Selection of a promising donor for developing zinc-biofortified rice based on genomic prediction model

Increasing zinc (Zn) concentrations in edible parts of food crops, an approach termed Zn-biofortification, is a global breeding objective to alleviate micro-nutrient malnutrition. In particular, infants in countries like Madagascar are at risk of Zn deficiency because their dominant food source, rice, contains insufficient Zn. Biofortified rice varieties with increased grain Zn concentrations would offer a solution and our objective is to explore the genotypic variation present among rice gene bank accessions and verify their performance under farmers' field conditions. A training set of 253 rice accessions was grown at two field sites in Madagascar. A genomic prediction model was developed from the above training set to predict brown rice Zn concentrations of 3,024 sequenced rice accessions. Predicted concentrations ranged from 17.1 to 40.2 ppm Zn with significant differences among rice sub-populations, of which *aus* group (n=201) had highest Zn concentrations (Fig. 1). The prediction accuracy of the developed model was evaluated using 61 previously untested accessions, and the relatively high coefficient of determination (R^2=0.55) between measured and predicted values confirmed the model validity (Fig. 2). Very high predicted grain Zn concentrations of accessions belonging to the *aus* sub-species were confirmed in additional field experiments, with one potential donor (IRIS313-9368) having more than twice the grain Zn compared to a local check variety (X265) (Fig. 3). We conclude that utilizing donors from the *aus* sub-species and employing genomic selection during the breeding process are the most promising approaches to raise grain Zn concentrations in rice.

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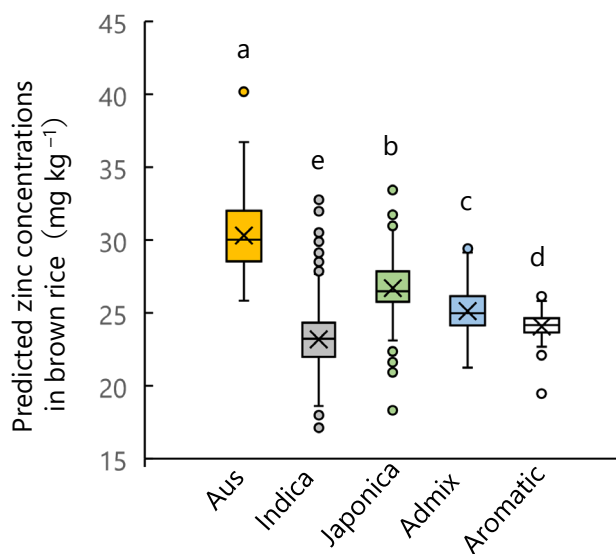*International Development (CIRAD)])*

Fig. 1. Predicted variations in brown rice zinc concentrations of 3,024 accessions from five rice sub-populations

Aus (n=201); Indica (n=1,089); Japonica (n=855); Admix (n=103); Aromatic (n=76). Different alphabets indicate significant differences in the means (shown in ×) among sub-populations by Tukey's HSD at $P<0.05$. The sub-populations were categorized by IRRI genebank.
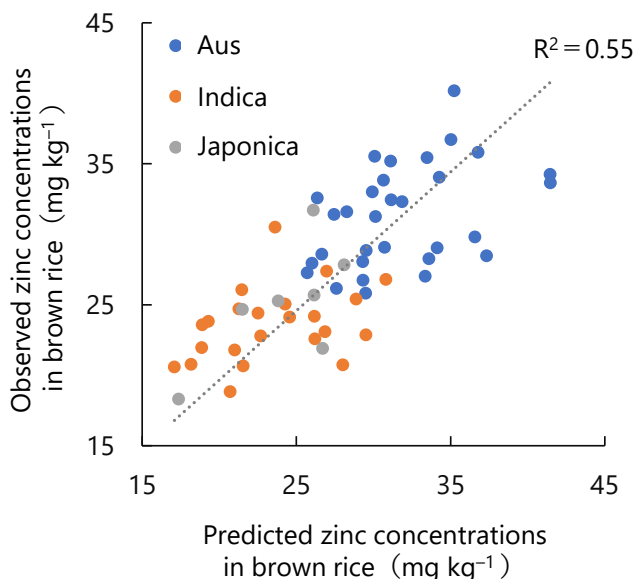

Fig. 2. Relationship between observed and predicted brown rice zinc concentrations of 61 unseen accessions
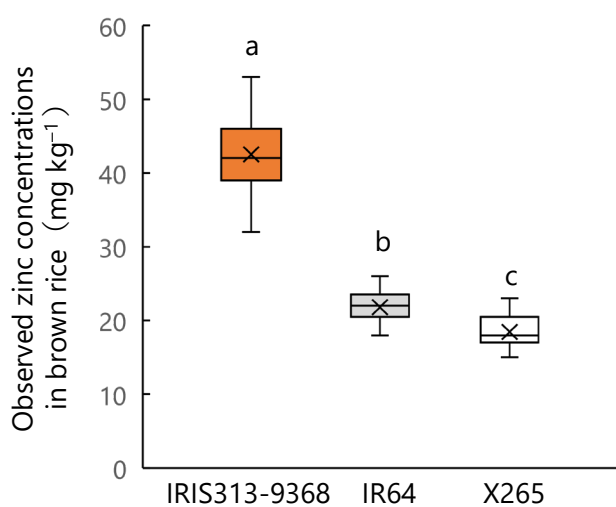

Fig. 3. Observed brown rice zinc concentrations of three rice accessions across 10 different growth conditions

IRIS313-9368: the aus type predicted to have high Zn concentration; IR64: a popular high-yielding lowland variety in the tropical region; X265: a leading lowland variety in Madagascar. Different alphabets indicate significant differences in the means (shown in ×) among sub-populations by Tukey's HSD at $P<0.05$.

Reference: Rakotondramanana et al. (2022) *Theoretical and Applied Genetics* 135: 2265−2278.
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