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Werkissa Yali *

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Review Article

Gene Pyramiding and its Importance in Modern Plant Breeding

Werkissa Yali

Ethiopian Institute of Agricultural Research, Chiro National Sorghum Research and Training Center, Chiro, Ethiopia.

***Correspondence Author:** Werkissa Yali, Ethiopian Institute of Agricultural Research, Chiro National Sorghum Research and Training Center, Chiro, Ethiopia.

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Abstract

Gene pyramiding is a breeding technique that involves putting together many genes with known effects on the qualities of interest. Plant breeders are frequently interested in enhancing multiple quantitative traits at the same time, such as yield, quality, and resistance to both biotic and abiotic stressors. Gene pyramiding is a crop breeding strategy that can be used to introduce new lines in both conventional and advanced molecular breeding programs. Gene pyramiding is a significant crop improvement approach. Gene pyramiding has allowed several genes to be integrated into a single plant via MAS to meet the aims of biotic or abiotic stress resistance, greater yield, and desired nutritional quality. MAS has a number of advantages over traditional phenotypic selection in plant breeding programs. With the advancement of molecular genetics and allied technology like as MAS, a new discipline of plant breeding gene pyramiding has emerged. The goal of gene pyramiding is to create a better phenotype by merging favored alleles into an ideal genotype. Gene pyramiding is a technique for combining beneficial genes from numerous parents into a single genotype of a certain feature. In general, this review focuses on gene pyramiding and approaches for sustainable crop development that have been successfully implemented in modern agriculture.

Keywords: gene pyramiding; marker assisted selection; plant breeding; resistance

Introduction

Gene pyramiding is an essential germplasm improvement approach (Chukwu et al., 2019). Gene pyramiding is a technique for combining numerous favorable genes from different parents into a single genotype (Ye & Smith, 2008). It is a breeding approach that involves putting together several genes that have a known effect on the trait of interest. In this sector, genetics has had a significant role. Plant breeding has taken on a new dimension with the introduction of genetic engineering and biotechnology, allowing for the development of crop varieties with more desired characteristics. A genotype having all of the target genes is the ultimate result of a gene pyramiding scheme (Wu et al., 2018).

During plant breeding, gene pyramiding is the simultaneous selection and/or introduction of numerous genes (Jiang, 2013). Humans have been trying to improve crops by selecting for desired features since the dawn of agriculture. The green revolution has resulted in significant improvements in productivity and quality of essential food crops all over the world. It is primarily used to improve existing elite cultivars for a few undesirable qualities for which large-effect genes have been found (Zhang, et al., 2018).

The merging of two or more resistance genes is known as gene pyramiding. Gene pyramiding would be aided by determining allelic relationships among resistant sources (Castro et al., 2003). Resistance is more persistent since it takes more mutations in the pathogen population to overcome the host plant's resistance. Gene pyramiding has a better chance of achieving long-term tolerance to biotic and abiotic stressors in crops. Resistance is often conferred by various resistance genes to different isolates, races, or biotypes. Combining their resistance expands the number of races available or isolates multiple characters in a variation at the same time (Joshi et al., 2010).

MAS (marker-assisted selection) is a technique for quickly introducing desirable features into new cultivars (Endo et al., 2020). Molecular markers, or DNA tags, that have been linked to traits of interest are especially useful for incorporating genes that are highly affected by the environment, genes for disease and pest resistance, and gene pyramiding, which is the accumulation of multiple genes for disease and pest resistance within the same cultivar (Miah, et al., 2013). Marker-Assisted Pyramiding is a combination of pyramiding and marker-assisted selection (Hsu et al., 2020).

In general, in addition to the epistatic effect, the creation of pyramid lines is a time-consuming and costly process. MAS-based gene pyramiding, on the other hand, may make it easier to efficiently pyramid genes into a single genetic backdrop (Srivastava, 2019). Breeders must consider the minimal population size that must be examined in order to have a good chance of attaining the desired genotype during pyramiding. By minimizing the number of generations that breeders must analyze to guarantee they have the appropriate gene combination, molecular marker genotyping can help with the gene pyramiding process (Oladokun et al., 2019). Breeders must combine features from numerous parents to develop exceptional lines and variations, a process known as gene pyramiding or stacking. Molecular indicators aid in the selection of the finest plants to work with (Dormatey et al., 2020).

Objectives of gene pyramiding

Gene pyramiding aims to achieve the following goals:

1. Improving trait performance by combining two or more complimentary genes

2. Introgression of genes from other sources to compensate for deficiencies

3. Increasing disease resistance and/or disease durability

4. Increasing the genetic diversity of cultivars that have been released

Method of gene pyramiding

Crop breeding has advanced significantly in recent years, and with the arrival of new molecular techniques, precision breeding is now possible in the shortest possible time (Suet al., 2019).

Conventional approach

Plant cultivars and germplasm have been developed using traditional breeding methods with great success (Bhat et al., 2021). Using cycles of backcrossing, gene pyramiding, pedigree breeding, or recurrent selection to introduce novel traits into elite varieties, traditional breeding techniques generate genetic variants by recombination or untargeted mutagenesis (Ahmar et al., 2020).

Back cross breeding is the finest method among the various conventional approaches. Backcross breeding is the result of a cross between a hybrid (F1 or segregating generation) and one of its parents (Bhoi et al., 2019). The hybrid and future generations' progenies are routinely backcrossed to one of the F1 parents (Gramlich, et al., 2018). Backcrossing is a repeating process that breeders use to transfer a target allele from a donor variety to a popular cultivar; regrettably, it is slow and uncertain. It takes four years or more to breed a plant that carries the necessary donor allele but otherwise resembles the popular cultivar (Mundt, 2018).

Recurrent backcrossing is a breeding technique for incorporating one or a few desirable features into an elite variety with a high number of desirable qualities but just a few that are lacking (Hasan, et al., 2015). Backcrossing's goal is to transmit one or more genes of interest from the donor parent into the enhanced variety's genetic background and regain the recurring parent genome (RPG). During backcrossing, some undesirable genomic areas (gene drag) from the donor parent can move into the backcross progenies along with the target gene. Six to eight backcrossings are required to remove the linkage drag and recover the recurrent parent genome (Jamaloddin et al., 2020).

Molecular Marker Assisted Selection

Marker assisted gene pyramiding is a branch of marker assisted selection that is very essential. It's been used successfully in a number of plant breeding initiatives, the majority of which involved pyramiding disease resistance genes with the principal impacts (Gupta et al., 2010). By minimizing the number of generations that breeders must analyze to guarantee they have the appropriate gene combination, molecular marker genotyping can help with the gene pyramiding process (Chukwu et al., 2019).

Gene Pyramiding MAS-based gene pyramiding may make it easier to successfully pyramid genes into a single genetic background (Joshi et al., 2010). The practice of mixing two or more genes from several parents to generate elite lines and varieties is known as gene pyramiding or stacking (Francis et al., 2012). Pyramiding is the process of stacking numerous genes, resulting in the expression of multiple genes at the same time in a number of organisms (Manyangarirwa et al., 2006).

Backcross breeding relies heavily on molecular markers to stack two or more genes linked to biotic stress resistance (Dormatey et al., 2020). MAS (marker-assisted selection) is a technique for quickly introducing desirable features into new cultivars. Molecular markers, or DNA tags, that have been linked to traits of interest are especially useful for incorporating genes that are highly affected by the environment, genes for disease and pest resistance, and gene pyramiding, which is the accumulation of multiple genes for disease and pest resistance within the same cultivar (Babuet al., 2004).

With the creation and availability of an array of molecular markers and dense molecular genetic maps in agricultural plants, marker assisted selection (MAS), which involves indirect selection of traits by picking the marker associated to the gene of interest, has become a reality (Lema, 2018). Resistance to diseases, insects, and nematodes, tolerance to abiotic stresses, quality criteria, and quantitative features are only a few of the agronomic traits that can benefit from molecular markers (Dormatey et al., 2020).

Gene pyramiding is one of the most important applications of DNA markers in plant breeding. Molecular markers are extremely useful for pinpointing genotypes that possess the stacked desirable genes (Chukwu et al., 2019). By selecting for two or more genes at a time, marker-assisted gene pyramiding (MAGP) has been proposed and used to improve disease and pest resistance (Quang et al., 2004). In comparison to conventional breeding, which takes at least six generations to recover 99.2 percent of the recurrent parent genome, gene stacking or pyramiding is a useful technique for transferring several desired genes or QTLs from different parents into a single genotype in the shortest possible time (two to three generations) (Collard et al., 2008).

Importance of the Gene Pyramiding Technique to Agricultural Sustainability.

In agricultural research, the word "gene pyramiding" refers to a breeding strategy for pest control and improved crop yields (Taverniers et al., 2008). Gene pyramiding is most commonly employed to increase qualitative features like disease resistance and insect resistance (Ashkani et al., 2015). Using the technique of gene pyramiding, which allows the breeder to insert more than one resistance gene into one genotype, plant breeders can increase the diversity of resistance genes as well as introduce numerous genes from different sources into cultivars (Cveji et al., 2020).

The process of gene pyramiding has made a significant contribution to modern agriculture. It has resulted in the development of disease, insect pest, and abiotic stress tolerance in plants, as well as increased output on a long-term basis (Bharadwaj, 2016). The goal of gene pyramiding is to create an ideal genotype that is homozygous for the beneficial alleles at all n-loci. Molecular markers aid in the selection of the finest plants to work with. Biological challenges such as bacterial blight, gall midge, and blast, as well as abiotic factors such as submergence and salt, have a significant impact on their productivity over the world (Joshi et al., 2010).

To ensure long-lasting resistance for sustainable crop production, modern breeding approaches focus on pyramiding many genes or QTLs into a single genotype (Nelson et al., 2018). The goal of a gene pyramiding technique is to combine genes that have been found in many parents into a single genotype. The use of DNA markers accelerates the pyramiding process by allowing comprehensive gene identification of the progeny at each generation (Langridge & Fleury, 2011). Gene pyramiding, in general, tries to create an ideal genotype that is homozygous for the favorable alleles at all loci. A marker-based breeding technique lowers phenotyping, provides more effective alternatives for controlling linkage drag, allows for the pyramiding of genes with very comparable phenotypic effects, and shortens breeding time (Jiang, 2013). For inbred line breeding aimed at improving qualities controlled by key genes, marker-based gene pyramiding is now the approach of choice (Ye & Smith, 2008). When breeding disease-resistant cultivars, the technique of gene pyramiding (i.e., introducing many disease-resistance genes into one genotype) can be used to lengthen the lifespan of new cultivars (Dormatey et al., 2020).

Gene pyramiding is the process of introducing multiple particular genes into a single plant (Chukwu et al., 2019). Plant breeders may seek to introduce a lot of genes for conferring resistance to different races of a disease into a cultivar since infections come in different races. This technique works in locations where plant breeding is centralized and where the production region that uses the cultivar with multiple resistance genes is separated from the rest of the country (Miah et al., 2013). The success of the latter technique would be harmed if single resistant gene cultivars were released alongside multiple gene cultivars at the same time (Scheben et al., 2017).

Conclusion

Gene pyramiding is a technique for combining several favorable genes from different parents into a single genotype. Modern plant breeding, which is based on inheritance principles, has become one of the most significant aspects of agricultural science and technology. The fundamental technique for successful gene pyramiding is to combine all of the elite genes from several parents into a single genotype. Gene pyramiding is an essential germplasm improvement approach. By minimizing the number of generations that breeders must analyze to guarantee they have the appropriate gene combination, molecular marker genotyping can help with the gene pyramiding process.

Gene pyramiding with marker technology can be integrated into existing plant breeding programs around the world, allowing researchers to access, transfer, and mix genes at a speed and precision never before imaginable. Gene pyramiding is an essential germplasm improvement approach. By minimizing the number of generations that breeders must analyze to guarantee they have the appropriate gene combination, molecular marker genotyping can help with the gene pyramiding process.

Conflicts of Interest:

There are no conflicts of interest declared by the authors.

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