



RESEARCH COMMUNICATION

Inheritance pattern of imazethapyr tolerance in rice F_2 and backcross progenies derived from KMP-175 $\times$ Robin

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Received: 29 March 2026; Accepted: 05 June 2026; Available online: Version 1.0: 04 August 2026

Cite this article: Pallavi M, Deepak CA, Maruthi PBP, Spoorthi SR, Sanketh AU, Sandesh GM, Jeevan S, Anil KR. Inheritance pattern of imazethapyr tolerance in rice F_2 and backcross progenies derived from KMP-175 $\times$ Robin. Plant Science Today. 2026; 13(sp5): 1-6. <https://doi.org/10.14719/pst.14761>

Abstract

Herbicide tolerance is an essential trait for efficient weed management in direct-seeded rice systems (DSR), where early weed competition severely reduces crop establishment and productivity. The present study aimed to elucidate the inheritance pattern of imazethapyr tolerance in rice using F_2 and backcross populations derived from the cross KMP-175 $\times$ Robin. Segregating populations were evaluated under field conditions following imazethapyr application at 20 and 30 days after sowing (DAS). In the F_2 population, 314 tolerant and 99 susceptible plants were recorded among 413 individuals, fitting the expected 3 : 1 Mendelian segregation ratio ($\chi^2 = 0.23$, $p = 0.63$), indicating single gene control. The BCP₁ population segregated into 67 tolerant and 61 susceptible plants, conforming to the expected 1 : 1 ratio ($\chi^2 = 0.28$, $p = 0.59$), whereas all 95 plants in the BCP₂ population exhibited tolerance. The segregation pattern across generations supports that imazethapyr tolerance in Robin is governed by a single dominant gene. Molecular validation using the RM6844 marker linked to the *AHAS* gene further supports this inheritance pattern. The monogenic dominant nature of the trait enables efficient selection and rapid introgression into elite cultivars. These findings provide a strong genetic basis for developing herbicide-tolerant rice cultivars suitable for direct-seeded production systems.

Keywords: *AHAS* gene; herbicide tolerance; imazethapyr; monogenic inheritance; rice breeding; direct-seeded rice

Introduction

Rice is a major staple crop for a large proportion of the global population and sustaining its productivity is increasingly challenging under conditions of labour scarcity, declining water availability and rising production costs. In this context, direct-seeded rice (DSR) has emerged as a promising alternative to conventional transplanted rice because it reduces labour and water requirements, shortens crop establishment time and improves operational efficiency (1, 2). Despite these advantages, weed infestation remains a major constraint in DSR systems, as the absence of standing water and reduced crop-weed competitive advantage during early growth stages favour heavy weed emergence (3). Severe weed competition in DSR can cause substantial grain yield losses, making effective weed management essential for the sustainability and profitability of this production system (1, 4).

Among the available weed management options, chemical control through herbicides is widely regarded as one of the most practical and economical approaches in DSR ecosystems (5). Imidazolinone herbicides are important due to their broad-spectrum control of grasses, sedges and broad-leaved weeds through inhibition of acetohydroxy acid synthase (AHAS), a key enzyme in the biosynthesis of branched-chain amino acids (6, 7). Herbicide tolerance to imidazolinones is generally associated with point mutations in the *AHAS* gene that reduce herbicide binding

without severely affecting normal enzyme activity. Such mutations have been identified and utilised in several crop species, including rice, wheat, maize, sunflower and canola, thereby enabling the development of herbicide-tolerant production systems (6, 8).

Understanding the inheritance of herbicide tolerance is important for its effective use in crop improvement programmes. When tolerance is governed by a single major gene, particularly with dominant or semi-dominant expression, the trait can be transferred more efficiently into elite cultivars through conventional breeding and marker-assisted backcrossing. Previous studies in rice and other crops have shown that tolerance to AHAS-inhibiting herbicides is frequently controlled by one major gene, which greatly facilitates selection in segregating generations and accelerates varietal development (6, 9, 10). Nevertheless, the inheritance pattern of herbicide tolerance must be validated in each breeding material and cross combination, as such information is critical for confirming gene action and designing an appropriate breeding strategy.

Despite the availability of herbicide-tolerant rice cultivars, the inheritance pattern of imazethapyr tolerance varies depending on genetic background and mutation type. Understanding gene action in specific crosses is critical for designing efficient breeding strategies and marker-assisted selection. However, limited information is available on the inheritance of imazethapyr tolerance in Indian rice germplasm, particularly involving locally adapted varieties such as

KMP-175. Therefore, elucidating the inheritance pattern of herbicide tolerance in this genetic background is essential for developing improved cultivars suitable for DSR ecosystems.

This study examines the inheritance pattern of imazethapyr tolerance in rice using F_2 and backcross progenies derived from KMP-175 $\times$ Robin. The objective was to determine segregation behaviour and infer genetic control through Mendelian analysis. Such information will be valuable for the effective incorporation of herbicide tolerance into breeding programmes aimed at improving weed management in direct-seeded rice under practical production conditions.

Materials and Methods

Plant materials and population development

The experimental material for the present study comprised two rice genotypes contrasting in their response to imazethapyr, namely Robin, a herbicide-tolerant mutant genotype and KMP-175, a herbicide-susceptible genotype. The parental lines were phenotypically confirmed for imazethapyr response by applying imazethapyr 0.4 % SL at 20 and 30 days after sowing (DAS). Genotypic validation was carried out using the RM6844 marker linked to the *AHAS* gene to confirm polymorphism between the tolerant and susceptible parents. The cross KMP-175 $\times$ Robin was made to generate segregating populations for inheritance analysis.

The F_1 plants were confirmed for hybridity using the *AHAS* gene-linked molecular marker RM6844 (Supplementary Fig 1). Genomic DNA was isolated using standardised CTAB method (11) from young leaf samples of the parents and F_1 plants and polymerase chain reaction (PCR) amplification was carried out using RM6844 primers. Only F_1 plants showing a heterozygous banding pattern were considered confirmed hybrids.

The confirmed F_1 plants were selfed to produce the F_2 population and backcrossed with both parents to generate backcross populations. Backcrossing with KMP-175 produced the BCP₁ population, while backcrossing with Robin produced the BCP₂ population. These generations were used for inheritance analysis of imazethapyr tolerance.

Screening for imazethapyr tolerance

The parental lines, F_1 , F_2 , BCP₁ and BCP₂ populations were evaluated for response to imazethapyr under field conditions. All generations were raised under recommended agronomic practices and screened with imazethapyr 0.4 % at 20 and 30 DAS. Herbicide response was assessed based on visible injury symptoms such as chlorosis, growth suppression and plant mortality. Plants were classified as tolerant or susceptible 20 days after the first herbicide application (12).

Segregation analysis

The segregation pattern of herbicide tolerance was analysed in the F_2 and backcross populations based on phenotypic classification of plants as tolerant or susceptible after herbicide screening. The observed segregation was tested against the expected Mendelian ratios using the chi-square (χ^2) test, with the F_2 population evaluated against the expected 3 : 1 ratio for a single dominant gene and the backcross populations evaluated against the expected ratios based on the assumed mode of inheritance.

The goodness-of-fit was assessed using chi-square analysis following standard procedures (13). Degrees of freedom were calculated as number of classes-1 and probability values were determined at 5 % significance level.

The chi-square value was calculated as:

$$\chi^2 = \sum \frac{(O-E)^2}{E}$$

Where, O is the observed frequency and E is the expected frequency. Calculated chi-square values were compared with tabulated values at the appropriate degrees of freedom to assess the goodness-of-fit and infer genetic control.

Results

Phenotypic confirmation and genotypic validation of parental lines

Phenotypic screening of the parental lines following application of imazethapyr 0.4 % at 20 and 30 DAS clearly differentiated the two genotypes for herbicide response. Robin exhibited tolerance with normal growth and survival after herbicide application, whereas KMP-175 showed susceptibility, characterised by severe herbicide injury and plant mortality (Fig. 1a).

Genotypic validation using the RM6844 marker linked to the *AHAS* gene also revealed clear polymorphism between the parental lines (Fig. 1b). Robin amplified a band of 200 bp, whereas KMP-175 produced a band of 160 bp. The contrasting marker pattern between Robin and KMP-175 supports their genetic differentiation at the *AHAS*-linked region and justifies their use as tolerant and susceptible parents for inheritance analysis. Similar use of molecular markers linked to the *AHAS* gene for identifying herbicide tolerance has been reported in rice and other crops (6, 7, 10).

Confirmation of F_1 hybridity using RM6844 marker

The F_1 plants derived from the cross KMP-175 $\times$ Robin was confirmed for hybridity using the *AHAS* gene-linked molecular marker RM6844. The true F_1 plants showed the presence of both parental bands (160 bp and 200 bp), confirming their heterozygous nature. Thus, the RM6844 marker effectively validated the hybridity of the F_1 plants and confirmed their suitability for further development of F_2 and backcross populations (10).

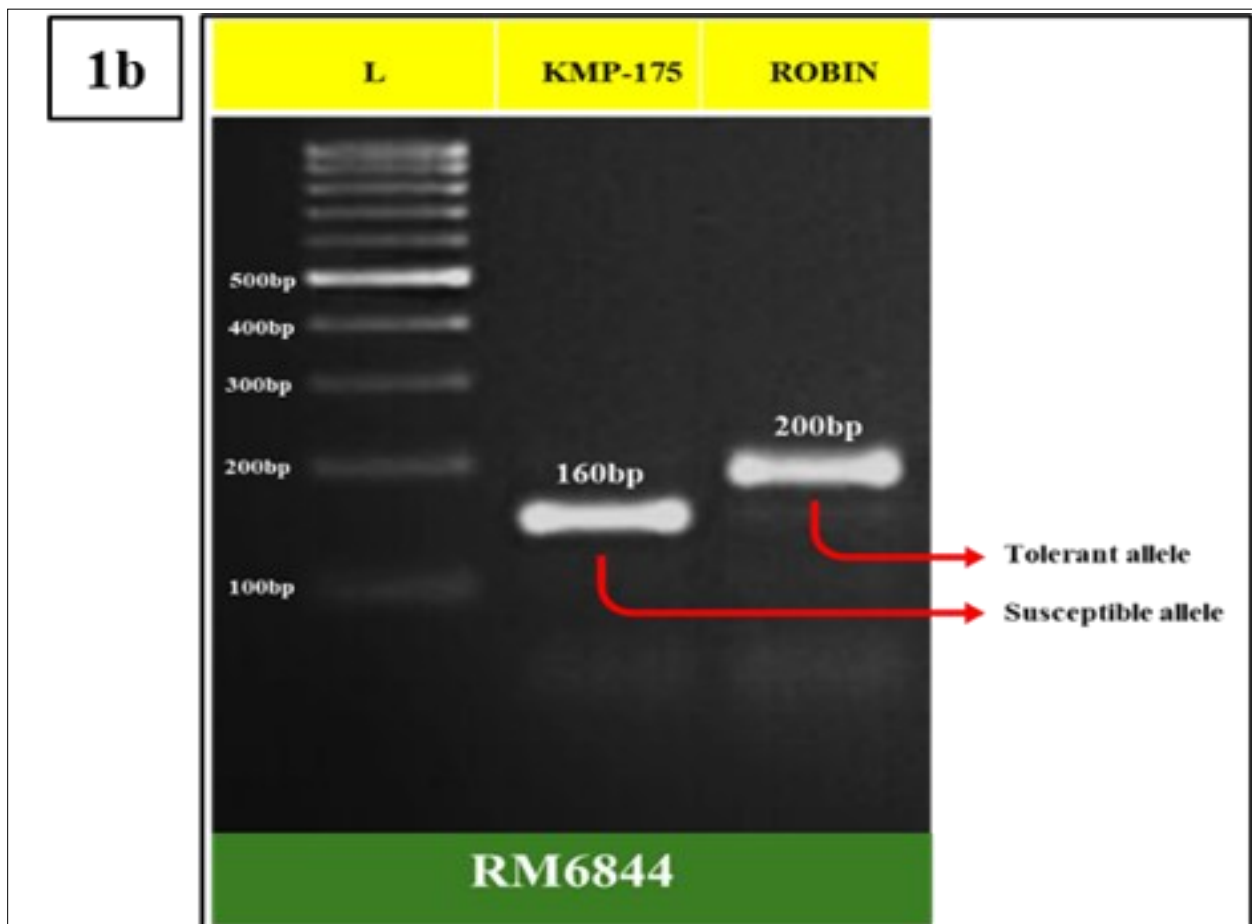
Segregation analysis of imazethapyr tolerance in F_2 and backcross populations

Clear segregation for imazethapyr tolerance was observed in the F_2 population derived from KMP-175 $\times$ Robin (Fig. 2, 3a, b). Among 413 plants screened, 314 exhibited tolerances, while 99 were susceptible. The observed segregation closely fitted the expected 3 : 1 ratio, suggesting monogenic dominant inheritance. The non-significant chi-square value further supports that the deviation from expected ratio was due to random variation (Table 1, Fig. 2). These results suggested that herbicide tolerance in Robin is controlled by a single dominant gene.

In the BCP₁ population ($F_1 \times$ KMP-175), 67 individuals were tolerant and 61 were susceptible out of 128 screened. The segregation pattern was tested against the expected 1 : 1 ratio and the chi-square value of 0.281 with a p -value of 0.596 indicated a good fit to the expected ratio (Table 1). In the BCP₂ population derived from the cross $F_1 \times$ Robin, all 95 plants screened were found to be

Table 1. Segregation of imazethapyr tolerance in the F₂ and backcross population derived from KMP-175 × Robin

Population	Total plants screened	Observed tolerant	Observed susceptible	Expected	Expected tolerant	Expected susceptible	X ² value	p value	Interpretation
F ₂	413	314	99	3 : 1	309.75	103.25	0.233	0.630	Fits 3 : 1 ratio
BCP ₁ (F ₁ × KMP-175)	128	67	61	1 : 1	64.00	64.00	0.281	0.596	Fits 1 : 1 ratio
BCP ₂ (F ₁ × Robin)	95	95	0	All tolerant	95.00	0.00	0.000	1.000	All plants tolerant as expected

**Fig. 1a.** Phenotypic response of parental plants to imazethapyr application.**Fig. 1b.** Molecular validation of imazethapyr tolerance using RM6844 marker.

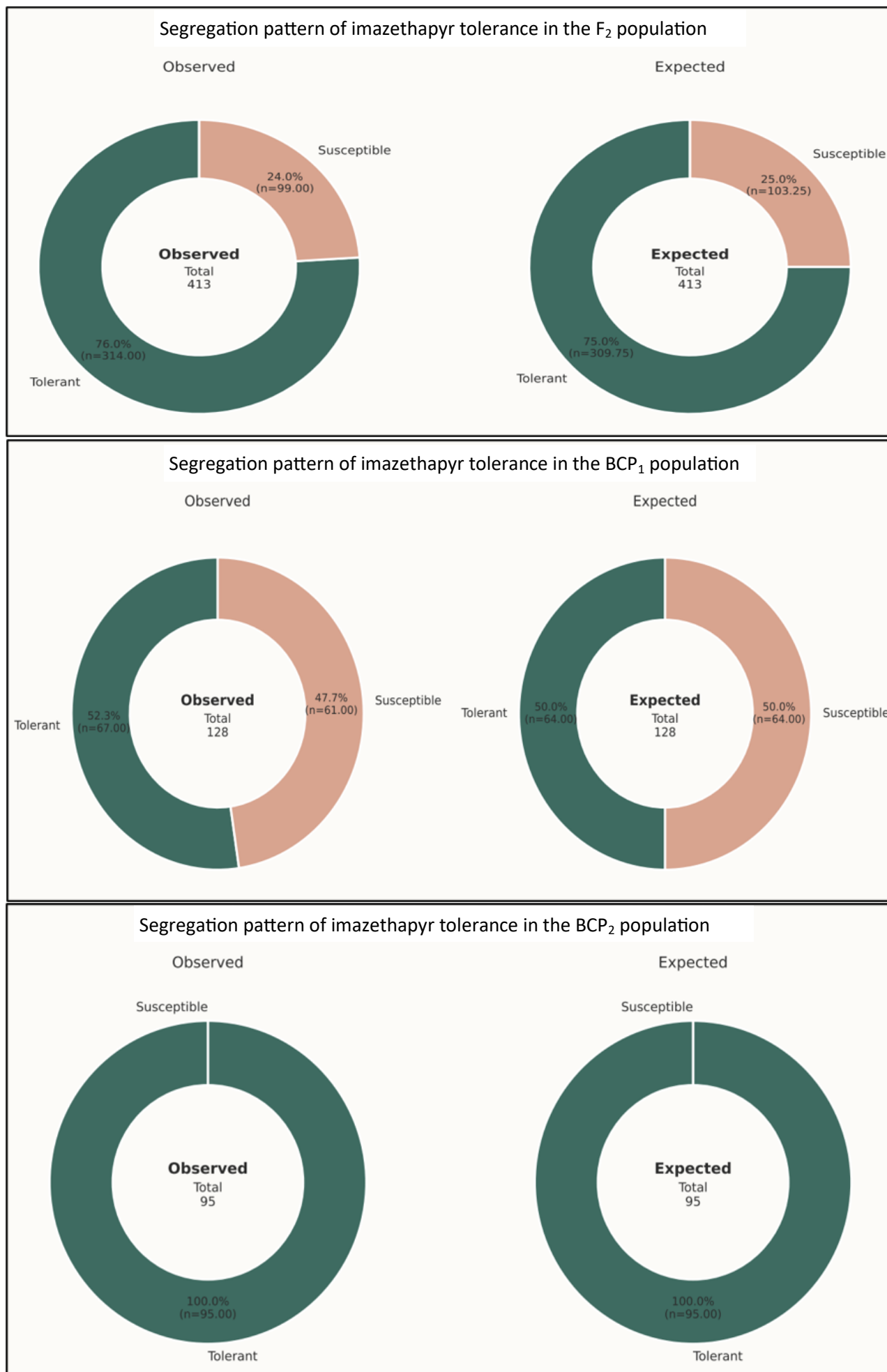


Fig. 2. Segregation pattern of imazethapyr tolerance in the F_2 and backcross population derived from KMP-175 $\times$ Robin.

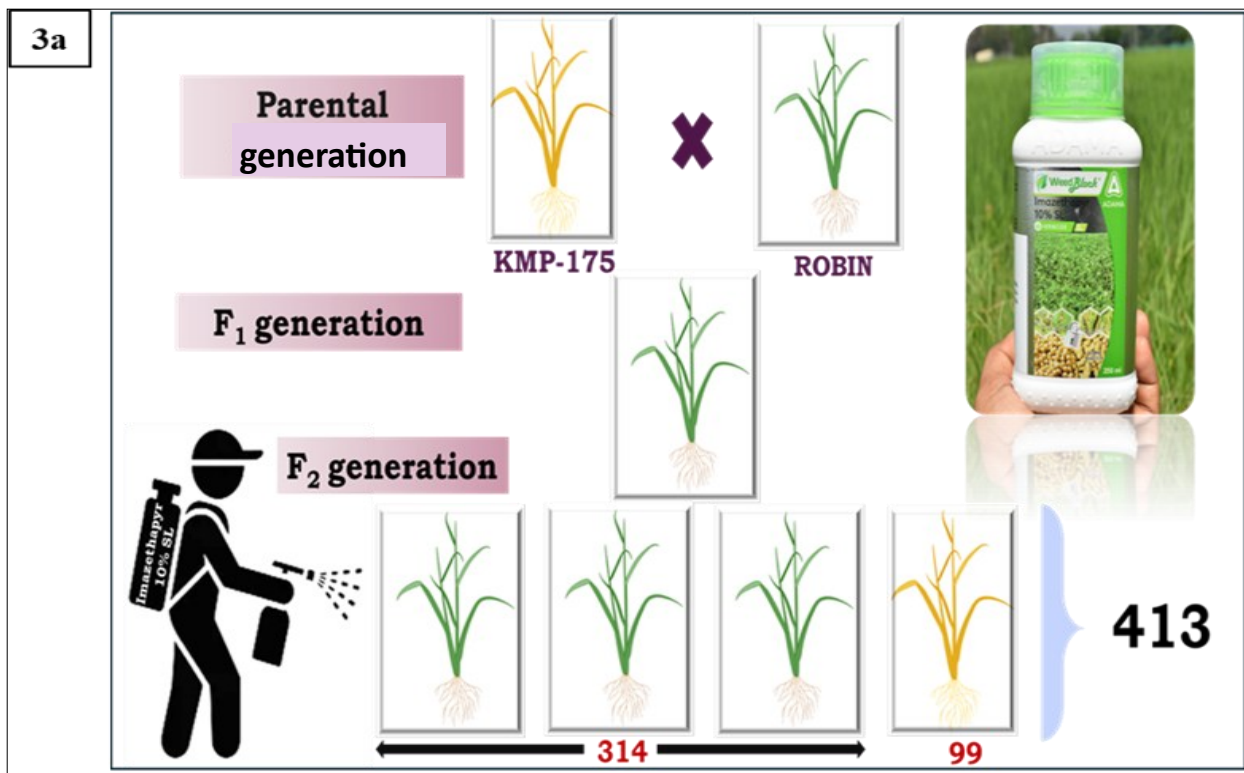


Fig. 3a. Observed segregation pattern of herbicide tolerance in the F₂ population.



Fig. 3b. Field view of segregation in F₂ population (Left) and BCP₁ generation.

tolerant and no susceptible plants were observed (Table 1). This segregation pattern was consistent with the expected response for a backcross involving the tolerant parent under single dominant gene inheritance. Overall, the segregation observed in the F₂ and backcross generations supports that imazethapyr tolerance in the cross KMP-175 × Robin is inherited as a monogenic dominant trait (Fig. 2).

Discussion

The segregation pattern observed in the present study indicated that imazethapyr tolerance in the cross KMP-175 × Robin is governed by a single dominant gene. The F₂ population fitted the expected 3 : 1 ratio, while the BCP₁ population conformed to the expected 1 : 1 ratio and the BCP₂ population showed the expected predominance of tolerant plants. These results collectively support the monogenic dominant inheritance of the trait.

The present findings are consistent with earlier reports describing *AHAS*-mediated herbicide tolerance in rice. Mutations in the *AHAS* gene generally confer dominant or semi-dominant inheritance through altered herbicide-binding affinity without major

impairment of enzyme function (6, 8). Previous studies reported single dominant inheritance of imazethapyr tolerance based mainly on F₂ phenotypic segregation (14). However, the present study further confirms this inheritance pattern in backcross generations (BCP₁ and BCP₂), providing stronger evidence for stable transmission during introgression breeding (10, 15).

It is also important to note that different allelic variants of *AHAS* may confer varying levels of tolerance, dominance expression, or cross-resistance depending on the mutation site and genetic background. In contrast to the present monogenic dominant pattern, herbicide tolerance in some crop systems has been reported as recessive or polygenic, especially when associated with non-target-site detoxification mechanisms.

Expression of herbicide tolerance under field conditions may also be influenced by environmental factors such as herbicide dose, plant growth stage, temperature and soil moisture, which can modify symptom severity. The combined phenotypic segregation and marker-based validation provide a consistent genetic framework for imazethapyr tolerance, supporting its effective deployment in rice breeding programmes.

Conclusion

The present investigation demonstrated that imazethapyr tolerance in the cross KMP-175 × Robin is governed by a single dominant gene. The F_2 and backcross segregation patterns supported monogenic inheritance, which will facilitate rapid selection and introgression. Molecular validation using RM6844 marker further strengthened the genetic interpretation. These findings provide a strong foundation for development of herbicide-tolerant rice cultivars suitable for direct-seeded rice systems.

Acknowledgements

The authors sincerely acknowledge the AICRP (Rice), ZARS, V.C Farm, Mandya for providing the necessary field and laboratory facilities and support to carry out the research work.

Authors' contributions

MP carried out the experiment and prepared the manuscript. BPMP and USA contributed to methodology formulation and experimental planning. SRS, and SGM and SJ contributed to the collection of phenotypic observations. RAK assisted in the preparation and arrangement of tables and figures. CAD supervised the study and provided critical revisions to the manuscript. All authors have read and approved the final version of the manuscript.

Compliance with ethical standards

Conflict of interest: Authors do not have any conflict of interest to declare.

Ethical issues: None

References

1. Rao AN, Johnson DE, Sivaprasad B, Ladha JK, Mortimer AM. Weed management in direct-seeded rice. *Advances in Agronomy*. 2007;93:153–255. [https://doi.org/10.1016/S0065-2113\(06\)93004-1](https://doi.org/10.1016/S0065-2113(06)93004-1)
2. Devkota M, Devkota KP, Khanda CM, Sayre KD, Maraseni TN, McDonald AJ, Lamers JPA. Increasing profitability, yields and yield stability through sustainable crop establishment practices in rice-based systems of the Eastern Gangetic Plains. *Agricultural Systems*. 2019;173:414–423. <https://doi.org/10.1016/j.agsy.2019.03.022>
3. Kraehmer H, Jabran K, Mennan H, Chauhan BS. Global distribution of rice weeds - a review. *Crop Protection*. 2016;80:73–86. <https://doi.org/10.1016/j.cropro.2015.10.027>
4. Chauhan BS. Weed ecology and weed management strategies for dry-seeded rice in Asia. *Weed Technology*. 2012;26(1):1–13. <https://doi.org/10.1614/WT-D-11-00105.1>
5. Chauhan BS, Opena J. Weed management and grain yield of rice sown at low seeding rates in mechanized dry-seeded systems. *Field*

Crops Research. 2013;141:9–15. <https://doi.org/10.1016/j.fcr.2012.11.002>

6. Tan S, Evans RR, Dahmer ML, Singh BK, Shaner DL. Imidazolinone-tolerant crops: history, current status and future. *Pest Management Science*. 2005;61:246–57. <https://doi.org/10.1002/ps.993>
7. Tranel PJ, Wright TR. Resistance of weeds to ALS-inhibiting herbicides: what have we learned? *Weed Science*. 2002;50(6):700–12. [https://doi.org/10.1614/0043-1745\(2002\)050\[0700:RROWTA\]2.0.CO;2](https://doi.org/10.1614/0043-1745(2002)050[0700:RROWTA]2.0.CO;2)
8. Yu Q, Powles SB. Resistance to AHAS inhibitor herbicides: current understanding. *Pest Management Science*. 2014;70(9):1340–50. <https://doi.org/10.1002/ps.3710>
9. Newhouse KE, Singh BK, Shaner DL, Stidham MA, Patterson FL. Mutations in corn (*Zea mays* L.) acetolactate synthase conferring resistance to imidazolinone herbicides. *Theoretical and Applied Genetics*. 1992;83:65–70. <https://doi.org/10.1007/bf00229227>
10. Shoba D, Raveendran M, Manonmani S, Utharasu S, Dhivyapriya D, Subhasini G, et al. Development and genetic characterization of a novel herbicide (imazethapyr) tolerant mutant in rice (*Oryza sativa* L.). *Rice*. 2017;10:10. https://ui.adsabs.harvard.edu/link_gateway/2017Rice...10...10S/doi:10.1186/s12284-017-0151-8
11. Doyle JJ, Doyle JL. A rapid DNA isolation procedure for small quantities of fresh leaf tissue. *Phytochemical Bulletin*. 1987;19(1):11–15.
12. Rao VS. *Principles of Weed Science*. Oxford and IBH Publishing Pvt. Ltd., New Delhi, India. 1992;P. 540.
13. Snedecor GW, Cochran WG. *Statistical Methods*, 8th edn. Iowa State University Press, Ames, Iowa, USA; 1989
14. Grover N, Kumar A, Yadav AK, Krishnan GS, Ellur RK, Bhowmick PK, et al. Marker assisted development and characterization of herbicide tolerant near isogenic lines of a mega Basmati rice variety, “Pusa Basmati 1121”. *Rice*. 2020;13(1):68.
15. Yu Q, Han H, Vila-Aiub MM, Powles SB. AHAS herbicide resistance endowing mutations: effect on AHAS functionality and plant growth. *Journal of Experimental Botany*. 2010;61(14):3925–34. <https://pubmed.ncbi.nlm.nih.gov/20627897/>

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