

Heavy metal science

In the 1980s scientists began laboratory studies on metal hyperaccumulator plants, i serious human diseases are the result of disruptions in metal homeostasis, for example Menke's disease, Wilson's disease, hemochromatosis and possibly Alzheimer and prion diseases. regulated network of metal homeostasis proteins. Existing knowledge of these proteins show a surprising extent of similarity between metal homeostasis networks in widely differing organisms, i.e. humans, yeast and plants. In the hyperaccumulator plant *Thlaspi caerulescens*, a metal-sequestering protein has previously been found to exhibit high similarity to its counterpart in *A. thaliana*, but is regulated differently. Advancing beyond these earlier results, the work published now on *A. halleri* has finally made it possible to achieve a global view of the complex metal homeostasis network in a metal hyperaccumulator plant.

The plant species *Arabidopsis halleri* is naturally found on soils heavily polluted with cadmium and zinc. It exhibits extreme metal tolerance and belongs to a small group of approximately 400 taxa of plants which accumulate heavy metals to extraordinary concentrations specifically in their above-ground biomass. These traits are potentially of great interest for the cost-effective clean-up of metal-polluted soils. Scientists at the Max Planck Institute of Molecular Plant Physiology in Potsdam and at the Leibniz Institute of Plant Biochemistry in Halle have pursued the mechanisms which underlie metal hyperaccumulation and tolerance at the molecular level. For this they exploited the fact that *A. halleri* is very closely related to the genetic model plant *A. thaliana*, of which the genome has been sequenced. In contrast to *A. halleri*, *A. thaliana* is metal sensitive and immobilises excess metal ions in the roots, thereby limiting the accumulation of metals in above-ground tissues.

Contrasting metal homeostasis of both species and their close genetic relationship enabled the researchers to compare gene messages (messenger RNA) of both species utilizing commercially available *A. thaliana* GeneChips. These chips contained probes for approximately one-third of the genes encoded in the genome of *A. thaliana*. The results led to the identification of the messages encoding proteins of key components of metal homeostasis, some more abundant in shoots and others more abundant in roots. The functions of these proteins, which could be demonstrated by the scientists or were derived from existing data, reflect very clearly the specific physiological functions of roots and shoots in the process of metal hyperaccumulation and tolerance in *A. halleri*. The role of the root is to detoxify metal ions and to maintain the metals in a mobile chemical form for translocation into the shoot of the plant. The shoot functions primarily in metal storage, which involves detoxification and sequestration of the metals. Specifically, in the roots the messages encoding a cellular zinc uptake protein, a protein that mobilizes metals from storage in root vacuoles and a nicotianamine synthase enzyme

are highly abundant. This latter enzyme catalyses the biosynthesis of a metal chelator molecule, nicotianamine, which can detoxify zinc and other metal ions in a mobile form through the formation of a stable metal complex. In the shoots the message levels for another isozyme of nicotianamine synthase are highly abundant. The researchers could again demonstrate an involvement in zinc detoxification. Furthermore the messages for several membrane proteins are highly abundant. One of these is likely to have a function in metal transport into shoot cells. The other two proteins are involved in the detoxification of zinc ions. It is probable that these proteins mediate the transport of metal ions from the cytoplasm into cellular compartments of lower metabolic activity, for example the plant cell central vacuole. Curiously, all these genes displayed high activity under all conditions, and not only when plants are challenged with heavy metals. This is consistent with the observation that leaves of *A. halleri* accumulate zinc even when the plant is growing on uncontaminated soils.

In the post-genome era genome sequences are becoming available of more and more organisms. This enables scientists for the first time to investigate the molecular basis of traits that enable some plants to grow under extremely hostile environmental conditions. This could help to improve crop yields in parts of the world where the climate or the soils are limiting or endangering agriculture, or develop healthier or more nutritious crops. Iron and zinc deficiency are two of the most common nutritional deficiencies. The knowledge of the molecular factors governing plant metal tolerance and accumulation could be instrumental in optimising metal contents in plant-derived foods by increasing essential metal contents, like those of iron and zinc, and reducing the accumulation of toxic metals like cadmium. Finally, if the ability to tolerate or hyperaccumulate metals can be transferred to a high-biomass Brassica plant, this could provide a technology for soil remediation.