

Phytosiderophores determine thresholds for iron and zinc accumulation in biofortified rice endosperm while inhibiting accumulation of cadmium

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Supporting information

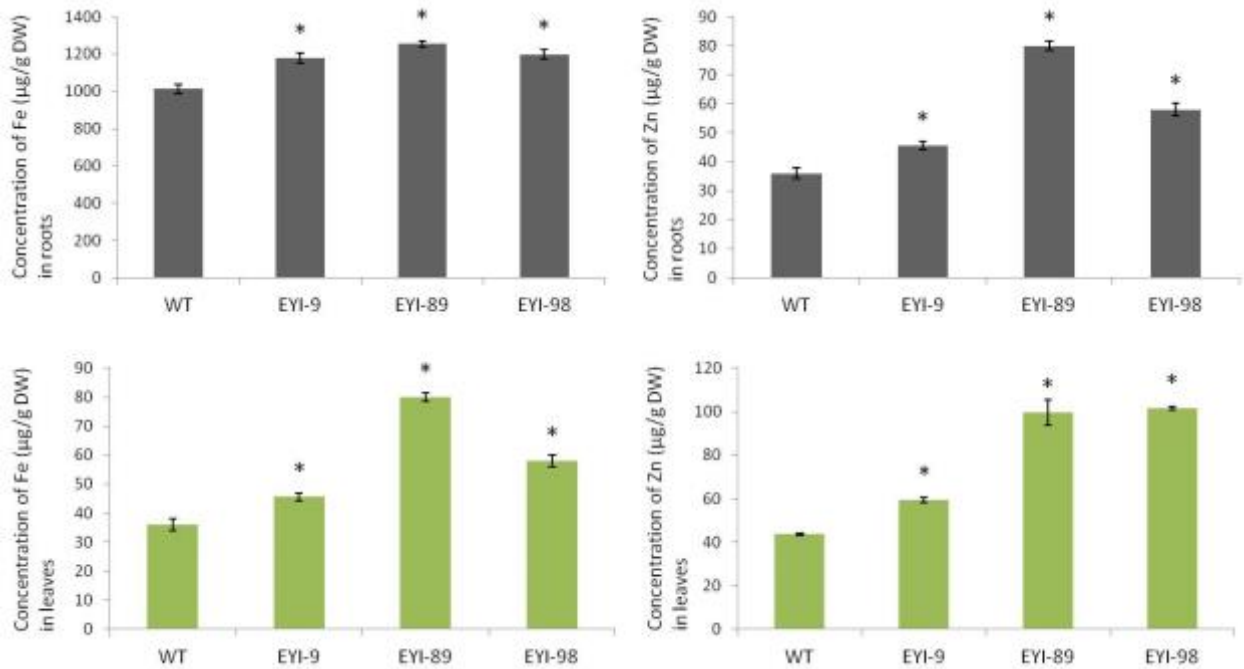


Fig. S1. Fe and Zn content ($\mu\text{g g}^{-1}$ DW) in roots and leaves of wild-type (WT) rice and three different T_1 transgenic lines co-expressing *OsNAS1* and *HvNAATb* (EYI-9, EYI-89 and EYI-98). DW = dry weight. Asterisks indicate a statistically significant difference between wild-type and transgenic plants as determined by Student's *t*-test ($p < 0.05$; $n = 6$). Roots and leaves from the wild-type and transgenic lines were harvested at the vegetative stage.

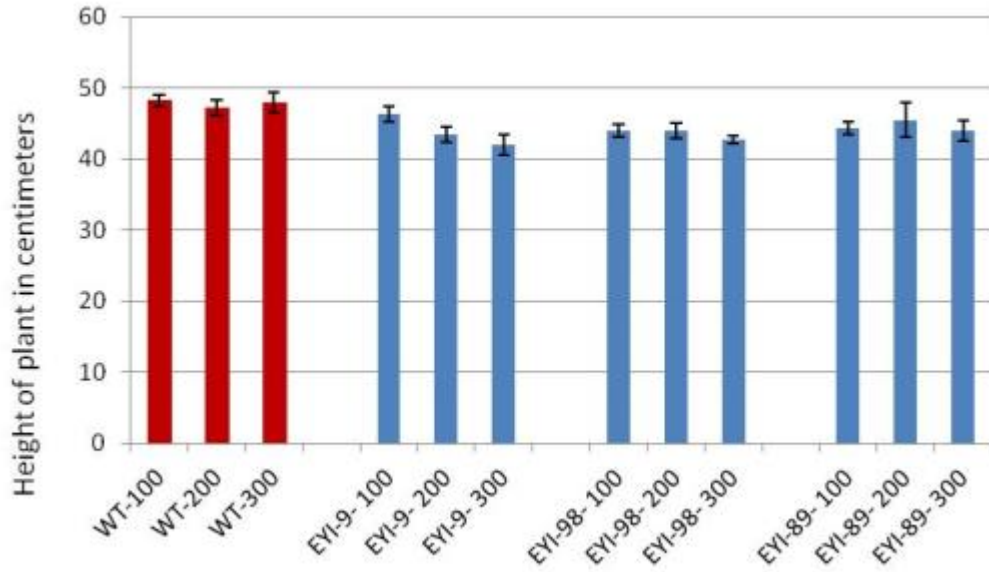


Fig. S2. Height of wild type and T₂ transgenic plants co-expressing *OsNAS1* and *HvNAATb* (EYI-9, EYI-89 and EYI-98). Data are means (n = 6).

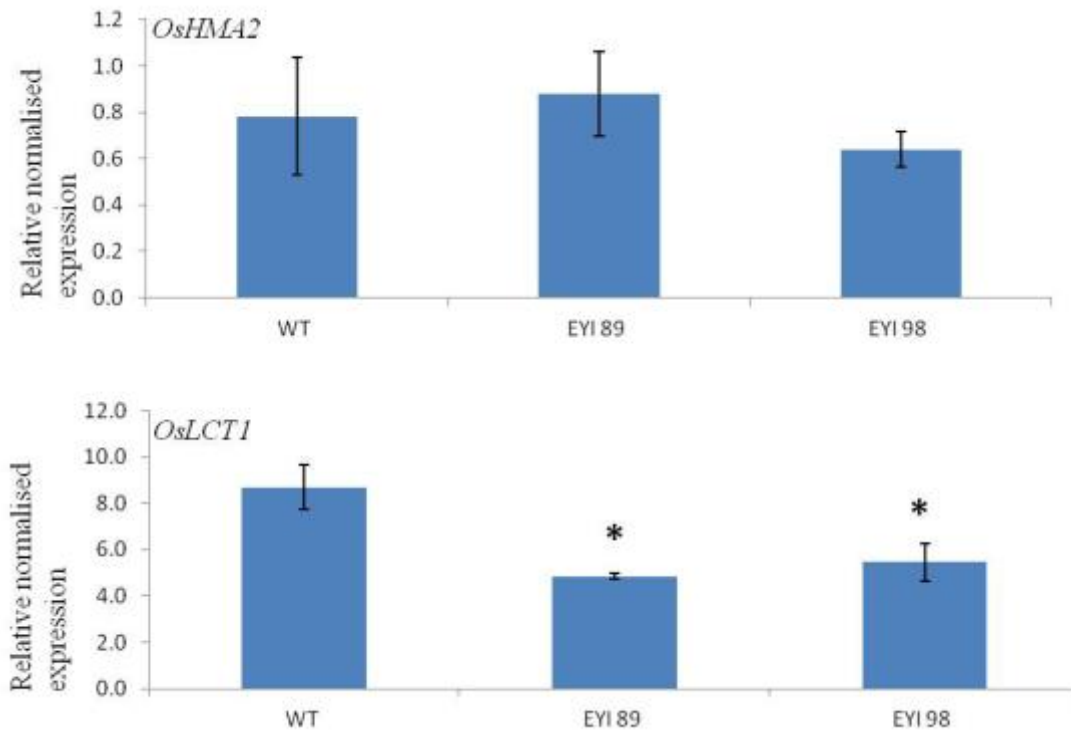


Fig. S3. Quantitative real-time RT-PCR analysis of *OsHMA2* and *OsLCT1* following the treatment of wild-type (WT) plants and T₃ transgenic lines co-expressing *OsNAS1* and *HvNAATb* (EYI-89, EYI-98) with 10 mM Cd at the grain-filling stage. Each value is the

mean of three independent experiments \pm SE. Relative transcript levels are normalized against *OsACTIN1*. Asterisks indicate a statistically significant difference between wild-type and transgenic plants as determined by Student's *t*-test ($p < 0.05$; $n = 3$). Gene-specific primers are listed in Supplementary Table S2. Both the wild-type and transgenic lines were grown under nutrient sufficient conditions, and the seeds were harvested at the grain-filling stage for total RNA isolation.

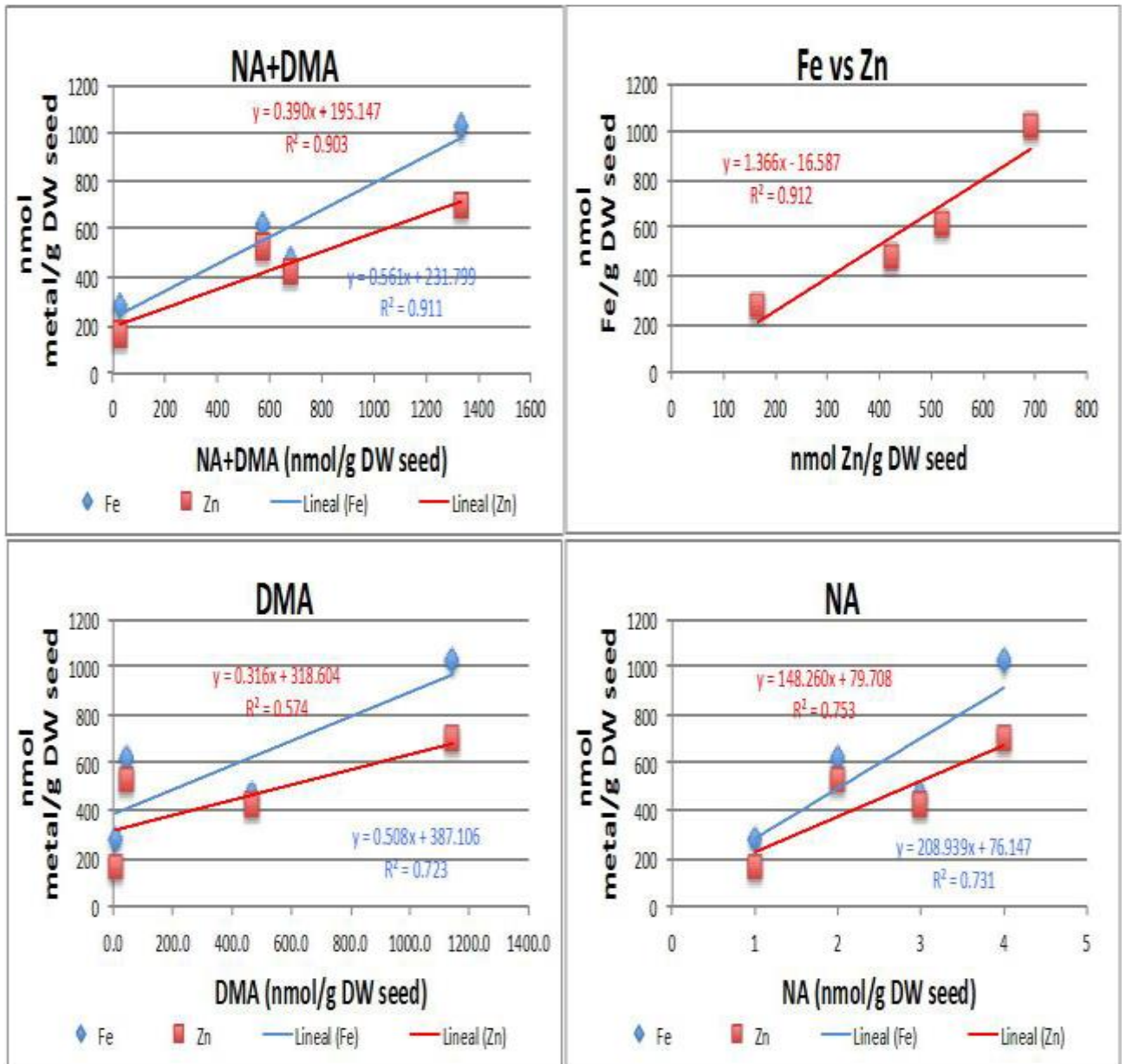


Fig. S4. Scatter graph and linear correlations between NA and/or DMA levels and Fe (blue diamonds) and Zn (red squares) levels in the unpolished seeds of wild-type plants and T₂ transgenic lines co-expressing *OsNAS1* and *HvNAATb* (EYI-9, EYI-89 and EYI-98).

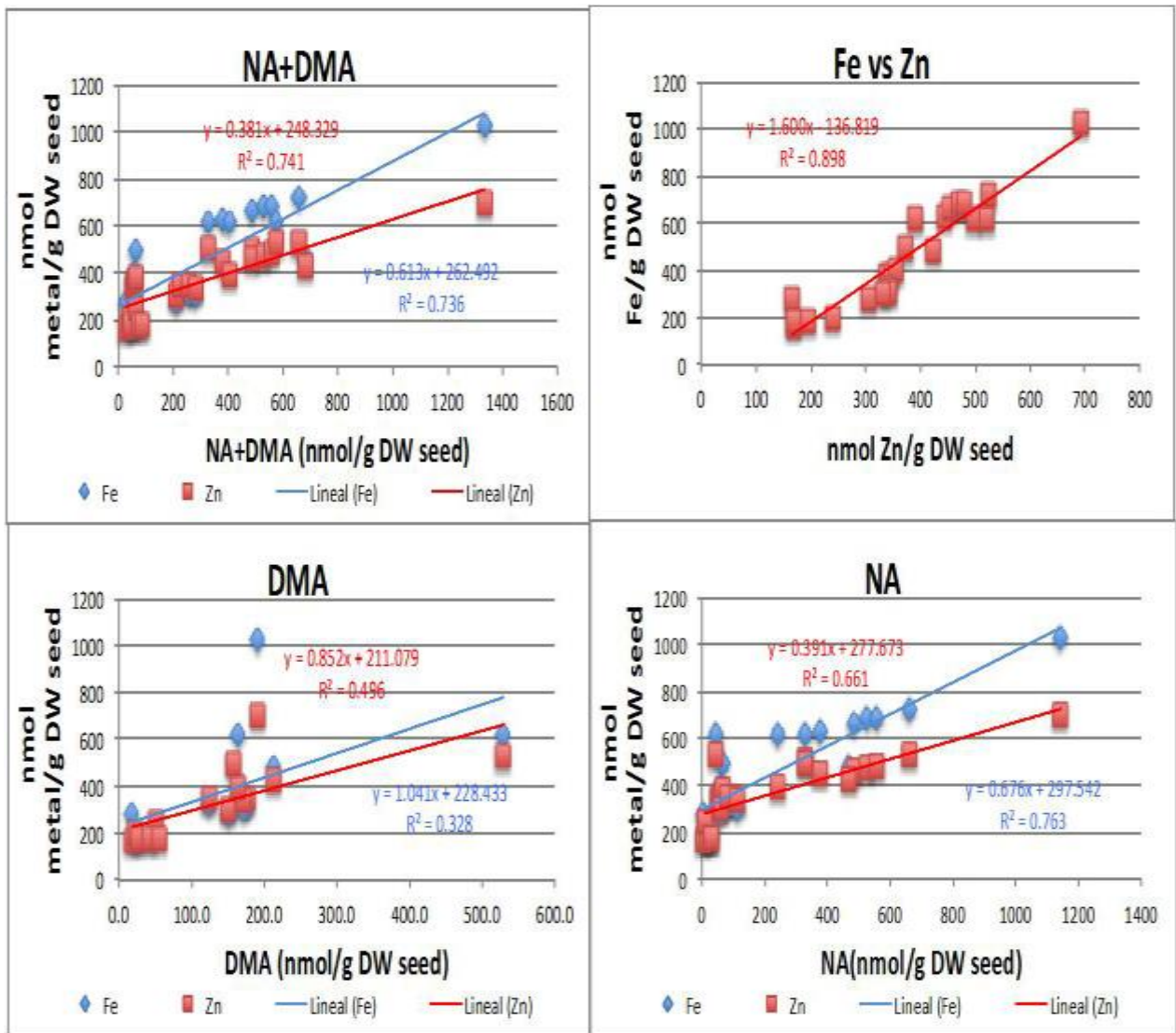


Fig. S5. Scatter graph and linear correlation between unpolished grain NA and/or DMA levels and Fe (blue diamonds) and Zn (red square) levels for the genotypes in Figure 2 and for those reported by others (Lee *et al.*, 2009; Johnson *et al.*, 2011; Lee *et al.*, 2011; Masuda *et al.*, 2012).

Gene	GenBank ID	Amplicon (bp)	Forward primer	Reverse primer
<i>Primers for cloning</i>				
<i>OsNAS1</i>	AB021746.2	999 bp	<i>OsNAS1</i> -BamHI-FOR AGG ATC CAT GGA GGC TCA GAA CCA AGA GGT CG	<i>OsNAS1</i> -HindIII-REV AAA GCT TCA TAA TAT AGT GCG CCT TTC GAT CGT CCG GCT GT
<i>HvNAATb</i>	AB005788.1	1656 bp	<i>HvNAATb</i> -BamHI-FOR AGG ATC CAT GGC CAC CGT ACG GCC AGA GAG CGA CG	<i>HvNAATb</i> -HindIII-REV AAA GCT TCT AGC AAT CAT CGC TCG CTC GAA TTT CTC
<i>Primers for real-time RT-PCR</i>				
<i>OsYSL15</i>	AB190923.1	78	CTGGTGCTGTTTGCTTGGGA	ATGAGCCCAGACGCAACAGC
<i>OsIRT1</i>	BAB85123.1	139	GCATCATGCAATTCGCTGC	CCTGAACAACCACGCTACAA
<i>OsZIP1</i>	AY324148.1	90	CGATGGTCCTCTTCTTCTGC	GTCGGGCTGCTCTCGTTGTA
<i>OsZIP4</i>	AB126089.1	107	TCCACCAGTTCTTTGAAGGC	CGGAGCAGTGAGGGAGAAGA
<i>OsVIT1</i>	NM_001059545.1	107	CCACAGCACAGAACGCCAT	GCTGAGGAATGGACGGTTT
<i>OsYSL2</i>	AB164646	169	GGTGGAGAGAGTTGTGGGTT	TCATTCCCGCACCAACATA
<i>OsFERRITIN1/ OsFERRITIN2</i>	AF519570.1/ AF519571.1	132	GCTTGAATGGAGGAGACTGTG	CTCCATTGCTACTGCGTGCT
<i>OsLCT1</i>	AB905364.1	100	GCTCAAGTGGATGGCGGACA	GCCACCATCTGTCTTGCTT
<i>OsHMA2</i>	AB697186.1	126	CGAGGAATACACCCGCATCAGC	CAAGCAGAGCCACGAAAAGAGC
<i>OsACTIN1</i>	AB047313.1	120	TCA TGT CCC TCA CAA TTT CC	GAC TCT GGT GAT GGT GTC AGC

Table S1. Genes and primers for cloning and quantitative real time RT-PCR analysis.

Line	Fe in unpolished seeds ($\mu\text{g/g DW}$)	Zn in unpolished seeds ($\mu\text{g/g DW}$)
EYI-9	26.35 *	47.49*
EYI-89	56.68*	77.80*
EYI-98	34.47*	58.7*
EYI-0.7	33*	43*
EYI-0.2	30*	42*
EYI-38	25*	37*
EYI-4	26.29*	28.02*
EYI-8	22.96*	21.57*
EYI-12	23.42*	23.24*
EYI-121	21.92*	22.77*
WT	15.33	18.51

Table S2. Fe and Zn content of unpolished seeds from wild-type (WT) and T₂ transgenic rice plants. DW = dry weight. Ten independent transgenic lines co-expressing *OsNAS1* and *HvNAATb* are shown. Asterisks indicate a statistically significant difference between wild-type and transgenic plants as determined by Student's *t*-test ($p < 0.05$; $n = 6$). Both the WT and transgenic lines were grown in nutrient sufficient conditions, and the seeds were harvested at physiological maturity.