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Establishing a bioinformatics pipeline to study drought stress related gene expression in rooibos (Aspalathus linearis)

Rooibos (Aspalathus linearis) is a medicinal plant endemic to South Africa, commonly used to make herbal tea. It produces a wide range of phenolic compounds, including the rare aspalathin and PPAC that have anti-diabetic and cardio-protective properties; therefore rooibos is considered a hot target for medical research. Due to the effects of climate change, such as increasing periods of drought and high temperatures, the rooibos plant stands to lose large swathes of its agricultural area. This spells disaster, as the plant is a major source of employment and one of the few cash-crops in the Cederberg Mountain region. Research into the genetics of drought tolerance in rooibos can aid in the establishment of marker assisted plant selection and breeding. The genome and diverse transcriptomes of rooibos have been sequenced by the medicinal plant genomics research team at UWC. Here, I am establishing a bioinformatics pipeline based on the standard RNA-Seq workflow to study gene expression in rooibos. I am using the program 'RSEM' to conduct transcriptome-wide differential gene expression analysis in leaf samples from a cultivated rooibos plant harvested in spring and in autumn, i.e before and after the hot, dry summer prevalent in the Cederberg Mountains. All computational analysis are performed at CHPC.

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Yes

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