



Gene Pyramiding: Durable Resistance in Crop Plants

(*Ravi Kishan Soni)

Research Scholar, College of Agriculture, Ummedganj (Agriculture University, Kota)

* soniravikishan@gmail.com

Gene pyramiding is the simultaneous selection for and/or introduction of multiple genes during plant breeding. The concept of gene pyramiding was first described by Watson and Singh (1953). Gene pyramiding is a standard breeding approach for combining several desirable genes/QTLs from multiple parents into a single genotype for a specific/multiple trait. A pyramid could be constructed with major genes, minor genes, defeated genes, effective genes, ineffective genes, race-specific genes, non-race specific genes or any other type of host gene that confers resistance.

Aim

- Improving trait performance by combining two or more complementary genes.
- Introgression of genes from other sources to correct for deficiencies.
- Increasing the durability of disease and/or disease resistance.
- Increasing the genetic diversity of cultivars that have been released.

Assumptions

- The locations of a group of genes of interest (target genes) as well as their linkage relationship are known.
- The genotype with favourable alleles at all loci of interest is specified as the target genotype for these genes prior to selection.
- These genes or markers associated to them can be used to determine an individual's genotype.
- There should be a collection of lines available that contain all of the target genes.

Types of Gene Pyramiding

Conventional technique

Genes are deployed in same plant one after other through Pedigree breeding (Cross between Resistant parents followed by continues selfing and selection) or Backcrossbreeding (repeated crossing between different resistant parents and elite genotype up to certain generation followed by selfing and selection) or Recurrent selection (intermitting and selection).

Disadvantages of Conventional Methods

- Minor gene phenotyping is difficult.
- The success of gene pyramiding is hampered by the inheritance model of the genes for the target traits, linkage, and/or pleiotropism between the target trait and other traits.
- The effect conferred by a recessive gene cannot be evaluated on heterozygous individuals and progeny testing is required.
- Linkage drag is unavoidable.

Molecular technique: Marker Assisted Gene Pyramiding

Phenotypic screening with indirect selection of diverse features is aided by the use of DNA markers that are firmly connected to target loci. Accelerating the process of conventional breeding and facilitating the improvement of attributes. MAS (marker-assisted selection) is a technique for quickly introducing desirable features into new cultivars. The goal of a gene pyramiding technique is to combine genes that have been found in many parents into a single genotype. In general, the gene pyramiding tries at the derivation of an ideal genotype that is homozygous for the desirable traits at all the loci.

Factors Affecting Gene Pyramiding

- (1) Population size: Muller (1923) and Sedcole (1977) proposed to use the equation: $N = \log_e(1-P)/\log_e(1-f)$. Where, N = Minimum population size, P = Desired probability of success (e.g. 99%, 95%, 90%), f = Frequency of the event (i.e., an individual plant having all desired alleles).
- (2) The number of genes and their combinations.
- (3) Phenotyping accuracy at the individual level
- (4) Inheritance model of the genes for the target characteristics, linkage and/or pleiotropism between the target characteristics and other characteristics.
- (5) Hybridization efficiency
- (6) Reproductive characteristics, a breeder's abilities to identify the desired genotypes, operating capital and interaction with foreign genes and its own genotype.

Fixation of pyramided genotype

A proposed approach for the fixation steps is to generate a population of doubled haploids (DH) from the root genotype. The genotypes are used to create a population of gametes, and their genetic material is doubled. As a result, there is a population of totally homozygous people in which the ideotype can be detected. After obtaining the root genotype, the optimal genotype may be produced in just one extra generation using this method. In other plant species, however, establishing a large population of DH is difficult and time-consuming. A possible alternative to this method is to self the root genotype directly to obtain the ideal genotype. Selfing the root genotype, on the other hand, will result in linkage breaks between the desired alleles, which will be difficult to detect because the linkage phase is rarely observable in selfed populations. As a result, it may cover too many generations, causing the gene pyramiding scheme to be stretched. Another alternative to all this methods would be to obtain a genotype carrying all advantageous alleles in coupling by crossing the root genotype with a parent containing none of the alleles. This confirms that the linkage phase of the offspring is known and the genotype can be derived without any mixing. The ideal genotype will be reached within two generations after the root genotype.

However, instead of crossing with a blank parent, a more simplified method would be to cross the root genotype with one of the founding parents. The linkage will still be known in such programmes, and genotypes that are homozygous for the target gene brought by the founding parent but heterozygous for other regions will be selected. The targeted genes do not need to be fixed afterwards, enhancing the chances of obtaining the optimum genotype. Backcross gene pyramiding with markers is referred to as marker assisted backcross gene pyramiding. This is by far the most widely acknowledged and effective form of gene pyramiding.

Benefits of Gene Pyramiding:

1. This method is widely used to combine several disease resistance genes for certain pathogen races.
2. Using traditional approaches, pyramiding is incredibly difficult to achieve.

3. Recognize phenotyping a single plant for different forms of seedling resistance almost impossible.
4. It's critical to cultivate 'durable' illness resistance against many races.
5. Improve existing elite cultivar.
6. Reduces extensive phenotyping.
7. Linkage drag can be controlled.
8. Reduces breeding duration.

Achivements

Crops	Crops Traits	Pyramided Genes
Rice	Blight resistance	Xa4, xa5, xa13, Xa21, Xa 5, Xa13 and Xa21
	Blast resistance	Pi(2)t, Piz5, Pi(t)a
	BPH resistance	Bph1 and Bph2
Wheat	Multiple resistance	Bacterial blight (Xa21), Sheath b light (RC7), Yellow stem borer Btfusiongene (cry1AB /cry1Ac)
	Leaf rust resistance	Lr41, Lr42, Lr43
	Aphid resistance	Gn2 and Gn4
	Cereal cyst nematode	CreX and CreY
Cotton	Insect pest resistance	Cry 1Ac, Cry 2Ac
	Bacterial and Sheath blight	chi11, tlp and Xa21
Pea	Nodulation ability	Sym9, Sym10
Barley	YMV resistance	rym4, rym5, rym9, rym11
	Stripe rust resistance	3 QTL
Soybean	SMV resistance	Rsv1, Rsv3, Rsv4
Potato	Late blight	R3a, R3b, R4, and Rpi- Smira1
Tobacco	Many plant viruses, RKN, TWF, BRR &fusarium wilt.	EN +N'

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