

A transcriptomics approach to understanding mechano-transduction by *Epichloë* symbionts of grasses.

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Fungal growth is influenced by many factors, and we have recently confirmed that mechanical signals are particularly important in inducing intercalary growth in the grass symbiont, *Epichloë festucae*. Hyphae growing in culture without mechanical disturbance extend exclusively through polar growth, however if subjected to mechanical force, compartments increase in length in proportion to the amount of stretch applied, and compartment division is accelerated compared to un-stretched controls. We are investigating the early biophysical processes that characterise hyphal responses to mechanical force. *E. festucae* hyphae were grown on amino-coated silicon membranes and physiologically-relevant stretching forces applied using a custom-designed stretching frame. The transcriptomes of stretched hyphae were compared to un-stretched controls growing on the same devices immediately after stretch (early response, ER) and 3 h after stretch (late response, LR). In the ER and LR, 105 and 403 genes were differentially expressed (DE) respectively. Fifty five percent of DE genes in the ER were also DE in the LR. Genes involved in reprogramming of primary metabolism and plasma membrane reorganisation were upregulated almost immediately (ER) in response to mechanical stretch, and genes encoding cell wall enzymes were DE in the cultures harvested later (LR). These findings will assist in determining hyphal responses to mechanical stretch and their role in regulating *E. festucae* physiology and growth in plants where hyphae are thought to be subjected to mechanical stretching forces.