GMR

Recent advances in gene pyrimiding with special reference to rice (*Oryza sativa* L.)

Anjali Singh*
Department of Genetics and Plant Breeding,
Acharya Narendra Deva University of Agriculture and Technology,
SRF, PPV&FR Authority, New Delhi, India

Corresponding author: Anjali Singh
E-mail: anjalisinghgpb@gmail.com

Genet. Mol. Res. 23 (2): gmr34060
Received: May 17, 2024
Accepted: May 24, 2024
Published: June 03, 2024

ABSTRACT

The improvement of sub-atomic hereditary qualities and related innovation like MAS has prompted the rise of another field in plant rearing quality pyramiding (IRRI).The term gene pyramiding is used in agricultural research to describe a breeding approach to achieve pest control and higher crop yield. Quality pyramiding focuses on the determination of an ideal genotype that is homozygous for the good alleles at all n-loci. Molecular markers aid in selecting the best plants with which to proceed.

Keywords: Pyramiding; MAS; MAB; Diseases

INTRODUCTION

Gene pyramiding: Quality pyramiding is characterized as a technique pointed toward collecting various beneficial qualities from numerous guardians into a solitary genotype for explicit characteristic.

Objectives

- Upgrading attribute execution by joining at least two corresponding qualities.
- Helping shortages by introgression of qualities from different sources.
- Expanding the solidness of infection and/or sickness obstruction.
- Expanding the hereditary premise of delivered cultivars.

For what reason to pyramid qualities?

- The issues of half breed rice.
- Breakdown of illness obstruction (impact, bacterial curse).
- Defenseless to bug bother (yellow stem drill and earthy colored planthopper).
- Cooking and eating quality.
- Steadily expanding requests to increment yield.

How to pyramid qualities?

Pyramiding is the collection of qualities into a solitary line or cultivar.

- A pyramid could be built with significant qualities, minor qualities, crushed qualities, successful qualities, ineffectual qualities, race-explicit qualities, non-race-explicit qualities, or some other kind of host quality that presents opposition. It includes:
    - Stacking of traits
    - Stacking of events
    - Stacking of genes
- A Genetically Modified Organism (GMO) and all subsequent identical clones resulting from a transformation process are called collectively a transformation event.
- On the off chance that more than one quality from another creature has been moved, the made GMO has stacking qualities (or stacked characteristics), and is known as a quality stacked occasion.

Kinds of quality pyramiding in plant rearing

Quality pyramiding is a harvest reproducing strategy that can be applied in traditional and high level sub-atomic rearing projects to present novel lines [1]. The customary strategy of harvest reproducing grows new yield assortments by utilizing conventional methods and routine regular cycles, when contrasted with present day and complex apparatuses of the ongoing time. The procedure includes consecutive quality pyramiding conveyed in a similar plant.

LITERATURE REVIEW

Interaction of planning a quality pyramiding methodology

Bringing every one of the helpful alleles into a solitary genotype is the general target of a quality pyramiding program. At the point when the quantity of parental lines containing the beneficial qualities (establishing guardians) is more than three, more than one intersection plan can bring about the age of the objective genotype. Subsequently, the quality pyramiding plan can be partitioned into two sections.

The initial segment is pointed toward cumulating one duplicate of all target qualities in a solitary genotype (called root genotype). The subsequent part is pointed toward fixing the objective qualities into a homozygous express, or at least, to get the objective genotype from the root genotype (Figure 1).

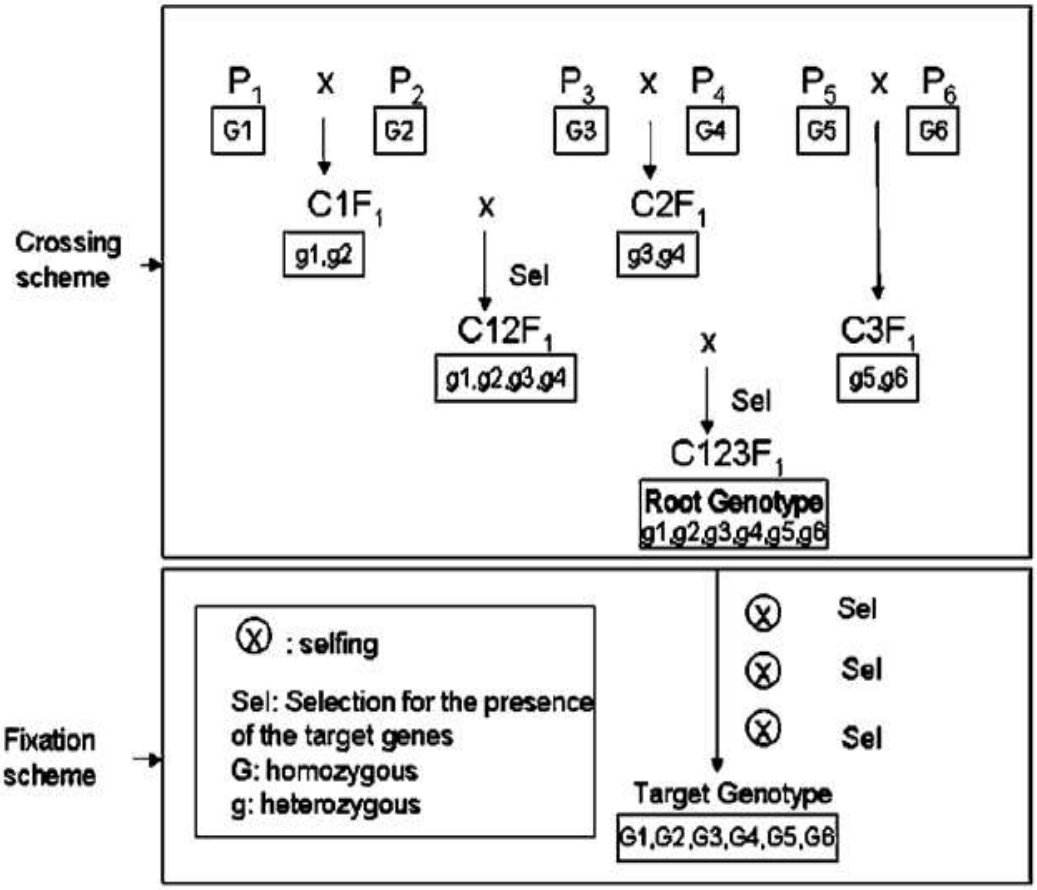

Figure 1: Diagramatic portrayal of a quality pyramiding plan cumulating six objective qualities from six parental lines.

Planning the obsession plan: Expecting that a genotype with a duplicate of the positive allele at every one of the designated loci (root genotype) is accessible, the plan of an ideal procedure is intended to track down the base number of ages for genotyping as well as phenotyping expected to fix every one of the loci for the helpful alleles inside the restriction of the biggest conceivable populace size relevant [2].

The most generally involved techniques for the creation of homozygous people are the improvement of Recombinant Ingrained Lines (RIL), and Multiplied Haploid (DH) populace. In this way, it is fitting to explore the practicality of accomplishing the goal utilizing RIL or DH. The goal of this step is to distinguish a determination conspires that prompts the creation of the objective genotype utilizing the base number of ages and the essentially suitable populace sizes in every one of the ages. The decision of the parent to utilize might be dependent upon specific contemplations relying upon the worth of the establishing guardians, the place of the loci, and so forth.

Planning the cross plan: An intersection plot which prompts the development of the root genotype should be planned in the event that the goal is reachable in light of the above step.

Marker-helped backcrossing

Reproducers move an objective allele from a contributor assortment to a famous cultivar by a redundant interaction called backcrossing; which, sadly, is slow and unsure. Rearing a plant that has the ideal benefactor allele yet in any case closely resembles the famous cultivar normally requires four years or longer.

Marker-helped rearing handles the two issues by permitting raisers to recognize youthful plants with the ideal quality and by working with the expulsion of stray contributor qualities from middle backcrosses. The outcome, in around two years, is a better assortment precisely like the famous cultivar aside from that it has the

moved worthwhile quality. On a basic level, this strategy can be applied to the rearing of any harvest or livestock. Markers are successful guides to choice in backcrossing in three ways:

- To begin with, markers can help choice on track alleles whose impacts are hard to notice phenotypically.
- Second, markers can be utilized to choose for uncommon offspring in which recombination close to the objective quality has delivered chromosomes that contain the objective allele and as minimal conceivable encompassing DNA from the giver parent.
- Third, markers can be utilized to choose intriguing descendants that are the after effect of recombination close to the objective quality, consequently limiting the impacts of linkage drag.

By and large, the marker helped backcross based quality pyramiding can be acted in three techniques. Marker helped backcrossing to be powerful, relies on a few variables, including the distance between the nearest markers and the objective quality, the quantity of target qualities to be moved, the hereditary base of the characteristic, the quantity of people that can be examined and the hereditary foundation in which the objective quality must be moved, the kind of sub-atomic marker(s) utilized, and accessible specialized offices (Figure 2).

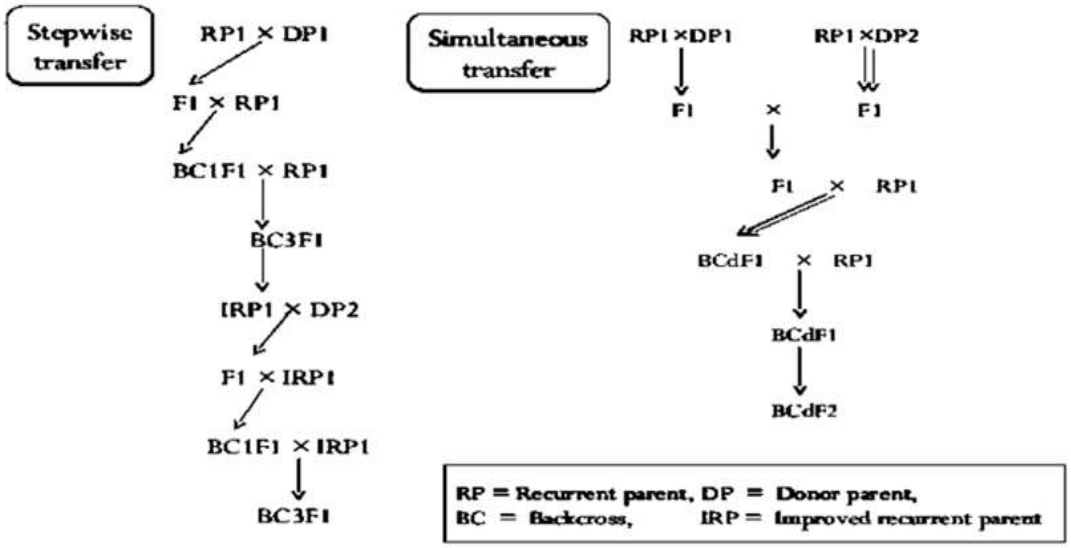

Figure 2: Diagram of marker-assisted backcrossing to transfer an objective allele into a popular cultivar.

Quality pyramiding different plan for backcrossing

- Introgression of Xa4, Xa7 and Xa21 for protection from bacterial curse in thermo-touchy hereditary male sterile rice (*Oryza sativa* L.) for the advancement of two-line half and halves.
- Marker helped introgression of bacterial curse obstruction in Samba Mahsuri, a tip top rice assortment:
  - Samba Mahsuri medium slim grain indica rice assortment.
  - Extremely well known among rancher and customers.
  - Profoundly powerless to numerous bug and sicknesses.
  - Synthetic control isn't viable.
- Improved Samba Mahsuri is the main assortment created by marker helped quality pyramiding.
- Rules for planning a productive quality pyramiding strategy.

Rules for planning a quality pyramiding crossing plan: Establishing guardians with less objective markers enter the timetable at prior stages. This rule depends on the accompanying realities:

- Once an objective quality has been integrated into a halfway genotype, genotyping should be finished in all later stages to guarantee its presence. Thusly, establishing guardians with more objective qualities ought to be utilized in later stage.

- Target qualities containing in an establishing guardian are in wanted linkage stage, which might be separated because of recombination. The more the meiosis included the lower the likelihood of keeping up with the ideal linkage.
- A cross that summons areas of strength for a linkage ought to be proceeded as soon as could really be expected. At the point when the objective qualities are connected, a quality connected in shock at certain phases of the pyramiding is undeniable and determination for recombinants is required. As the recurrence of recombinant sort is dependably lower than that of the parental kinds, bigger populace sizes are expected to recuperate the ideal recombinant.
- More crosses ought to be directed at every age assuming genotyping cost is low and the basically pertinent populace size is huge. At the point when the greatest number of crosses is performed at every age, the quantity of ages expected to create the root genotype is decreased and accordingly the complete length of the pyramiding program is diminished.
- One cross for every age is required assuming the essentially appropriate populace size is little or it is high to genotyping cost. In this sort of crossing plan, from the second era the beneficial genotype is framed by a recombinant gamete delivered by the chose genotype in the last age and a gamete of the recently presented parent.

Techniques for improving the proficiency of the obsession step

- **Going between chosen people:** As previously mentioned, the outcome of a quality pyramiding procedure relies upon getting the objective genotype inside the time span and cost characterized by raisers regardless of between mating between chosen people at every age helpful alleles in all target loci is absent at any age, crossing two plants with all that reciprocal genotypes can be utilized to get the program. Going between integral genotypes may likewise accelerate the reproducing system regardless of whether a palatable genotype is available.
- **Crossing the root genotype to a genotype with a few beneficial qualities:** Crossing the root genotype to a first class line without the ideal qualities can likewise be utilized to change the unfortunate stage over completely to the helpful one. This will successfully lessen the necessary populace size in resulting ages. This thought can be reached out to ages before the arrangement of root genotype.
- **Propelling every single acceptable genotype:** In certain ages multiple (to some degree heterozygous) genotype can possibly deliver the genotype wanted for the future. These agreeable genotypes might have various frequencies and different offspring sizes are expected to best understand their true capacity. The most effective system will be the one that advances the most acceptable genotype (less loci are isolating, and the isolating loci are in the helpful linkage stage) at every age.

Proficiency of quality pyramiding

Virtual experiences and hypothetical computations have given useful assets to examining the effectiveness of quality pyramiding programs. Three distinct quality pyramiding plans, one in view of a flowing family, and two in light of the request for crosses of the establishing guardians were assessed to check the transmission probabilities of the objective qualities and the cumulated populace size required in each plan [3].

Fundamental variables influencing quality pyramiding

Qualities of the objective characteristics/qualities: At the point when the qualities to be pyramided are practically very much portrayed and markers utilized for determination equivalent to the actual quality (amazing markers), quality pyramiding will find true success. For subjective qualities constrained by one or a couple of qualities, the recognizable proof of the qualities and firmly connected markers is simpler given phenotyping is painstakingly directed. A couple of markers for every quality can be utilized for following the presence/nonappearance of the objective qualities. At the point when the objective qualities are QTL with moderate or little impacts, pyramiding might find actual success because of the accompanying reasons. First and foremost, the distinguished QTL might be bound to be a bogus positive. Furthermore, mistaken QTL restrictions bring about the need to choose for more marker loci covering enormous genomic sections to be sure that target QTL alleles are held in chosen offspring. Thirdly, QTL impacts might be well defined for a specific hereditary foundation.

Regenerative qualities: The spread capacity of a not entirely set in stone by the quantity of seeds delivered by a solitary plant.

- Propagation capability of a crop is determined by the number of seeds produced by a single plant.
- A fairly large F2 population can be obtained by collecting seed from many F1 plants of the cross between two homozygous parents, from F3 generation seed can only be collected from a single plant.
- Efficiency of hybridization may be an important constraint for some crop species.
- When wild relatives are used as donor of desirable genes, many more reproduction related constraints may exist including cross incompatibility between wild species and cultivated crop (Figure 3).

Figure 3: Quantity of seeds delivered by a solitary plant.

Operating capital: All breeding programmes are operated within the limits of available operating capital. Therefore, reducing the overall cost is always an important consideration when choosing a strategy. In addition to the use of the most economic mating and testing approaches, other factors affecting the cost also need to be considered. In the context of gene pyramiding, cost affects both what can be achieved and how to achieve Increasing the numbers of generations (duration) will it. Increasing the number of generations (duration) will reduce the pressure on population size required in each generation and may result in the reduction of the total cost. However, increasing the duration delays the release of the new cultivar and consequently reduced market share.

Coordinating quality disclosure, approval and pyramiding

At the point when the statement of a quality is constrained by different qualities with generally little impacts, it is a quantitatively characteristic. The majority of the significant agronomic attributes, for example, yield, stress obstruction and quality are quantitative. Qualities for quantitative characteristics are more challenging to attributes. Quantitative Characteristics Loci (QTL) planning utilizing intentionally produced planning populaces, for example, F2 plants, backcross plants, Recombinant Innate Lines (RIL), Backcross Ingrained Lines (BIL) or Multiplied Haploid Lines (DHL), as well as a linkage map developed utilizing sub-atomic markers are presently the standard methodology for distinguishing QTL controlling quantitative quality. A huge populace size is expected to give adequate discovery power.

Progressed backcross QTL examination (Stomach muscle QTL): The high level backcross QTL investigation (Stomach muscle QTL) was proposed by Tanksley and Nelson (1996) to at the same time recognize and introgress positive alleles from unadapted benefactors into tip top foundation. The overall Stomach muscle QTL investigation is involved the accompanying trial stages:

- Creating a world class by contributor mixture,
- Backcrossing to the first class parent to deliver BC populace which is exposed to marker/or phenotypic determination against unwanted contributor alleles,
- Genotyping BC2 or BC3 populace with polymorphic atomic markers,
- Assessing the isolating BC F22 or BC F23 populace for qualities of interest and QTL investigation,
- Choosing objective genomic districts containing helpful giver alleles for the development of NILs in the first class hereditary foundation and,
- Assessment of the agronomic characteristics of the NILs and tip top parent controls in recreated conditions.

Introgression Lines (ILs): ILs is delivered by precise backcrossing and introgression of marker-characterized outlandish sections behind the scenes of first class assortments. Distinguishing QTL qualities utilizing ILs doesn't need linkage map development or refined factual examination for QTL, this is a more easy to understand technique for reasonable rearing projects and furthermore for natural science.

Utilitarian Markers: Markers connected to the QTL distinguished by linkage planning utilizing one or a couple of populaces might possibly be helpful in quality pyramiding on the grounds that various subsets of QTL will be polymorphic in every populace, and the linkage stages between the marker and QTL alleles can vary even between firmly related genotypes. The linkage stages likewise will in general be more predictable in the event that the wellspring of QTL is from a genetic stock which is exceptionally unmistakable from the one utilized by the reproducers. Accordingly, markers connected to novel alleles from fascinating germplasm or wild family members are bound to be effectively executed.

DISCUSSION

Further developed Tapaswini having four BB opposition qualities pyramided with six qualities/QTLs, obstruction/resilience to biotic and abiotic stresses in rice, [4]. Rice, a significant food crop, is filled in a large number of natural circumstances and experiences huge yield misfortunes as it is continually presented to a great many ecological and biotic burdens. The commonness of various biotypes/strains has required gathering of various obstruction qualities/QTLs into first class genotypes to give a more extensive size of opposition. The ongoing review reports fruitful pyramiding of qualities/QTLs that give resilience/protection from Submergence (Sub1), Saltiness (Saltol), impact (Pi2, Pi9) and nerve midge (Gm1, Gm4) to enhance the four bacterial scourge obstruction qualities (Xa 4, xa5, xa13, Xa21) present in superior Tapaswini, a world class cultivar. The exact exchange of qualities/QTLs was achieved through compelling closer view choice and reasonable quality pyramids were recognized. Foundation choice was worked on utilizing morphological and grain quality attributes to improve the recuperation of the intermittent parental genome.

In the bioassays, the pyramids showed more elevated levels of opposition/resilience against the objective anxieties. The original component of the review was effective pyramidization and exhibition of the capability of ten qualities/QTLs in another genotype. This achievement can animate a few such investigations to understand the maximum capacity of sub-atomic plant reproducing as the establishment for rice improvement.

Pyramiding of three bacterial curse opposition quality for wide range obstruction in profound water opposition assortment [5]. Jalmagna is a well-known deep-water rice assortment, great yield under waterlogged condition and the assortment is profoundly vulnerable to bacterial curse illness. The three significant BB obstruction qualities pyramided lines displayed elevated degree of opposition and are supposed to give solid opposition under profound water circumstance. High closeness in agro-morphologic characteristics. Nonattendance of opposing impacts for yield and different characters were seen in the best pyramided lines. Marker helped pyramiding of two earthy colored plant hopper opposition quality into world class rice cultivars.

Utilization of atomic markers in ID and portrayal of protection from rice impact in India [6]. Phenotyping of NRVs against leaf impact and atomic evaluating and hereditary variety for significant impact obstruction qualities will help in judicious utilization of these varieties. The current review gave an outline of the hereditary variety of the eighty rice assortments for leaf impact opposition. Moreover, the exact assessment of impact opposition qualities in rice assortments, and the marker loci acquired are exceptionally enlightening and proficient in the determination of parental lines and advancement of new rearing populace.

- The data got from the phenotypic response and hereditary fluctuation of the assortments will be especially helpful for legitimate determination of assortments in various impact inclined regions and could likewise be used in quality arrangement and quality pyramiding based on commonness of *M. oryzae* races.
- Moreover, a portion of the assortments had other impact obstruction qualities, could be utilized in planning of qualities and in the use of marker helped choice.
- Being adjusted to specific ecologies, and having coevolved with the nearby populace of the impact growth,

these safe assortments will be potentially taken advantage of which enjoy more upper hands over other unfamiliar opposition givers right now being utilized in the reproducing programs.

- Besides, these assortments have been reared with great agronomic attributes alongside various illness and bug opposition and abiotic stress resistance.

Impacts of pyramiding quantitative opposition qualities pi21, Pi34, and Pi35 on rice leaf impact sickness, [7]. Improvement of safe cultivars has been a successful strategy for controlling rice impact infection brought about by *Magnaporthe oryzae*. Quantitative impact opposition qualities might offer sturdy obstruction in light of the fact that the determination strain on *M. oryzae* to defeat obstruction is low because of the qualities' moderate weakness. Since the impacts of individual obstruction qualities are somewhat little, pyramiding these qualities in rice cultivars is a promising strategy. Here, we utilized close isogenic and backcross lines of rice cultivar Koshihikari with single-or two-quality mixes of impact opposition qualities (pi21, Pi34, and Pi35) to assess the concealment of leaf impact. The seriousness of the illness was evaluated all through the disease cycle. Opposition changed among the lines: Pi35 presented the most grounded obstruction, while Pi34 showed the most fragile impacts. Two sorts of joined quality connections were noticed, and they fluctuated based on quality blend and normal for the contamination:

- The mix of two obstruction qualities was more powerful than both of the qualities separately or
- The mix of two opposition qualities was like the level of the best obstruction quality in the pair. The best quality mix for the concealment of leaf impact was pi21+Pi35.

Marker-helped introgression of three predominant impact obstruction qualities into a fragrant rice cultivar [8]. Current high yielding rice assortments have supplanted the majority of the conventional cultivars in late past. Mushk Budji, is one such short grained landrace known for its fragrance and impeccable quality, in any case, is exceptionally powerless to impact sickness that has prompted significant decrease in its space. Mushk Budji was crossed to a triple-quality giver line, DHMAS 70Q 164-1b and completely finished marker-helped closer view and foundation choice in first and second backcross ages that assisted with consolidating impact opposition qualities Pi54, Pi1 and Pita. Marker-helped foundation determination was completed utilizing 78 SSR and STS markers that assisted with lessening linkage haul around the qualities Pi54, Pi1 and Pita to 2.74, 4.60 and 2.03 Mb, respectively. The three-quality lines in BC2F2:3 were genotyped utilizing 50 K SNP chip and uncovered over 92% genome comparability to the RP. 2-D gel measure recognized differentially communicating 171 protein spots among a bunch of backcross inferred lines, of which 38 spots showing match score of 4 assisted us with computing the proteome recuperation. The better lines communicated protection from impact under fake and regular field conditions.

CONCLUSIONS

- Molecular marker offer incredible breadth for working on the proficiency of traditional plant reproducing.
- Gene pyramiding may not be the most appropriate technique when numerous QTL with little impacts control the characteristics and other strategy, for example, marker helped repetitive determination ought to be thought of.
- With MAS based quality pyramiding. It is currently feasible for reproducer to lead many rounds of choice in the year.
- Gene pyramiding with marker innovation can coordinate into existing plant rearing programmed everywhere.
- This will assist reproducer with getting around issues connected with bigger rearing populace, replication in assorted conditions and accelerate the improvement of advance lines.
- As a future push improvement of programming for QTL planning and negligible populace necessity computation, planning of illness obstruction quality in significant harvests, distinguish the new assets of positive opposition qualities and advancement of stable/solid opposition assortments of Rice.

REFERENCES

1. Chu Z, Fu B, Yang H, Xu C, Li Z, et al. (2006a). Targeting xa13, a recessive gene for bacterial blight resistance in rice. *Theor. Appl. Genet*. 112: 455-461.

2. Ji ZJ, Yang SD, Zeng YX, Liang Y, Yang CD, et al. (2016). Pyramiding blast, bacterial blight and brown plant hopper resistance genes in rice restorer lines. *J. Integr. Agric*. 15: 1432-1440.

3. Khush GS, Mackill DJ and Sidhu GS (1989). Breeding rice for resistance to bacterial leaf blight. In: IRRI (ed) Bacterial blight of rice. IRRI, Manila, Philippines. 207-217.

4. Sundaram RM, Chatterjee S, Oliva R, Laha GS, Cruz LJE, et al. (2014). Update on Bacterial Blight of Rice: Fourth International Conference on Bacterial Blight. *Rice*. 7: 12.

5. International Rice Research Institute (2019). Rice knowledge Bank.

6. Zhou YL, Uzokwe VNE, Zhang CH, Cheng LR, Wang L, et al . (2011). Improvement of bacterial blight resistance of hybrid rice in China using the Xa23 gene derived from wild rice (*Oryza rufipogon*). *Crop. Prot*. 30: 637-644.

7. Chukwu SC, Rafii MY, Ramlee SI, Ismail SI, Oladosu Y, et al. (2019). Marker-assisted selection and gene pyramiding for resistance to bacterial leaf blight disease of rice (*Oryza sativa* L.). *Biotechnol. Equip*. 33: 440-455.

8. Ashkani S, Rafii MY, Shabanimofrad M, Ghasemzadeh A, Ravanfar SA, et al. (2016). Molecular progress on the mapping and cloning of functional genes for blast disease in rice (*Oryza sativa* L.): Current status and future considerations. *Crit. Rev. Biotechnol*. 36: 353-367.