

## The Rooibos Genome Program: computational requirements

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While plant genome analysis is gaining speed worldwide, few plant genomes have been sequenced and analyzed on the African continent. Yet, this information holds the potential to transform diverse industries: it unlocks medicinally and industrially relevant biosynthesis pathways for bioprospecting and can boost innovation of plant breeding and plant protection strategies. Considering that South Africa is home to the highly diverse Cape Floristic Region, local establishment of methods for plant genome analysis is essential. The Medicinal Plant Genomics Program was initiated at UWC in 2016 with the sequencing of the diverse transcriptomes and the genome of rooibos (*Aspalathus linearis*); an endemic South African medicinal plant species commonly known as a beverage – rooibos tea. Here, I provide insight into the computational requirements essential for the analysis of this relatively large eukaryotic genome (1.2 Gbp). Biocomputational data analysis, spanning base calling and quality filtering of the raw data ( $\approx 2.5$  Tb), genome and transcriptome assembly, and subsequent structural and functional genome annotation, was completed locally at CHPC in Cape Town.

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