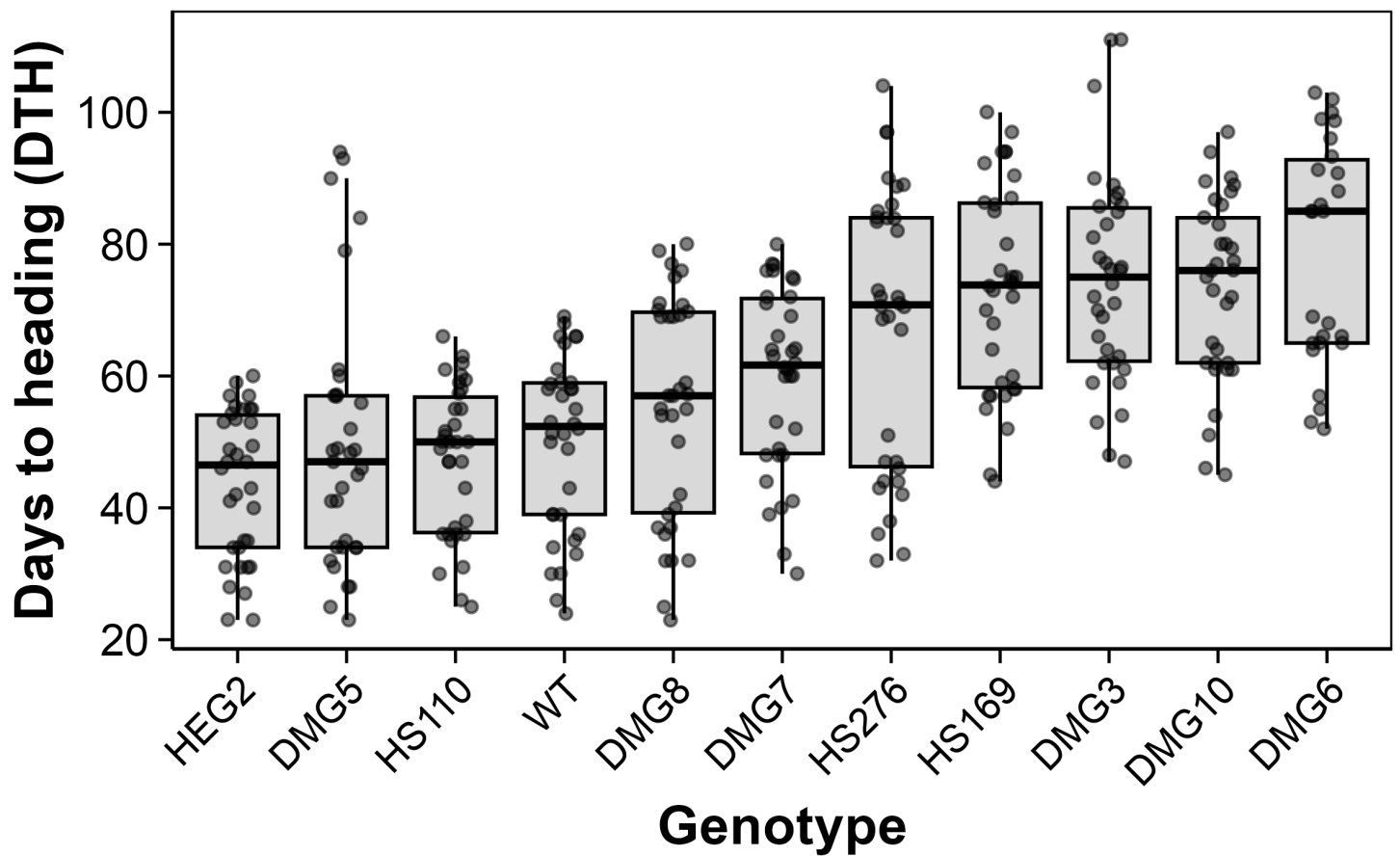
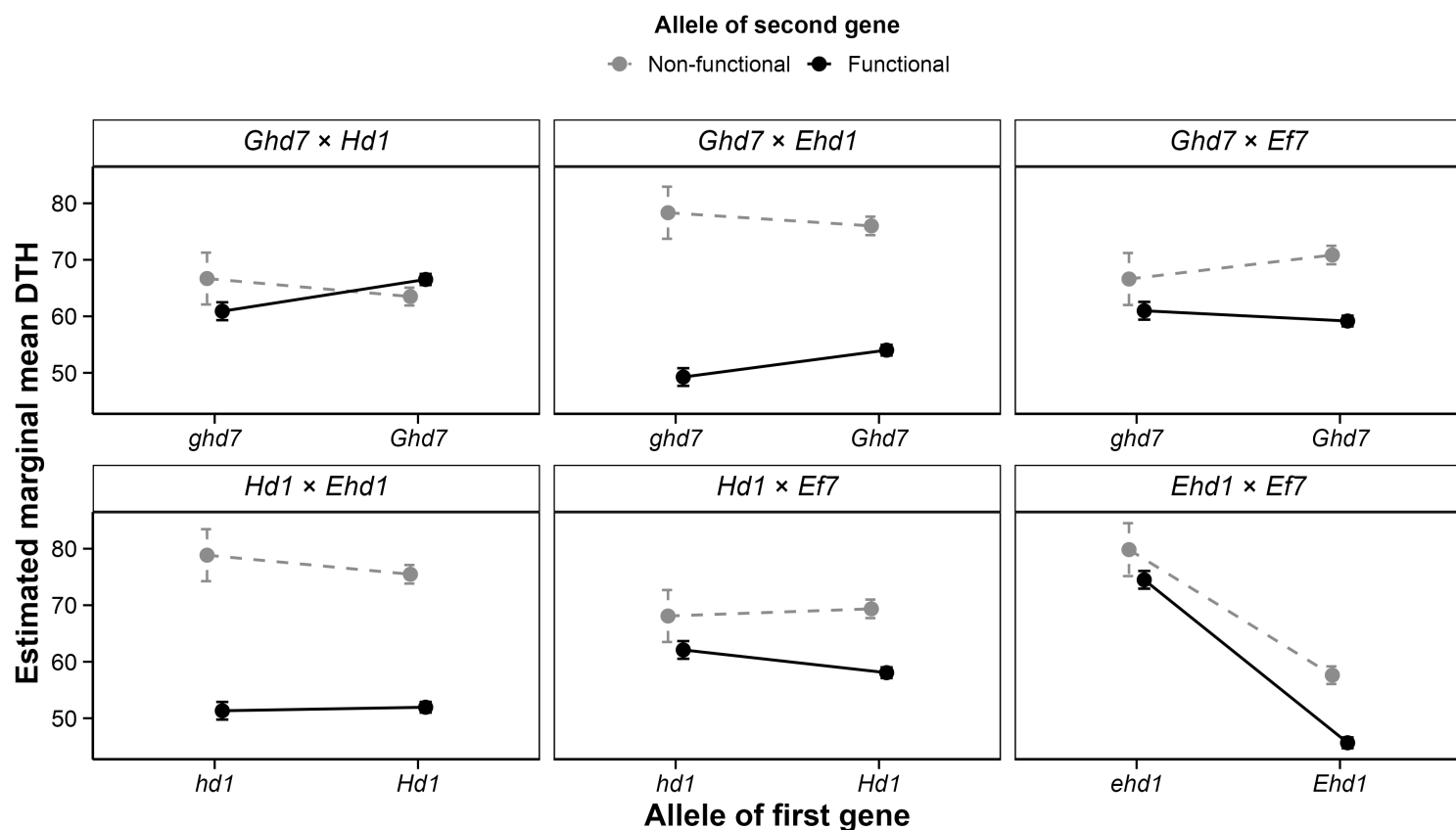




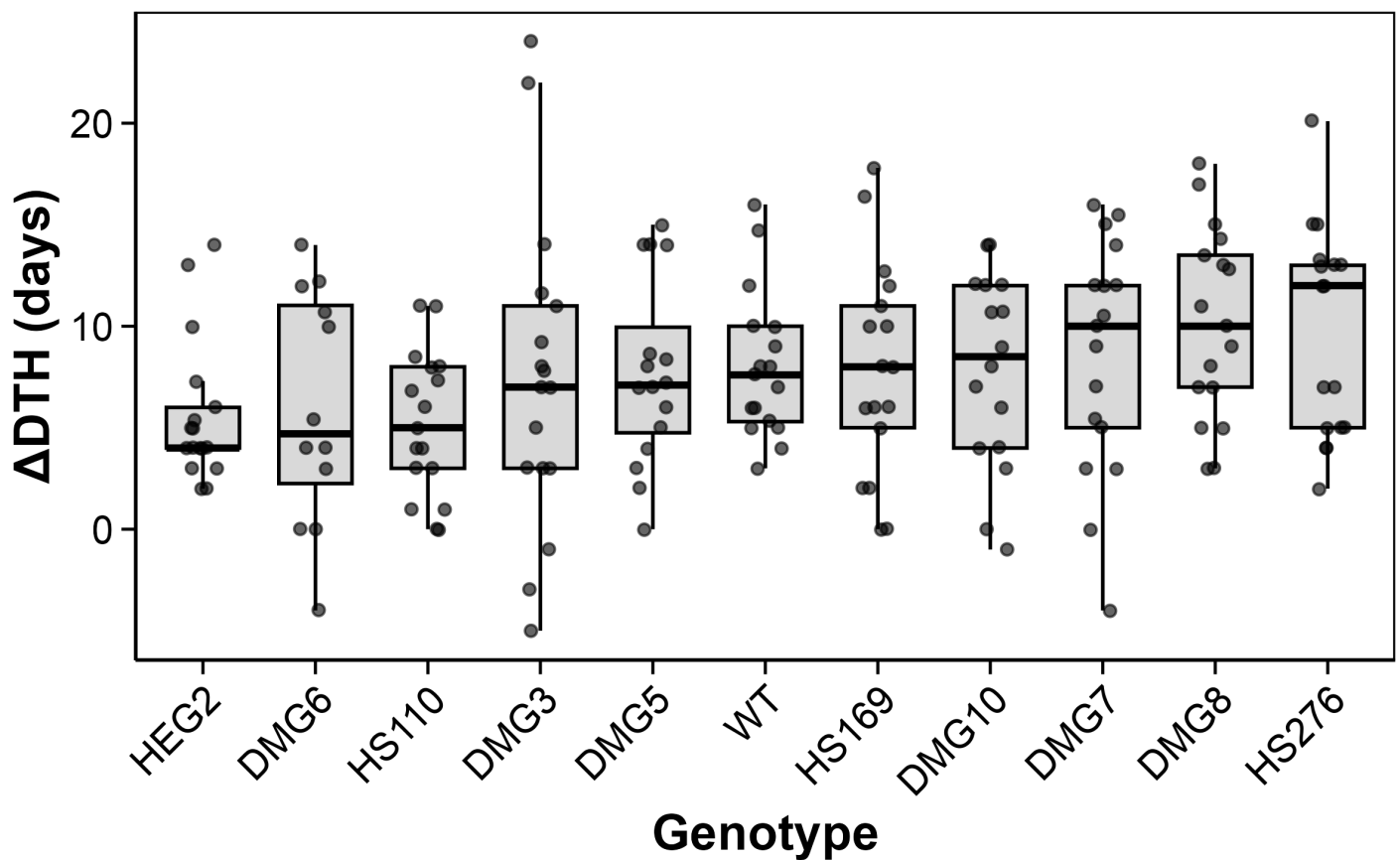
Supplemental Fig. S1. Observed DTH distribution by genotype

Boxplots show the distributions of observed DTH values for each genotype across fertilizer conditions and site-by-year environments. The center line, box, and whiskers represent the median, interquartile range, and values within 1.5 times the interquartile range, respectively. Dots indicate individual observations. This figure presents observed distributions only and does not indicate statistical comparisons among genotypes.



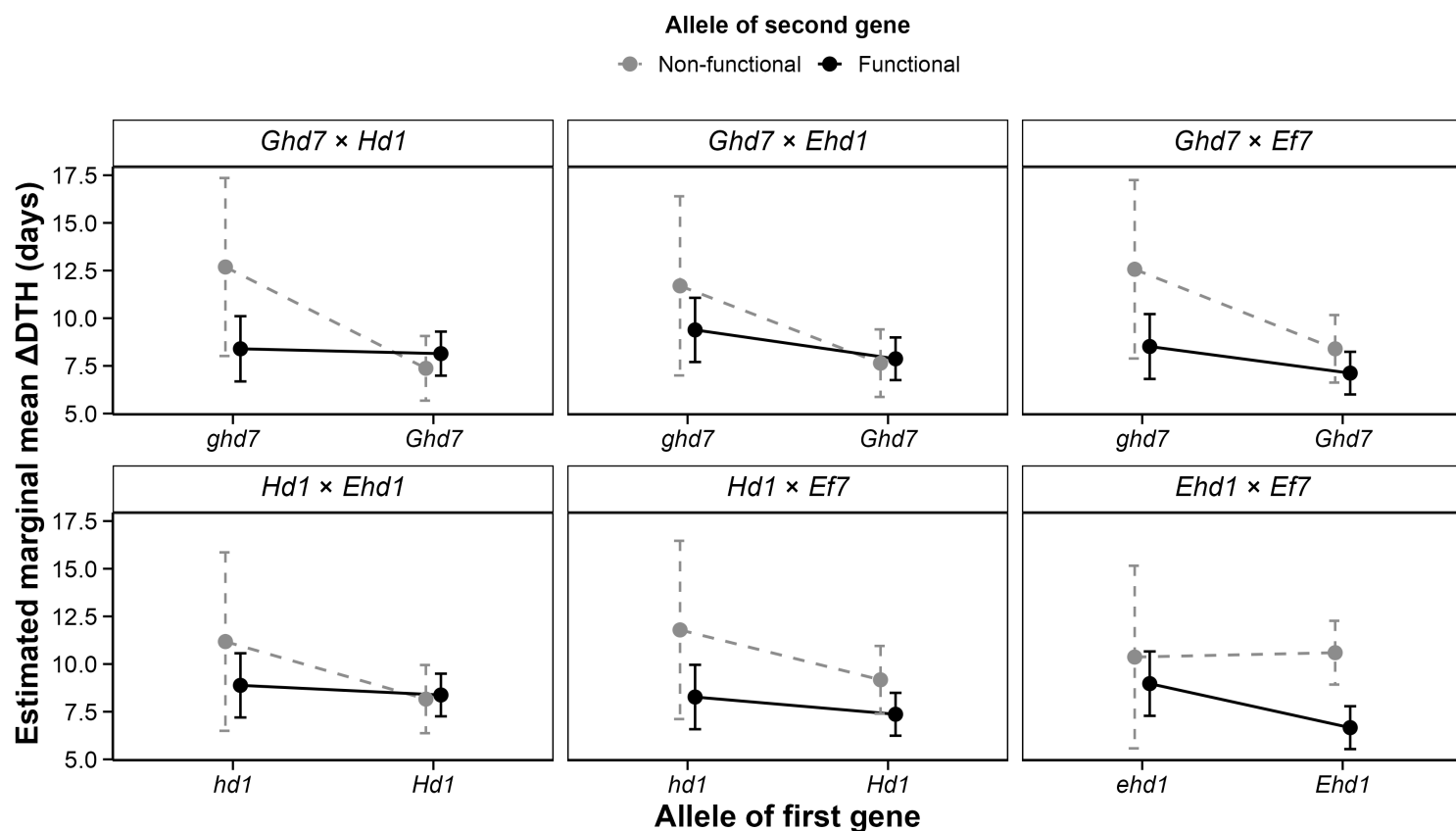
Supplemental Fig. S2. Pairwise gene interaction effects on DTH

Estimated marginal mean DTH for all pairwise combinations among *Ghd7*, *Hd1*, *Ehd1*, and *Ef7*. Points represent estimated marginal means from the two-gene interaction DTH model, and error bars indicate 95% confidence intervals. Lines connect estimates across the allelic states of the first gene, grouped by the allelic state of the second gene.



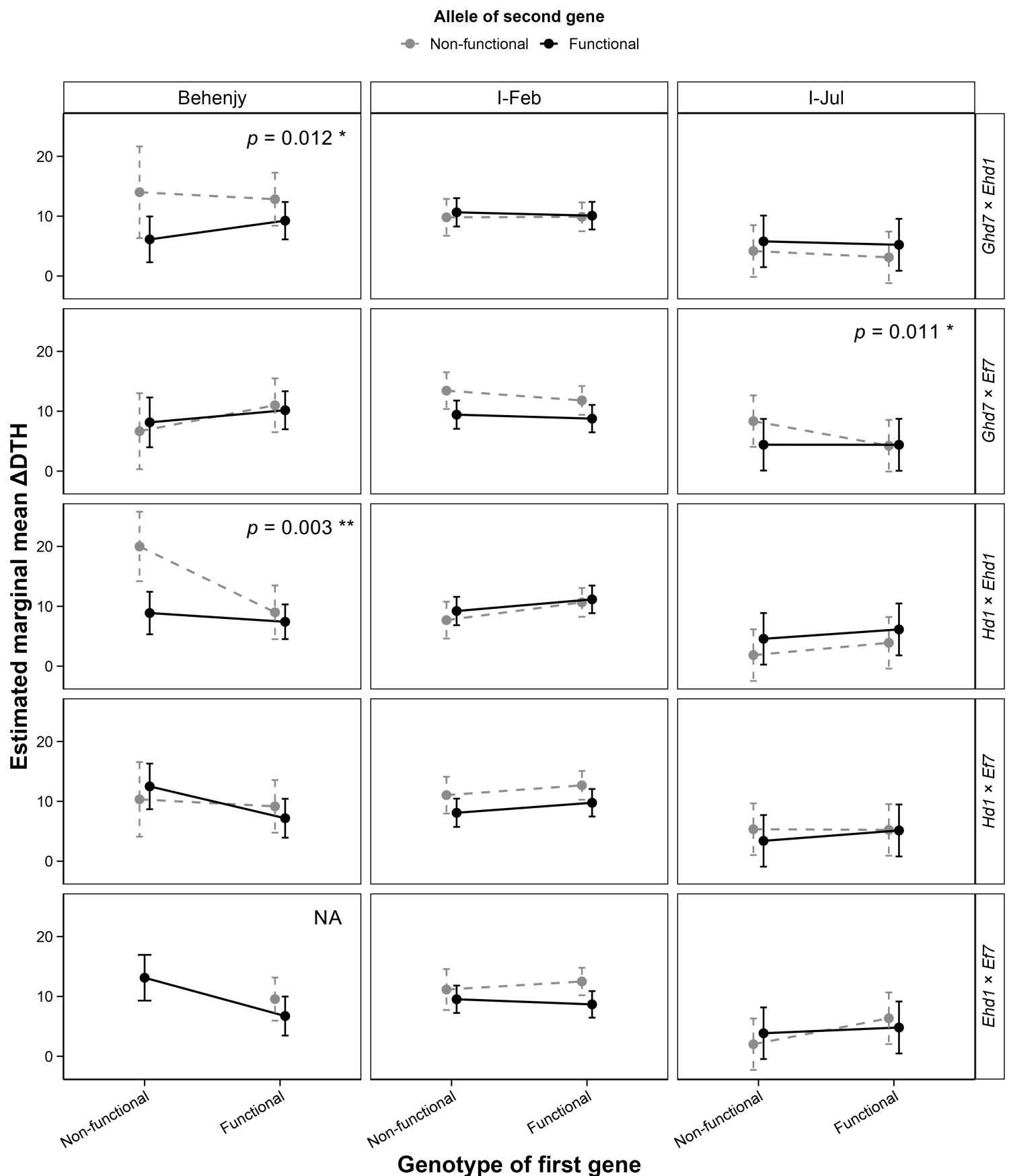
Supplemental Fig. S3. Observed Δ DTH distribution by genotype

Boxplots show the distributions of observed Δ DTH values for each genotype, and dots indicate individual paired observations. Δ DTH was calculated as DTH under LF treatments minus DTH under NF treatments for each genotype within the same site-by-year environment and block. The center line, box, and whiskers represent the median, interquartile range, and values within 1.5 times the interquartile range, respectively. This figure presents observed values only; model-estimated marginal means and statistical comparisons among genotypes are not shown.



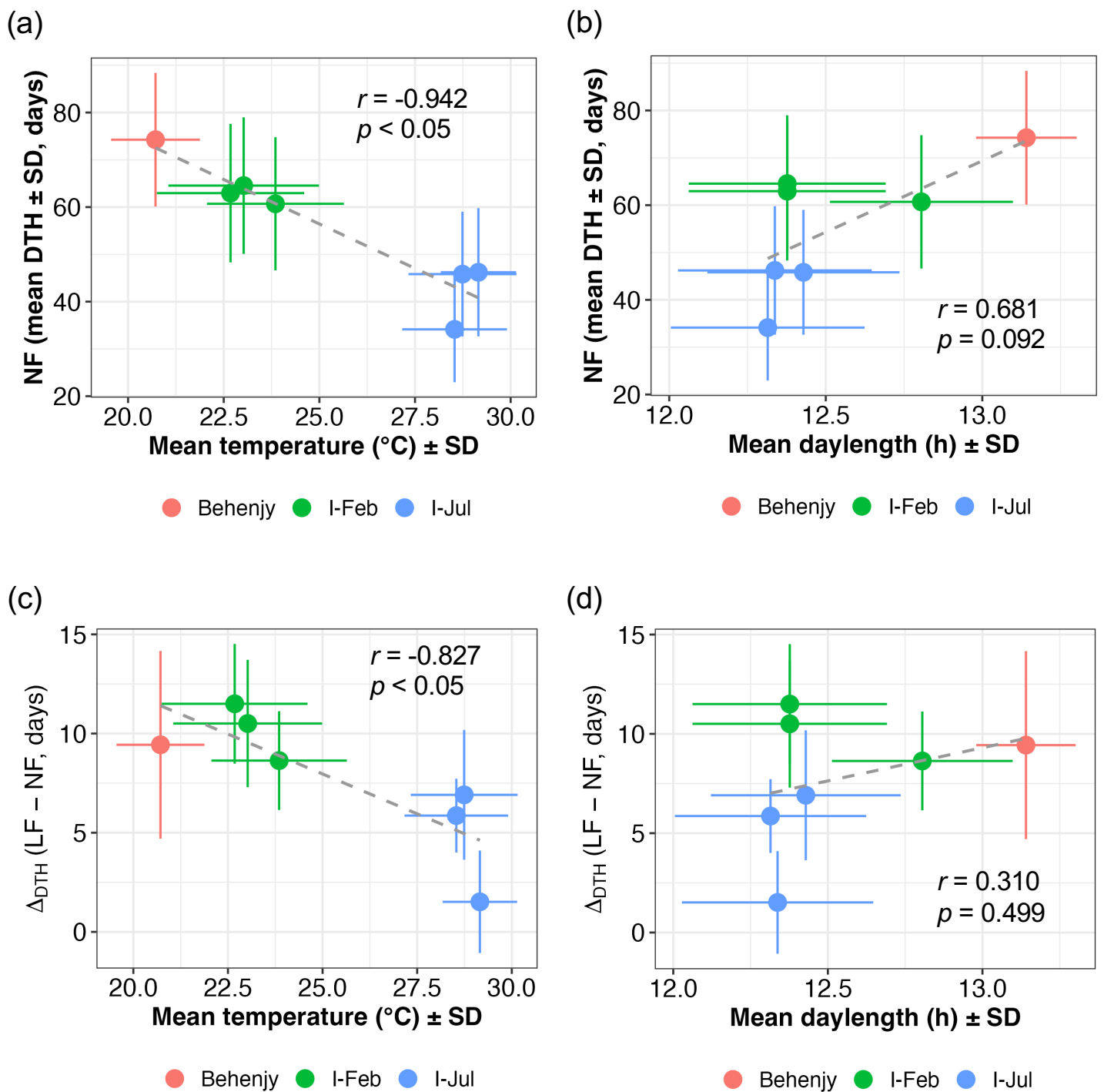
Supplemental Fig. S4. Pairwise genetic interaction effects on Δ DTH

Estimated marginal mean Δ DTH for all pairwise combinations among *Ghd7*, *Hd1*, *Ehd1*, and *Ef7*. Points represent estimated marginal means from the two-gene interaction Δ DTH model, and error bars indicate 95% confidence intervals. Lines connect estimates across the allelic states of the first gene, grouped by the allelic state of the second gene.

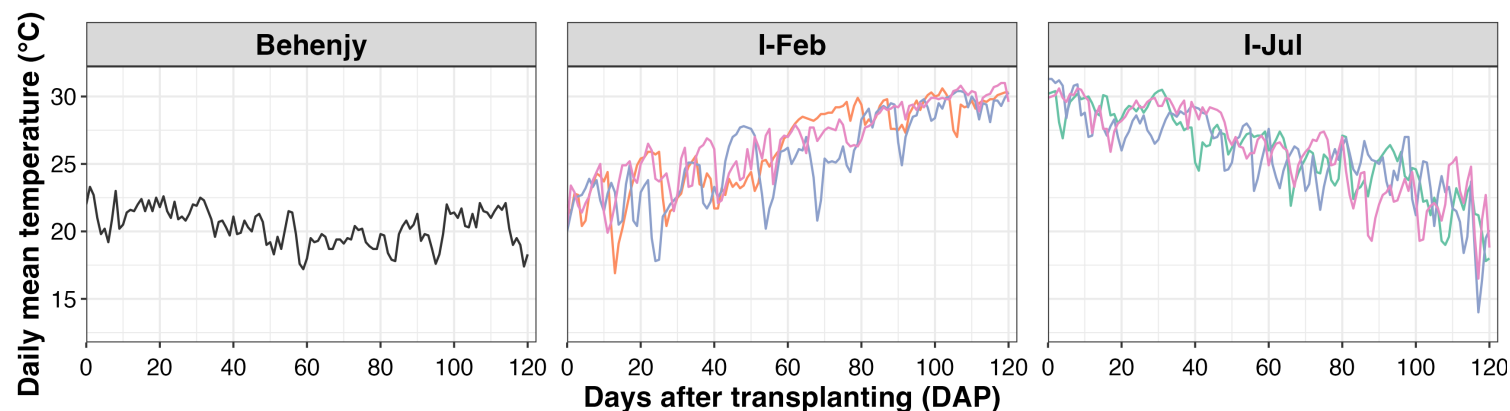


Supplemental Fig. S5. Site-specific pairwise gene interaction effects on Δ DTH

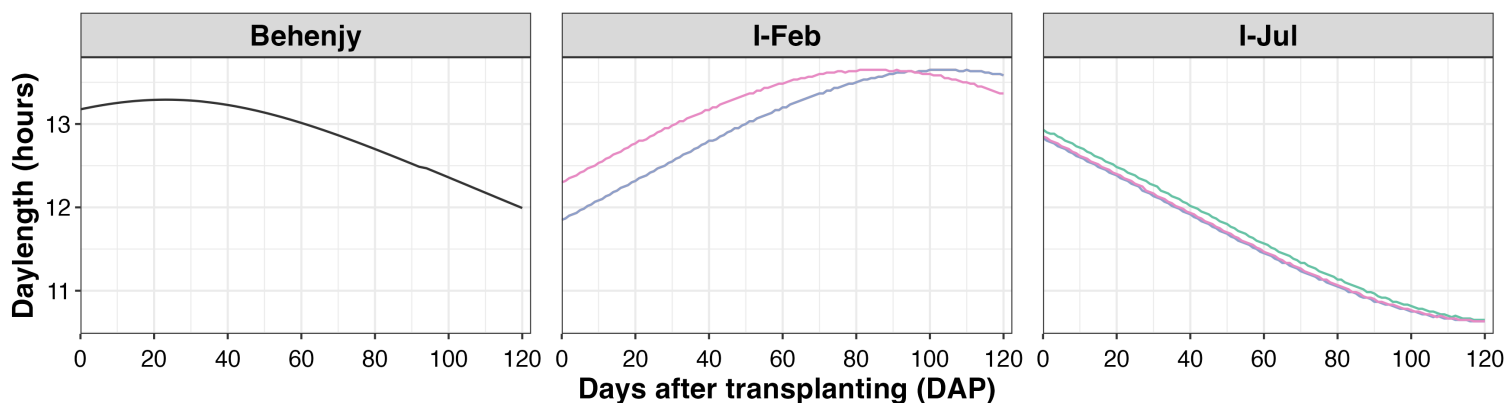
Estimates were obtained from focused site-specific models for each pairwise interaction. Year was treated as a random effect for I-Feb and I-Jul. For Behenjy, which had one year of data, a linear model without the Year random effect was used. P values and asterisks indicate significant interaction terms in the corresponding site-specific model (* $P < 0.05$, ** $P < 0.01$). Panels without annotations indicate non-significant interaction terms. NA indicates that the corresponding interaction term was not estimable because of missing data or incomplete allele combinations. These analyses were exploratory and intended to visualize site-specific $G \times G$ patterns.



Supplemental Fig. S6 Correlation between days to heading (DTH) under noraml-fertilizer (NF) conditions and (a) mean temperatures or (b) mean daylengths during the 45-days period after transplanting, and correlation between Δ_{DTH} (the difference of DTH between NF and LF) and (c) mean temperatures or (d) mean daylengths during the same period. Each point represents the mean values across 11 genotypes cultivated in each year. Correlation coefficients (r) were calculated using Pearson's correlation.



Behenji (2024) & Ishigaki (by year) — Behenji — Year 2020 — Year 2021 — Year 2022 — Year 2023



Behenji (2024) & Ishigaki (by year) — Behenji — Year 2020 — Year 2021 — Year 2022 — Year 2023

Supplemental Fig. S7 Daily mean temperature and daylength from transplanting in each environmental condition and each year. I-Feb and I-Jul indicate Ishigaki February sowing season and Ishigaki July sowing season, respectively.

Supplemental Table S1. Site-specific gene and pairwise gene interaction effects on Δ DTH.

I-Feb			I-Jul		Behenjy	
Term	<i>F</i> value	<i>P</i>	<i>F</i> value	<i>P</i>	<i>F</i> value	<i>P</i>
<i>Ghd7</i>	2.010	0.160	2.064	0.156	0.043	0.837
<i>Hd1</i>	0.007	0.933	0.566	0.454	4.028	0.057
<i>Ehd1</i>	0.000	0.991	4.793	0.032 *	7.153	0.014 *
<i>Ef7</i>	4.032	0.048 *	0.917	0.342	1.904	0.181
<i>Ghd7:Hd1</i>	5.645	0.020 *	1.133	0.291	3.886	0.064
<i>Ghd7:Ehd1</i>	0.033	0.855	0.009	0.923	7.724	0.012 *
<i>Ghd7:Ef7</i>	0.807	0.372	6.825	0.011 *	0.042	0.839
<i>Hd1:Ehd1</i>	0.008	0.929	0.758	0.387	11.749	0.003 **
<i>Hd1:Ef7</i>	0.468	0.496	1.582	0.213	0.042	0.839
<i>Ehd1:Ef7</i>	1.457	0.231	2.397	0.127	NA	NA

Note: Site-specific exploratory models were used to evaluate additive gene effects and pairwise gene interactions associated with Δ DTH. Year was fitted as a random effect for I-Feb and I-Jul. For Behenjy, which had one year of data, a linear model without the Year random effect was used. *P* values are shown for each term. NA indicates that the term was not estimable. Asterisks indicate the significance of the *Ghd7* × *Hd1* interaction term in each site-specific model (* *P* < 0.05; ** *P* < 0.01; *** *P* < 0.001).

Supplementary Table S2. Allele-specific markers used to genotype four heading-time loci. Lowercase *italics* indicate loss -of-function alleles. Amplicon sizes are for IRGSP-1.0.

Locus / Gene	Chr.	RAP_ID	Variant typology	Previous nomenclature / allele origin	Allele origin Reference	Assay type	Amplicon size (bp) (IRGSP1.0)		Restriction enzyme	cut	Annealing (°C)	Forward primer	Reverse primer
							WT	Mut					
<i>E17 (Hd17)</i>	6	Os06g0142600	16bp deletion	HS276 (<i>e17</i>)	Saito et al. 2012	PCR-RFLP	207	191	<i>Afa</i> I (<i>Rsa</i> I)	mutant	56°C	CATCAGCCACAACATATGGGTGCTCCTGG	ATCTCCAAATGCCACTTGGATGTGACATG
<i>Hd1 (Se1)</i>	6	Os06g0275000	Transposon insertion	HS110 (<i>se1</i>)	Yano et al. 2000	PCR	455	888	-	-	56°C	GCTGCGATCTTTAGGC	CTCCAGCAGGTGTCAGG
<i>Ghd7 (E1)</i>	7	Os07g0261200	Transposon insertion	Aikoku (<i>e1</i>)	Saito et al., 2019	Allele specific-PCR (3 primers mix)	350	450	-	-	56°C	CGTTTCAGCAATAGCATTATGG	TCAGCGAGATCGATGACTTG
												GACGCACAAATGGAGCACGAAC	
<i>Ehd1 (E1)</i>	10	Os10g0463400	Transposon insertion	HS169 (<i>eh1-h</i>)	Saito et al., 2009	PCR	145	578	-	-	56°C	GCCTCATTTTCTTTGTGATGTATGTACC	CGGTAGGAAAGAACGCATC

Supplemental Table S3 Cropping site, year, sowing date and transplanting date in each environment.

Site	Site	Year	Season	Sowing date	Transplanting date
Ishigaki_Feb. sowing	Ishigaki	2021	First	9 Feb. 2021	9 Mar. 2021
(I_Feb)	Ishigaki	2022	First	9 Feb. 2022	9 Mar. 2022
	Ishigaki	2023	First	28 Feb. 2023	28 Mar. 2023
Ishigaki_Jul. sowing	Ishigaki	2020	Second	21 Jul. 2020	18 Aug. 2020
(I_Jul)	Ishigaki	2022	Second	26 Jul. 2022	23 Aug. 2022
	Ishigaki	2023	Second	25 Jul. 2023	22 Aug. 2023
Behenjy	Behenjy	2024	Single	23 Oct. 2023	28 Nov. 2023

Supplemental Table S4 The soil chemical properties under NF and LF conditions in the Ishigaki field.

Contents	Unit	Field	
		Low Fertilizer (LF)	Normal Fertilizer (NF)
pH	—	7.3	7.3
Ammonium nitrogen	mg/100g	0.2	0.4
Nitrate nitrogen	mg/100g	0.3	0.3
Total nitrogen_mass-fraction	mg/100g	0.5	0.7
Truog-available phosphate	mg/100g	1.0	19.0
Exchangable potassium	mg/100g	8.0	63.0
Exchangable magnesium	mg/100g	27.0	52.0
Exchangable calcium	mg/100g	809.0	549.0
Phosphorus absorptive coefficient	—	1000.0	1100.0
Cation exchange capacity	me/100g	10.0	13.5

Note: LF was characterized by lower available phosphate than NF, although other soil chemical properties also differed between conditions.