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Erratum: Meta-QTL and haplo-pheno analysis reveal superior haplotype combinations associated with low grain chalkiness under high temperature in rice

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KEYWORDS

starch metabolism, grain chalkiness, meta-QTL analysis, haplotype, haplo-pheno analysis, granule bound starch synthase I, starch synthase IIa

An Erratum on

Meta-QTL and haplopheno analysis reveal superior haplotype combinations associated with low grain chalkiness under high temperature in rice

By Kumari A, Sharma D, Sharma P, Sahil, Wang C, Verma V, Patil A, Imran M, Singh MP, Kumar K, Paritosh K, Caragea D, Kapoor S, Chandel G, Grover A, Jagadish SVK, Katiyar-Agarwal S and Agarwal M (2023). *Front. Plant Sci*. 14:1133115. doi: 10.3389/fpls.2023.1133115

Due to a production error, Figure 1 was a repeat of Figure 7 in the published article.

The corrected Figures appear below.

The publisher apologizes for this mistake.

The original version of this article has been updated.

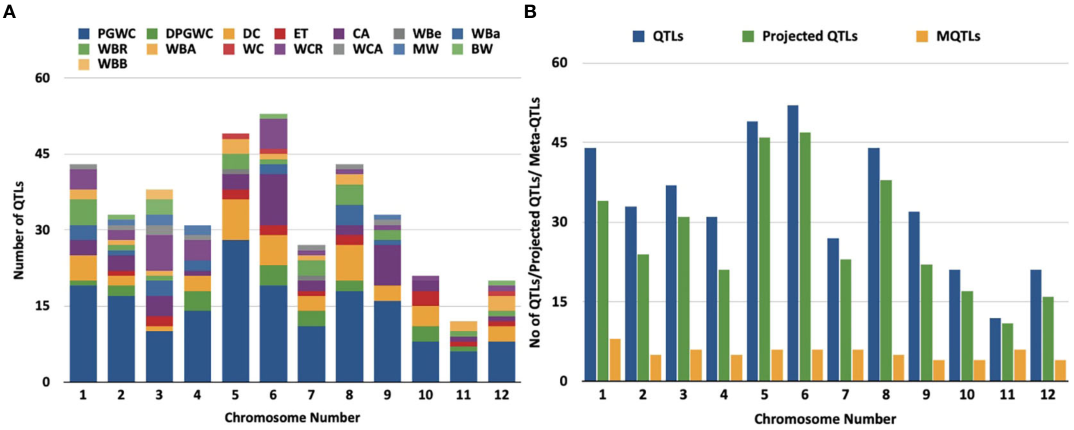

FIGURE 1
Distribution of QTLs and meta-QTLs associated with rice grain chalk on different chmmosomes of rice, **(A)** Trait-wise distribution of initial QTLs used for the meta-QTL analysis, (PGWC, Percentage Grain with Chalkiness; DPGWC, Degree of Percentage Grain with Chalkiness; DC, Degree of Endosperm Chalkiness; ET, Endosperm Transparency; CA, Chalkiness Area; WBe, White Belly; WBa, White Back; WBR,; WBA, White Back Area; WC, White core; WCR, White core rate; WCA, Whlte core area; MW,Mi1ky white; BW, Basal White; WBB, White Back and Basal). **(B)** The distribution of QTLs, projected QTLs and meta-QTLs on twelve rice chromosomes.

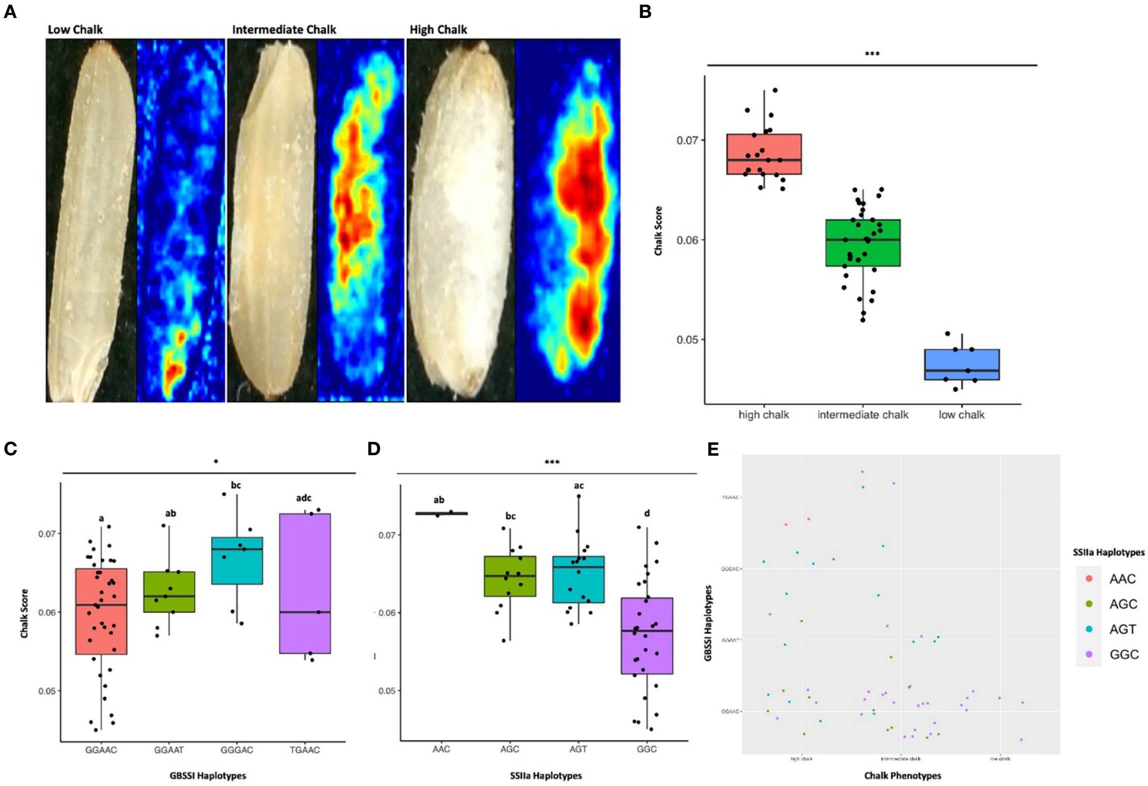

FIGURE 7
Haplo-pheno analysis of Granule Bound Starch Synthase I and Starch Synthase II a, **(A)** Rice seed scans and their corresponding heat maps highlighting the chalky area (red) in less chalk, intermediate chalk and high chalk seed types. **(B)** Box plot depicting the chalky score of 60 rice genotypes (grown in two crop seasons) categorized as high, intermediate and low chalk **(C)** Box plot of the chalk score data categorized according to the GBSS I haplotypes. **(D)** Box plot of the chalk score data categorized according to the SSIIa haplotypes. **(E)** Comparison of the haplotypic combination of GBSS I and SSIIa. One-way ANOVA was conducted for determining the statistical significance of haplotype means. Chalk score data designated with the same alphabet are not significantly different at $p \leq 0.1$(.) or $p \leq 0.05$ (*) or $p \leq 0.001$ (***) as per Turkey *Post hoc* test for Honest Significance Difference (HSD) analysis.