



Enhancing Groundnut Resilience: Marker-Assisted Backcrossing for Foliar Disease Resistance in TMV 2 Peanut Variety

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Groundnut (*Arachis hypogaea* L.), a vital oilseed crop, suffers significant yield losses due to foliar diseases like late leaf spot (LLS) and rust. The conventional TMV 2 peanut variety, though popular for its quality and adaptability, is highly susceptible to these diseases. Recent advancements in marker-assisted backcrossing (MABC) have enabled the precise introgression of disease resistance traits. This article presents the application of MABC to develop LLS- and rust-resistant backcross lines in TMV 2 using donor GPBD 4. The successful deployment of SSR markers linked to resistance QTLs and field-based validation led to the development of promising lines with superior yield and disease resistance. The integration of molecular markers with traditional breeding offers a powerful path to sustainable groundnut improvement in the face of climate and disease challenges.

Keywords: Groundnut, marker-assisted backcrossing, late leaf spot, rust resistance, TMV 2, GPBD 4, molecular breeding, peanut improvement.

Introduction

Groundnut, an essential oilseed crop globally and in India, is cultivated over 25 million hectares with an annual production of approximately 45 million tonnes (FAOSTAT, 2016). It is not only a significant source of edible oil but also provides protein-rich food and income to millions of smallholder farmers. However, the productivity of groundnut is severely constrained by foliar fungal diseases, notably late leaf spot (LLS) caused by *Phaeoisariopsis personata* and rust caused by *Puccinia arachidis*. These diseases, often occurring together, can lead to yield losses exceeding 70% (Subrahmanyam et al., 1984). Among the popular groundnut cultivars in India, TMV 2 is widely grown for its uniform kernels, premium oil quality, and adaptability across regions. Yet, its high susceptibility to foliar diseases has limited its long-term viability. The integration of molecular markers with backcross breeding offers a solution to improve TMV 2's disease resistance without compromising its desirable agronomic traits.

The Role of Marker-Assisted Backcrossing in Groundnut Breeding

Marker-assisted backcrossing (MABC) enables the targeted transfer of specific genetic regions (quantitative trait loci or QTLs) associated with desired traits from a donor genotype to an elite recipient background. In this case, the donor GPBD 4, known for its high resistance to LLS and rust, was used to improve TMV 2 through MABC.

This approach accelerates breeding cycles and enhances precision by:

- **Foreground selection:** Screening for disease resistance genes using SSR markers.
- **Background recovery:** Ensuring the recipient genotype's genome is largely retained.
- **Field evaluation:** Confirming resistance and agronomic performance under disease pressure.

Genetic Basis of Resistance

Two major QTL regions controlling resistance were identified:

- **A03 chromosome:** Conferring 67.98% resistance to LLS and 82.62% to rust.
- **A02 chromosome:** Contributing an additional 62.34% resistance to LLS (Kolekar et al., 2016).

Markers such as GM2009, GM2079, GM2301, GM1839, and IPAHM103 were tightly linked to these regions and used for genotypic selection throughout the breeding program.

Materials and Methods: The Breeding Strategy

Between 2012 and 2015, the researchers crossed TMV 2 (recurrent parent) with GPBD 4 (donor parent) and carried out three cycles of backcrossing. A combination of PCR-based marker analysis and phenotypic screening was used to identify lines carrying resistance alleles.

The breeding scheme included:

- Development of F1, BC1F1, BC2F1, and BC3F1 populations.
- Foreground selection using SSR markers for resistance.
- Evaluation under disease epiphytotic conditions created using the spreader row technique.
- Assessment of disease scores (1–9 scale) and yield traits.

Results and Selection of Superior Lines

The breeding program successfully identified several lines that exhibited strong resistance and yield gains. Notable findings included:

- **TMG-29 and TMG-46**, advanced backcross lines (BC1F4), exhibited a **disease score of 3.0** for both LLS and rust compared to 7.0 and 8.0 in TMV 2.
- These lines recorded **71.0% and 62.7% higher pod yield**, respectively, over TMV 2.
- Superior lines like **TMG-22-1, TMG-32-19, and TMG-51-2** in F4 generation also demonstrated improved disease resistance and yield.
- Field traits like **shelling percentage, test weight, and kernel quality** were retained or improved in these lines.
- Morphologically, these backcross lines maintained the **erect growth habit and uniform pod appearance** typical of TMV 2.

Molecular Validation and Genetic Recovery

The backcross lines were screened for the presence of donor alleles at the targeted loci:

- **TMG-29 and TMG-46** carried resistant-type alleles at all five SSR marker loci.
- Additional lines like **TMG-48 and TMG-49** had partial allele matches but showed intermediate resistance.

Advanced genotyping (unpublished ddRAD-Seq data) revealed that TMG-46 shared 99.99% genomic similarity with TMV 2, confirming the successful recovery of the recurrent parent's background with added disease resistance.

Implications for Breeding and Cultivar Development

The success of this program demonstrates that **MABC is a viable and efficient strategy** for improving elite but disease-susceptible varieties like TMV 2. Benefits include:

- **Retention of consumer-preferred traits** such as pod quality and taste.
- **Reduction in chemical fungicide use**, supporting environmental sustainability.
- **Genetic uniformity**, ensuring ease of varietal adoption by farmers.
- Enhanced potential for **multilocation release**, with the lines currently undergoing national evaluation.

Comparative Insights from Other Studies

Similar efforts in groundnut and other crops confirm MABC's effectiveness:

- Varshney et al. (2014) improved rust resistance in **ICGV 91114, JL 24, and TAG 24**.
- Pasupuleti et al. (2016) enhanced both foliar disease resistance and oleic acid content.
- Simpson et al. (2003) reported nematode resistance through MAS in peanut.

These studies collectively suggest that molecular breeding is becoming a mainstream approach for crop improvement, especially for complex traits influenced by multiple genes.

Future Prospects and Recommendations

The successful development of resistant TMV 2 lines through MABC opens new opportunities:

- **Genome-wide selection** and **marker-assisted recurrent selection (MARS)** could be integrated to improve complex traits like drought tolerance.
- **High-throughput genotyping platforms** and **next-generation sequencing** can further accelerate breeding cycles.
- **Integration with speed breeding** and **digital phenotyping** could cut generation times and improve selection efficiency.
- **Participatory varietal selection (PVS)** involving farmers can enhance adoption and feedback-driven improvement.

Conclusion

The integration of marker-assisted backcrossing with traditional breeding methodologies has demonstrated immense potential for developing foliar disease-resistant peanut lines. The improved TMV 2 derivatives—TMG-29 and TMG-46—represent a breakthrough in sustaining productivity, enhancing resilience, and maintaining consumer acceptance in groundnut cultivation. As climate and disease challenges intensify, molecular breeding stands out as a vital tool for ensuring food and economic security for millions of farmers worldwide.

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