De novo assembly and characterization of *Monsonia burkeana* leaf transcriptome

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Monsonia (*Monsonia burkeana* Planch. ex Harv) is one of the most valuable tea and traditional medicinal plants used in Southern Africa. In spite of its wide usage by the local inhabitants, there is very little or no genomic and transcriptomic information regarding this plant in literature. To provide understanding of the naturally occurring tea and drug specific products and the key pathways responsible for the biosynthesis of these molecules, we sequenced the leaf transcriptome using Illumina MiSeq platform. This generated 800 MB 300x300 paired-end 2,590,652 reads that were assembled *de novo* in to 46757 transcript sequences. Blast based annotation of the assembled transcripts revealed best hits for homology in other species covering more than 17,800 genes. Functional GO annotation and KEGG pathways showed the enzymes that were involved in the biosynthesis of secondary metabolites. A total of 93 KEGG pathways with 15 functional categories and associated genes encoded by more than 90% of the coding transcripts are responsible for the biosynthesis of primary and secondary metabolites. Caffeine metabolism, flavonoid and phenylpropanoid biosynthesis and xenobiotics biodegradation, terpenoids and polyketides metabolism are named but few were identified in association with tea quality and therapeutic drugs. More than 80 different gene families such as cytochrome p450 and protein kinase were identified to potentially encode for enzymes related with the biosynthesis of secondary metabolites in various pathways. This data gives insight into the M. *burkeana* leaf tissue in harboring tea and drug specific bioactive chemicals.

Biography

Adugna A Woldesemayat has completed his PhD in 2015 from the University of the the Western Cape (UWC), South Africa in Bioinformatics and is currently a Post-doctoral research fellow at the University of South Africa (UNISA), Science Campus, Florida, South Africa. He is currently In-charge of the next generation sequencing (NGS) data analysis and suppervises postgradate students. He has published several papers in reputed journals.

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