NICIS

NATIONAL INTEGRATED
CYBERINFRASTRUCTURE SYSTEM

CHPC

Contribution ID: **99**   Type: **Talk**

Use of high-throughput sequencing to uncover resistance mechanisms in sugarcane

Wednesday, 4 December 2019 12:00 (20 minutes)

The sugarcane industry is an important agricultural activity in South Africa generating an annual estimated average direct income of R14 billion. Economic loss due to Eldana saccharina (eldana), a lepidopteran stemborer, is estimated to be R1 billion per annum. Commercial sugarcane cultivars (Saccharum spp. hybrids), have different susceptibility ratings to eldana, varying from low to high risk of sustaining economically damaging infestations. The South African Sugarcane Research Institute has utilised the resources of the Centre for High Performance Computing in an approach involving high-throughput RNA sequencing (RNA-seq) to identify early and late response genes that are differentially expressed in two sugarcane cultivars possessing contrasting resistance phenotypes when challenged with eldana herbivory. The results will be used to identify molecular mechanisms involved in the successful defence response and identify candidate genes which are most likely to be useful in breeding for resistance to eldana.

HPC content:
Annotation and assembly is a computationally intensive process that requires considerable CPU time and effort. Various bioinformatic tools were used for the de novo transcriptome assembly and the differential expression analyses required in this project.

Supported Student

Primary author: Mrs JACOB, Robyn (South African Sugarcane Research Institute)

Presenter: Mrs JACOB, Robyn (South African Sugarcane Research Institute)

Session Classification: HPC Applications

Track Classification: Bioinformatics and Biological Sciences