A comparative gene co-expression analysis using self-organizing maps on two congener filmy ferns identifies specific desiccation tolerance mechanisms associated to their microhabitat preference

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Background: Filmy-ferns (Hymenophyllaceae) are poikilohydric, homoiochlorophyllous desiccation-tolerant (DT) epiphytes. They can colonize lower and upper canopy environments of humid forest. Filmy-ferns desiccate rapidly (hours), contrasting with DT angiosperms (days/weeks). It has been proposed that desiccation tolerance in filmy-ferns would be associated mainly with constitutive features rather than induced responses during dehydration. However, we hypothesize that the inter-specific differences in vertical distribution would be associated with different dynamics of gene expression within the dehydration or rehydration phases. A comparative transcriptomic analysis with an artificial neural network was done on Hymenophyllum caudiculatum (restricted to lower canopy) and Hymenophyllum dentatum (reach upper canopy) during a desiccation/rehydration cycle. Results: Raw reads were assembled into 69,599 transcripts for H. dentatum and 34,726 transcripts for H. caudiculatum. Few transcripts showed significant changes in differential expression (DE). H. caudiculatum had ca. twice DE genes than H. dentatum and higher proportion of increased-and-decreased abundance of genes occurs during dehydration. In contrast, the abundance of genes in H. dentatum decreased significantly when transitioning from dehydration to rehydration. According to the artificial neural network results, H. caudiculatum enhanced osmotic responses and phenylpropanoid related pathways, whilst H. dentatum enhanced its defense system

responses and protection against high light stress. Conclusions: Our findings provide a deeper understanding of the mechanisms underlying the desiccation tolerance responses of two filmy ferns and the relationship between the species-specific response and the microhabitats these ferns occupy in nature. © 2020 The Author(s).

Gene co-expression

Homoiochlorophyllous

Hymenophyllaceae

Neural network

Poikilohydric

RNA-seq transcriptome

Temperate rainforest

Chile

chromosomal mapping

desiccation

ecosystem

fern

gene expression

gene expression profiling

genetics

physiological stress

Chile

Chromosome Mapping

Desiccation

Ecosystem

Ferns

Gene Expression

Gene Expression Profiling

Stress, Physiological