components in the plant cell for edits. The newer technologies need more complex technical skill sets and screening is a challenge given the absence of markers and still is in infancy. Other improvements include TREE (transient reporter for editing enrichment) to purify single edited cells in real time (Standage-Beier et al. 2019). A simple next generation of hybrid seed technology is developed using CRISPR-edited GMS maintainer by knocking out or inactivating ZMMS26 (Zea mays Male Sterile 26 gene) and a DS RED marker. The hemizygous mutated MS 26 gene is sterile and the maintainer line is already labelled by DsRED (red fluorescent protein) and easy to sort (Qi et al. 2020). Maher et al. (2019) showed that a combination of developmental regulators (like WUS, ipt, STM- SHOOT MERISTEMLESS) is sufficient to induce shoot formation thus circumventing tissue culture methods. Then, a combination of DRs and gene editing reagents created edited shoots. The strategy was used in dicot crops like Arabidopsis, tobacco, potato, grape and tomato. Consumer resentment in some areas of the world resulted in low to no penetration of GM technology. Therefore, emphasis on non-vector, non-integration of foreign DNA in the primary or initial stage of GE development would be beneficial. Here, we look into available technique to undertake DNA-free editing.

DNA-Free Editing and Nanotechnology For quite some time, nanotechnology-based material is being used in agrochemical formulations which are aimed at plant nutrition, crop protection, abiotic and biotic stress resistance (Sanzari et al. 2019). These nano-materials are particles ranging from 1 to 100 nm and are chemically or physically linked. Thus, nanoparticles could be used in the delivery of Cas9 protein-gRNA or mRNA (Cas9)-gRNA load inside the cell for genome editing (Jeevanandam et al. 2018). The basic requirement of nanoparticle in genome editing is that the material must be permeable, can accumulate the cargo and should be able to retain the payload for extended period of time (Blanco et al. 2016). However, the uptake of nanoparticle (NP) is very unpredictable (Sanzari et al. 2019). Zhao et al. (2017) reported magnetofection technology in cotton involving pollen, magnetic particle and electromagnetic field. This technique has the advantage of being independent of the tissue culture protocol and genotype. Commonly used gene-coating material and cargo include polymers (polyethyleneimine, phenyl boronic acid or cell-specific aptamer, a combination thereof including functionalised graphene oxide), nanoclay, liposome (lipid like nanoparticles), gold nanoparticles, nanoscrew and coreshell. Cargo delivery involves Agrobacterium-mediated transformation including agrolistics, adenovirus and lentivirus (see Wei et al. 2020 and Nguyen et al. 2020 for details). The emergence of delivery methods of nanotechnology assisted delivery is considered a breakthrough technology. While commonly used Cas9 causes double-stranded breaks in the 4th base pair of PAM sequence, which is then repaired by NHEJ or HDR (Wu et al. 2014). However, HDR is active in dividing cells and therefore rare (Devakota, 2018). The Cas9 protein is about 160 kDa (Mout et al. 2017) which when co-delivered with RNP for DNA-free genome editing poses a challenge due to its shear size, and in such situation, Cas9 mRNA may help as well as limit the off-target editing due to its limited stability in the plant cell. Further, the Cas9 protein is positively charged and poses challenge for encapsulation in nanoparticles. The encapsulation of lipid in the outershell of the nanoparticle improves its stability and better protects the DNA and protein from degradation by cellular nucleases and protease. Also, see Chakraborty and Vora (2020). The supremacy of NHEJ over HDR has limited application in plants owing to concerns about possible off-targets (Anshari et al. 2020). With the discovery of base editing, this can transform one base to the other without breaks and foregoing the need for a repair template. Base editing can be categorised into broadly four generation. Initially, BE1 was invented with fusing cytidine deaminase, BE2 was an improvement over BE1 in that it
incorporates uracil DNA glycosylase inhibitor (UGI), BE3 is dCas9 replaced by nCas9 (nickase) while BE4 has rat/lam-
prey/human APOBEC1 with nickase (for detailed review,
Bhattacharya et al. 2019). NHEJ is preferred approach where loss of function of a gene is desired (Monsur et al. 2020).
Nowadays, both adenine and cytidine base editors are avail-
able which facilitates base conversion (by deamination) in a
narrow window (see Nishida et al. 2016). Like DNA, RNA
editing is done via REPAIR (RNA editing for programmable
A to I then to G) and RESCUE (RNA editing for specific C to
U exchange). However, to reduce the possible off-targets,
guanine mismatches is incorporated in gRNA design (Bhattacharya et al. 2020; Monsur et al. 2020). Another strategy is to intro-
duce uracil DNA glycosylase inhibitor (UGI) into base editor
(Komor et al. 2016). In another recent development, Liu et al.
(2020) invented a very fast CRISPR (vfCRISPR) on demand
system targeted on living cells with the goal of inducing DSBs
with a high resolution. The vfCRISPR system helps in
targeting single allele and eliminating off-target activity.
Primarily, the vf system works on a caged RNA strategy,
which prevents Cas9 from cleaving the DNA strand until ac-
tivated by light, thus facilitating precise breaks. Therefore,
SNP variation in the crop genome is linked to variation in
traits and this knowledge can be successfully exploited to
create designer crops through base editing (Li et al. 2018).
Traditionally, exploiting such SNPs variation through conven-
tional breeding would take several years and CRISPR/Cas can
achieve the same in less time. Wang et al. (2020) developed a
series of APOBEC-Cas9 fusion induced deletion system
(AFIDS) which when combined with human APOBEC3A
(A3A) with uracil glucosidase and a AP lyase results in a
robust editing system. This results in predictable, multi-
nucleotide targeted deletions within the protospacer window
in rice and wheat. The SWEET14 (Sugar Will Eventually Be
Exported Transporters 14) deletion mutants obtained in this
study had significantly smaller blight lesions than 1 or 2 bp
INDELS, while in wheat, the same group found three predict-
able mutants of miR396 that averted formation of mature
RNA.

Social Impact No formal study depicting the perception of
gene-edited crops on consumer sentiments was conducted
in India till date. However, there are studies available across
globe on the social and consumer perception. Earlier, Wehlan
and Lema (2017) noted that GE caused dilemma in the minds
of policyholders in issues relating to regulatory and safety com-
pliance. Furthermore, due to the absence of exogenous DNA in
the final product despite using biotechnological intervention is
an additional challenge for enforcing regulatory requirements.
Thus, such decision-making will lead to the use of many social
science tools to arrive at logical conclusion. Lassoud et al.
(2019) published the results of a comprehensive study to esti-
mate the cost and time involved for commercialising gene
edited crops when they are regulated just like GMO vs. when
GE crops are treated at par with conventional crops. The survey
results shows that in the first scenario (like GM), this will cost
US$24.5 M and take 14 yr. In the second scenario (non-regu-
lated), it will fetch US$10M and can be completed in just 5 yr.
There was no significant difference between products devel-
oped in North America and Europe based on existing regula-
tions. In another survey conducted in Costa Rica, it was found
that though consumers have low knowledge about genome
editing but are ready to accept the product owing to high per-
ceived produce, quality and disease resistance (Gatica-Arias
et al. 2019). While in a study by Kato-Nitta et al. (2019) in
Japan, it was found that consumers were more positively in-
clined toward genome-edited crops than genetically modified
(GM) crops. Also, the perception widened when choice was
between conventionally breed crops and GM crops. Thus, GE
crops seem to have a positive edge. A study in Germany con-
ducted on the same topic of GE found that stakeholders in value
chain of wheat perceived celiac-safe and fungal tolerant trait
positively. Whelan et al. (2020) observed that GE resulted in
diverse range of products options and wide participation of
many start-ups and SMEs. This will result in faster adoption
of technology, i.e. faster bench to market. Website 5 n.d.gives
detailed up-to-date information on GE in human and agriculture
space.

Future of GE Crops As Nucciu et al. (2018) discussed, the
efforts undertaken over the past 20 yr in developing drought
tolerant crops emphasising that regulations and the fact that
food security advantages can accrue from modern biotechno-
logical interventions including gene editing. GE may be seen
positively by general public than in the past. Some notable
products in the past developed worldwide through GM ap-
proaches include Monsanto’s DROUGHTGUARD (Website
2 n.d.), Corteva’s AQUAMAX (Website 3 n.d.) and NX1-4T
sugarcane (Website 4 n.d.). A comprehensive list of global
pipeline of biotech crops is reviewed by Parisi et al. (2016),
from arable to speciality crops. Xu et al. (2019) noted that
there must be continuous discussion between developers,
breeders and consumers in the GE product development
space. Further, the type of delivery agents used to regenerating
mutants should be emphasised. Therefore, it is expected that
the new plant breeding technologies could fill the unfulfilled
promise in accelerating crop improvement efforts. Further, the
cost of developing gene editing crops is less than that of GM
crops, owing largely due to no to low regulatory cost depend-
ling on designated marketplace.

Conclusion

Farmers need new improved varieties to increase crop yield
and feed the Nation and the Globe. Plant breeders are
equipped with various tools including marker assisted molecular breeding and genomics to name a few for the purpose. Competition between breeding community is intense given the globalisation of the world economy and warrants adoption of new technique to achieve the desirable end results (please see Zimny et al. 2019). Genome editing has been here for the last decade or so, particularly targeted oligonucleotide mutagenesis, meganucleases, zinc fingers and TALENS. However, due to their complexity, it did not result in any new crop product in India though many examples exist outside the country. Particular interest in this field is amplified by the recent discovery of CRISPR/Cas9 GE system. CRISPR/Cas9 is simple, versatile, low cost and stood to democratise the field of GE. In the absence of a clear road map, fresh investments by various parties are unlikely, especially from the past GM experience. India has come up with a draft regulation for genome editing. Further, other interested parties like ICAR (Indian Council of Agriculture Research) and NAAS (National Academy of Agricultural Science) have shown positive intention to make the road map simple (NAAS 2020). SDN-1 and 2 edits are likely to be less regulated, barring few traits like herbicide tolerance and can show up in farmer’s field hopefully soon. SDN-3 gene replacements are likely to be treated at par with GM. Food security is paramount for the world’s second most populous country. It is hoped that GE tool kit will be included in the plant breeding strategies sooner than later.

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