

Assembling the mitochondrial genome of Rooibos (*Aspalathus linearis*)

Rooibos (*Aspalathus linearis*) is an economically important medicinal plant endemic to South Africa. It provides diverse pharmacological and nutraceutical benefits, and was shown to alleviate stress, allergy, diabetes and cardiovascular disease symptoms, and to boost the immune system. To understand the genomic background of these medicinal properties, diverse transcriptomes and the nuclear genome of rooibos have been sequenced by the Medicinal Plant Genomics Research team at UWC. The genomic DNA samples also included mitochondrial and chloroplast DNA which provides an opportunity to study the organelle genomes of this plant. The mitochondrial genome may provide insight into the phylogenetic evolution of rooibos. It can also be used to study how plant mitochondrial genomes are involved in stress response, the mechanisms behind horizontal gene transfer and the different replication modes of plant mitochondrial genomes. However, the assembly of plant mitochondrial genomes is difficult because they contain large repeat sequences. My project focuses on the establishment of a computational pipeline for plant mitochondrial genome assembly using short and long read sequencing data. Here, I describe application of GetOrganelle to assemble the mitochondrial genome of rooibos from short read Illumina sequencing data.

Student?

Yes

Supervisor name

Dr Uljana Hesse

Supervisor email

uhesse@uwc.ac.za

Primary author: Ms LEE, Casey (University of the Western Cape)

Co-authors: HESSE, Uljana (University of the Western Cape); MGWATYU, Yamkela (University of the Western Cape, Department of Biotechnology, Robert Sobukwe Road, Bellville, 7535, South Africa)

Presenter: Ms LEE, Casey (University of the Western Cape)

Session Classification: Micro-talks

Track Classification: Bioinformatics and Biological Sciences