



Transcriptomic Next-Generation Sequencing approach to assessing biostimulant priming of *Arabidopsis thaliana* during drought stress

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Biostimulants are becoming a significant part of the global agrochemical industry. Europe currently holds the greatest market share, where an estimated 6.2 million hectares are treated with biostimulants (Calvo et al. 2014). When applied, biostimulants enhance plant biomass, improve crop quality, and mitigate numerous environmental stress challenges. Many of the available biostimulants fall within the classifications required for organic agriculture, and are independent of fertilizer and plant protection product legislation. Crucially, these products when used in conjunction with crop management strategies, offer solutions to the ever-growing pressures to limit usage of other products in the agrochemical sector.

Drought stress is one of the primary environmental factors affecting global crop productivity. Under stress conditions crop plants energy expenditure is directed to defence, resulting in unfavourable economic effects such as germination inhibition, growth rate reduction, early senescence, and ultimately yield losses. Therefore, identifying plant biostimulant products which can improve the plant's tolerance and or mitigate the resulting growth and yield losses, is a high priority.

Plant priming is a physiological state that allows the plant to better tolerate a future stress than that of a non-primed plant. Natural priming involves a mild environmental stress, which the plant then 'remembers' in subsequent future stress allowing a more efficient response that benefits plant health and survival. Much of the priming processes involve epigenetic regulation, which acts to alter and differentially regulate gene expression in plants exposed to environmental stimuli.

Our work has exploited Next Generation Sequencing (NGS) technology to assess the genome-wide transcriptional profiles of the model plant, *Arabidopsis thaliana* after application of biostimulants, and at a key stage of early onset drought stress. We identified differentially expressed genes in each of the treatments and analysed the corresponding molecular pathways activated by the biostimulants, both in the presence and absence of drought stress.