

## Retrograde Signaling in Plants: its nature and contributing pathways

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Plastid-to-nucleus signaling is important to coordinate plastid and nuclear gene expression. Transcriptomic as well as genetic studies suggest several pathways which contribute to this retrograde signaling cascade: tetrapyrrole biosynthesis, plastidial gene expression, redox imbalance induced pathways, reactive oxygen species (ROS) signaling and metabolic signatures. However, the hierarchy of these pathways, their contribution to retrograde signaling cascades as well as the nature of the retrograde signal remain elusive. Additionally, the answer to a retrograde signal has been shown to be of high complexity. To elucidate the complex interplay, identify hierarchies and the nature of the retrograde signal, a systems biology approach is needed.

For this purpose, we conducted a meta-analysis of several experiments targetting different pathways by introducing mutations or specific treatments to wildtype plants in *Arabidopsis thaliana*. The expression of mutant versus wildtype plant or untreated versus treated wildtype plant was analyzed for each experiment, generating for each experiment a list of significantly differentially expressed genes. Subsequently, these lists were the basis for calculating intersections between the experiments. All experiments share a set of 39 differentially expressed genes ( $p=2.56 \times 10^{-5}$ ), which might represent a core response modul of retrograde signaling. These genes are mainly responsive to ABA, Auxin, ROS and sugar signals. Since the precursors of ABA, but not ABA itself, are synthesized in the chloroplast and the synthesis of Auxin takes place outside the chloroplast, the results allow to hypothesize that the core retrograde signal might be ROS or sugar-driven.

## References

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