

# Oxidative stress response in *Arabidopsis thaliana* after exposure to uranium: the role of glutathione

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## Introduction

Uranium is a heavy metal and radionuclide with **greater risk for chemical toxicity** than radiological. Due to anthropogenic pollution **2-5 mg/kg uranium** occurs in the earth's crust. It is known that uranium induces **oxidative stress** in plants. This is a condition with an **imbalance** in the production and elimination of **reactive oxygen species (ROS)**, causing cellular **damage** such as oxidized DNA bases and lipid peroxidation. The plant developed a defence mechanism to cope with oxidative stress of which glutathione is an important element. However, the role of GSH under uranium stress is not fully understood. Therefore, the objective of this work is to further analyse the role of GSH in *Arabidopsis thaliana* plants under uranium stress.

## Materials & methods

*Arabidopsis thaliana* plants were cultivated in a **hydroponic set-up** during 18 days after which they were **exposed during 3 days to different uranium concentrations (0, 3, 6.25, 12.5, 25 or 50 µM)**. After harvesting the plants, the **transcriptome was sequenced** at the University of Antwerp (Illumina HiSeq2000 + Truseq™ RNA sample prep kit) and the **Differentially expressed genes were identified** (cut-off values: |Log2 Fold Changes| > 1 & False discovery rate < 0.05). The differentially expressed genes were analysed in a **GO enrichment analysis** using the web-based tool **Metascape** [2]. The analyses were done separately for up- and downregulated genes.

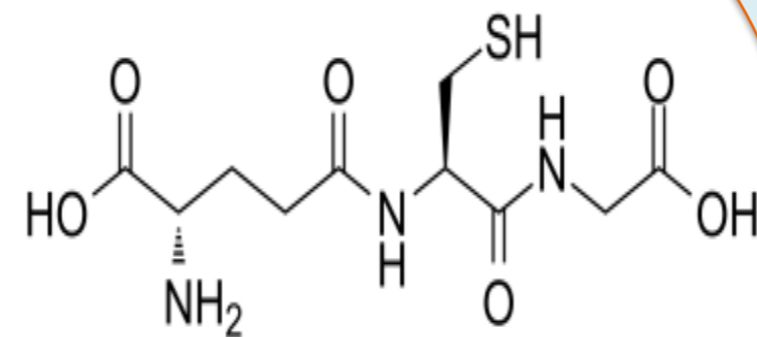


Figure 1: Glutathione structure [1]



Figure 2: *Arabidopsis thaliana* [3]



Figure 3: Hydroponic set-up [4]

## Results & discussion

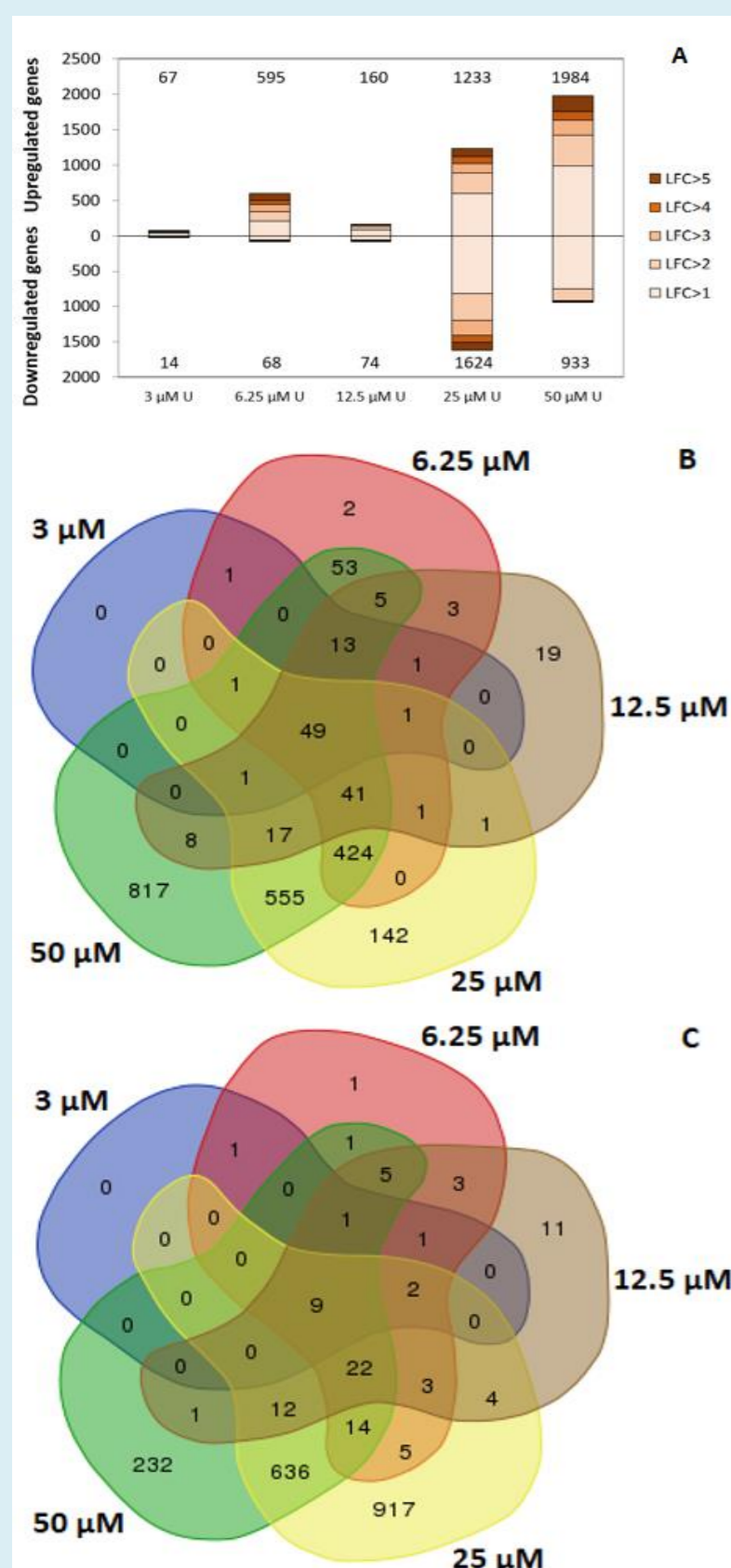


Figure 4: Results of *Arabidopsis thaliana* after exposure to different uranium concentrations: (A) Differentially expressed genes; (B) Venn diagram upregulated genes; (C) Venn diagram downregulated genes.

- 3-12.5 µM U: limited amount of affected genes
- 25-50 µM U: more affected genes → different (higher) stress response
- 49 Commonly upregulated genes between all conditions. 1088 Genes common between 25 and 50 µM U
- 0, 2, 19, 142, 817 Uniquely upregulated genes
- 9 Commonly upregulated genes between all conditions. 693 Genes common between 25 and 50 µM U
- 0, 1, 11, 917, 232 Uniquely upregulated genes

U  
0, 3, 6.25, 12.5, 25, 50 µM

S metabolism

Disturbed S homeostasis

Preserve sulfur for primary metabolism

Glutathione

Detoxification

Enzymatic defence ↑

U possibly detoxified by direct quenching with role for GSTU3/4/12

Importante role for GSTs

Redox homeostasis

Oxidative stress starting from 6.25 µM

No important role for AsA-GSH cycle?

Possible decreased U translocation

Metal homeostasis

Phytochelatin

Role for MYB49 in limiting U uptake?

Disturbed metal homeostasis (Cu, Fe...)

## Conclusion

- No differentially expressed genes related to: GSH synthesis, AsA-GSH and phytochelatin
- Important role for GSTs and peroxides in both detoxification and redox homeostasis
- Uranium may be detoxified by direct quenching with a role for GSTU3/4/12

## Perspectives

- Cad2-1 mutant (GSH deficient) with analyses such as uranium uptake, lipid peroxidation, enzymatic activity and growth
- Cad1-3 mutant (phytochelatin deficient)
- Investigate specific genes with the (in this work) already developed primers
- Measure GST enzymatic activity

## Bibliography

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