

Genetic Analysis of Mineral Accumulation in *Arabidopsis thaliana* and *Brassica rapa*

Mark G.M. Aarts¹, Artak Ghandilyan¹, Jian Wu^{1,2}, Juan Du³, Henk Schat⁴, Rifei Sun², Maarten Koornneef¹, Hong-Qing Ling³, Xiaowu Wang²

¹ Laboratory of Genetics, Wageningen University, Arboretumlaan 4, 6703 BD, Wageningen, The NETHERLANDS (mark.aarts@wur.nl)

² Institute of Vegetables and Flowers, Chinese Academy of Agricultural Sciences, P.R. CHINA

³ Institute of Genetics and Developmental Biology, Chinese Academy of Sciences, P.R. CHINA

⁴ Ecology and Physiology of Plants, Faculty of Biology, Vrije Universiteit, The NETHERLANDS

INTRODUCTION

Zinc and Fe are essential micronutrients required by all organisms for their function in many cellular processes. Zinc and Fe deficiency is also a serious problem for the human population causing wide-spread malnutrition. Improving Zn and Fe content in edible plant parts can provide a solution to reduce this malnutrition. Unfortunately, little is known so far about the genes that are relevant or even crucial for modifying Zn or Fe accumulation in plants. We used a genetic approach to identify quantitative trait loci (QTL) that are involved in the accumulation of nutrients, including Zn and Fe, in *Arabidopsis thaliana*, which is the general plant reference species, and *Brassica rapa*, which is a related vegetable crop species of economic importance, especially in eastern Asia, where Zn and Fe malnutrition is prominent.

METHODS

Genetically segregating populations consisting of 158, resp. 120 Recombinant Inbred Lines (RILs) for *A. thaliana* Landsberg *erecta* (*Ler*) x Cape Verde Island (*Cvi*) and *Ler* x Kondara (*Kond*) populations and 183 Doubled Haploid (DH) lines for Heading Chinese Cabbage (*B. rapa* ssp. *pekinensis*) were grown in soil and in 0.5 x Hoagland's hydroponic medium and sampled as seeds, leaves or roots (*A. thaliana*) and leaf (*B. rapa*). Both populations were genotyped using polymerase chain reaction (PCR) -based genetic markers. Seed phytate (*Arabidopsis* only) and nutrient contents were determined by Atomic Absorption Spectroscopy (AAS) or Inductively Coupled Plasma-Atomic Emission Spectroscopy (ICP-AES). These data were used as trait data for QTL analysis in both species.

RESULTS AND DISCUSSION

Initially, the frequency distribution of nutrient contents in the set of RILs was examined for *Arabidopsis* (Fig 1). The QTLs were obtained for the accumulation of 6 different cationic nutrients (Ca, Fe, K, Mg, Mn, Zn) and the anti-nutrient phytate in seed, leaves and roots of *A. thaliana* *Ler* x *Kond* RILs, grown in soil and hydroponic cultures. Compared to a previous analysis of a *Ler* x *Cvi* RIL population grown in soil by Vreugdenhil et al. (2004), relatively few QTL were found to be common in both populations, and when comparing the soil-grown plants. Further fine-mapping to identify involved genes is in progress and focuses on two QTLs controlling phytate and Zn/Fe seed content, both located on the top of chromosome 3.

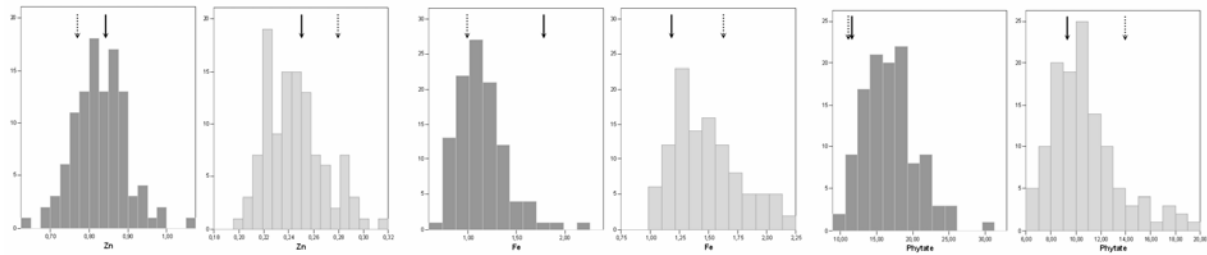


Figure 1. Frequency distributions for seed Zn, Fe and phytate content of soil (dark grey) and hydroponically grown (light grey) *Arabidopsis* RIL populations. The vertical axes indicate the frequencies and the horizontal axes indicate nutrient (mMol g⁻¹ dry weight) and phytate content (µg g⁻¹ dry weight).

We previously found that the Zn, Fe and Mn content of *B. rapa* leaves varied between 23.2-155.9; 60.3-350.1 and 20.9-53.3 µg g⁻¹ dry weight, respectively, when plants were grown in a hydroponic medium containing 2 µM Zn. There was little variation in average nutrient contents between different cultivar groups (Table 1). The analysis of a segregating *B. rapa* population detected seven significant QTLs that explain 11-18% of the variance found for individual nutrient contents (Na, Mg, P, Mn, Zn and Sr) by Multiple-QTL Model (MQM) mapping. The explained variance per locus is relatively low, indicating that the number of major QTLs for nutrient content is limited.

Table 1. Average Zn, Fe or Mn content (µg g⁻¹ d. wt.) in shoots of a number of *B. rapa* accessions according to cultivar groups. Data are presented as means ± S.E.

| Cultivar group | No. acc. | Zn | Fe | Mn |
|-------------------------------------------------------|----------|---------|----------|--------|
| Chinese cabbage (sp. <i>pekinensis</i>) | 44 | 60 ± 30 | 142 ± 50 | 32 ± 7 |
| Pak Choi (sp. <i>chinensis</i>) | 37 | 69 ± 24 | 118 ± 46 | 34 ± 5 |
| Caixin (sp. <i>parachinensis</i>) | 15 | 60 ± 21 | 125 ± 72 | 37 ± 5 |
| Wutacai (sp. <i>narinosa</i>) | 4 | 83 ± 50 | 153 ± 48 | 45 ± 7 |
| Turnip (sp. <i>rapa</i>) | 5 | 44 ± 10 | 145 ± 48 | 39 ± 6 |
| Mizuna (sp. <i>nipposinica</i>) | 3 | 75 ± 10 | 142 ± 37 | 44 ± 5 |
| ZiCaitai (sp. <i>chinensis</i> var. <i>purpurea</i>) | 2 | 80 ± 15 | 185 ± 67 | 34 ± 0 |

CONCLUSIONS

There was sufficient genetic variation in *A. thaliana* and *B. rapa* to allow QTL analysis for nutrient accumulation traits that could eventually lead to the identification of important Zn- or Fe-homeostasis genes for future marker assisted breeding purposes.

REFERENCES

- Vreugdenhil, D., Aarts, M.G.M., Koornneef, M., Nelissen, H., and Ernst, W.H.O. (2004) Natural variation and QTL analysis for cationic mineral content in seeds of *Arabidopsis thaliana*. *Plant, Cell, Environ.* 27: 828-839.