

Erratum to: Identification of novel rice low phytic acid mutations via TILLING by sequencing

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In Table 3, there were three errors in the values reported for the “100-grain weight” column, which affect three parts of the manuscript. The authors apologize to the readers of Molecular Breeding for all inconveniences caused by these mistakes. The paper should be modified as follows:

1. In Abstract section, the sentence starting with “Evaluation of these lines...” should read as “Evaluation of these lines indicates that one of the ITPK mutants (46 % InsP₆ reduction) and one of the MRP mutants are similar to wild-type plants in seed weight, germination, and seedling growth”.
2. In Results section, under the heading “Grain weight, germination, and seedling growth of *lpa* mutants”, the first two sentences should read as “Although none of the homozygous *lpa* mutants exhibited obvious developmental defects, the IPTK splice mutant and the A1427T MRP mutant did show a significant reduction in grain weight (Table 3). Compared to wild type, the IPTK splicing site mutant and the A1427T MRP mutant had a 5 and 15 % reduction in 100-grain weight, respectively”.
3. In Discussion, the sentence starting with “In this study, two severe *lpa* mutants....” should read as “In this study, two severe *lpa* mutants (ITPK splicing site and *OsMIK*) showed significant delays in germination and seedling growth”.

The online version of the original article can be found under doi:[10.1007/s11032-014-0127-y](https://doi.org/10.1007/s11032-014-0127-y).

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Table 3 Comparison of seed dry weight and phosphorus contents of rice mutants and wild-type (Nipponbare)

Gene	Mutant line	100-grain weight (g) ^a	P contents (mg g ⁻¹ seed)			InsP ₆ reduction
			InsP ₆ ^b	Pi ^b	Total P ^b	
Wild type	Nipponbare	2.37 ± 0.02	2.55 ± 0.18	0.53 ± 0.15	3.30 ± 0.11	–
OsMIK (Os03g5276) [†]	Nonsense	2.35 ± 0.05	0.65 ± 0.21*	2.55 ± 0.33*	3.03 ± 0.51	74 %
ITPK (Os09g34300)	Splice	2.27 ± 0.03*	0.82 ± 0.40*	1.88 ± 0.21*	3.25 ± 0.21	68 %
	Substitution (P522L)	2.30 ± 0.14	1.38 ± 0.65*	1.75 ± 0.50*	3.31 ± 0.78	46 %
MRP (Os03g04920)	Substitution (L733F)	2.39 ± 0.08	1.79 ± 0.69*	1.25 ± 0.33*	3.55 ± 1.11	30 %
	Substitution (A1427T)	2.02 ± 0.07**	2.04 ± 0.78*	1.05 ± 0.32*	3.44 ± 0.51	20 %

Mutant line: Nonsense mutation, Splice; splicing site altered, Substitution (amino acid substitution and position in peptide)

All values are means and standard deviation from three independent assays

*, ** Significant difference from wild type by a Student's *t* test at the level of $P = 0.05$ and $P = 0.01$, respectively

[†] *lpa* control (Kim et al. 2008b)

^a 100-grain weight was measured from manually counted 100 grains from three homozygous *lpa* mutants

^b Total P, phytic acid P, and inorganic P are expressed as phosphorus (atomic weight $P = 31$) concentration to facilitate comparison