Table 1 Suppl. Average activities of α-amylase [μmol(maltose) g^{-1}(protein) min^{-1}], pyruvate decarboxylase (PDC) [μmol(NADH) g^{-1}(protein) min^{-1}], alcohol dehydrogenase (ADH) [μmol(NADH) g^{-1}(protein) min^{-1}], and phosphofructokinase (PFK) [μmol(NADH) g^{-1}(protein) min^{-1}]; and relative quantification (RQ) values of genes - *calcineurin B-like protein-like protein kinase 15* (*CIPK15*), *rice amylase 3D* (*Ramy3D*), *myeloblastosis related protein S1* (*MYBS1*), *sucrose nonfermenting 1 related protein kinase* (*SnRK1A*), *ethylene insensitive 3-like 1a* (*OsEIL1a*), transcription factors - ethylene responce factors 63 and 71 (ERF63, ERF71), and proteins - expansins A2, A4, A7, and A12 (EXPA2, EXPA4, EXPA7, EXPA12 in different Assam rice genotypes IR-64, RKB, and KHO.

ID	Enzyme and gene name	Enzyme activities and RQ values		
		IR-64	RKB	KHO
1	α-amylase activity	13.2	32.2	21.27
2	PDC activity	1.45	2.75	3.62
3	ADH activity	23	27	20
4	PFK activity	1.45	3.64	4.33
5	CIPK-15	1	0.41	0.43
6	RAmy3D	1	2.59	2.69
7	MyBS1	1	10.22	2.59
8	SnRK1A	1	2.6	2.29
9	OsEIL1a	1	3.2	2.2
10	EXPA7	1	2.3	0.76
11	EXPA12	1	0.18	0.11
12	EXPA2	1	2.57	0.16
13	EXPA4	1	0.37	0.3
14	ERF63	1	2.75	2.91
15	ERF71	1	4.8	2.87

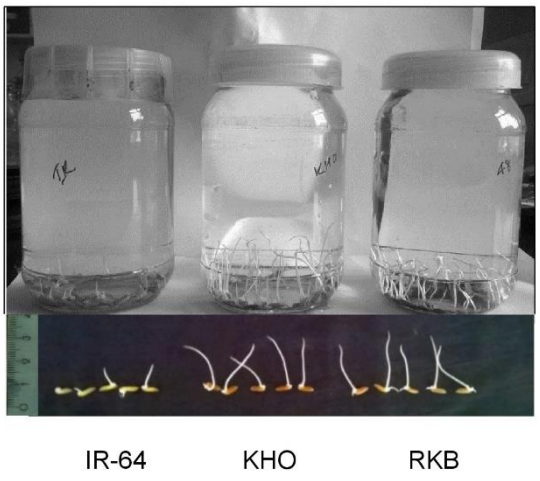
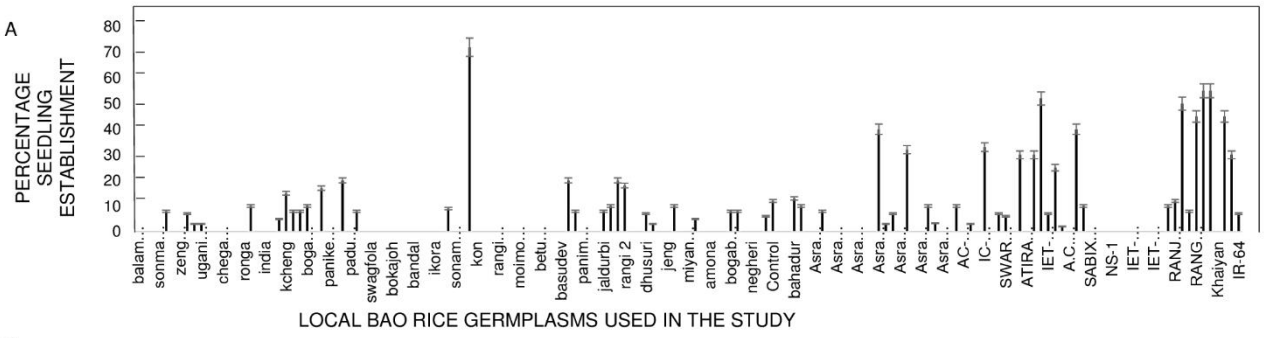


Fig. 1 Suppl. Photographs of 4-d-old seedlings of rice genotypes IR-64, KHO, and RKB differing in anaerobic tolerance.



B

Germplasms	%Anaerobic germination	Water head Reach (days)	% Establishment
Khaiyan	0	0	0
Ma zhan (red)	30	9	30
Khao hlan on	58	9	45
Rangdharkekua	78	11	72
IR-64	8	15	0

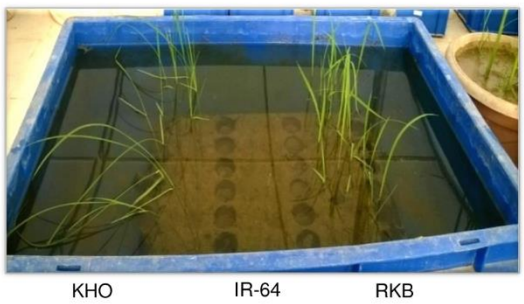


Fig. 2 Suppl. *A* - Initial screening deep water rice Assam local landraces for germination and early growth in anaerobic conditions caused by flooding with respect to genotypes KHO (positive control) and IR-64 (negative control). Rangdhakekua bao (RKB) was observed to have a high establishment percentage. *B* - Comparison of the tolerance of different genotypes in terms of germination percentage, days to touch standing water head, and establishment percentage. *C* - Photographs of 12-d-old seedlings of genotypes KHO, IR-64, and RKB grown under anaerobic conditions.

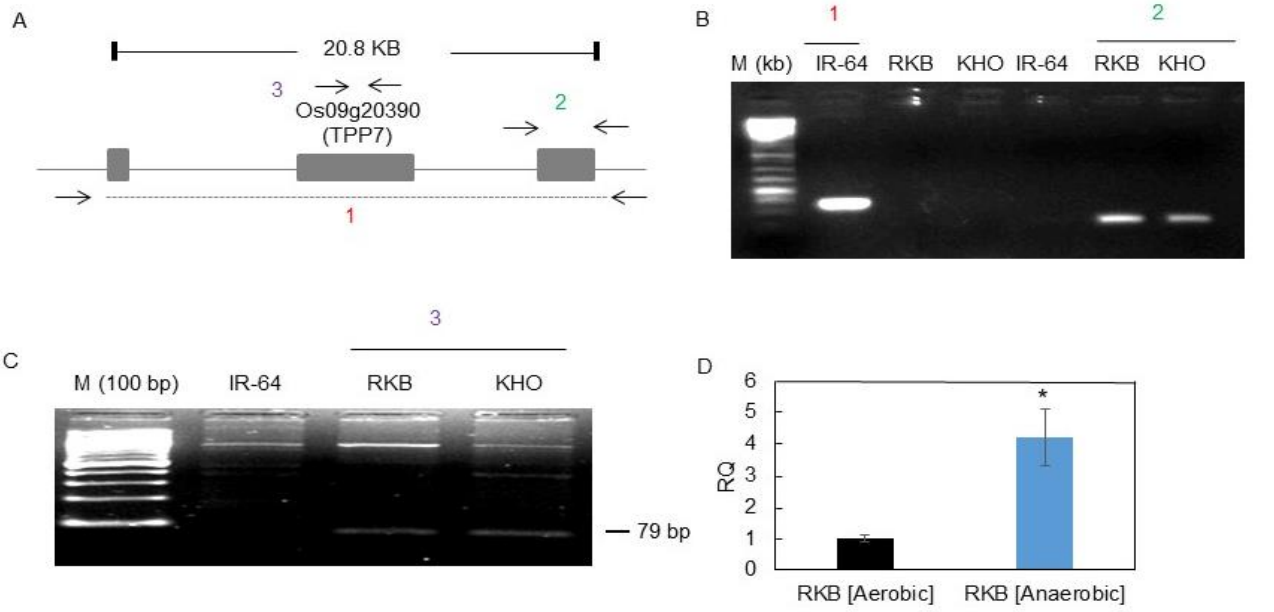


Fig. 3 Suppl. *A* - A schematic diagram showing the presence or absence of a 20.8 kb deletion according to Kretzschmar *et al*. (2015). A flanking marker from outside the border of quantitative trait locus would generate an amplified product. 1 - absence of 20.8 kb deletion, 2 - 20.8 kb deletion, 3 - amplified product. *B* - The presence of amplified product (1) in a genotype IR-64 and its absence in genotypes KHO and RKB. *C* - Amplified product (3) for confirming the presence of *trehalose phosphate phosphatase 7* (*TPP7*) in the genotypes KHO and RKB (2). *D* - Total mRNA accumulation of *TPP7* in the genotype RKB under aerobic and anaerobic stress conditions were determined using quantitative real time reverse transcription PCR. RQ - relative quantification. Means ± SDs of three biologically independent experiments, each with duplicate samples. Statistical significance (*) set at $P < 0.05$; one-way *ANOVA*, followed by the Tukey's honestly significantly difference *post hoc* test.