International Journal for Research in Applied Sciences and Biotechnology

ISSN: 2349-8889
Volume-8, Issue-1 (January 2021)

www.ijrasb.com

https://doi.org/10.31033/ijrasb.8.1.10

Application Techniques of Molecular Marker and Achievement of Marker Assisted Selection (MAS) in Three Major Crops Rice, Wheat and Maize

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ABSTRACT

With the discovery of new genetic technology, the researcher focuses on using DNA molecular markers to improve new varieties worldwide. Such as resistance to biotic and abiotic stresses and enhancing quality and quantity at different plant breeding fields. Conventional breeding selection is based on phenotype data selection, time-consuming, and has a high chance of linkage drag. Thus, DNA molecular marker method usage is faster, easy, and not expensive than conventional breeding programs. This review focused on applying molecular markers such as genetic diversity analysis, the genotype of identification and fingerprinting, gene tagging and mapping, QTL analysis, and marker-assisted selection. In another part of this review, we focused on MAS's achievements related to improving agronomic traits, quality traits, and biotic/abiotic stresses for three major cereal crops like Wheat, Rice, and Maize.

Keywords- Molecular Markers, Marker Assisted Selection (MAS), Crop Improvement.

I. INTRODUCTION

Cereal crops are the most important source that supplies food and producing raw material for industrial use. Still, meaning full space are still remains among the yields and food consumption of crops worldwide. Thus Plant insects, disease, and non-capable environment conditions often cause serious losses of crop yield. On the other hand, rapidly growing up world population will cause a shortage of food worldwide. To prevent food shortage, the breeders require developing new varieties continuously with high quality, quantity, resistance to biotic and abiotic stresses, etc. thus; plant breeding plays the main role in reach the above objects e Molecular markers. During the last two decades, many varieties develop. The important genetic tools for plant breeders nowadays and using molecular marker related to all major crop species [Tazeb. A., 2018]. In general, the target genes do not reflect themselves by molecular markers. Still, they may serve as signals or flags and use them as chromosome landmarks to facilitate the introgression of genes associated with economically beneficial characteristics. MAS is a molecular method in which the classification index dependent on genotypic data selects parental lines for intercrossing [Collards et al., 2005]. In order to incorporate various target characteristics into a single line or genotype, the traditional breeding system requires more breeding cycles.

In comparison, in a single genotype, MAS displays the goal characteristic more reliably in less selection cycles with less inadvertent errors. Thus, MAS is time and requires less capital to boost high productivity crops. MAS is a perfect access for improving crop production and protecting crops from different stresses [Oliveira et al., 2008]. More ever, the breeders want to increase selection efficiency that allows to discrimination the best genotypes in all crop improvement programs. The report showed when the selection is based only on phenotypic assess, the breeders usually oppose the problem of genotype-environment interaction, which may hide desirable genotypes that will make selection harder than [Stromberg et al, 1994]. Therefore, the breeders are trying to decrease the interaction between genotype and environment by stratification of the selection scheme [Gardner et al., 1961] or to make an indirect selection of yield using the correlation among agronomic characters [Collins et al., 1965] in addition to produce selection efficiency through progeny test [Lonnquist et al., 1964]. Generally, these conventional techniques have been contributed to obtain more precise at the time of selection; however due to the increased use of resources on the one hand and new demand and challenges for crop productivity on the other have open way for the development of new molecular tools that have increased selection efficiency. The use of numerous molecular marker techniques to facilitate the effectiveness and screening of linkage maps in plants helps breeders with linkage maps to handle applied research in order to classify and define genetic diversity in commercially valuable plant species. The key explanations for encouraging the use of molecular marker approaches in crop improvement programs are the expense and heritability of the indicators, which is much lower in the cost than the conventional selection system [Winter et al., 1995] as well as the recommended usage of molecular markers for crop improvement is their applications onto trait selection with low heritability. Identification of complicated inheritance such as stresses resistance and

the introgression of gene coming from exotic or native germplasm [Sari-Gorla et al., 1999]. In top of that other potential usage of the markers assessment of genetic connectedness among breeding material and population, Recognition and fingerprint of genotypes [Kumar et al, 2014] and recognition of correlated with controls of morphological characters meaningful agronomic characteristics marker-assisted sorting and identification of sequences of essential candidate genes for potential study in plant breeding programmes [Kumar et al, 2014]. Perfect must be able to show high level of polymorphism, ease of allele detection, co-dominant, distributed thoroughly throughout the genome, neutral, economical, ease to use and reproducibility. These marker polymorphisms should be expressed in every cells and tissues of the plant without regard to the stage of development [Smulders and De Klerk, 2011].

Over long period, plant-breeding combine with usage and development of molecular markers has push up the crop yield and better productivity. Using marker technique, identifying targeted loci and its amplification in crop plants is commonly used for further utilization. Many disease resistance genes, resistance to stresses, and quality traits like nutrient uptake and water use efficiency are major foci of plant breeding attempt as forecast population growth has put pressure on the environment for increasing food production. Therefore, plant-breeding will plays key role together with molecular markers for increasing crop yield. [Ahmad et al, 2017]

Truthfully, varieties of varieties have already been published for the usage of MAS items sometimes in cereal plant species [Varshney et al., 2006]. Some good examples of the production of MAS and molecular markers in the wheat rice and maize species were seen in Table 1 and 2.

II. APPLICATIONSOFMOLECULARMARKERTECHNIQUESINCROPIMPROVEMENT

Therefore, odd molecular instruments have recently been created to demonstrate their utility in functional plant breeding to promote the characterization, detection and modification of genetic variation on economically relevant agronomic characteristics. Therefore, the novel molecular marker applications in crop improvement programmes are described below:

- Study of genetic variation
- Identification of genotypes and their fingerprinting
- Tagging/mapping of chromosomes
- Analysis of a quantitative feature locus [QTL]
- Supported collection marker [MAS]

2.1. Genetic Diversity Analysis:

Analysis of the scope and distribution of genetic variation in a crop species is necessary to understand the developmental connection between sample and accessions to genetic resources in organized fashion for breeding objectives. Thus, molecular methods of multiple plant organisms are superior methods for evaluating genetic variation. Since molecular markers have provided very useful information about crop germplasm, this information is much important for plant breeders to make decisions about the utility of germplasm especially in the search for unusual and rare genes. A crop species of restricting genetic base is plain lyimprobably to harbor novel genes e.g. those that provide resistance to biotic and abiotic pressures.

Several types of molecular marker techniques have been used for genetic studies in crop plants such as AFLPs, RFLPs, RAPDs and SSRs, among many classes of molecular techniques, [SSR] markers are applicable and valuable because of their ability to cope with plant genetics and breeding, for example, in many applications, co dominant inheritance, positive genome coverage relative abundance, and multiallelic nature. Further on, 31 varieties of cassava were evaluated by Elias et al [Elias et al., 2000] by using AFLP marker for genetic diversity. In similar perspective, five more limited AFLP primer variations used on 60 breadfruit samples were taken into account, and then enhanced a total of 414 bands in 85persent, which was polymorphic. Interestingly, genetic gap difference takes place from 0.0044 to 0.3376. However, as seen by Study of Molecular Variance [AMOVA] e.g. 57.45 percent than [42.55 percent] across populations, broad populations appear to have a greater variety. It has been shown that RAPD markers are very useful to test genetic variation in a very succinct way for genetic breeding and cassava germplasm [Colombo et al., 2000]

Furthermore, 53 wheat cultivars were genotyped using 24 SSR markers in Polish Wheat's for genetic similarity assessment. Analysis on SSR marker inhibits allowed DNA polymorphisms to be embraced by one SSR marker, resulting in a total of 166 alleles ranging from 3 to 13 alleles with an estimate of 7.22 per indicator. Previous research found that winter cultivars redeemed a great deal of variability relative to spring cultivars .They found that SSR primers yield a massive amplification of an average of 12.31 alleles per locus for a total of 357 distinct alleles. Their research showed that the genetic difference existed between 11 geographical regions with a ratio of 73 percent and 27 percent, respectively. At the same period, the genetic information of hexaploidy wheat landraces was shown in a separate North Oman research by SSR-based geographical origin diversity research that conducted a maize population analysis using 30 microsatellite markers for genetic diversity. Owing to the collection of genetic variety deficits in terms of the total number of alleles per locus, the population did not change substantially with the amount of genetic variation. Genetic distances check the favorable results of one recurring selection period, since the synthetic is more differentiated relative to the initial population has also been genotyped 82 established genotypes of sugarcane from seven geographical domain applying a set of 12

ISSR markers so as to apprise the extent of molecular genetic diversity. The ISSR primers intensify the maximum of 149 distinct alleles with an average of 12.41 allerles per locus. Thus, the ISSR fingerprint in this study recognized genetically rare genotypes that are muchprominent source of diverse sugarcane germplasm [Adebabay et al. 2017].

2.2. Fingerprinting of Genotypes and Identification:

Profiling of DNA fingerprint is so necessary for varietal recognition as well as for verifying germplasm variability. Thus, DNA fingerprint information is important for determining genetic diversity, characterization of accessions in germplasm collections, and the safety of germplasm assets [Kumar et al, 2014]. Molecular markers are commonly used in various crops for DNA fingerprinting of cultivars and breeding programs. The technology of Molecular marker has potentially require for improving purity estimation in crop hybrids. For example, Mongkolporn et al. studied the genetic purity of 3 F1 chilly hybrid varieties using two molecular marker ISSR and RAPD. They mention that analysis of RAPD remarkably detected all three F1 hybrids, while ISSR detected only two. As a result, we can say that the RAPD marker procedure can produce many markers/alleles than the ISSR system. In a general manner, all the valid molecular tools from the essayist and eagerly employable RAPDs, ISSRs, DNA amplification fingerprinting [DAF] to the more exact and strong AFLPs, microsatellites/SSRs and RFLP analyses have been used for the identification of almost related lines as well as high product varieties. Thus, different molecular marker techniques are ideal for recognition of nearly related genotypes that vary in some of the morphological traits.

2.3. Mapping /Gene Tagging:

The fascinating application of molecular markers now a day, as a tool for locating genes managing agronomic ally significant characters via linkage to mapped DNA sequences. Gene tagging exhibit to the mapping of genes that-commercially significantly close to known markers. Phenotypic estimation at the cellular level or the whole organism level provides information, which can determine gene location on chromosomes that confer the phenotype of interest. Thus, molecular markers are extremely close linked to genes look like a label that is useful for selecting of a gene by indirect way in plant breeding programs with molecular map construction; we can detect or tag number of genes that are commercially importance like stress tolerance resistance to disease, resistance to insect, genes of fertility restoration, yield improvement traits tagged a gene responsible for the resistance of powdery mildew ol-1 in tomato on chromosome 6 by using SCAR and RAPD markers. Gene tagging is a pre-requisite step for [MAS] and gene cloning by map-based [kumar et al, 2014].

2.4. Study for Quantitative Trait Locus (QTL);

A portion of the genetic element that is responsible for the absorption of a quantitative trait's phenotypic heterogeneity is called quantitative trait loci [QTL]. Thus, a QTL genuinely mentions a portion of the genome compared to a gene that one or more usable genes may overcome. QTL-mapping is the organization between the values of observed trait and existence markers allele that have been mapped to linkage map is analysis. Whenever it becomes meaningfully clarify that The correlation witch is found not displaying several method effects, it is declared to occur and detect the QTL. We may also approximate the size of the QTL witch's allelic result observed. This information can be utilised through indirect filtering usage by evaluating the instances of the QTL breeder for its use. Whenever selection is calculated by applying molecular markers called marker-assisted selection on genetic material recovered [MAS]. Thus, according to QTL analysis requires the followings;

- Cross p1 and p2 to produce population for mapping
- Identification of polymorphic markers between parents
- Create markers data
- Generating of linkage maps related to molecular markers
- Collection of phenotypic data related to QTL trait
- Mapping of QTLs [Association of markers with QTL]

2.5. Marker Assisted Selection [MAS]:

With the appearance of [MAS], fresh breeding tools are found for making selection of breeding populations easier and more precise. With these breeding tools, heritable traits are able to link with DNA segments responsible for that trait. These segments of QTLs or DNA might be specified with special techniques in the laboratory. In the selection program the breeder can select a trait easier with the help of a marker. According to the fundamental requirements for [MAS] in the breeding program are below;

- Finding of markers which might be linked with desirable traits
- Confirm the valid markers in the breeding population and also in parents
- If there is no validity of markers, need to design and make it valid before usage [if there is no valid data of mapping populations so it needs two to four-year for generation of marker and making it valid]
- Designing of breeding and selection strategy
- For detecting all significant alleles to be examined the need to arrange a minimum
- Need to keep scrupulous records
- Need to test for traits fixation

III. MAS AND DEVELOPMENTS OF VARIETIES

By using MAS, a lot of varieties become developed, such as stresses resistance like biotic/abiotic. In various crop plants, like maize, wheat, rice, pearl millet and barley, grain yield and quality improvements

have been made ["Dwivedi et al. 2007; Jena and Mackill 2008; Prasanna et al. 2010: Gupta et al. 2010"].

3.1. MAS and Rice development

Several essential germplasm lines were effectively used in breeding, contributing to commercially relevant varieties. MAS originated and prepared rice substances and published varieties with major characteristics, along with the traditional breeding scheme. Most of the genes used in MAS and variety production such as disease tolerance are "Xa23, Xa21, Xa4, Pi l, Pi-1, Pi-2, Pi-25, Pi-33, R-sb2t, R-sbzt, etc.", genes correlated with grain consistency such as "Lgc1, Wx, Frg, badh2" sterility gene [Rf5] and date heading. Kernel quality characteristics including kernel weight, kernel width/kernel length, basmati fragrance, and bacterial blight resistance [MABC] were coupled with high amylase content through the use of marker aided back cross [MABC]. Improvement of submergence resistance [Sub 1 gene] varieties through the use of MAS previously recorded from Thailand and their adaptation for deep water paddy cultivation in eastern India has been tested. Deeds of MABC-enhanced resistance varieties were evaluated to infer the role of Sub1 in different genetic backgrounds. Quick and high-accuracy of MABC inserted the sub1 loci into a rain fed lowland rice variety BR11, which is Bangladesh's super variety. Approximately 100 distinct genes were established at the end of 2015. Among these hundred genes, 14 genes "Pi1, Pi2, Pi9, Pi20[t], Pi33, Pi39, Pi40[t], Pi47, Pi48, Pi54rh, Pi56, Piz, Piz-t, and Pigm" have been added linked to their wide resistance "[Hayashi et al., 2010; Huang et al., 2011; Das et al., 2012; Hua et al., 2012, 2015; Liu et al., 2013]". These markers help rice development in Asian countries from 11 to 34 percent by supplying hybrid and inbred varieties. This has an effect on an expected grain product rise of 0.8 million metric tonnes ["worth US$20.5 million"] per one cropping season of paddy rice in China's key Indonesia, Philippines and India by cultivating tolerance to bacterial blight from hybrid/inbred varieties [Leung et al. 2004].

3.2. MAS and Maize development

By the use of MAS different varieties of maize has been developed world wide such as 'Vivek Quality Protein Maize [QPM] Hybrid 9'in India. The variety was improved by selection of phenotypic endosperm adapters in parental lines and the use of marker-assisted transfer of the O_2 gene [CM145 and CM212] of Vivek Hybrid 9. The same path was used for the adapting of early maturing inbred lines to the mountainous regions of India for the development of QPM of different elite line [Gupta et al, 2009] while the same concept was further on extended by Khanduri et al [2010] who elaborated that there are 6QPM types of 6 elite inbred lines namely "CM150, CM139, CM 140, CM151, CM138, CM137" Three single-cross hybrids, such as PEEHM5 "[CM150 □ CM151], PEHM2 [CM137 □ CM138], Parkash [CM139 □ CM140]", were categorically taken into account as parents. Five elite lines, "CM137, CM138, CM139, CM140 and CM212" is pyramidized for the resistance of turcicum leaf blight [Exserohilum turcicum] and Polysora rust ["Puccinia polysora"] of major genes/QTL. In China, pipeline MAS products are conducting comparable attempts on MAS for the generation of QPM lines and significant QTL transition for sugarcane mosaic virus [SCMV] resistance.

Identified many SNPs that are significantly correlated with the three resistance characteristics of Mediterranean maize borer attack. Significantly linked to these SNPs were 10 tunnel length [TL], eleven kernel resistance [KR] SNPs, and four-stem harm SNPs [SD].

Fifteen QTLs located on six chromosomes for maize weevil [MW] originating from the cross of Population 84 were identified and Kilima examined F6 RIL families using composite interval mapping [CIM]. Research reveals that these regions are capable of utilising MW resistance in tropical maize in breeding programmes for MAS.

3.3. MAS and Wheat development

MAS is also being included in national and foreign breeding projects every day. The joint wheat programme of the Chinese Academy of Agricultural Sciences [CAAS] and CIMMYT, working along with numerous provincial programmes in mainland China, plays a leading role in the improvement of molecular markers in order to establish valid molecular markers from other programmes across the world . This program's key aim was to clone the Psy 1 genes correlated with yellow pigment in flour on chromosomes 7A and 7B for the production of useful markers dependent on allélic varieties and then legalise them in Chinese cultivars of wheat. More than 80 markers are now being used to target characteristics such as consistency, disease tolerance, plant height, kernel weight, and adaptation, including these markers and markers developed by other programmes worldwide. Actually, the use of molecular markers for parental line characterization increases the efficiency of selection in backcross segregating species and promoting in progressed lines the presence of gene products. Three lines improved by the MAS in local experiments were checked and strong productivity characteristics with remarkable efficiency of two parents were combined "Zhonghu He, personal communications". 42 characteristics/genes including rust resistance genes "Lr9, Lr19/Sr25, Lr24/Sr24, Lr34/Yr18, Lr46/Yr29, Lr47, Sr26, Sr32, Sr33 and Sr36" selected by the Western Australia Wheat Breeding Program for germplasm enhancement and variety production by MAS. At 54 locus [Pm1-Pm54], almost 82 intended genes immune to powdery mildew have been established, including "Pm1a-Pm1e at Pm1, Pm3a-Pm3g at Pm3, Pm4a-Pm4d at Pm4, Pm5e-Pm5, Pm8, Pm17, and Pm24a-Pm24b at Pm24a-Pm24b [Hao et al., 2015]". The United Statute introduces wheat Fields genomics, which requires MABC, to unify 27 different disease and pest resistance genes and 20 advantageous pest and breeding performance alleles into 180 lines appropriate for the

main wheat production regions in the US [Dubcovsky-Around 2004]. This comprises more than 3,000 MABC, generating 240 backcross-derived lines, and even releasing 45 MAS derived lines. [1] For grain texture pinB-D1b, [2] for stripe rust resistance and grain protein quality Gpc-B1/Yr36, [3] for leaf rust resistance Lr47, [4] for resistance to all three rusts Lr37/Yr17/Sr38, and [5] for Hessian fly resistance H13. The germplasm was improved for a form of phenotype utilizing different genes. In MAS-supplemented wheat breeding programmes similar to CIMMYT, 25 separate markers of genes correlated with tolerance to protein content, insect pests, and other agronomic characteristics were used [William et al. 2007]. However, for the crossing block test at CIMMYT to design crosses aspired to transfer/stacking of genes, a total of 20 markers were used for Ppd, Rht, Vrn and immunity genes against infections. In Europe, these markers were used to screen resistance in comparison to soil-borne viruses and to detect the spectrum of rust resistance loci, verbalization and photoperiod genes ["Ppd and Vrn1, 2 and 3"], dwa ["Fhb1 and Fhb2"]. The release of Lillian ["DePauw et al. 2005"], which is responsible for the increase grain protein content gene ["GPC-B1"], and Goodeve [DePauw et al. 2009], which controls the orange blossom wheat midge resistance gene ["Sm1"], has almost led to MAS. The implementation of desirable rust and efficiency characteristics utilizing DH in combination with MAS technologies led to the improvement of an economically important line extracted from "Stylet" within 5 years. compared to the creation of a classical breeding system variety that took 12 years. For wheat farmers in the US, the durum wheat variety derived from the MAS 'Westmore' regulating Yr36 gene responsible for stripe rust resistance is also economically true.

While there are just a few studies that greatly illustrate MAS usage in plant breeding systems, the technology has provided its potential as a method for promoting traditional crop plant genetic improvement. Several successful examples are available for the MAS program, which, by numerous breeding companies, has released several industrially valuable varieties globally. Examples of plant breeding of suitable lines in the public sector pipeline that will be true in the future are also effective.

3.4. Steps required in MAS

- Molecular markers Validation. Need to Extract individual's DNA and determine trait and marker relationship one to one.
- Extraction of DNA at seedling stage form population and put to use MAS. Need selection of individuals based on the presence of desired molecular markers for the trait of interest. Related to other traits, the selection process might be based on the methods of classical breeding. Least possible amount of individuals to be examined might be as per the determined strategy and statistical compensation.

3.5. Achievement of Marker-Assisted Selection

In plant pathology, molecular techniques are now well established as an effective tool for the indirect selection of challenging traits in plant breeding at the stage of the seedling. This technology accelerates the typical process of plant breeding and thereby strengthens dynamic characteristics that traditional monoculture farming cannot readily enhancement. This analysis studies MAS's achievement in different biotic and abiotic resistance plants, particularly in some major crops. MAS is widely used nowadays to improve varieties that resistance against pest, drought, and disease in rice, Maize, and wheat. Enormous commercial losses caused by diseases, for breeding resistant and economically relevant rice, wheat and maize varieties, pest and drought researchers have been involved in using molecular marker breeding access and MAS. Only plant diseases alone induced a 20% decrease in food and cash crop production from biotic and abiotic tension. In various crop varieties, particularly cereals, a high proportion of genes/QTLs regulating agronomic characteristics and consulting resistance to both abiotic/biotic stresses were established and tagged, using molecular markers. The achievement of MAS is not limited to variety improvement alone. In reality, the MAS items were already liberated as varieties in the case of certain cereal species [Varshney. et al., 2006]. For rice, maize and wheat species, good examples of MAS production are described in [table 1].

Table 1: A few instances of MAS for plants tolerant of breeding stress.

Crop	Genetic /QTLs	Form of biotic/abiotic pressure	Source
RICE	Xa4, xa5 & Xa21	B.L.B	Jeung et al., [2006]
RICE	Xa21, xa13 & xa5	B.L.B	Pradhan et al., [2015]
RICE	Piz-5 & Pi 54	B.L.B	N.K.Singh et al., [2012]; V.K. Singh et al., [2012]
RICE	Bph27[t] & Bph3	Brown Plant Hopper [B.P.H]	Liu et al., [2016a, 2016b]
RICE	RM 201	Drought	Lang and Buu [2008]
RICE	Sub1	Water logging	Nandi et al., [1997]

ISSN: 2349-8889
Volume-8, Issue-1 (January 2021)

www.ijrasb.com https://doi.org/10.31033/ijrasb.8.1.10

RICE	qTIL2 and qTIL4	Water logging	Nagai et al., [2012]
RICE	Qsct-11	Cold	Chen and Li. [2005]
RICE	qCTF7,qCTF8, qCTF12	Cold	Shinada et al., [2013]
RICE	qCTS12a	Cold	Da Cruz et al., [2013]
WHEAT	Fh61 & Qfhs.ifa-5A	Fusarium head blight [FHB]	Miedaner et al., [2006]
WHEAT	Sr25, SrWeb & Sr50	Stem rust	Yadav et al., [2015]
WHEAT	Lr19 & Lr24	Leaf rust	Singh et al., [2004]
WHEAT	Gb3	Green bug	Weng et al. [2005]
WHEAT	H9	Hessian fly	Kong et al. [2005]
WHEAT	QLt.ksu.1D, QFv/fm.ksu-3B,QChl.ksu-3B, Gyp.ksu-4A	Drought	Kumar et al. [2012]
WHEAT	Fr1 and Fr2	Cold	Snape et al. [1997]
MAIZE	RP3	Rust	Wisser et al. [2006]
MAIZE	p1	Corn earworm	Butron et al. [2001]
MAIZE	qMrdd1	Maize rough dwarf disease	Tao et al. [2013]
MAIZE	q2.09HR & q5.03HR	Head smut	Li et al. [2015]
MAIZE	Root-ABA1	Root development under water stress	Giuliani et al. [2005]

Table 2: Some examples of Molecular markers were produced in wheat, maize and rice for different characteristics.

S. No.	Genetic /Locus	In parenthesis, alleles and anticipated product scale	Trait to which FMMs belong Evolved	Source
Wheat Agronomic Traits				
1	Rht-B1	Rht-B1a [237], Rht-B1b [237]	Reduced plant height	[Ellis et al., 2002], [Zhang et al., 2006]
2	Rht- D1	Rht-D1b [264], Rht-D1a [254]	Reduced plant height	[Ellis et al., 2002]
3	Ppd- D1 TaGW2-6A TaSus2-2B	Ppd-D1a [713], Ppd-D1b [490] TaGW2-6A [949], aGW2-6A [418] Happa-H [423], Hap-L [381]	Photoperiod sensitivity Grain weight Grain weight	[Beales et al., 2007] [Su et al., 2011] [Jiang et al., 2011]
4	VRN-D1	vrn-D1 [1671], vrn-D1 [997]	Vernalization	[Fu et al., 2005]
5	VRN-H1	vrn -H1 [474], vrn -H1 [403]	Vernalization	[Fu et al., 2005], [Jia et al., 2004]
6	VRN-B3	vrn-B3	Vernalization	[Fu et al., 2005]
7	VRN-A1	Vrn-A1 [1068] and vrn-A1 [552]	Vernalization	[Fu et al., 2005]
Quality Traits				
1	Talox-B1	SNP based markers LOX16 [489 bp] and LOX18 [791 bp]	Processing quality	[Geng et al., 2012]
2	Glu-A3	gluA3a [529], gluA3b [894], gluA3d [967], gluA3e [158], gluA3f [552], gluA3g [1345], gluA3ac [573]	Processing quality	[Wang et al., 2009]

3	Ppo-D1	Ppo-A1a [685], Ppo-A1b [876]	Polyphenol oxidase activity	[He et al., 2007]
4	Psy1	YP7B-1 [156], YP7B-2 [428], YP7B-3 [884], YP7B-4 [716]	Yellow pigment content	[He et al., 2008]
5	TaZds-D1	TaZds-D1a, TaZds-D1b [981]	Yellow pigment content	[Zhang et al., 2011]
6	TaZds-A1	TaZds-A1a [183], TaZds-A1b [179]	Yellow pigment content	[Dong et al., 2012]
Maize Agronomic Traits				
1	Dwarf8	InDel markers: MITE, 18-bp deletion, 2-bp InDel, 3-bp InDel, 6-bp InDel. SNP markers: C/G SNP, C/T SNP, C/T SNP, C/T SNP, G/T, SNP, G/A SNP & C/G SNP	Flowering time	[Andersen et al., 2005]
Quality Traits				
1	PSY1	PSY-SNP7 [A/C SNP] & PSY1-IDI [378 bp InDel]	Provitamin A content	[Azmach et al., 2013]
2	LCYE	LCYE-50 TE [285 bpInDel], LCYE-SNP [G/ SNP] & LCYE-30 InDel [8 bpInDel]	C Provitamin A content	[Azmach et al., 2013]
3	crtRBI1	crtRBI-50 TE [397/206 bpInDel], crtRBI-InDel4 [12 bpInDel], crtRBI-30 TE [325/1250 bp InDel]	Provitamin A content	[Azmach et al., 2013]
4	DGAT1-2	SNP17 [G/T], SNP19 [T/C], InDel20 [3 bp/9 bp & InDel37 [3 bp]	Oil content	[Chai et al., 2012]
5	ZmcrtRB3	SNP based marker	α-carotene content	[Zhou et al., 2012]
6	Bm3	InDel based marker Digestibility	Forage quality for	[Lu¨bberstedt et al., 2005]
Rice Agronomic Traits				
1	GS3	C/A SNP based CAPS marker	Grain length	[Fan et al., 2009]
2	S5	InDel based marker [AD1], SNP based marker [AC2]	Spikelet fertility	Ji- et al., 2010
3	GS3	SNP based marker [DRR-GL]	Kernel length and elongation	Ramkumar, et al., 2010
Quality Traits				
1	Waxy	SNP based derived CAPS marker	Endosperm amylase content	[Yamanaka et al., 2004]
2	badh2	803 bp deletion based marker [FMbadh2-E4-5], 8 bp deletion based marker [FMbadh2-E7], 7 bp deletion based marker [FMbadh2-E2]	Fragrance	[Bradbury et al., 2005; Sakthivel et al., 2009; Shao et al., 2011;Shi et al., 2008]
3	Frg	SNP based marker	Fragrance	[Jin et al., 2003]
4	Lgc1	Two InDel based [InDel-Lgc1-1and InDel-Lgc1-2] markers	Low glutenin content	[Chen et al., 2010]
5	Waxy	SNP based marker	Amylose content	[Ayres et al., 1997]

IV. CONCLUSION

The conventional breeding selection approach is completely phenotype-based, time-consuming, and has a strong linkage drag risk. It suggests that the MAS may be a meaningful tool to aid plant breeders purchasing the target of improving food quality, supplying crops immune to biotic and abiotic stress, and improving antioxidant and nutrient foods. The existing hurdles need to be well examined in order to enhance the practicality of marker aided collection and suitable solutions can also be improved [Collard and Mackill, 2008]. Suppose MAS, by using high throughput markers is being used in a conventional breeding methods. In that case, it can be proved as an advantageous tool for overcoming the risk of climate change and reducing future challenges of food deficiency that might be happened [Devi, E. L et al., 2017].

The extension and usage of DNA-based indicators utilizing high-performance marker finding is expected for current advances in molecular biology and biotechnology, and genotyping is now a relatively new area and more interesting proposition. One of the achieve excellent of DNA markers will be a new development of common genomic instruments to promote crop breeding, utilizing high throughput access that has the ability to perform comprehensive genomic experiments entirely, cheaply, reliably and rapidly with high sensitivity [Tazeb. A.2018]. Molecular markers are essential genetic resources for breeders for the collection of genetic variability, the detection of genetic differences. For virtually all large crop plant varieties, forms of molecular markers and vast amounts have been improved the last two decades have gone. Molecular markers identify genetic variation that has been critical for both identifying genome dynamics and improving the efficiency of breeding. Du to comprehensive global attempt identification of tightly related molecular markers to large amounts of agronomic characteristics and tolerance to abiotic/biotic stresses in a major cropspecies, it was possible [Garrido-Cardenas et al., 2017].

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