Identification of novel genes responsible for As^{5+}(砷) detoxification in rice

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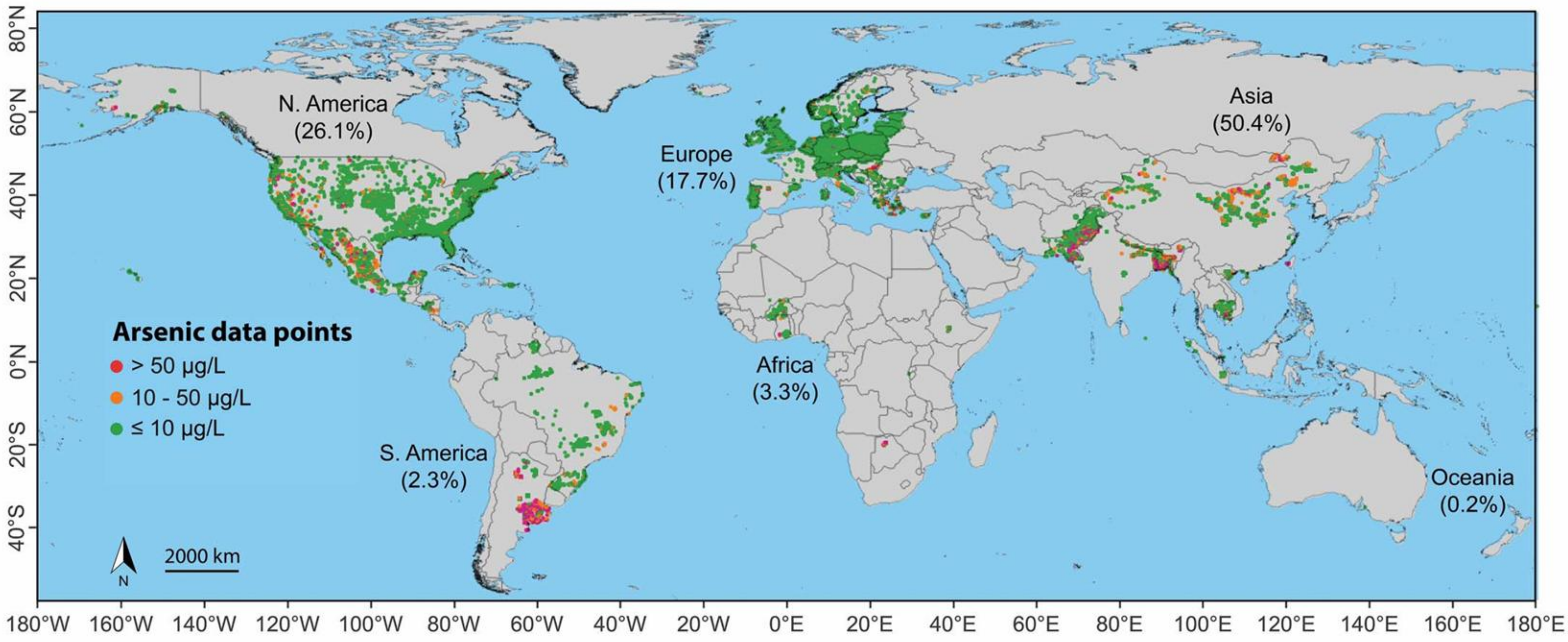
13 March 2026 Launceston

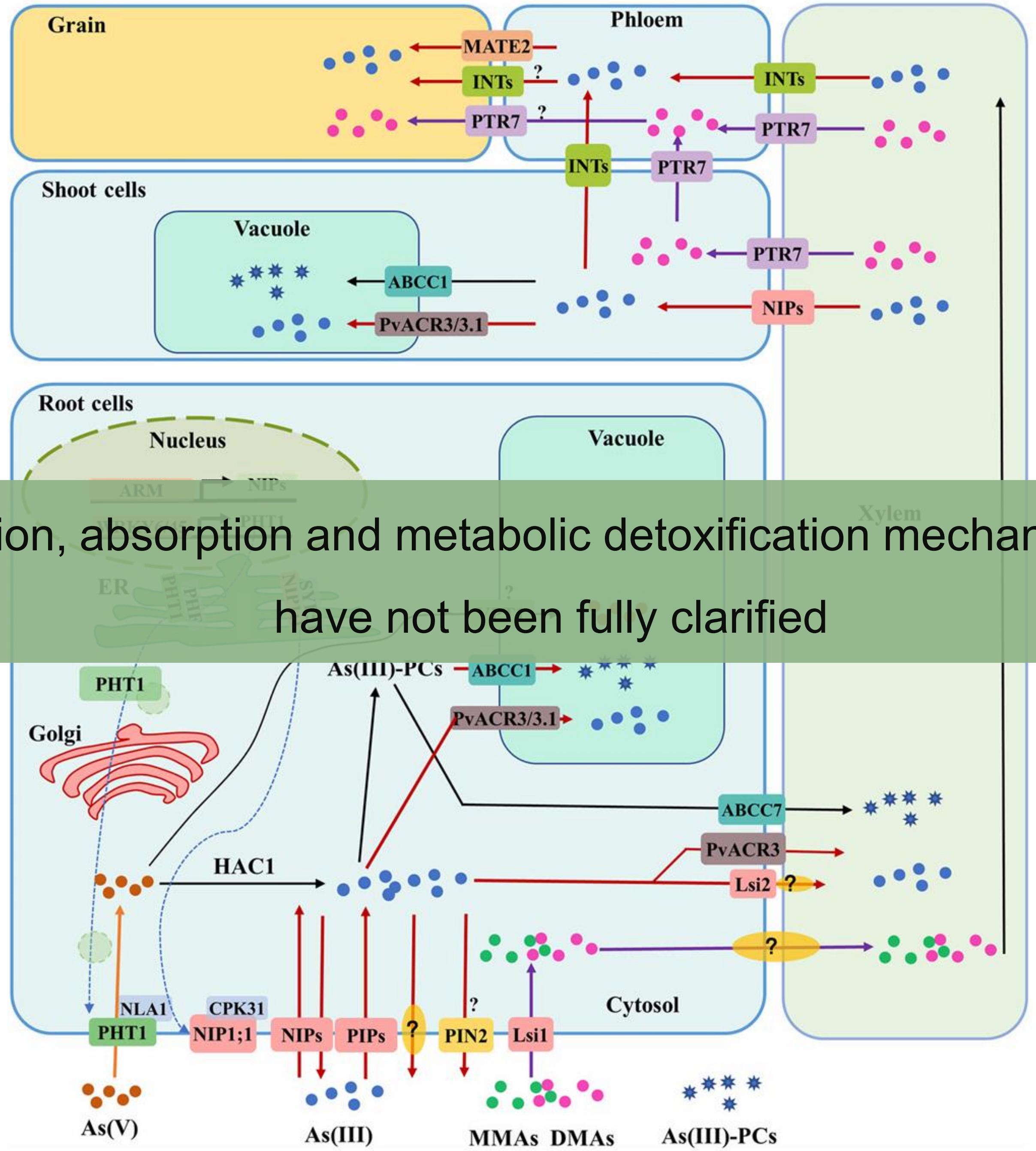
Background

Arsenic pollution in agricultural soils and irrigation water is becoming increasingly serious



(Podgorski and Berg, 2020)

Background



The signal perception, absorption and metabolic detoxification mechanisms of arsenic in rice have not been fully clarified

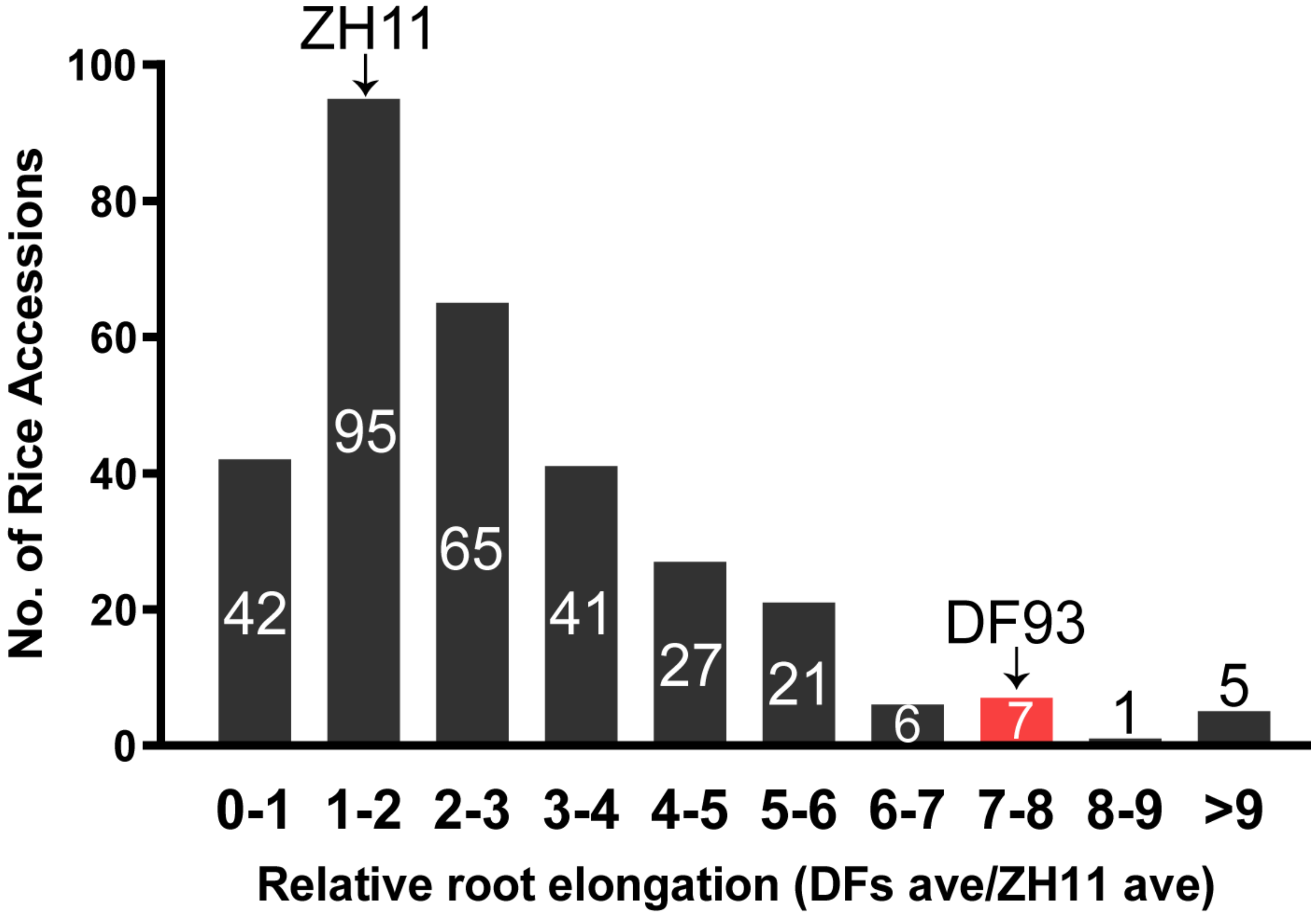
(Zhao et al, 2020)

Research content

1. To identify novel genes related to arsenate tolerance and detoxification in rice.

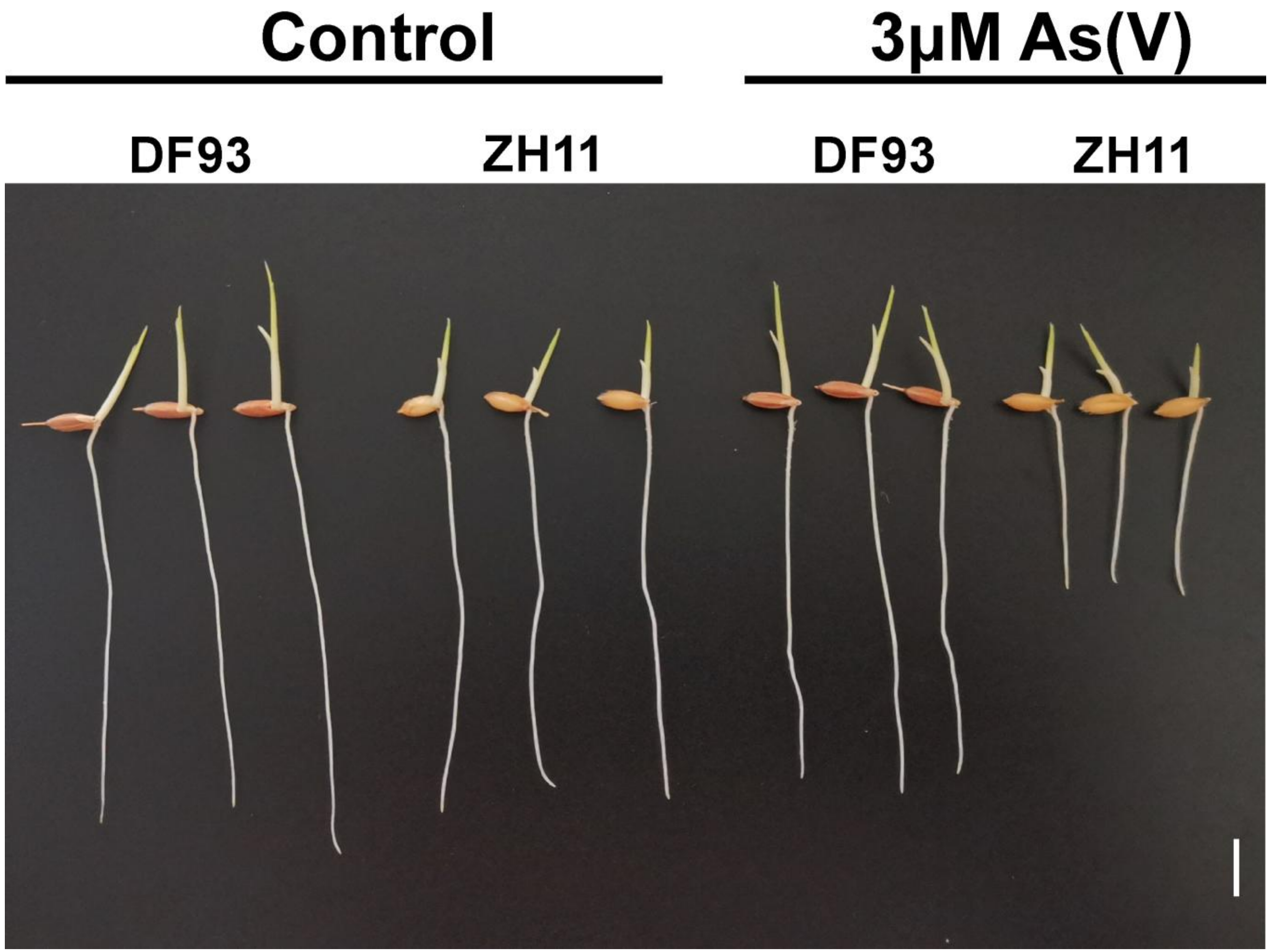
2. To explore the natural variation of arsenate tolerance

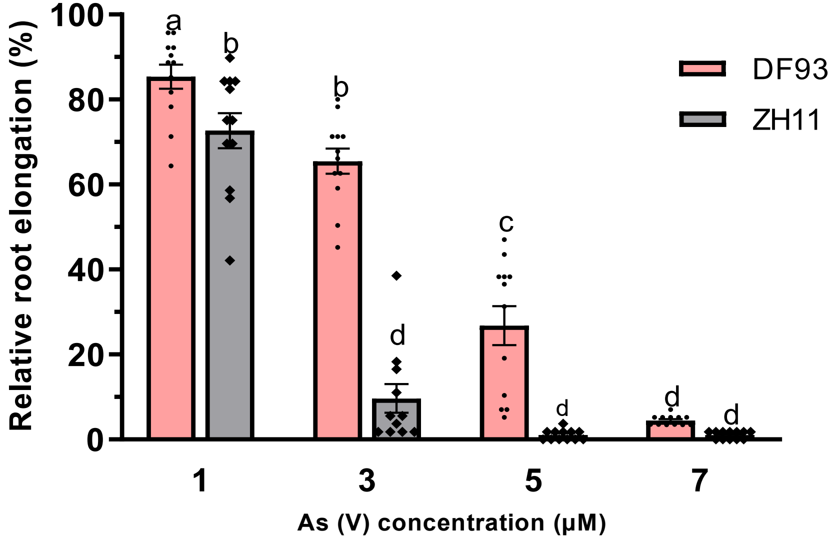
Natural variation of As(V) tolerance of 310 rice genotypes

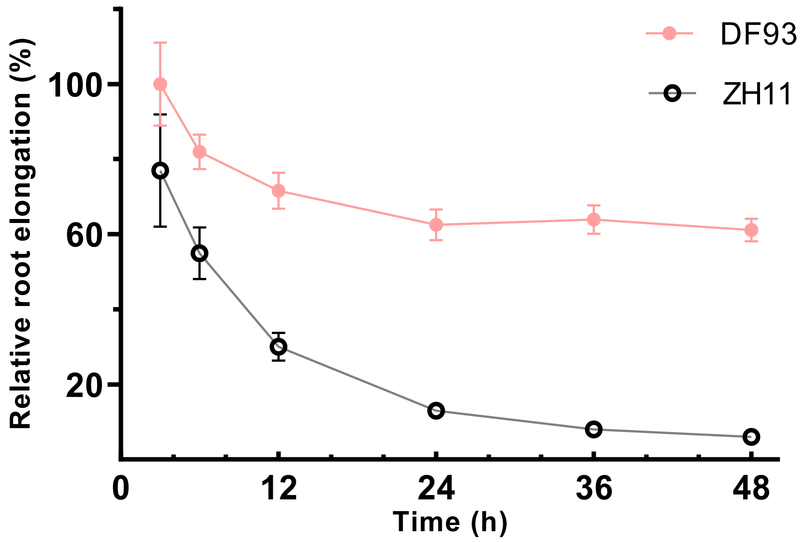


2.5 μM AsV for 24 h

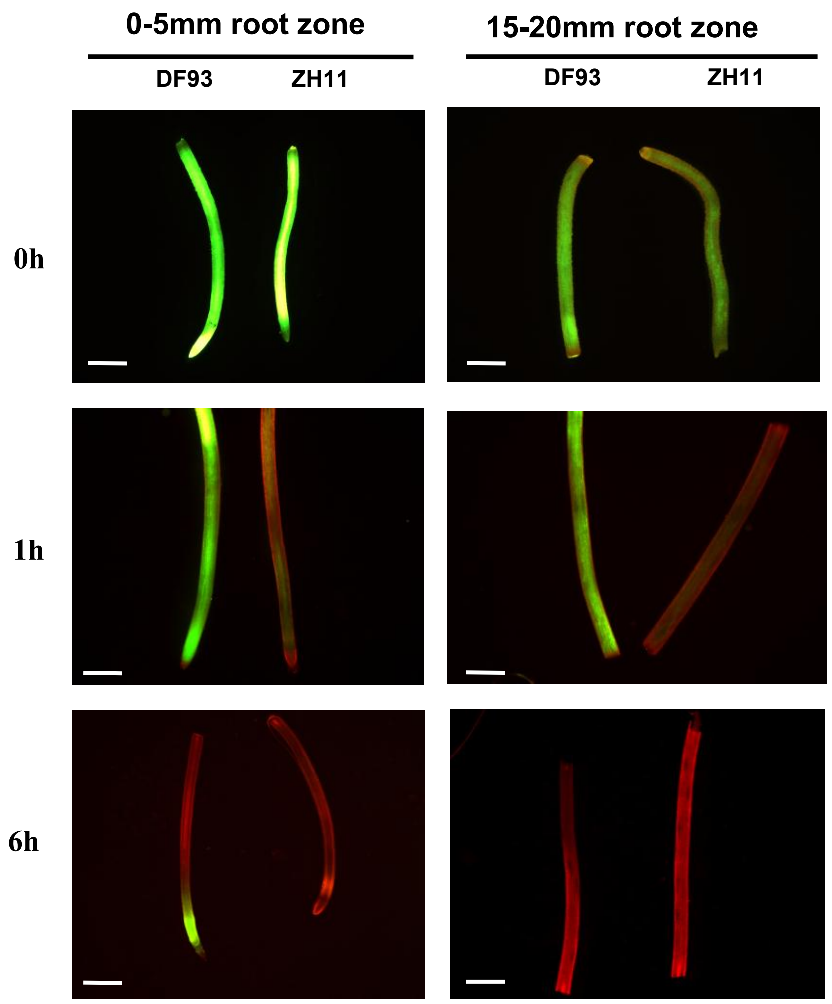
DF93 - an arsenate-tolerant genotype



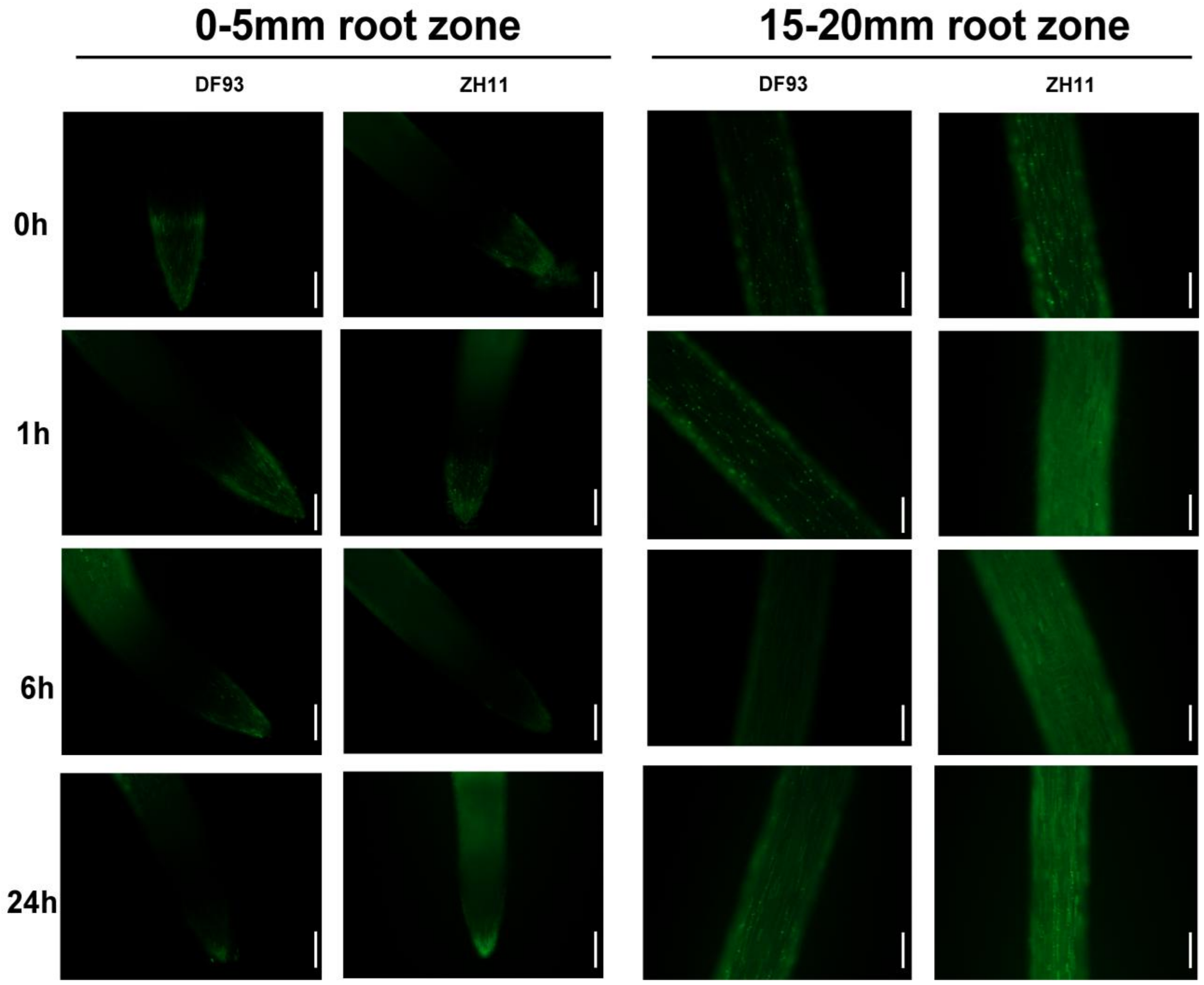




Root cell viability was much higher in DF93 than that in ZH11



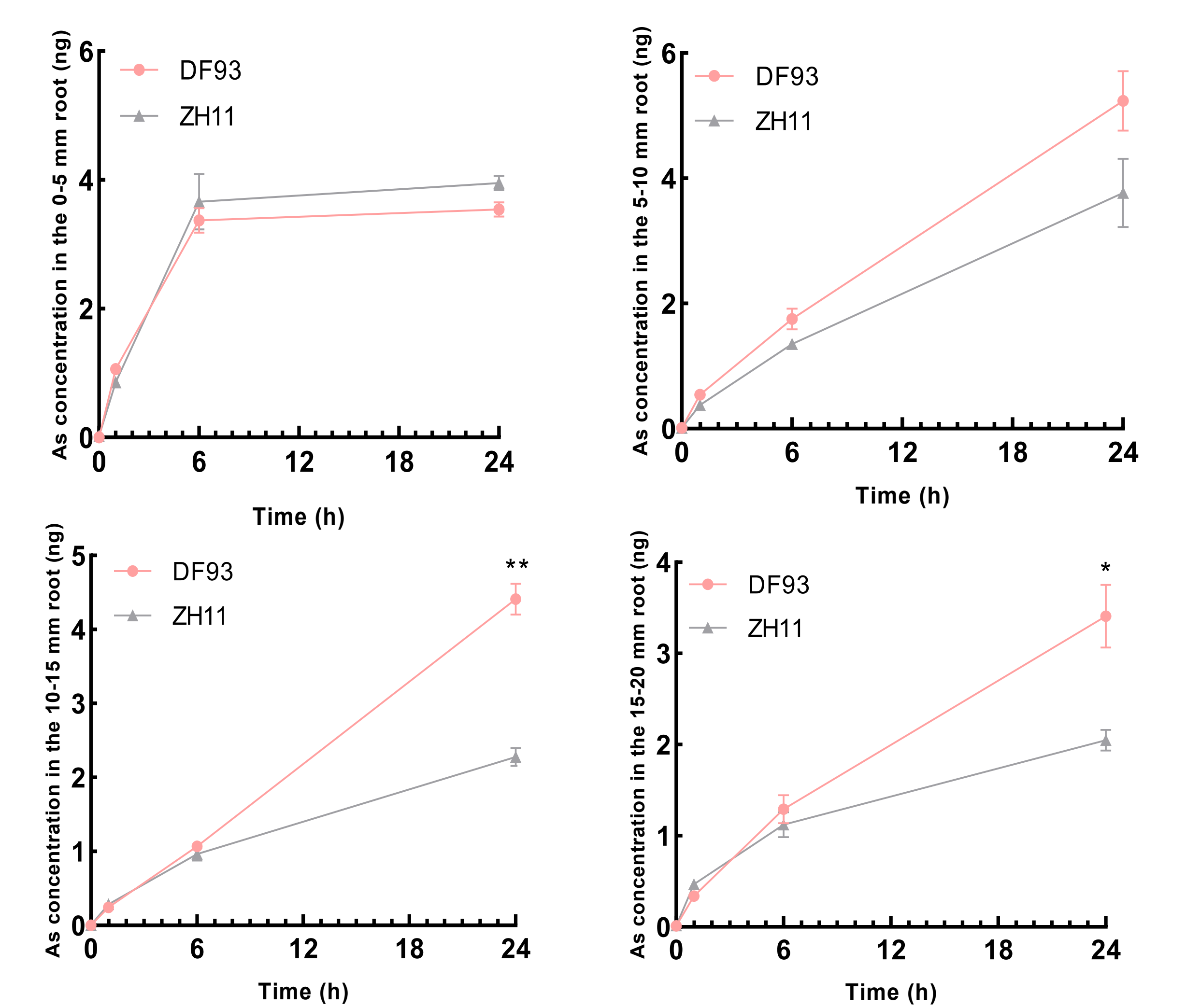
Fluorescein Diacetate (FDA) -Propidium Iodide (PI) staining
Red:dead cells Green: live cell



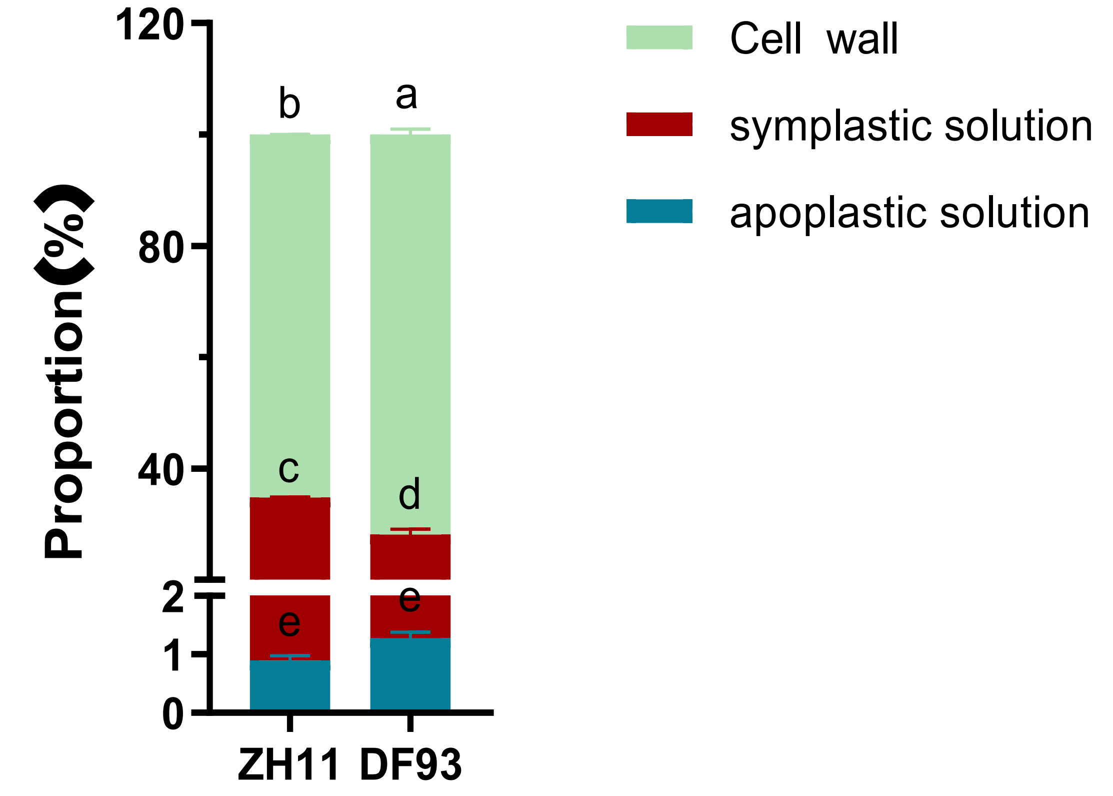
Reactive oxygen species staining

Differential As accumulation between DF93 and ZH11

As content in different root tip zone

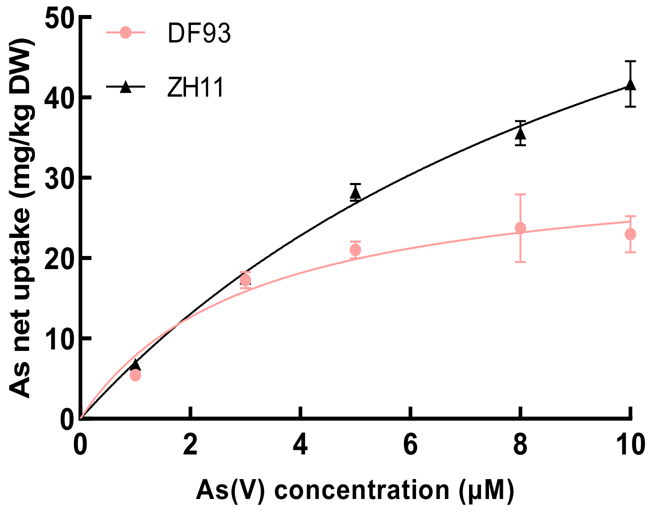


As content in root cell sap

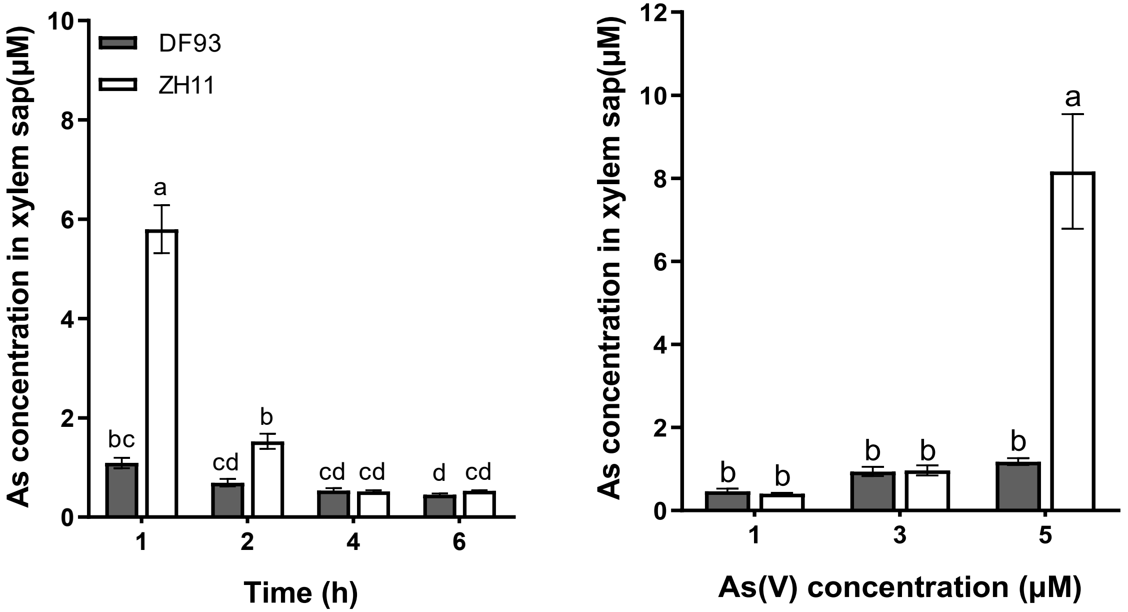


Differences in As(V) uptake, transport, and efflux

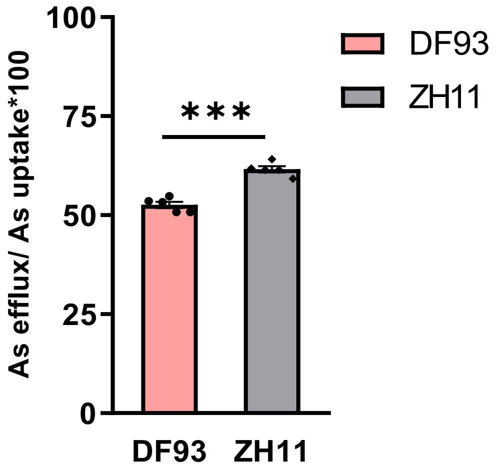
- **Net uptake**



- **Xylem sap**

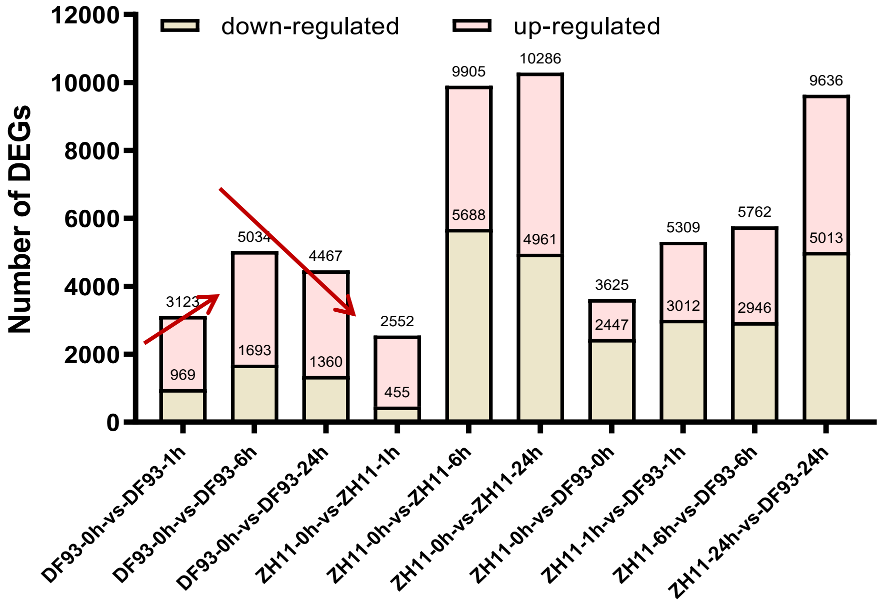


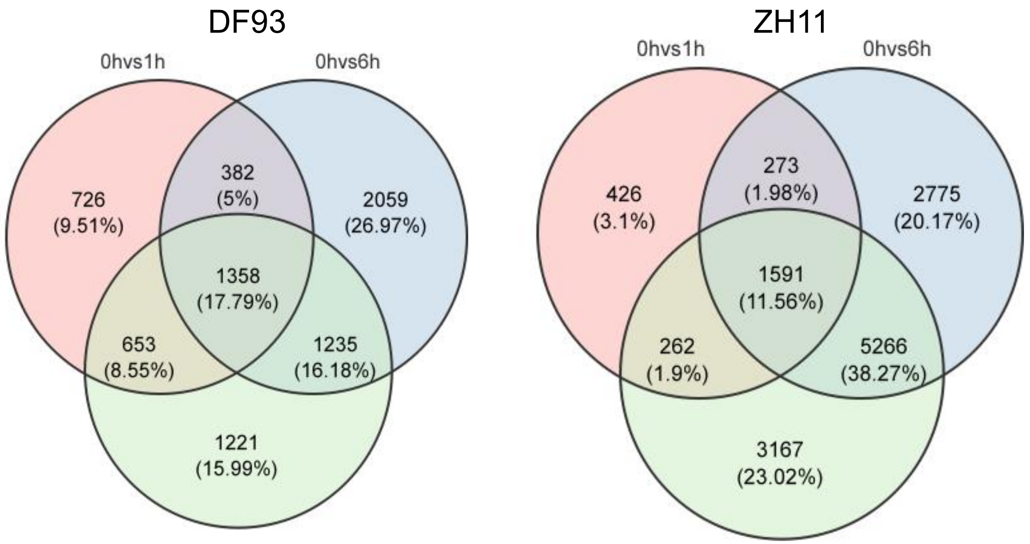
- **Efflux**

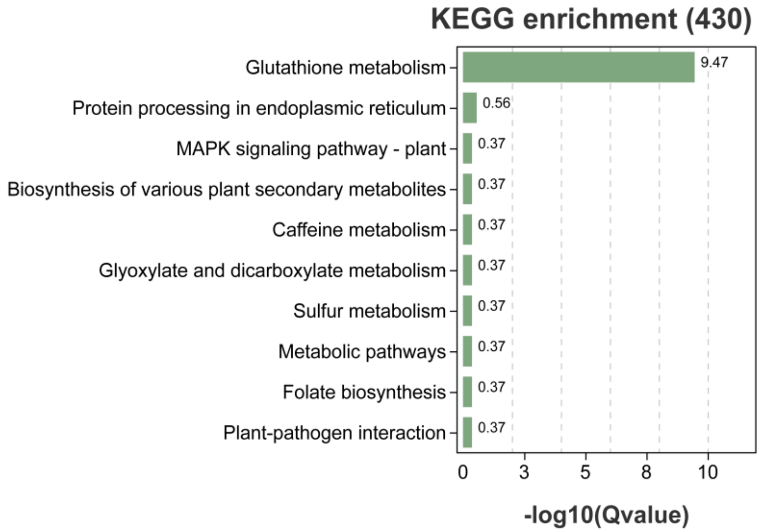


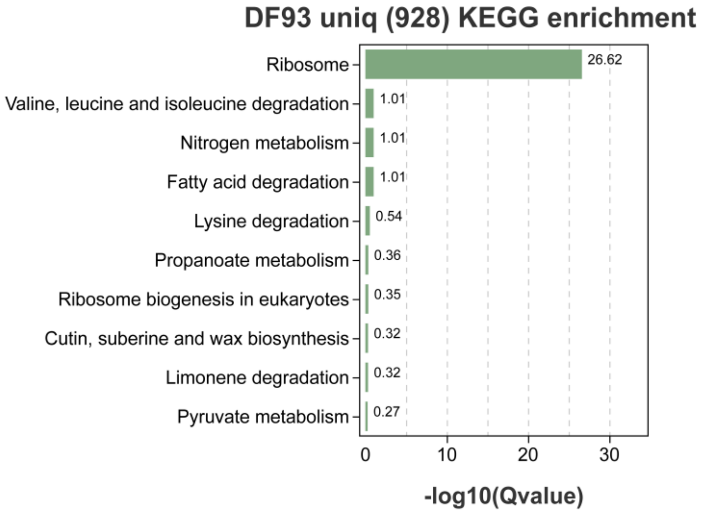
➢ **The differential root uptake and xylem loading capacity of As may be main factors determining the contrasting As(V) tolerance in DF93 and ZH11, rather than the efflux capacity.**

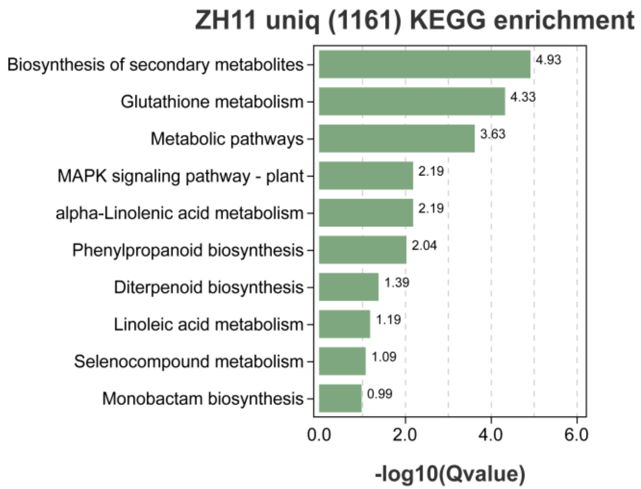
Transcriptome analysis of two genotypes in response to As(V) stress





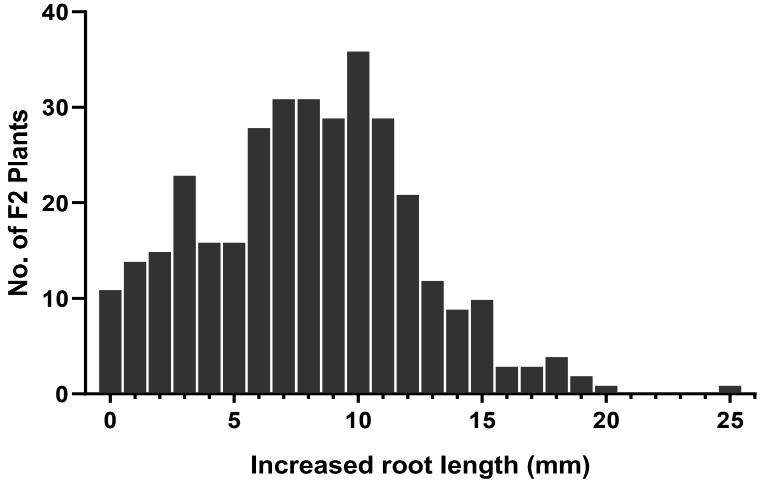


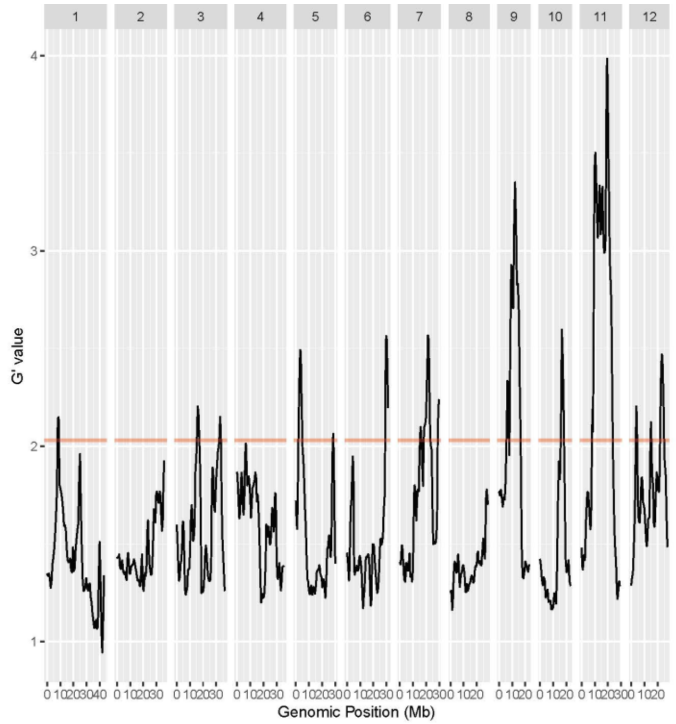




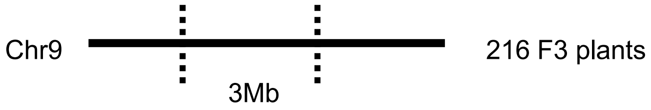
- **The 928 DEGs unique to DF93 were mainly relevant to protein synthesis, metabolism and ribosomes.**

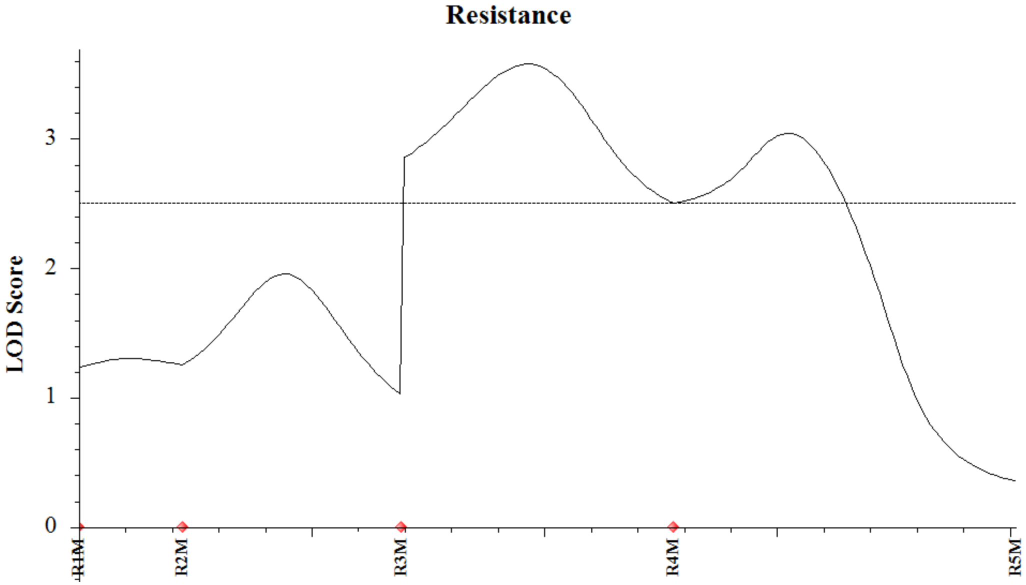
Identification of candidate genes through BSA-seq



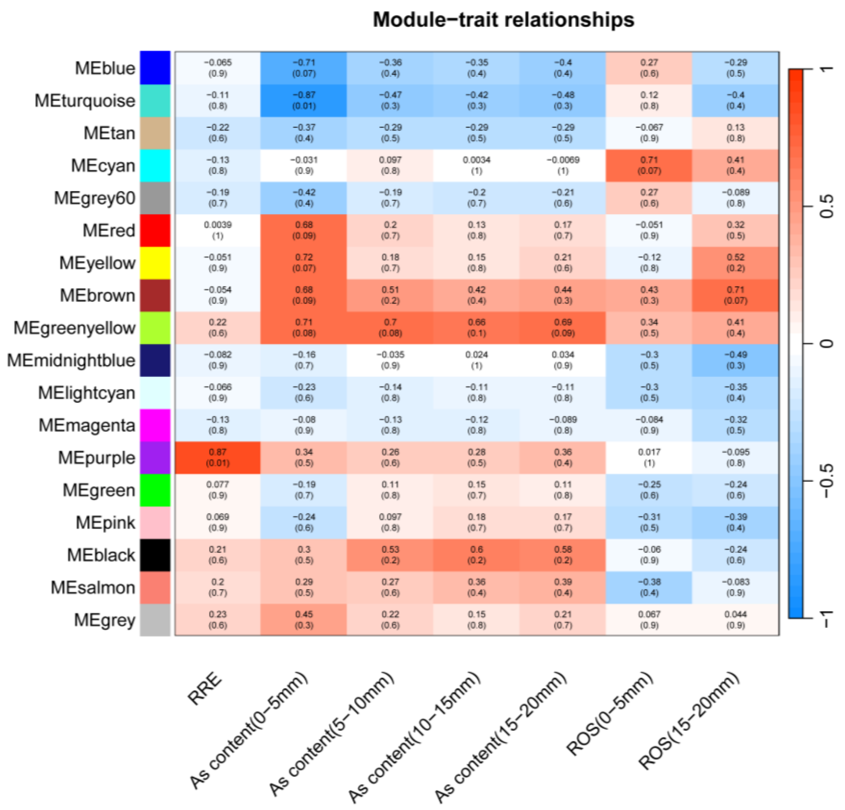


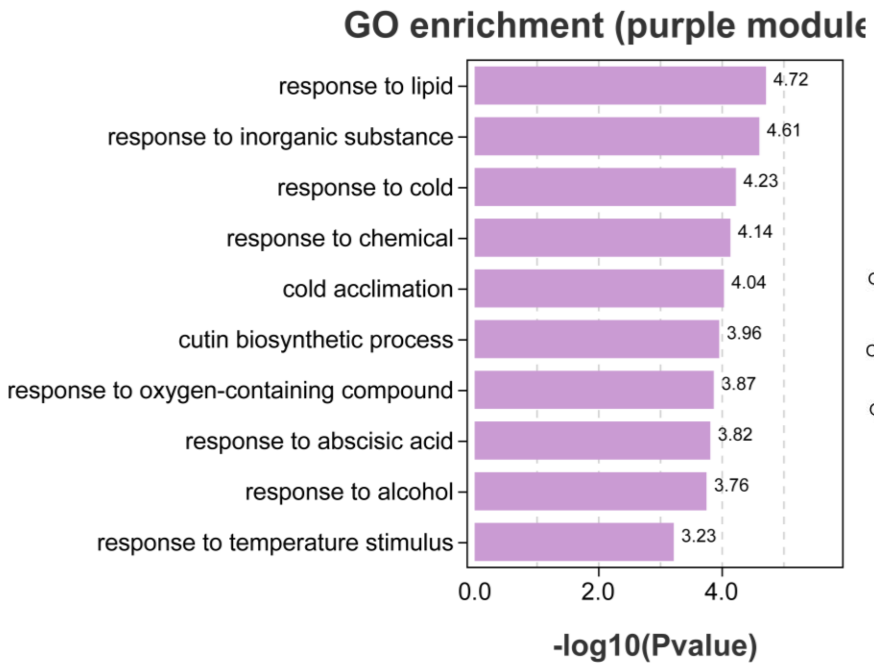
Mapping

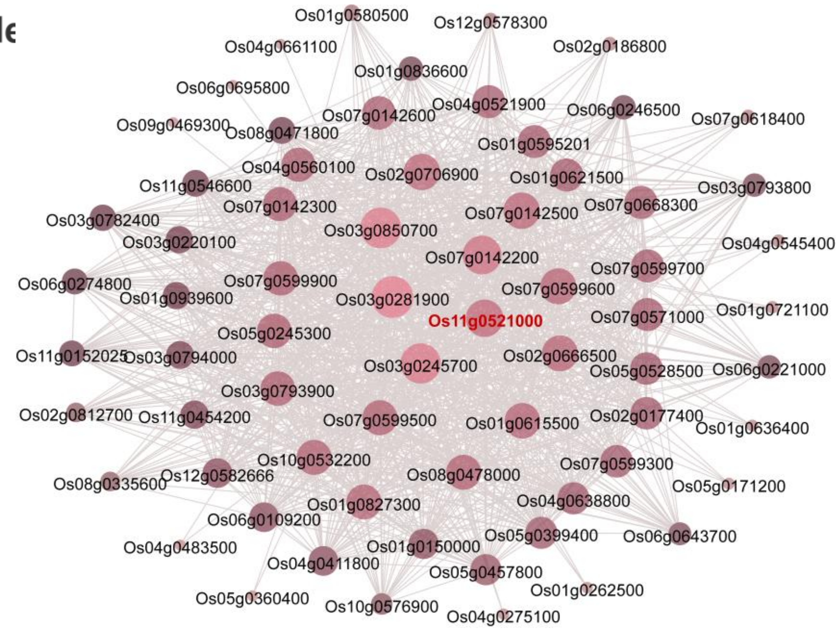




Identification candidate genes through intergrated BSA- & RNA-seq

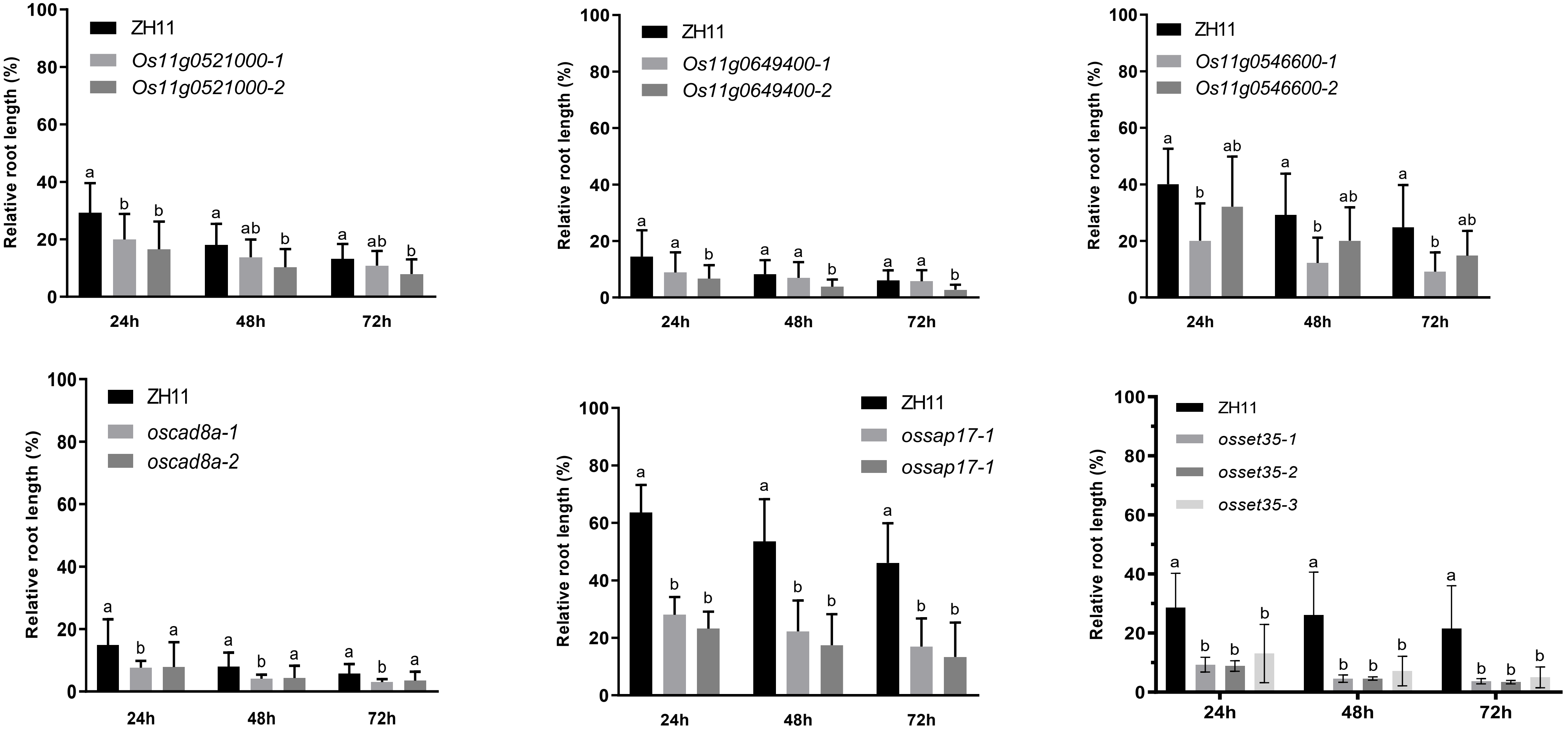






- **The combination of BSA-Seq and RNA-Seq analysis identified six candidate genes. WGCNA analysis mainly selected the genes in the purple module related to the root length phenotype.**

Knockout of the candidates lead to increased sensitivity to As(V)



Further verification of the candidate -*OsSAP17*

AN1-type zinc-finger protein

***OsSAP17*(LOC_Os09g21710)**

Target1: ACGGAGGCGTTCCCGGACCT**GGG**

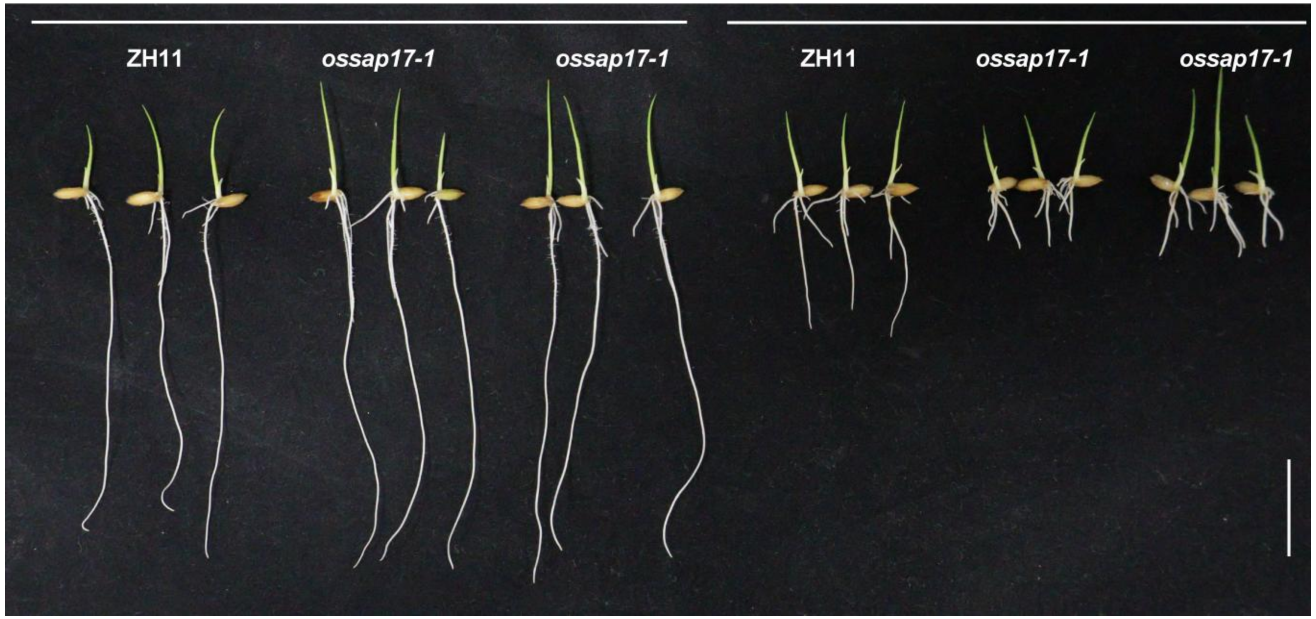
Target2: AGCCGTGGTCCCGGTACGTC**CGG**

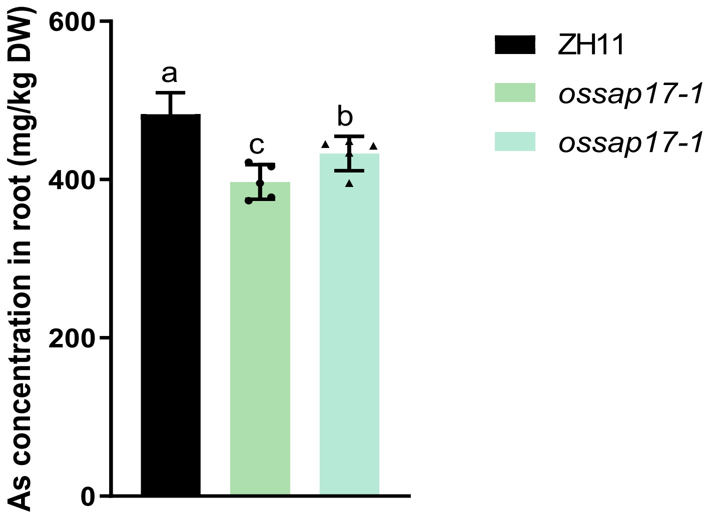
Target3: AGAAGGTGTGCCTCAAGCAC**CGG**

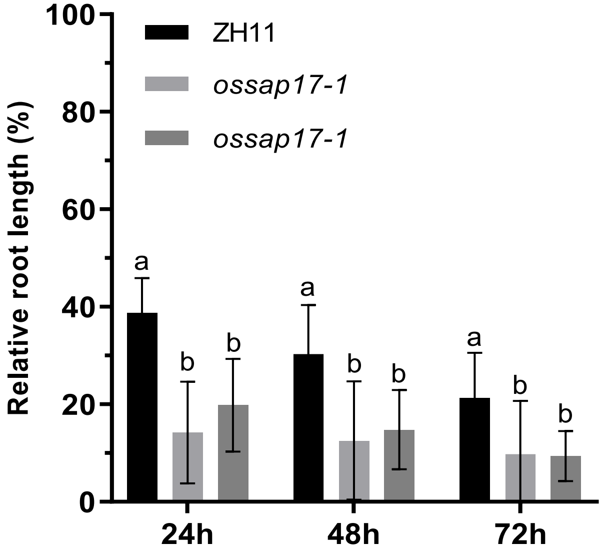
ZH11: CCCGGACCTGGG....AAGGTGTGCCTCAAGCACCGGTTCCCCGCCGAC

ossap17: CCCGGATC---CACCGGTTCCCCGCCGAC (**C-T,-360bp**)

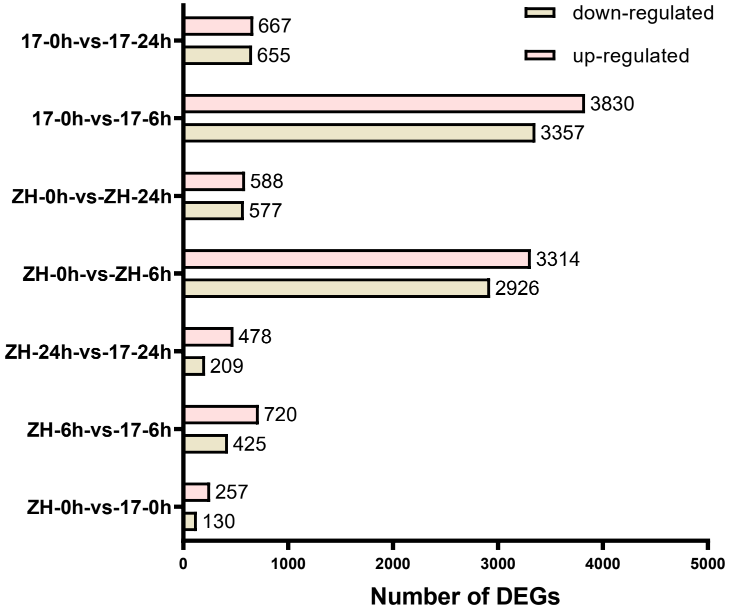
CK **2.5 μM As (V)**

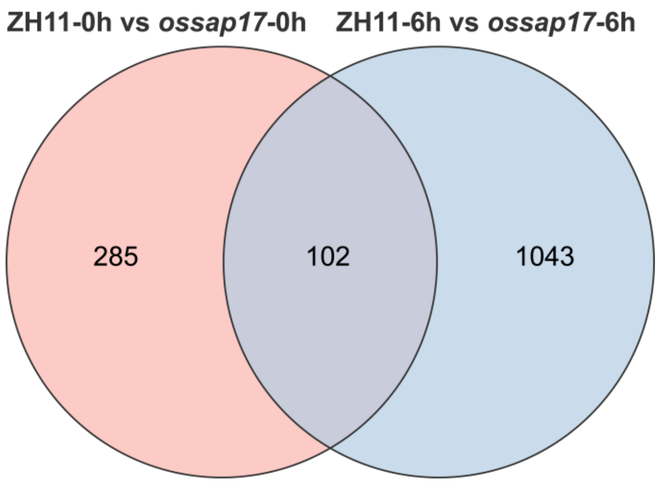


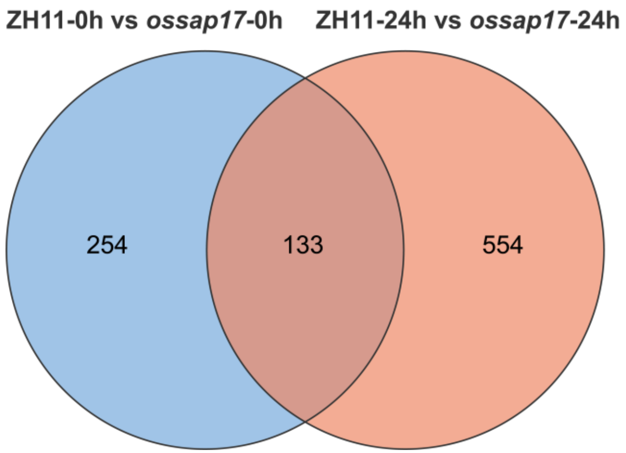


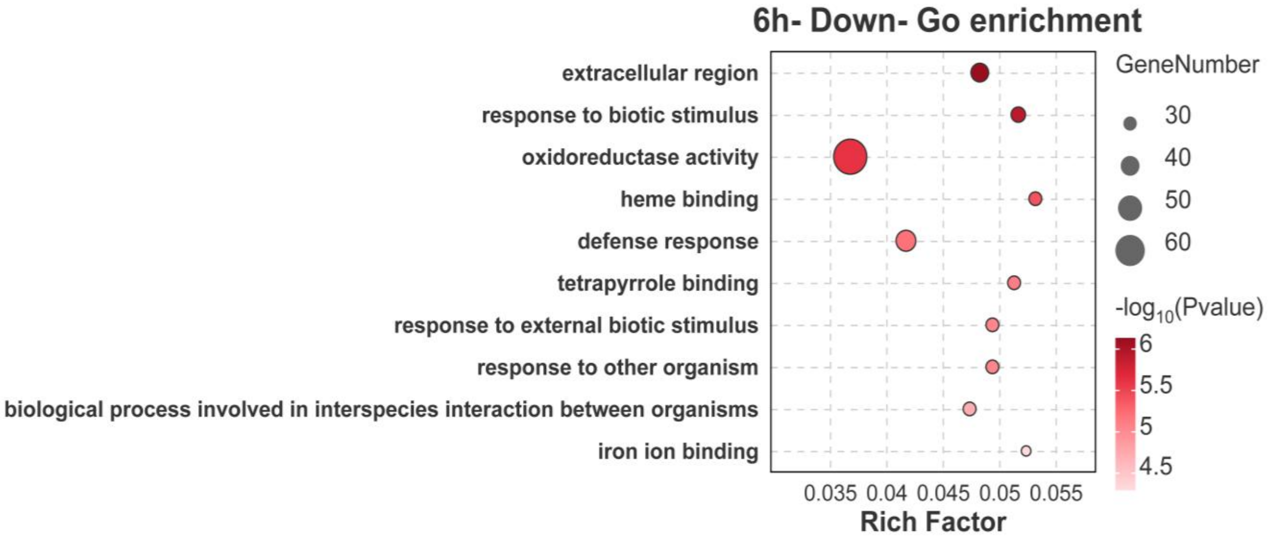


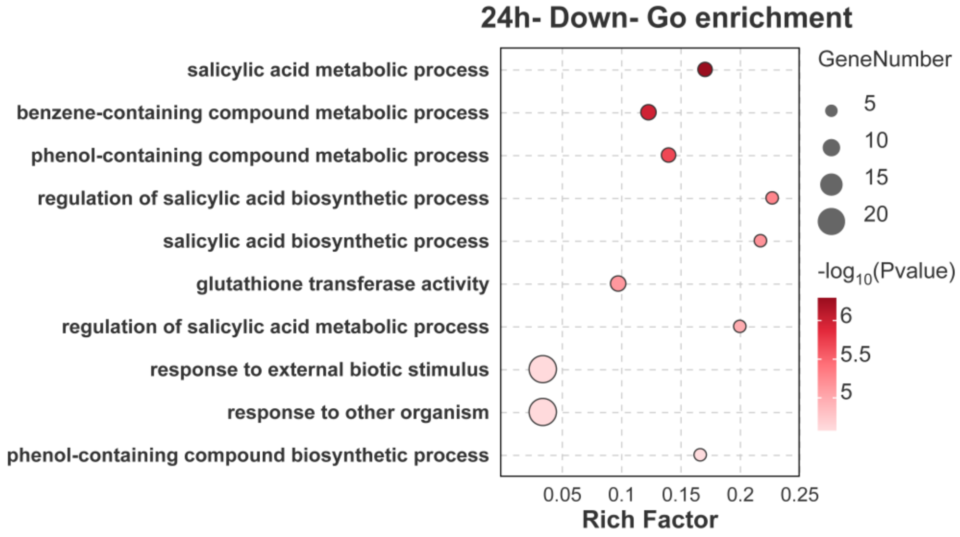
Transcriptomic analysis of *ossap17* mutants











Summary

- **The differences in root absorption and xylem loading capacity of arsenic, as well as cell wall adsorption, may be the main factors determining the differences in arsenate tolerance between DF93 and ZH11.**

- **Compared with ZH11, DF93 could respond to arsenate stress signal faster.**

- **OsSAP17 may respond to arsenate stress by regulating the redox balance and hormone signaling in rice.**

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