

Gene Pyramiding Through Marker Assisted Backcross Method

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SUMMARY

The gene pyramiding through MABC technique has contributed enormously to modern agriculture. It has led to tolerance development in plants for diseases, insect pests, and abiotic stresses and productivity enhancement on a sustainable basis. Molecular marker genotyping can facilitate the gene pyramiding process by reducing the number of generations that breeders must evaluate to ensure they have the desired gene combination. Despite the tremendous advancement of gene pyramiding, there are still challenges that need to be addressed to improve its implementation and vast impact. Gene pyramiding through MABC should be cost effective, and technical collaboration and financial support make this more viable for developing countries to use for improvement of their local germplasm.

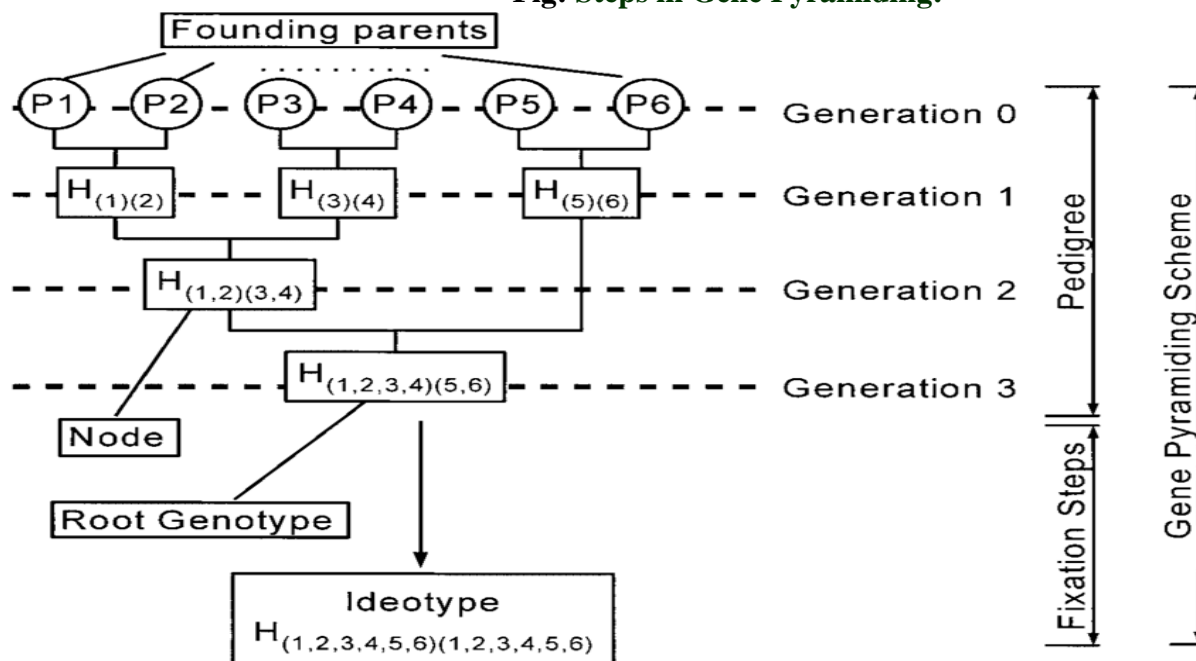
INTRODUCTION

In modern agriculture, conventional crop-breeding techniques alone are inadequate for achieving the increasing population's food demand on a sustainable basis. Thus, to meet the increasing food demand, smart and rapid crop-breeding tools are required to simultaneously improve multiple agronomic and nutritional traits. The advancement of molecular genetics and related technologies are promising tools for the selection of new crop species. Gene pyramiding through marker-assisted selection (MAS) and other techniques has accelerated the development of durable resistant/tolerant lines with high accuracy in the shortest period of time for agricultural sustainability.

What is Gene Pyramiding?

Gene pyramiding is defined as a method aimed at assembling multiple desirable genes/QTLs from multiple parents into a single genotype for specific/multiple trait through conventional breeding (Xu *et al.*, 2012).

Fig: Steps in Gene Pyramiding:



Steps in Gene Pyramiding:

- Founding parents
- Node genotype
- Root genotype
- Ideotype
- Fixation step

Objectives of Gene Pyramiding Scheme:

- Enhancing trait performance by combining two or more complementary genes.
- Remedying deficits by introgression genes from other sources.
- Increasing the durability of disease resistance.
- Broadening the genetic basis of the released cultivar.
- Genotype building.

Different Level of Selection:

- Foreground Selection
- Recombinant Selection
- Background Selection

Practical Application:

- For trait which is simply inherited but difficult to phenotype.
- For quantitative trait for which major contributing genes identified already.
- For genes which have very similar phenotypic effect.
- Necessary to cumulate & fix the target gene rapidly.

Case Study

Varshney *et al.* (2016) transferred “QTL-hotspot” containing quantitative trait loci (QTL) for several root and drought tolerance traits in chickpea (*Cicer arietinum* L.) through MABC into JG 11 (leading variety in India) from the donor parent ICC 4958. Foreground selection with up to three SSR markers and background selection with up to ten AFLP primer combinations was undertaken. Root trait phenotyping of ILs showed higher rooting depth (RDp) in all 29 ILs, better root length density (RLD) in 26 ILs, and higher root dry weight (RDW) as compared to the recurrent parent, JG 11.

Yadawad *et al.* (2017) introgressed two leaf rust resistance genes, Lr24 and Lr28 in bread wheat variety DWR 162 by Marker Assisted Backcrossing (MABC). The near isogenic line of PBW 343 was used as a donor. The MABC approach employed one SSR marker, Xwmc313 and one SCAR marker SCS421 with its locus linked to Lr28 and two SCAR markers, SCS719 and SCS 1302 linked to Lr24 for foreground selection to select plants carrying Lr24 and Lr28 genes. Marker assisted background selection and field evaluation of BC2F2 plants revealed high yield potential of selected plants along with leaf rust resistance and no yield penalty was apparent.

Goswami *et al.* (2018) reported the improvement of an elite QPM inbred, HKI1128Q of maize (*Zea mays* L.) for proA using marker-assisted introgression of crtRB1 favourable allele. Severe segregation distortion for crtRB1 was observed in BC1F1, BC2F1 and BC2F2. Background selection by 100 SSRs revealed mean recovery of 91.07% recurrent parent genome varying from 88.78% to 93.88%. Introgressed progenies possessed higher mean β carotene (BC: 9.22 μ g/g), β -cryptoxanthin (BCX: 3.05 μ g/g) and provitamin A (proA: 10.75 μ g/g) compared to HKI1128Q (BC: 2.26 μ g/g, BCX: 2.26 μ g/g and proA: 3.38 μ g/g).

Shasidhar *et al.* (2020) used MABC in groundnut (*Arachis hypogaea* L.) to improve three popular Indian cultivars (GJG 9, GG 20, and GJGHPS 1) for foliar disease resistance (FDR) and high oleic acid content. A total of 22 BC3F4 and 30 BC2F4 introgression lines (ILs) for FDR and 46 BC3F4 and 41 BC2F4 ILs for high oleic acid were developed. Phenotyping of these ILs revealed FDR scores comparable to the resistant parent, GPBD 4, and ILs with high (~80%) oleic acid in addition to high genome recovery.

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