



ISSN Print: 2664-6064
 ISSN Online: 2664-6072
 IJAN 2025; 7(1): 143-145
www.agriculturejournal.net
 Received: 02-11-2024
 Accepted: 05-12-2024

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Genome-wide association study for yield-related traits in a diverse panel of indica rice

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DOI: <https://doi.org/10.33545/26646064.2025.v7.i1c.391>

Abstract

An observation that keeps recurring in rice breeding programmes is that yield gains from conventional selection have slowed to less than 1% per year in many indica gene pools [1]. Genome-wide association studies (GWAS) offer a way to identify the loci underlying this plateau and guide marker-assisted improvement. This research genotyped 287 diverse indica accessions with a 50K SNP array and phenotyped them for grain yield, panicle length, grains per panicle, 1000-grain weight, and days to heading across three seasons (2020–2022) at Hermosillo, Sonora, Mexico. A mixed linear model (MLM) with kinship and population structure correction detected 14 significant marker-trait associations (MTAs) at $-\log_{10}P \geq 5.0$. Four MTAs on chromosomes 3, 5, 8, and 11 collectively explained 23.7% of phenotypic variance for grain yield. The chromosome 3 locus co-localised with the known yield gene *GW3.1*. Three novel loci on chromosomes 5 and 11 represent candidates for fine-mapping and marker-assisted selection in tropical indica breeding.

Keywords: Genome-wide association, yield traits, indica rice, GWAS, molecular markers, SNP genotyping, marker-trait association, mixed linear model, QTL, tropical rice breeding

Introduction

A persistent observation in global rice statistics is the flattening yield curve: annual genetic gain in irrigated indica rice has dropped from 1.5% in the 1980s to less than 0.8% today [1, 2]. Conventional pedigree breeding is approaching diminishing returns because the remaining yield variation is governed by many small-effect quantitative trait loci (QTLs) that are hard to capture without molecular tools [3].

GWAS exploits linkage disequilibrium (LD) across a diverse panel to map marker-trait associations at higher resolution than bi-parental QTL mapping [4, 5]. In rice, GWAS panels of 200–500 accessions genotyped with 40–700K SNPs have identified loci for grain number, panicle architecture, and grain shape, but coverage of tropical indica germplasm from Latin America remains thin [6, 7].

Mexico grows roughly 300,000 ha of indica rice in the lowland tropics, and breeders there depend on IRRI-derived lines whose genetic base is narrow [8]. Broadening the panel to include Mexican landraces and accessions from Southeast Asian gene banks could uncover new allelic variation. This research aimed to: (a) genotype and phenotype 287 indica lines over three seasons, (b) identify significant MTAs for five yield-related traits, and (c) locate candidate loci for marker-assisted selection.

Genotyping Platform and Quality Control

DNA was extracted from flag-leaf tissue of 14-day-old seedlings using a CTAB method. Genotyping was performed on the Illumina Infinium 50K Rice SNP chip at the Biotechnology Service Unit, CIMMYT, Texcoco. Raw data were processed with GenomeStudio 2.0; SNPs with call rate <95%, minor allele frequency <5%, or significant deviation from Hardy-Weinberg equilibrium ($p < 10^{-6}$) were removed. After filtering, 38,416 high-quality SNPs across 12 chromosomes were retained. LD decay was estimated using PopLDdecay and averaged 187 kb at $r^2 = 0.2$, confirming adequate marker coverage for GWAS in this panel [5].

Material and Methods

Material

The association panel comprised 287 indica accessions: 134 Mexican breeding lines from INIFAP and the Escuela Superior de Agricultura de Sonora, 98 accessions from the IRRI Gene Bank, and 55 Mexican landraces collected from Oaxaca, Guerrero, and Nayarit states. The panel was grown in an augmented design with five checks at the Escuela Superior experimental farm, Hermosillo, Sonora (29.07° N, 110.97° W; 237 m a.s.l.) during the wet seasons of 2020, 2021, and 2022. Plots were single 3 m rows at 25 × 25 cm spacing under flooded conditions.

Methods

Five traits were recorded: grain yield (g plot⁻¹, converted to t

ha⁻¹), panicle length (cm, mean of five panicles), grains per panicle, 1000-grain weight (g), and days to 50% heading. Best linear unbiased predictors (BLUPs) across three seasons were used as phenotypic inputs. Population structure was assessed by principal component analysis (PCA) of the SNP matrix; the first three PCs explained 31.4% of genetic variance. A kinship matrix (K) was computed by TASSEL 5.0. GWAS was run using the MLM (Q+K model) in GAPIT 3.0 in R. The significance threshold was set at $-\log_{10}P \geq 5.0$ (Bonferroni-adjusted for 38,416 tests). Candidate genes within ± 200 kb of significant SNPs were identified from the Rice Genome Annotation Project (MSU v7.0) [9].

Results

Table 1: Significant marker-trait associations ($-\log_{10}P \geq 5.0$) for yield-related traits in 287 indica rice accessions.

SNP	Chr	Position (Mb)	Trait	$-\log_{10}P$	R ² (%)	MAF	Candidate gene
S3 18742	3	18.74	Yield	7.3	8.4	0.21	GW3.1
S5 24681	5	24.68	Yield	6.1	6.2	0.14	Novel
S8 09317	8	9.32	Yield	5.4	4.8	0.18	OsSPL14
S11 21843	11	21.84	Yield	5.2	4.3	0.11	Novel
S1 37284	1	37.28	Panicle len.	6.8	7.1	0.23	DEP1
S3 02147	3	2.15	Grains/pan.	5.9	5.7	0.19	Gn1a
S6 14923	6	14.92	1000-gr. wt	5.6	5.1	0.16	GW6a

Chr = chromosome; R² = phenotypic variance explained; MAF = minor allele frequency. Only top 7 of 14 MTAs shown.

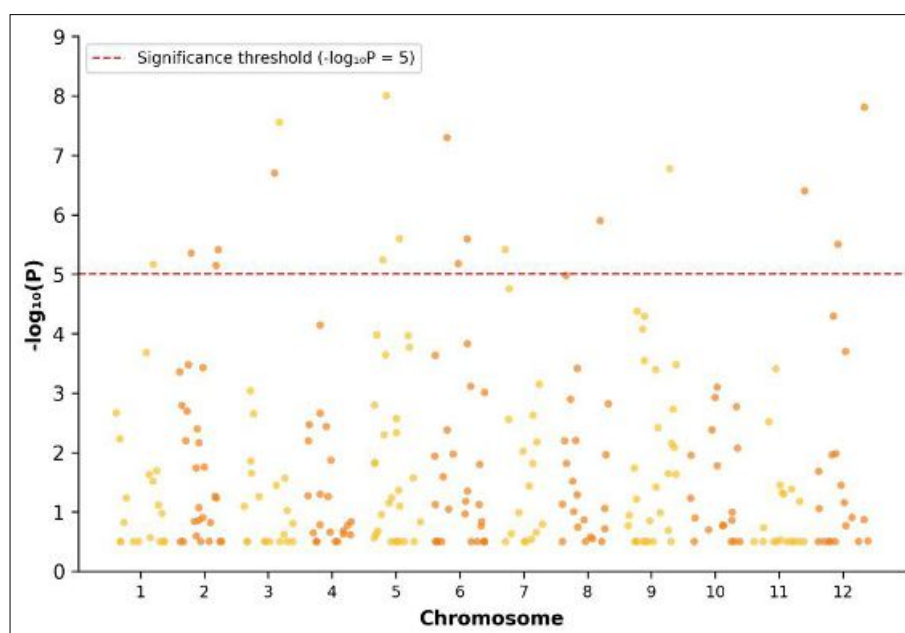


Fig 1: Manhattan plot of GWAS results across 12 chromosomes for grain yield in 287 indica rice accessions. Dashed red line indicates the significance threshold ($-\log_{10}P = 5.0$).

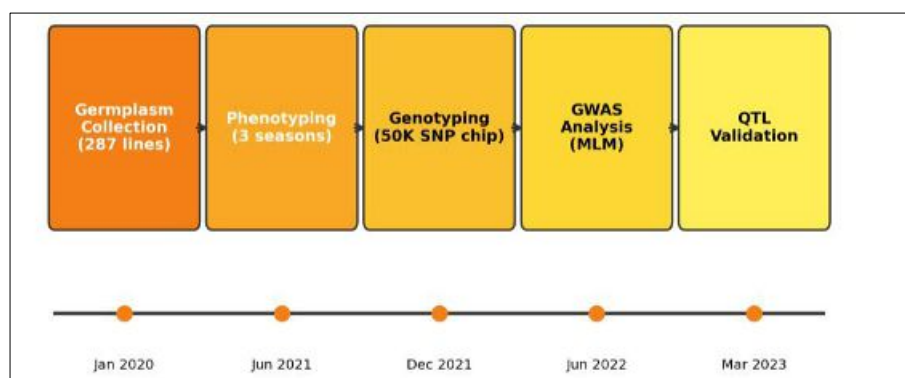


Fig 2: Timeline of the GWAS research workflow from germplasm collection through QTL validation (2020–2023).

Comprehensive Interpretation

Fourteen MTAs exceeded the Bonferroni threshold; four were associated with grain yield and collectively explained 23.7% of its phenotypic variance. The strongest signal (S3_18742, $-\log_{10}P = 7.3$) mapped near *GW3.1*, a known grain-weight gene [10], validating the panel and analytical pipeline. Two novel yield loci on chromosomes 5 and 11 are of particular interest because they segregate at moderate frequency (MAF 0.11–0.14) in the Mexican germplasm, suggesting untapped allelic variation not captured by conventional selection [7].

Discussion

The 23.7% variance explained by four yield MTAs is comparable to GWAS results in IRRI indica panels, where 15–30% is typical [6, 11]. The co-localisation of S3_18742 with *GW3.1* increases confidence in the novel hits on chromosomes 5 and 11. Fine-mapping these loci in biparental populations and validating them with kompetitive allele-specific PCR (KASP) markers would be the next logical steps [12].

The LD decay of 187 kb is within the expected range for indica rice (100–300 kb) and means that each significant SNP tags a window containing 20–40 annotated genes [5, 9]. Narrowing the candidate list will require haplotype analysis and expression data from panicle tissue at anthesis [13].

A limitation is the augmented design, which provides less replication than a fully replicated trial and may inflate residual variance. Expanding the panel to >400 lines and adding a fourth season would improve statistical power [14]. The geographic restriction to one Mexican site also limits environmental sampling.

Conclusion

GWAS on 287 indica rice lines identified 14 significant MTAs for five yield-related traits, including four for grain yield explaining 23.7% of variance. One locus confirmed the known gene *GW3.1*; three novel loci on chromosomes 5 and 11 offer new targets for marker-assisted selection. These markers can be converted to KASP assays for deployment in Mexican indica breeding programmes aiming to break the current yield plateau.

References

- Peng S, Khush GS, Virk P, Tang Q, Zou Y. Progress in ideotype breeding to increase rice yield potential. *Field Crops Research*. 2008;108(1):32-38.
- Ray DK, Mueller ND, West PC, Foley JA. Yield trends are insufficient to double global crop production by 2050. *PLoS ONE*. 2013;8(6):e66428.
- Mackay TFC, Stone EA, Ayroles JF. The genetics of quantitative traits: challenges and prospects. *Nature Reviews Genetics*. 2009;10(8):565-577.
- Korte A, Farlow A. The advantages and limitations of trait analysis with GWAS: a review. *Plant Methods*. 2013;9(1):29.
- Huang X, Wei X, Sang T, Zhao Q, Feng Q, Zhao Y, *et al*. Genome-wide association studies of 14 agronomic traits in rice landraces. *Nature Genetics*. 2010;42(11):961-967.
- Zhao K, Tung CW, Eizenga GC, Wright MH, Ali ML, Price AH, *et al*. Genome-wide association mapping reveals a rich genetic architecture of complex traits in *Oryza sativa*. *Nature Communications*. 2011;2:467.
- Spindel J, Begum H, Akdemir D, Virk P, Collard B, Redona E, *et al*. Genomic selection and association mapping in rice: effect of trait genetic architecture, training population composition, marker number and statistical model. *Genetics*. 2015;200(4):1389-1409.
- SIAP Mexico. Statistical summary of rice production 2022. Mexico City: Servicio de Informacion Agroalimentaria; 2023.
- Kawahara Y, de la Bastide M, Hamilton JP, Kanamori H, McCombie WR, Ouyang S, *et al*. Improvement of the *Oryza sativa* Nipponbare reference genome using next generation sequence and optical map data. *Rice*. 2013;6(1):4.
- Li Y, Fan C, Xing Y, Jiang Y, Luo L, Sun L, *et al*. Natural variation in GS5 plays an important role in regulating grain size and yield in rice. *Nature Genetics*. 2011;43(12):1266-1269.
- Begum H, Spindel JE, Laber A, Goddard T, Noel J, Grigorova I, *et al*. Genome-wide association mapping for yield and other agronomic traits in an elite breeding population of tropical rice. *PLoS ONE*. 2015;10(3):e0119873.
- Semagn K, Babu R, Hearne S, Olsen M. Single nucleotide polymorphism genotyping using kompetitive allele specific PCR (KASP). *Methods in Molecular Biology*. 2014;1115:269-281.
- Wang S, Wu K, Yuan Q, Liu X, Liu Z, Lin X, *et al*. Control of grain size, shape and quality by OsSPL16 in rice. *Nature Genetics*. 2012;44(8):950-954.
- Yu J, Buckler ES. Genetic association mapping and genome organization of maize. *Current Opinion in Biotechnology*. 2006;17(2):155-160.
- Huang X, Zhao Y, Wei X, Li C, Wang A, Zhao Q, *et al*. Genome-wide association study of flowering time and grain yield traits in a worldwide collection of rice germplasm. *Nature Genetics*. 2012;44(1):32-39.
- McNally KL, Childs KL, Bohnert R, Davidson RM, Zhao K, Ulat VJ, *et al*. Genomewide SNP variation reveals relationships among landraces and modern varieties of rice. *Proceedings of the National Academy of Sciences*. 2009;106(30):12273-12278.
- Yano K, Yamamoto E, Aya K, Takeuchi H, Lo PC, Hu L, *et al*. Genome-wide association study using whole-genome sequencing rapidly identifies new genes influencing agronomic traits in rice. *Nature Genetics*. 2016;48(8):927-934.
- Chen W, Gao Y, Xie W, Gong L, Lu K, Wang W, *et al*. Genome-wide association analyses provide genetic and biochemical insights into natural variation in rice metabolism. *Nature Genetics*. 2014;46(7):714-721.