

Combined 'omics' approaches to dissect the roots' iron uptake system in soybean plants

Marta W. Vasconcelos¹, Carla S. Santos¹, Adelaide Machado²
Carla Pinheiro^{2,3}, Cândido Pinto Ricardo²

¹ Centro de Biotecnologia e Química Fina - Laboratório Associado, Escola Superior de Biotecnologia, Universidade Católica Portuguesa/Porto, Rua Arquitecto Lobão Vital, Apartado 2511, 4202-401 Porto, Portugal; ² Instituto de Tecnologia Química e Biológica António Xavier, Universidade Nova de Lisboa, Oeiras, Portugal; ³ Faculdade de Ciências e Tecnologia, Universidade Nova de Lisboa, Caparica, Portugal



Introduction

When growth conditions are adverse, such as in calcareous soils, iron (Fe) solubility is very low, resulting in the development of Iron Deficiency Chlorosis (IDC). To cope with this problem, legumes and other plants activate a root Fe reductase enzyme, increasing Fe uptake capacity. As we have consistently observed a "patchy" phenotype in the root reducing regions, the main objective of this work was to understand if this phenomenon is regulated at the transcriptional and post transcriptional level.

Methods

Soybean plants were grown under Fe depletion (0 μM) and Fe deficiency (10 μM) in hydroponic conditions, for 14 days. Fe deficiency chlorosis was visualized in the shoots (Fig. 1) and root reductase activity was measured (Fig. 2). Agarose localization assay was also performed in order to visualize and isolate Fe reducing and Fe non-reducing root zones (Fig. 3). Root samples were collected for transcriptomic and proteomic analysis.

Results / Discussion

Foliar Analysis



Fig. 1 – Visualization of Fe deficiency chlorosis development in Fe depleted (A) and Fe deficient (B) plants.

Both treatments were under high levels of stress and developed severe chlorosis.

Reductase Activity

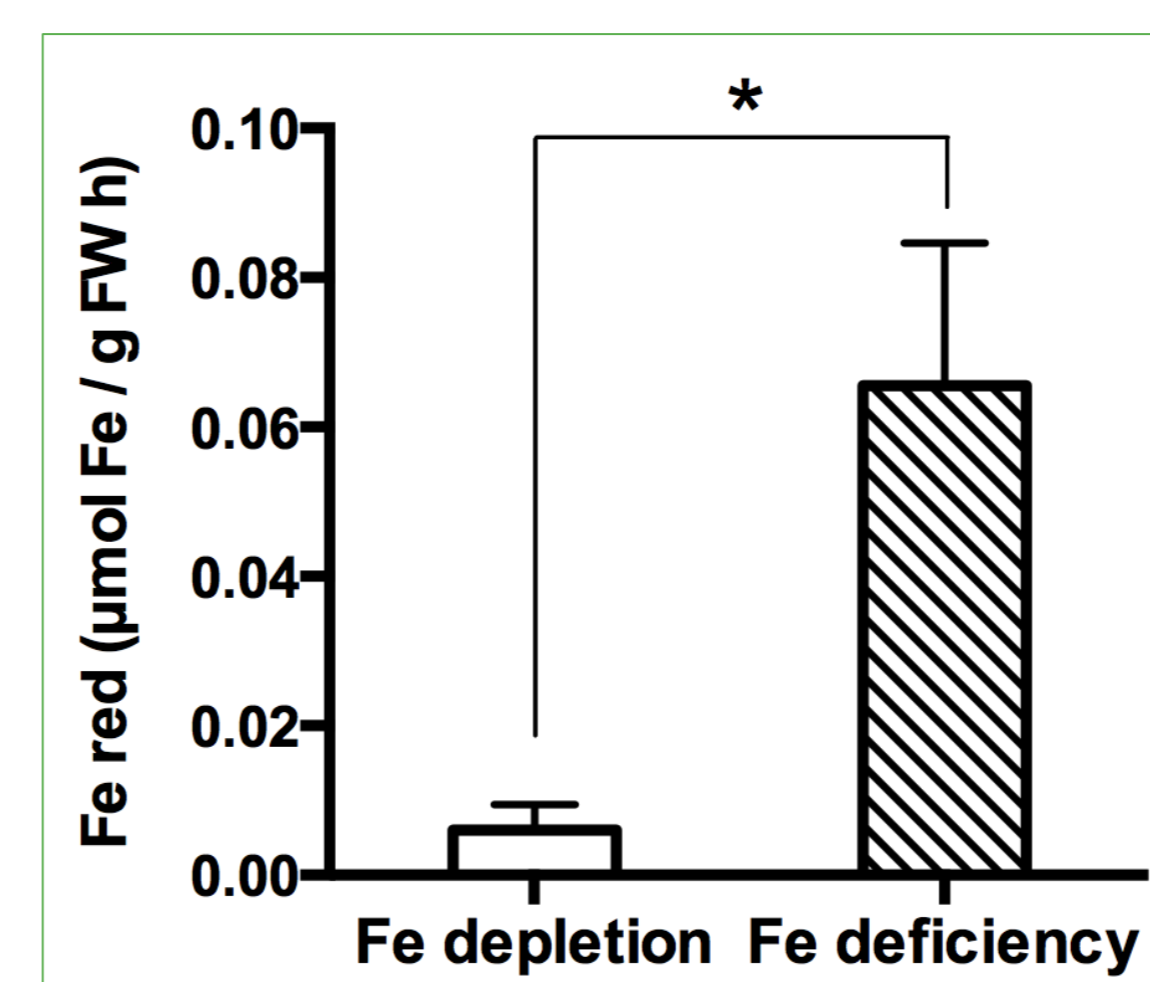
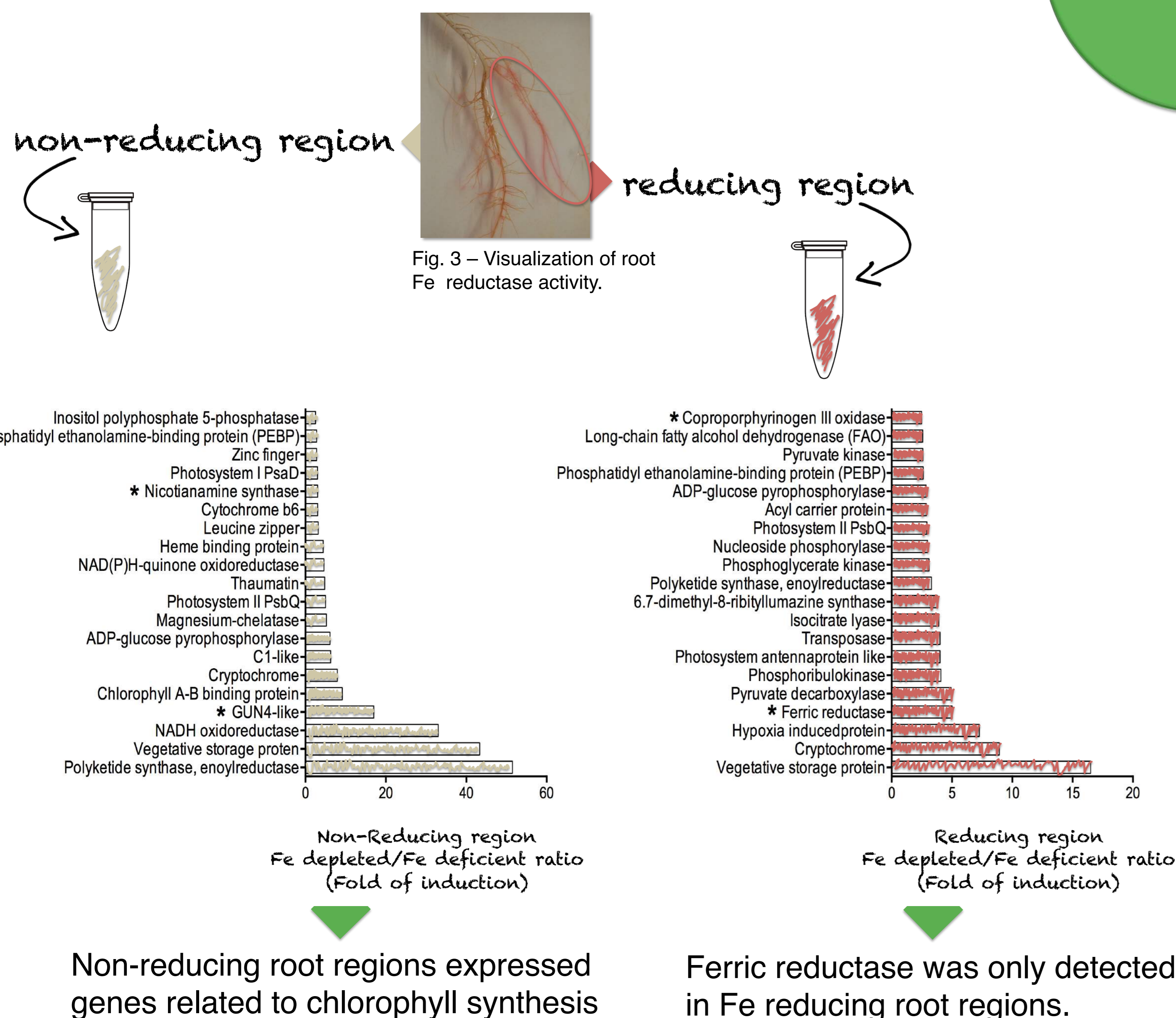


Fig. 2 – Root Fe reductase activity in Fe depleted (A) and Fe deficient (B) plants.

Reductase enzyme might require a minimum amount of Fe to function, hence the low activity under Fe depletion!

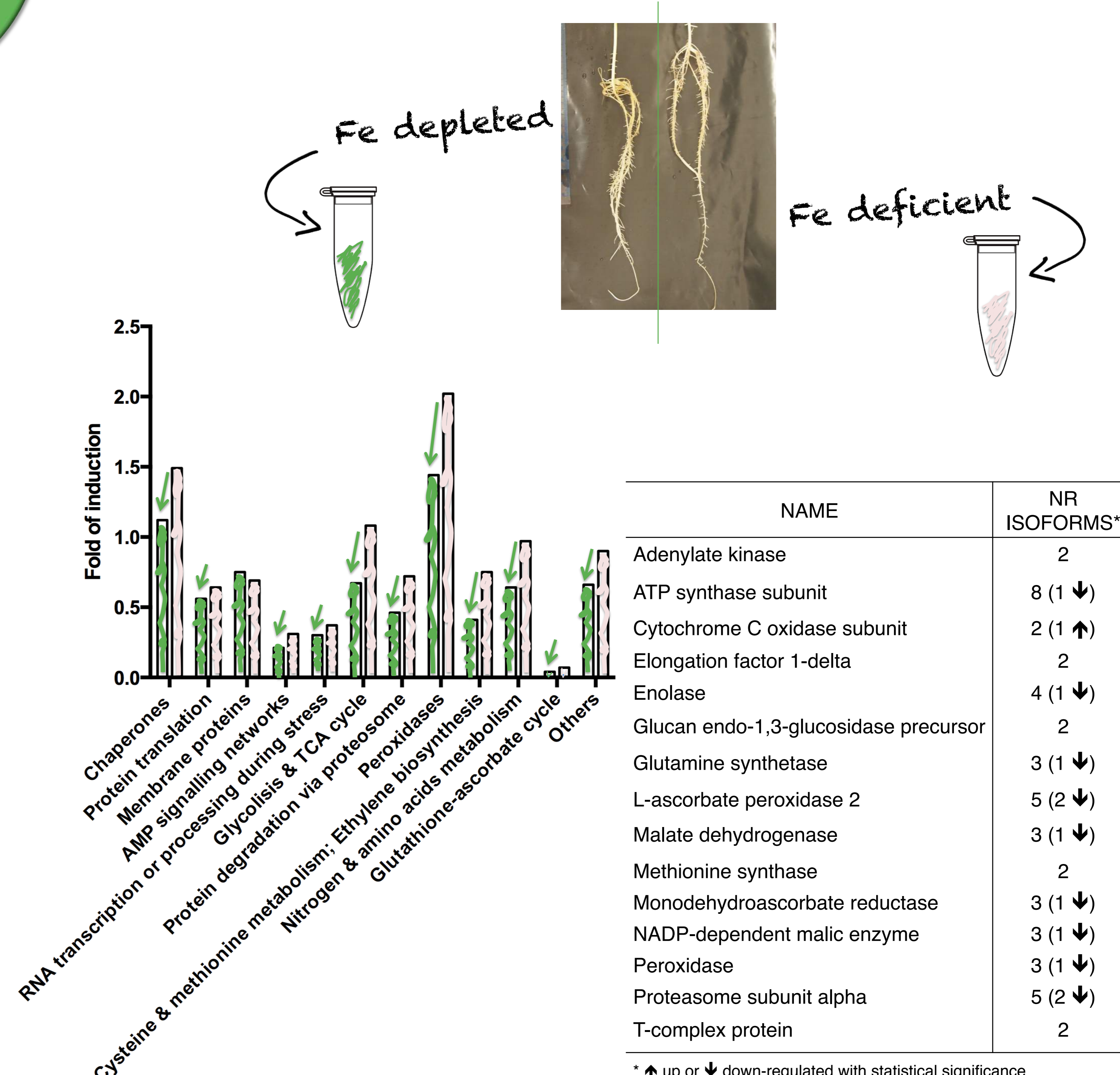
TRANSCRIPTOMICS

Technique: Illumina Hiseq2000
Analysis: Differentially expressed genes in distinct root parts



PROTEOMICS

Technique: Gel based proteomics
Analysis: Protein profiling of total root in different Fe conditions



Conclusions

- ◆ At the transcriptional level, all samples expressed several redox genes including quinone reductases, heme containing proteins, cytochrome P450 and oxidoreductases.
- ◆ Proteomics data revealed major shift in metabolism, since 39% of the detected proteins were shown to be responsive to Fe depletion. A massive down-regulation of metabolism was observed (89% of the detected proteins).

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