# Transcriptomics and Proteomics: Tools for Optimising Phytoremediation Activities

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Negligent industrial development has greatly contributed to environmental pollution through the contamination of water and soil by xenobiotic organic chemicals. Remedial strategies to deal with chemical pollution require reliable methods to identify and monitor contamination, as well as effective procedures to attenuate or to eliminate the pollutant. In the food chain, plants are ideally placed as early bio-indicators of environmental pollution as they experience and respond to environmental toxicants sooner than organisms at higher trophic levels. Furthermore, some plants are capable of detoxifying anthropogenic chemicals by metabolic transformation and could prove useful for the remediation of contaminated water and soil: so-called phytoremediation.

So far research technologies aimed at developing plants for bio-indication/bio-monitoring and for remediation have largely relied on standardised chemical and biochemical procedures to evaluate phytotoxicity, metabolic fate and persistence of organic pollutants in plants. The next stage in the evolution of these plant-based technologies is the improvement and optimisation of any innate phytoremediation activities identified in selected plants.

In general, uptake followed by metabolism and compartmentation is responsible for the detoxification of organic xenobiotics in plants. These are complex cellular systems that may be organised in well-defined pathways and are often controlled by large families of genes. In order to elucidate complex traits such as detoxification, an emerging idea is to make use of global approaches such as the new “omic” technologies to identify molecular changes in plant tissues exposed to specific organic xenobiotics. From expression profiles at the messenger RNA level, transcriptomics permit the identification of function-related gene clusters and at the protein level proteomics provide information on where, when and at what level specific proteins accumulate.

We conclude that these global approaches may be a useful way of widening screening capability to identify appropriate molecular markers that can be used to improve detoxification activity.

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