

## Supplemental Figures and Tables

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Genomic prediction accounting for genotype by environment interaction offers an effective framework for breeding simultaneously for adaptation to an abiotic stress and performances under normal cropping conditions in rice.

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The following supporting information is available for this article:

**Figure S1:** Correlation matrix between performance in each condition (continuous flooding – CF and alternate wetting and drying – AWD) and response variables (response index and slope of the joint regression) for the three traits considered: days to flowering (FL), nitrogen-balance index (NI), and panicle weight (PW). The reference (RP) and progeny (PP) populations are in green and grey, respectively.

**Figure S2:** Single environment and multi-environment (M1 and M2) predictive abilities in cross validation experiments with 40% of untested entries in the reference population obtained with three statistical models (GBLUP, RKHS-1, RKHS-2). Continuous flooding and alternate wetting and drying water management conditions are in blue and orange, respectively. Three traits are presented: days to flowering (FL), nitrogen balance index (NI) panicle weight (PW). The letters in each panel represent the results of Tukey’s HSD comparison of means and apply to each panel independently. The means differ significantly ( $p$ -value  $< 0.05$ ) if two boxplots have no letter in common.

**Table S1:** Variance components and the associated statistic (F-value for fixed effects and Z-value for random effects) of days to flowering (FL), nitrogen balance index (NI), and panicle weight (PW). Separate analysis of each population and each water management system (continuous flooding – CF and alternate wetting and drying – AWD).

**Table S2:** Variance components and the associated statistic: F-value for fixed effects and Z-value for random effects) of days to flowering (FL), nitrogen balance index (NI), and panicle weight (PW). Separate analysis of each population pooled over water management conditions (continuous flooding – CF and alternate wetting and drying – AWD).

**Table S3:** Variance components for the joint regression for days to flowering (FL), nitrogen balance index (NI), and panicle weight (PW). Results are shown for the reference and progeny populations.

**Table S4:** Mean genomic predictive abilities in the reference population for the response variables (index and slope) and the performance within each condition (continuous flooding – CF and alternate wetting and drying – AWD). The results for days to flowering (FL), nitrogen balance index (NI) and panicle weight (PW) are presented. Two statistical models (GBLUP and RKHS) were used.

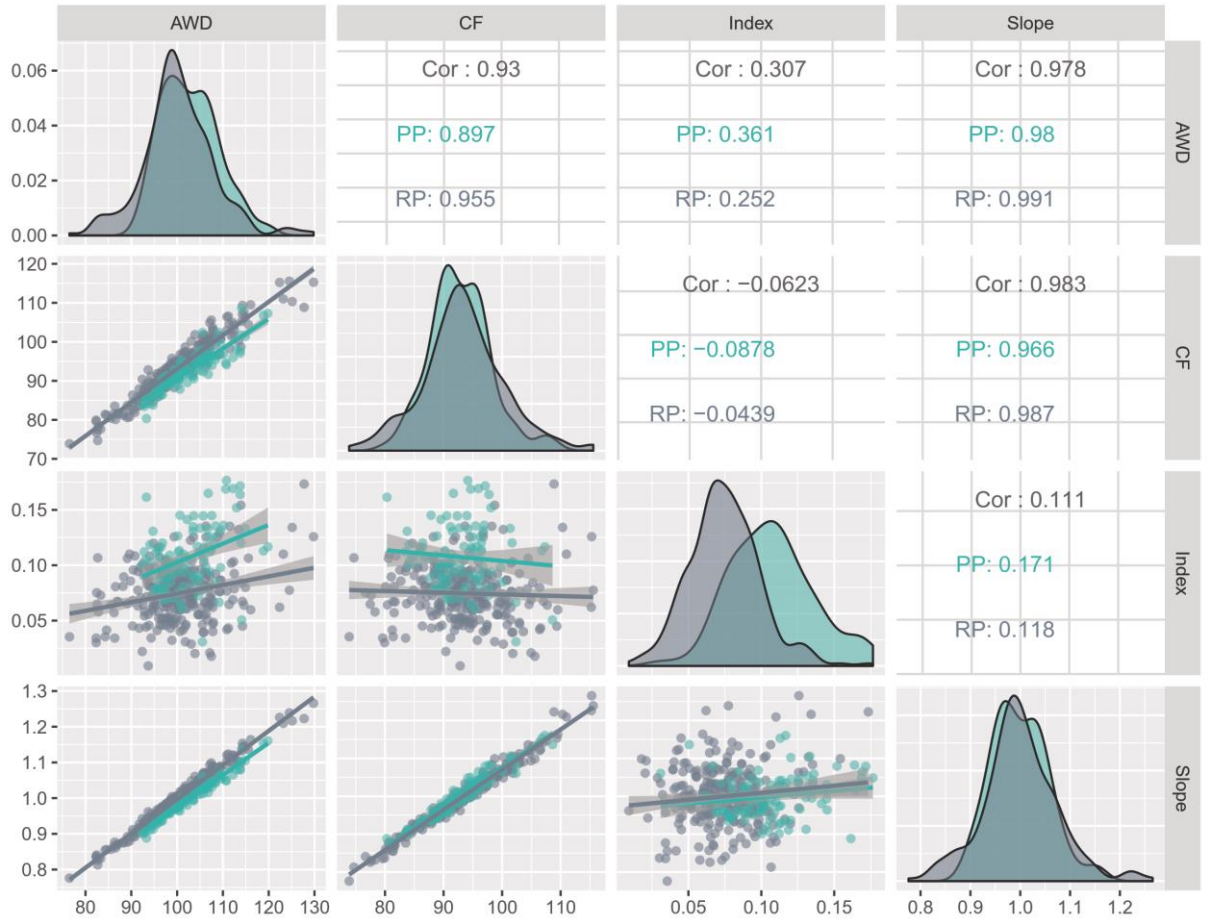
**Table S5:** Genomic predictive abilities for across population validation for the response variables (index and slope) and the performance within each condition (continuous flooding – CF and alternate wetting and drying – AWD). The scenarios used to define the training set are S1 (only the parents), S2 (100 individuals of the RP selected with CDmean) and S3 (the whole RP). Results for days to flowering (FL), nitrogen balance index (NI) and panicles weight (PW) are presented. Two statistical models (GBLUP and RKHS) were used.

**Table S6:** Mean genomic predictive ability of the performance within each condition (continuous flooding – CF and alternate wetting and drying – AWD) using single or multi-environment models in the reference population. For multi-environment models, two methods of cross-validation were used: M1 and M2. In addition to genomic predictive ability, the phenotypic predictive ability evaluated as the correlation between the performances in the two conditions using the same random sampling as in M2 cross-validation are provided. Results for days to flowering (FL), nitrogen balance index (NI) and panicle weight (PW) are presented. Two statistical models (GBLUP, RKHS) were used in single environment prediction and three (GBLUP, RKHS-1 and RKHS-2) in multi-environment prediction.

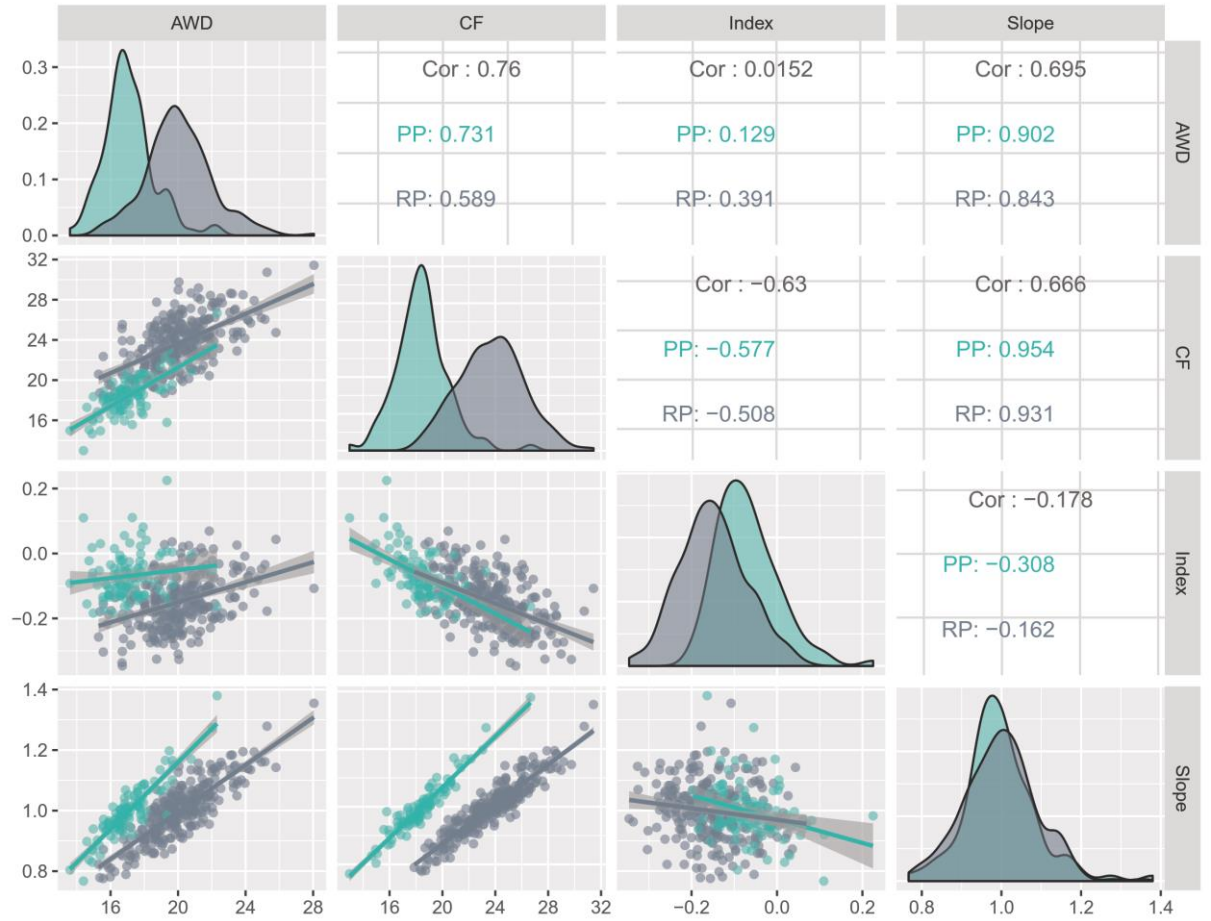
**Table S7:** Genomic predictive abilities of the performance within each condition (continuous flooding – CF and alternate wetting and drying – AWD) using single or multi-environment models for across population validation. The scenarios used to define the training set are S1 (only the parents), S2 (100 individuals of the RP selected with CDmean) and S3 (the whole RP). Results for days to flowering (FL), nitrogen balance index (NI) and panicle weight (PW) are presented. Two statistical models (GBLUP,

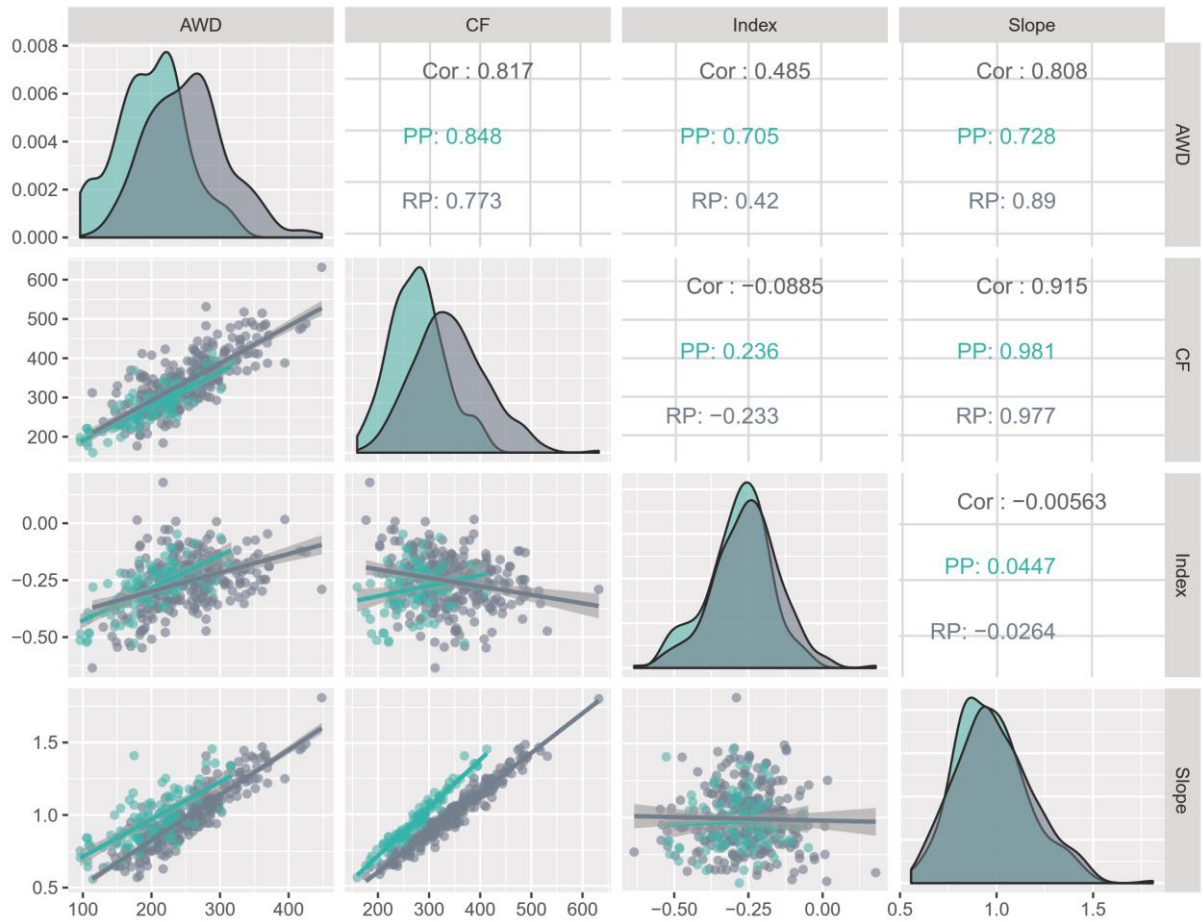
RKHS) were used in single environment prediction and three (GBLUP, RKHS-1 and RKHS-2) in multi-environment prediction.

**FL**

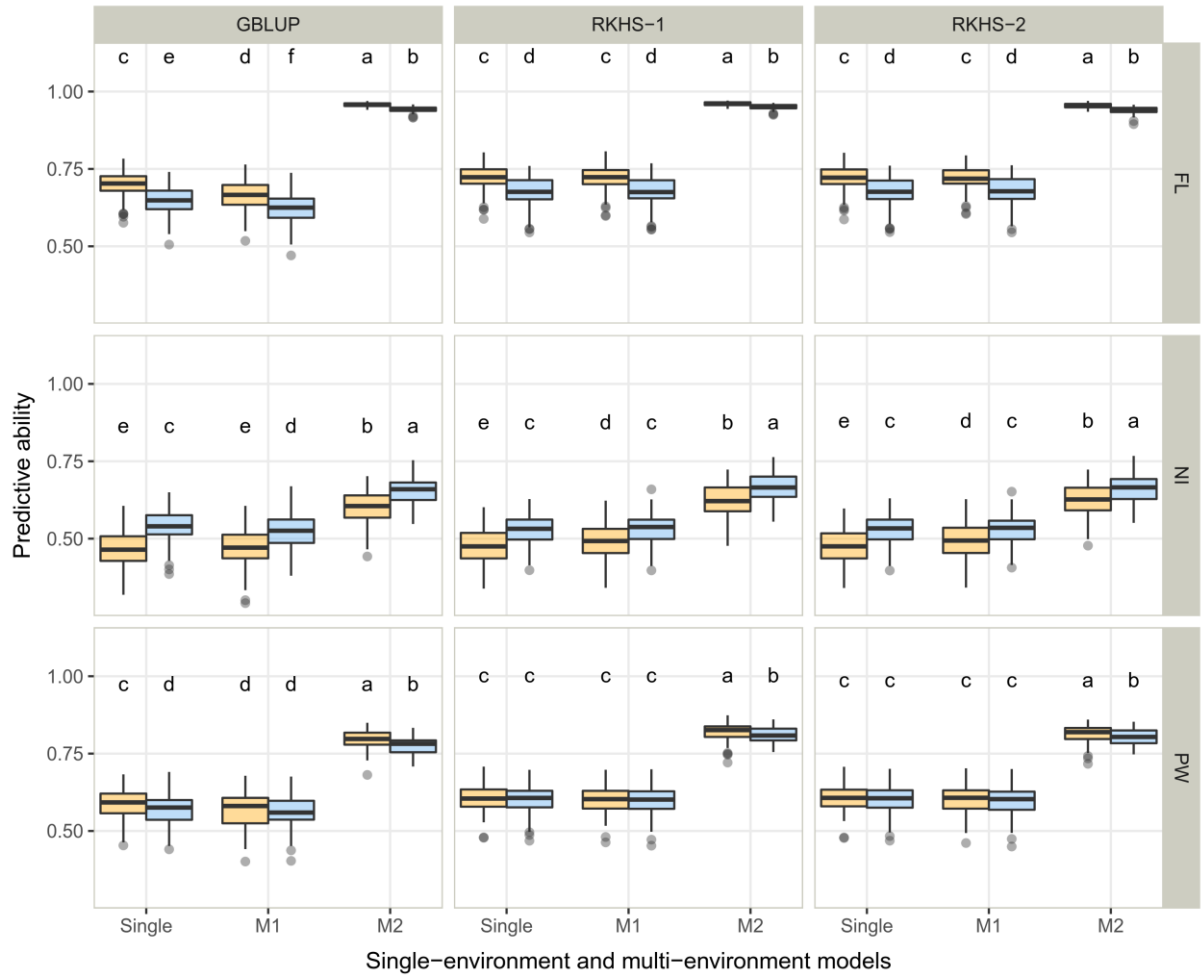


**NI**



**PW**

**Figure S1:** Correlation matrix between performance in each condition (continuous flooding – CF and alternate wetting and drying – AWD) and response variables (response index and slope of the joint regression) for the three traits considered: days to flowering (FL), nitrogen-balance index (NI), and panicle weight (PW). The reference (RP) and progeny (PP) populations are in green and grey, respectively.



**Figure S2:** Single environment and multi-environment (M1 and M2) predictive abilities in cross validation experiments with 40% of untested entries in the reference population obtained with three statistical models (GBLUP, RKHS-1, RKHS-2). Continuous flooding and alternate wetting and drying water management conditions are in blue and orange, respectively. Three traits are presented: days to flowering (FL), nitrogen balance index (NI) panicle weight (PW). The letters in each panel represent the results of Tukey's HSD comparison of means and apply to each panel independently. The means differ significantly ( $p$ -value < 0.05) if two boxplots have no letter in common.

**Table S1:** Variance components and the associated statistic (F-value for fixed effects and Z-value for random effects) of days to flowering (FL), nitrogen balance index (NI), and panicle weight (PW). Separate analysis of each population and each water management system (continuous flooding – CF and alternate wetting and drying – AWD).

Population	Trait	Condition	Fixed / Random	Source	Estimate	Standard error of the estimate	F or Z statistic	p-value
Reference	FL	AWD	Fixed	Year			1700.49	<.0001
			Random	Genotype	57.6813	5.5461	10.4	<.0001
				Year * Genotype	10.9007	1.2604	8.65	<.0001
				Residual	11.2789	0.4755	23.72	<.0001
		CF	Fixed	Year			753.03	<.0001
			Random	Genotype	47.7834	4.2925	11.13	<.0001
				Year * Genotype	4.3612	0.5405	8.07	<.0001
				Residual	5.9523	0.2501	23.8	<.0001
	NBI	AWD	Fixed	Year			82.39	<.0001
			Random	Genotype	4.9925	0.7344	6.8	<.0001
				Year * Genotype	1.2169	0.568	2.14	0.0161
				Residual	14.7108	0.6268	23.47	<.0001
		CF	Fixed	Year			87.34	<.0001
			Random	Genotype	6.1702	1.0147	6.08	<.0001
				Year * Genotype	4.0852	0.8514	4.8	<.0001
				Residual	16.7468	0.7088	23.63	<.0001
	PW	AWD	Fixed	Year			191.12	<.0001
			Random	Genotype	3435.39	390.5	8.8	<.0001
				Year * Genotype	949.48	189.58	5.01	<.0001
				Residual	3142.66	140.95	22.3	<.0001
		CF	Fixed	Year			39.66	<.0001
			Random	Genotype	5088.95	505.4	10.07	<.0001
				Year * Genotype	850.38	150.39	5.65	<.0001
				Residual	2437.24	105.68	23.06	<.0001
Progeny	FL	AWD	Fixed	Year			642.63	<.0001
			Random	Repetition			3.91	0.004
				Genotype	35.1488	6.0138	5.84	<.0001
				Year * Genotype	8.1658	1.7861	4.57	<.0001
		CF	Fixed	Year			656.75	<.0001
			Random	Repetition(Year)			7.84	<.0001
				Genotype	23.1957	3.9792	5.83	<.0001
				Year * Genotype	7.3783	1.1809	6.25	<.0001
				Residual	2.2718	0.1648	13.78	<.0001
	NBI	AWD	Fixed	Year			92.76	<.0001
			Random	Repetition(Year)			15.69	<.0001
				Genotype	3.0271	0.5762	5.25	<.0001
				Year * Genotype	0			
		CF	Fixed	Year			234.1	<.0001
			Random	Repetition(Year)			3.87	0.0043
				Genotype	4.1183	0.7624	5.4	<.0001
				Year * Genotype	0.696	0.3059	2.28	0.0114
				Residual	3.7236	0.2808	13.26	<.0001
	PW	AWD	Fixed	Year			224.57	<.0001
			Random	Repetition(Year)			36.36	<.0001
				Genotype	2487.8	408.02	6.1	<.0001
				Year * Genotype	466.32	93.7984	4.97	<.0001
		CF	Fixed	Year			19.33	<.0001
			Random	Repetition(Year)			51.44	<.0001
				Genotype	2698.52	435.18	6.2	<.0001
				Year * Genotype	415.49	88.7666	4.68	<.0001
				Residual	554	40.3973	13.71	<.0001

**Table S2:** Variance components and the associated statistic: F-value for fixed effects and Z-value for random effects) of days to flowering (FL), nitrogen balance index (NI), and panicle weight (PW). Separate analysis of each population pooled over water management conditions (continuous flooding – CF and alternate wetting and drying – AWD).

Population	Trait	Fixed / Random	Source	Estimate	Standard error of the estimate	F or Z statistic	Respective p-value
Reference	FL	Fixed	Year			1634.20	<.0001
			Condition			2294.10	<.0001
			Condition*Year			731.78	<.0001
		Random	Genotype	52.01	4.73	10.99	<.0001
			Year*Genotype	5.19	0.70	7.40	<.0001
			Condition*Genotype	0.32	0.35	0.91	0.1805
			Condition*Year*Genotype	2.49	0.47	5.31	<.0001
			Residual	8.63	0.26	33.53	<.0001
	NBI	Fixed	Year			2.06	0.1526
			Condition			476.53	<.0001
			Condition*Year			217.82	<.0001
		Random	Genotype	4.66	0.70	6.62	<.0001
			Year*Genotype	1.83	0.49	3.74	<.0001
			Condition*Genotype	0.92	0.43	2.16	0.0155
			Condition*Year*Genotype	0.81	0.54	1.49	0.068
			Residual	15.75	0.47	33.28	<.0001
	PW	Fixed	Year			36.59	<.0001
			Condition			914.07	<.0001
			Condition*Year			212.19	<.0001
		Random	Genotype	3961.99	395.27	10.02	<.0001
			Year*Genotype	15.53	118.61	0.13	0.4479
			Condition*Genotype	312.42	135.38	2.31	0.0105
			Condition*Year*Genotype	869.37	167.40	5.19	<.0001
			Residual	2787.24	87.08	32.01	<.0001
Progeny	FL	Fixed	Year			843.72	<.0001
			Rep(Year)			8.25	<.0001
			Condition			1168.88	<.0001
			Condition*Year			23.54	<.0001
		Random	Genotype	27.46	4.69	5.86	<.0001
			Year*Genotype	5.30	1.17	4.51	<.0001
			Condition*Genotype	1.68	0.69	2.45	0.0072
			Condition*Year*Genotype	2.49	0.71	3.51	0.0002
			Residual	7.01	0.36	19.52	<.0001
	NBI	Fixed	Year			268.27	<.0001
			Rep(Year)			8.56	<.0001
			Condition			85.02	<.0001
			Condition*Year			22.22	<.0001
		Random	Genotype	3.25	0.59	5.48	<.0001
			Year*Genotype	0.32	0.17	1.81	0.0352
			Condition*Genotype	0.32	0.18	1.79	0.037
			Condition*Year*Genotype	0.00			
			Residual	4.78	0.24	19.91	<.0001
	PW	Fixed	Year			47.35	<.0001
			Rep(Year)			64.92	<.0001
			Condition			689.06	<.0001
			Condition*Year			261.44	<.0001
		Random	Genotype	2394.72	390.55	6.13	<.0001
			Year*Genotype	163.54	66.14	2.47	0.0067
			Condition*Genotype	194.30	69.46	2.80	0.0026
			Condition*Year*Genotype	260.52	67.47	3.86	<.0001
			Residual	584.89	30.06	19.45	<.0001



**Table S3:** Variance components for the joint regression for days to flowering (FL), nitrogen balance index (NI), and panicle weight (PW). Results are shown for the reference and progeny populations.

Population	Trait	Joint regression parameters	Estimates	Standard error of the estimates	Z statistics	p-values	Confidence limits	
							Lower	Upper
Reference	FL	$\mu_i$	0					
	FL	$\beta_i$	1.0055	0.08439	11.91	<.0001	0.8586	1.1938
	NI	$\mu_i$	0					
	NI	$\beta_i$	1.0063	0.08462	11.89	<.0001	0.859	1.1951
	PW	$\mu_i$	357.34	2651.71	0.13	0.4464	39.2821	1.89E+89
	PW	$\beta_i$	1.0327	0.09148	11.29	<.0001	0.8745	1.2383
Progeny	FL	$\mu_i$	0					
	FL	$\beta_i$	1.003	0.144	6.96	<.0001	0.7712	1.3581
	NI	$\mu_i$	0					
	NI	$\beta_i$	1.007	0.1448	6.95	<.0001	0.7741	1.3641
	PW	$\mu_i$	2033.77	2511.54	0.81	0.209	457.74	432973
	PW	$\beta_i$	1.0045	0.1504	6.68	<.0001	0.7644	1.3792

**Table S4:** Mean genomic predictive abilities in the reference population for the response variables (index and slope) and the performance within each condition (continuous flooding – CF and alternate wetting and drying – AWD). The results for days to flowering (FL), nitrogen balance index (NI) and panicle weight (PW) are presented. Two statistical models (GBLUP and RKHS) were used.

Phenotype	Model	FL		NI		PW	
		Mean	SE	Mean	SE	Mean	SE
Index	GBLUP	0.29	0.12	0.21	0.11	0.43	0.10
Index	RKHS	0.30	0.13	0.17	0.12	0.48	0.09
Slope	GBLUP	0.69	0.08	0.59	0.08	0.62	0.07
Slope	RKHS	0.72	0.08	0.59	0.08	0.64	0.07
AWD	GBLUP	0.71	0.08	0.47	0.10	0.62	0.07
AWD	RKHS	0.74	0.08	0.48	0.09	0.63	0.06
CF	GBLUP	0.66	0.08	0.56	0.08	0.59	0.08
CF	RKHS	0.70	0.08	0.55	0.08	0.62	0.07

**Table S5:** Genomic predictive abilities for across population validation for the response variables (index and slope) and the performance within each condition (continuous flooding – CF and alternate wetting and drying – AWD). The scenarios used to define the training set are S1 (only the parents), S2 (100 individuals of the RP selected with CDmean) and S3 (the whole RP). Results for days to flowering (FL), nitrogen balance index (NI) and panicles weight (PW) are presented. Two statistical models (GBLUP and RKHS) were used.

Phenotype	Scenario	Model	FL	NI	PW
Index	S1	GBLUP	0.24	0.16	0.17
		RKHS	0.15	-0.10	0.14
	S2	GBLUP	-0.01	0.04	0.19
		RKHS	0.00	-0.06	0.15
	S3	GBLUP	0.24	0.17	0.17
		RKHS	0.21	0.12	0.25
Slope	S1	GBLUP	0.30	0.25	0.51
		RKHS	0.38	0.04	0.56
	S2	GBLUP	0.20	0.35	0.32
		RKHS	0.22	0.36	0.32
	S3	GBLUP	0.32	0.43	0.45
		RKHS	0.37	0.45	0.52
AWD	S1	GBLUP	0.32	0.25	0.51
		RKHS	0.37	0.03	0.54
	S2	GBLUP	0.23	0.27	0.39
		RKHS	0.25	0.24	0.40
	S3	GBLUP	0.34	0.36	0.42
		RKHS	0.37	0.38	0.49
CF	S1	GBLUP	0.27	0.19	0.48
		RKHS	0.37	-0.03	0.56
	S2	GBLUP	0.14	0.27	0.28
		RKHS	0.16	0.29	0.31
	S3	GBLUP	0.28	0.39	0.42
		RKHS	0.36	0.41	0.52

**Table S6:** Mean genomic predictive ability of the performance within each condition (continuous flooding – CF and alternate wetting and drying – AWD) using single or multi-environment models in the reference population. For multi-environment models, two methods of cross-validation were used: M1 and M2. In addition to genomic predictive ability, the phenotypic predictive ability evaluated as the correlation between the performances in the two conditions using the same random sampling as in M2 cross-validation are provided. Results for days to flowering (FL), nitrogen balance index (NI) and panicle weight (PW) are presented. Two statistical models (GBLUP, RKHS) were used in single environment prediction and three (GBLUP, RKHS-1 and RKHS-2) in multi-environment prediction.

Conditions	Type	Model	FL		NI		PW	
			Mean	SE	Mean	SE	Mean	SE
AWD	Single	GBLUP	0.71	0.08	0.47	0.1	0.61	0.07
		RKHS	0.74	0.08	0.48	0.09	0.63	0.06
	M1	GBLUP	0.67	0.08	0.48	0.1	0.6	0.07
		RKHS-1	0.74	0.08	0.5	0.1	0.63	0.06
		RKHS-2	0.73	0.08	0.5	0.09	0.63	0.07
		GBLUP	0.96	0.01	0.59	0.09	0.8	0.04
		RKHS-1	0.96	0.01	0.62	0.09	0.84	0.04
		RKHS-2	0.96	0.01	0.62	0.09	0.83	0.04
	Phenotype		0.96	0.01	0.57	0.1	0.78	0.05
CF	Single	GBLUP	0.66	0.08	0.56	0.08	0.59	0.08
		RKHS	0.7	0.08	0.55	0.08	0.62	0.07
	M1	GBLUP	0.63	0.09	0.54	0.09	0.59	0.08
		RKHS-1	0.69	0.08	0.55	0.09	0.62	0.07
		RKHS-2	0.69	0.09	0.55	0.08	0.61	0.07
		GBLUP	0.95	0.01	0.65	0.07	0.78	0.04
		RKHS-1	0.95	0.01	0.66	0.07	0.82	0.04
		RKHS-2	0.95	0.01	0.66	0.07	0.82	0.04
	Phenotype		0.95	0.01	0.58	0.09	0.77	0.06

**Table S7:** Genomic predictive abilities of the performance within each condition (continuous flooding – CF and alternate wetting and drying – AWD) using single or multi-environment models for across population validation. The scenarios used to define the training set are S1 (only the parents), S2 (100 individuals of the RP selected with CDmean) and S3 (the whole RP). Results for days to flowering (FL), nitrogen balance index (NI) and panicle weight (PW) are presented. Two statistical models (GBLUP, RKHS) were used in single environment prediction and three (GBLUP, RKHS-1 and RKHS-2) in multi-environment prediction.

Condition	Scenario	Model	Type	FL	NI	PW
AWD	S1	GBLUP	Single	0.32	0.252	0.513
		GBLUP	Multi	0.307	0.362	0.435
		RKHS	Single	0.365	0.027	0.537
		RKHS-1	Multi	0.379	0.036	0.521
		RKHS-2	Multi	0.375	0.087	0.546
	S2	GBLUP	Single	0.227	0.268	0.391
		GBLUP	Multi	0.284	0.338	0.255
		RKHS	Single	0.248	0.239	0.398
		RKHS-1	Multi	0.259	0.301	0.333
		RKHS-2	Multi	0.281	0.293	0.36
	S3	GBLUP	Single	0.339	0.364	0.423
		GBLUP	Multi	0.358	0.418	0.338
		RKHS	Single	0.371	0.379	0.494
		RKHS-1	Multi	0.389	0.439	0.463
		RKHS-2	Multi	0.387	0.462	0.478
CF	S1	GBLUP	Single	0.269	0.189	0.48
		GBLUP	Multi	0.199	0.196	0.504
		RKHS	Single	0.369	-0.034	0.562
		RKHS-1	Multi	0.356	-0.031	0.57
		RKHS-2	Multi	0.356	-0.029	0.578
	S2	GBLUP	Single	0.144	0.271	0.282
		GBLUP	Multi	0.202	0.316	0.306
		RKHS	Single	0.158	0.285	0.314
		RKHS-1	Multi	0.168	0.33	0.322
		RKHS-2	Multi	0.184	0.312	0.347
	S3	GBLUP	Single	0.284	0.391	0.417
		GBLUP	Multi	0.295	0.324	0.443
		RKHS	Single	0.362	0.405	0.517
		RKHS-1	Multi	0.354	0.362	0.516
		RKHS-2	Multi	0.36	0.389	0.526