

# Fine-tuning of root growth by a potentially novel molecular mechanism

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In spite – or rather, because – of their sessile lifestyle, plants can adjust their growth in order to evade or adapt to stressful conditions and objects – light deficiency, water scarcity, or even just a particularly annoying underground stone blocking the root from growing further. The mechanisms behind this developmental response involve many different components with various roles and are a topic of ongoing research by plant biologists around the world.

Like any other biological function, this too is guided by information that is encoded in the genes, which are translated into proteins, the “executive” molecules that perform virtually all tasks. Every cell contains a complete copy of the organism’s genes, but developmental changes like this require that each cell expresses different ones and in different amounts, in a coordinated manner. This coordination of gene expression depends on strict regulation by certain proteins called transcription factors. One particular group of transcription factors that are similar to one another, collectively called “class III HD-zip” transcription factors, directs many different developmental processes in plants, including the growth of the root. In the model plant species *Arabidopsis thaliana*, which is the most common flowering plant in biological studies worldwide, this group of transcription factors has five members, and the ways that they can control root growth and development have only recently started to unravel.

In order to have clues about how any transcription factor controls a biological function, scientists monitor which genes are activated or silenced upon alterations of its activity. When this was done for the class III HD-zip transcription factors in the *Arabidopsis* root, a gene that encodes a glutaredoxin was detected. Glutaredoxins are enzymes that interact with other proteins and catalyse a very specific type of chemical reactions in the cell, redox reactions – where there is exchange of energy between molecules. Each glutaredoxin is specific in its target proteins, which in turn act as switches that are turned on or off by redox modifications. Therefore glutaredoxins can have a targeted impact on the total cellular activity by directing the redox energy to specific target proteins, introducing the concept of “redox control”. Although this specific protein is not experimentally confirmed to have glutaredoxin function, it is designated as such because it is structurally similar to known glutaredoxins.

By tagging this glutaredoxin with a fluorescent protein and analysing its presence in *Arabidopsis* seedlings, we detected it in cells near the tip of the root, supporting our suspicion that it may have a role in this site. To determine whether a gene is important for a trait, it is common to examine plants with blocked or altered function of that gene. When we examined *Arabidopsis* seedlings with blocked function of this glutaredoxin, we found they had shorter roots than normal, which confirms that it has an actual role in root growth. However, if the function of class III HD-zip transcription factors itself is disturbed, the function of the glutaredoxin had a much smaller effect on root growth. This could be because of other root growth mechanisms controlled by the class III HD-zip transcription factors, which can “mask” the glutaredoxin’s effect. Therefore, this glutaredoxin may act to support root growth in normal or close to normal conditions.

Although the general impact of redox on root growth is not a new concept, the involvement of glutaredoxins in root growth has only recently emerged. The discovery of this glutaredoxin’s role in root growth may demonstrate a novel manner in which the plant can harness redox energy and channel it appropriately, in order to enhance the plasticity of its development. Before drawing conclusions though, we still need to confirm its function as a glutaredoxin experimentally. It would also be interesting to determine if this pathway intersects with other known mechanisms of root growth control or if it involves new, unknown components. Identification of its target proteins would provide useful data towards this goal.