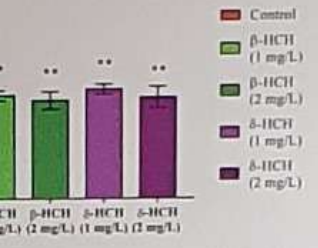


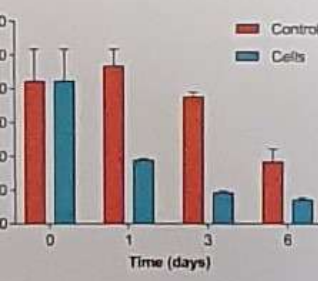
Sphingomonas paucimobilis UT26
 for which homologs have been
 in red boxes.

for 10 days of exposure to HCH



10 days-exposure to α-HCH and γ-
 isomers of β-HCH and δ-HCH isomers.

γ-HCH isomers but was hardly
 press.



HCH.
 of toxic intermediates.

mechanism for iron regulation through the slippery plant iron sensor.

BACKGROUND

Iron uptake in dicotyledonous plants is controlled by a hierarchy of transcription factors (FIT) and transcription factors (AHA2), (FRO2) to Fe²⁺ levels compared to this

RESULTS

A comparison of iron uptake and mobilization in Medicago truncatula following the complexity of the network gave three (2 and 3) that were in



1. Proteomics and Metabolomics: riboflavin

M. truncatula induces at transcript, protein and metabolite levels riboflavin and a new derivative accounts for 75% of

Root Responses of *Medicago truncatula* Plants Grown in Two Different Iron Deficiency Conditions: Changes in Root Protein Profile and Riboflavin Biosynthesis

Characterization of Flavins in Roots of Fe-Deficient Strains of *Medicago truncatula* with a Focus on *Medicago truncatula*

Proteomics and mutant analysis: a new derivative accounts for 75% of the total riboflavin in roots of Fe-deficient *Medicago truncatula* plants

Genetically Exclusive Alterations in Secondary Metabolism of *Medicago truncatula* are Crucial for the Uptake of Insoluble Iron Compounds

Chlorophyllin 8-Hydroxylase-Mediated Furoxanthin Production is Crucial for Iron Mobilization

Mutant analysis and biochemistry: the

BTSL-LIKE (BTSL) proteins were closely correlated to the master regulator of Fe uptake, FIT. Biochemical analysis demonstrated that these unstable proteins ubiquitinate and promote

BTSLs negatively regulate transcription