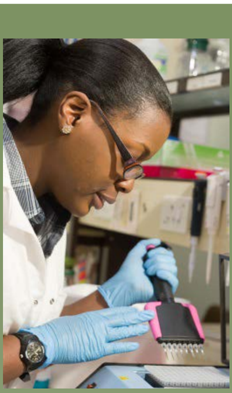
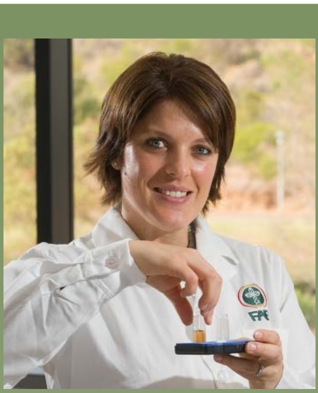
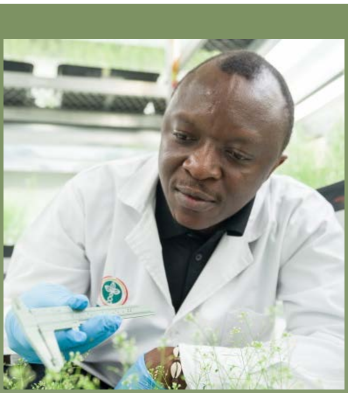




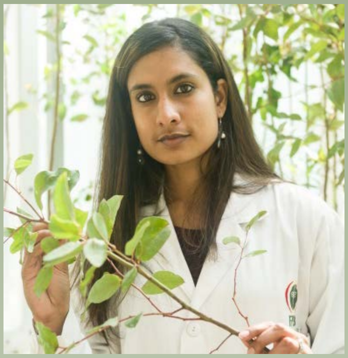


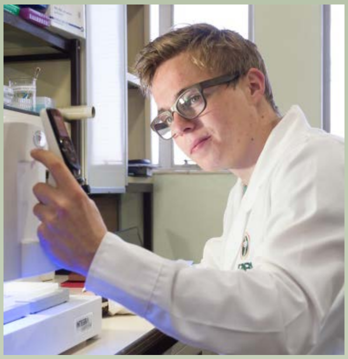
The Forest Molecular Genetics (FMG) Programme

The Forest Molecular Genetics (FMG) Programme, headed by Prof. Zander Myburg, is based at the University of Pretoria's Department of Genetics and is affiliated with the Forestry and Agricultural Biotechnology Institute (FABI) and the Genomics Research Institute (GRI). Our research focuses on the genetic control of wood development in fast-growing plantation trees, primarily *Eucalyptus* and tropical pines grown in South Africa. Furthermore, we study defence mechanisms in forest trees with a view to protect trees from pests and pathogens. We use a number of research and technology platforms, namely: genomics, bioinformatics, high-throughput DNA marker analysis, functional genetics, as well as wood phenotyping. We work in close collaboration with South African forestry companies, such as Sappi, Mondi, Hans Merensky and York Timbers to develop human capacity and resources for the application of tree biotechnology in operational tree improvement programmes. This research is supported by grants from the National Research Foundation (NRF), the Technology and Human Capacity for Industry Programme (THRIP), the Forest Sector Innovation Fund (FSIF) and the Department of Science and Technology (DST) of South Africa.

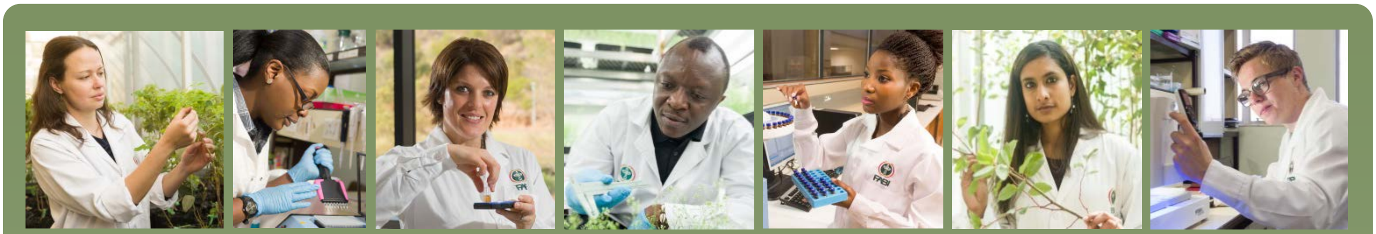
For more information or to submit an application, please contact
the FMG Project Coordinator, Mrs Marja O'Neill, at
marja.oneill@up.ac.za, telephone: 012 420 6377

http://www.fabinet.up.ac.za/index.php/research-groups/forest-molecular-genetics





Forest Molecular Genetics (FMG)



BSc(Hons)/MSc Bioinformatics & Biotechnology Positions Available 2016

The Forest Molecular Genetics (FMG) Research Programme offers the following BSc(Hons)/MSc Bioinformatics/Biotechnology positions for 2016:

Systemic defence responses in *Eucalyptus* (Biotechnology project). This project involves the use of the QuantStudio OpenArray Platform to investigate the systemic defense responses of *Eucalyptus* grandis to pathogen attack. We aim to determine if hormone signaling pathways are perturbed by the primary challenge and whether these changes provide enhanced protection against secondary pathogen attack. This project involves real-time PCR based expression profiling, phytohormone analysis, plant pathology trials and bioinformatics analyses. Main supervisor: Dr Sanushka Naidoo

Identification, characterisation and expression analysis of chromatin-regulating factors in *Eucalyptus grandis* (Bioinformatics project). Despite the central importance of epigenomics in trait properties and development, little is known about the mechanisms by which epigenomic modifications are regulated. A wealth of chromatin readers, writers and erasers of epigenomic marks have been described, together comprising the machinery by which cells write and interpret the epigenetic code. This bioinformatics project will identify and functionally categorise *E. grandis* homologs of known chromatin-regulating factors, and identify candidates linked to wood formation using existing transcriptomics resources. Main supervisor: Dr Steven Hussey

Transcriptome-wide allele-specific expression (ASE) analysis in interspecific hybrids of *Eucalyptus (*Bioinformatics project). Single nucleotide polymorphism (SNP) markers along the coding region of a gene allows partitioning of RNA-seq data into the two alleles carried by each individual. This NRF-supported bioinformatics project will use existing genome resequencing data of two parental trees and transcriptome sequences of 127 progeny to perform haplotype (allelic) phasing followed by quantification of ASE of each gene. Main supervisor: Prof. Zander Myburg

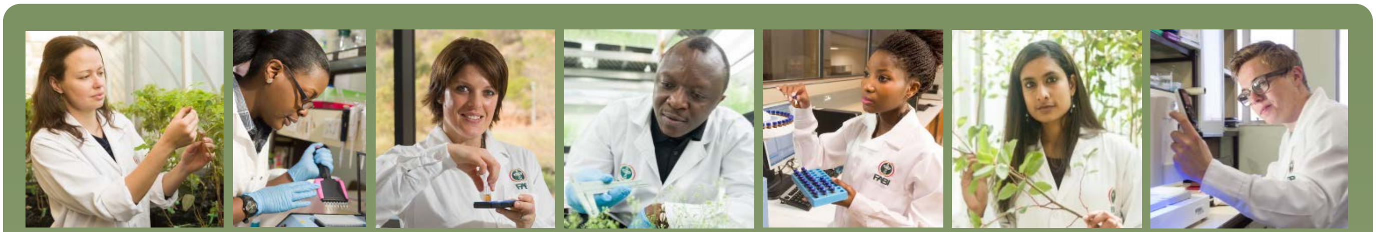
Bioinformatics resources for analysis and visualization of genetic mapping data in *Eucalyptus* (Bioinformatics project). This bioinformatics project will contribute to the development of bioinformatics resources (a module of the *Eucalyptus* Genome Integrative Explorer (EucGenIE, www.eucgenie.org) for management and visualization of genetic mapping data (DNA markers, genetic maps, QTLs, eQTLs). The project is supported by NRF and forestry industry. Main supervisor: Dr Nanette Christie

Detection and quantification of alternative splicing in *Eucalyptus* secondary cell wall biosynthesis genes (Bioinformatics project). This NRF and industry-supported bioinformatics project will entail identification of alternative splicing and a detailed isoform-specific gene expression analysis of secondary cell wall biosynthesis genes in *Eucalyptus* using RNA-Seq data. The project is supported by NRF and forestry industry. Main supervisor: Dr Nanette Christie

Construction of a custom 256-SNP genotyping OpenArray resource for *Eucalyptus* hybrid introgression breeding (Biotechnology project). Interspecific hybridization followed by backcross introgression of specific genomic regions tagged by SNP DNA markers offers the opportunity to develop *Eucalyptus* clonal varieties tailored for specific environments, while maintaining superior growth and wood properties. In this project, a custom OpenArray with species discriminating DNA markers will be developed for backcross breeding of *Eucalyptus* hybrids. Main supervisor: Prof. Zander Myburg

Positions in FMG are supported by bursary additions from industry and THRIP (in addition to NRF and other bursaries). For more information or to submit an application, please contact the FMG Project Coordinator, Mrs Marja O'Neill, at marja.oneill@up.ac.za

Forest Molecular Genetics (FMG)



MSc Positions Available 2016

The Forest Molecular Genetics (FMG) Research Programme offers the following MSc positions for 2016:

Disparate terpene defence mechanisms in two *Pinus* species in response to *Fusarium circinatum*
The project aims to investigate and model the main defense responses in *Pinus patula* and *P. tecunumanii* to *Fusarium circinatum.* More specifically, we aim to verify the model over a time-course of infection and couple this with analysis of the terpenes in pine. We will also be able to identify pathogen specific transcripts over the time-course of infection by mapping reads to the pathogen genome. This project involves the development of a QuantStudio OpenArray for high-throughput gene expression analysis, transcriptome analysis of the pathogen, targeted metabolite analysis and plant pathology trials. Main supervisor: Dr Sanushka Naidoo

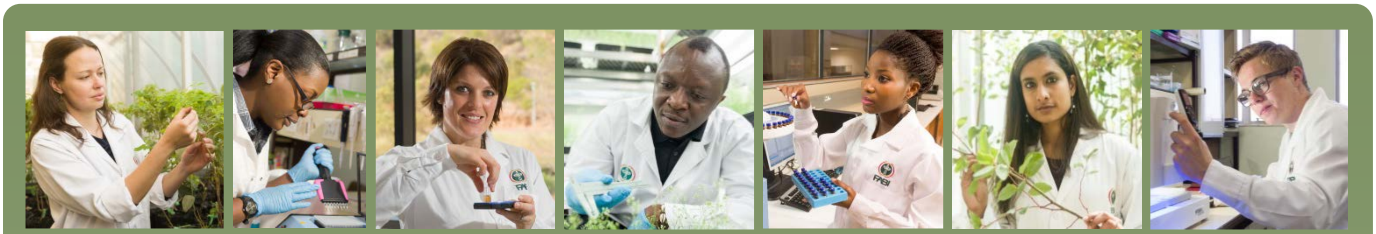
Genome-wide analysis of chromatin accessibility regulating gene expression in *Eucalyptus grandis* tissues. The dynamic packaging of genomic DNA and its association with regulatory proteins, collectively known as chromatin, has a profound influence on development. Accessible chromatin regions, identified by DNase I nuclease hypersensitivity (DH), can be used to identify novel enhancer elements and tissue-specific chromatin configurations. This epigenomics project will use DNase-seq and RNA-seq to characterise the accessible chromatin landscape of various *E. grandis* tissues, identify tissue-specific DH sites and model gene expression. Main supervisor: Dr Steven Hussey.

High-throughput SNP marker analysis and linkage mapping of wood biopolymer processing traits in *Eucalyptus*. Nested association mapping (NAM) is a powerful approach to dissect quantitative genetic variation by combining linkage analysis within families and genome-wide association (GWAS) across families. This DST and industry (Sappi) supported project will entail high-density SNP mapping and QTL analysis in the F1 hybrid progeny of *Eucalyptus grandis* and *E. urophylla*. Main supervisor: Prof. Zander Myburg

A genome-diversity atlas for commercially grown *Eucalyptus* species. Knowledge of the genome diversity of *Eucalyptus* tree species is essential for understanding population genetics and evolution of these species and for guiding gene conservation and molecular breeding. This Forestry Sector Innovation Fund (FSIF) supported project will generate a Genome Diversity Atlas for the main commercially relevant eucalypt species cultivated in South Africa. Main supervisor: Prof. Zander Myburg

Positions in FMG are supported by bursary additions from industry and THRIP (in addition to NRF and other bursaries). For more information or to submit an application, please contact the FMG Project Coordinator, Mrs Marja O'Neill, at rmarja.oneill@up.ac.za

Forest Molecular Genetics (FMG)



PhD Positions Available 2016

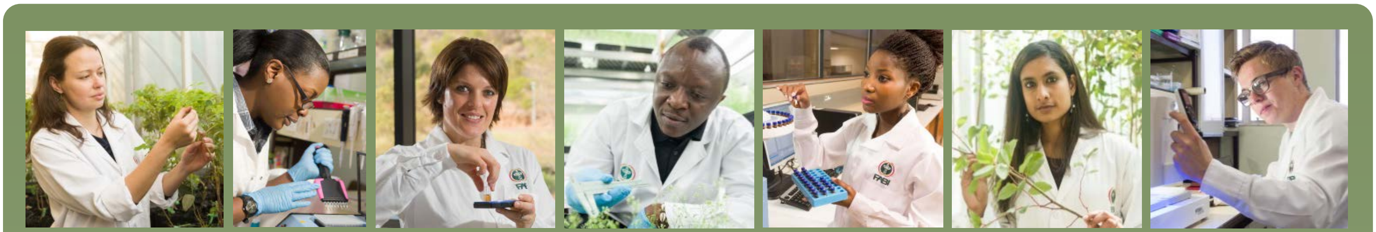
The Forest Molecular Genetics (FMG) Research Programme offers the following PhD positions for 2016:

Identification of transcriptional networks regulating secondary cell wall biogenesis in *Eucalyptus grandis* through *cis-element* mining of key transcription factors. Transcriptional networks are defined by interactions between transcription factors and their cognate *cis*-regulatory DNA elements. In *Arabidopsis*, transcriptional networks can be predicted *in silico* based on known TF-*cis* element recognition, especially when combined with information on conserved noncoding sequences (CNSes). In this project, the candidate will identify DNA sequences bound *in vitro* by key secondary cell wall-related transcription factors in *E. grandis* using SELEX, and integrate this information with *E. grandis* CNS data to predict and model secondary cell wall transcriptional networks. Main supervisor: Dr Steven Hussey.

Interaction of genome and epigenetic variation affecting the viability and heterosis of *Eucalyptus* hybrid clones. Genetic (DNA) and epigenetic (DNA methylation) patterns of variation are affected by interspecific hybridization and long term propagation of clonal varieties. This industry (Mondi) supported project will investigate the accumulation of genomic variation (by genome-wide resequencing) and epigenetic variation (by genome-wide methylation sequencing) associated with clonal propagation and environmental variation in two F1 hybrid clones of *E. grandis* and *E. urophylla*, one of which has exhibited unexplained sudden death syndrome. Supervisors: Prof. Zander Myburg and Dr Steven Hussey

Positions in FMG are supported by bursary additions from industry and THRIP (in addition to NRF and other bursaries). For more information or to submit an application, please contact the FMG Project Coordinator, Mrs Marja O'Neill, at rmarja.oneill@up.ac.za

Forest Molecular Genetics (FMG)



Postdoctoral Positions Available 2016

The Forest Molecular Genetics (FMG) Research Programme offers the following postdoctoral positions for 2016:

Population genomics and molecular breeding of tropical pine species. What genomic diversity underlie species and provenance differentiation, as well as hybrid vigour and disease resistance in tropical pine species such as *Pinus patula* and *P. tecunumanii*? This population genomics project will involve development and application of exome capturing and next-gen DNA sequencing technology for genome-wide genotyping, population genomics analysis and molecular breeding of tropical pine species grown in South Africa and South America. The project is supported by forestry industry and the Forestry Sector Innovation Fund (FSIF) of South Africa. Main supervisor: Prof. Zander Myburg

Molecular characterization of proteins involved in carbon partitioning during xylogenesis. A systems biology and biotechnology project is available investigating proteins involved in carbon import/export and metabolism in organelles during wood formation. Through systems genetics approaches we have identified several organellar transporters and enzymes of unknown function that we hypothesize act on key metabolites to impact carbon utilization for secondary cell wall synthesis. The project will investigate the effects of these genes on the plant's physiology and cell wall properties. Main supervisor: Dr Eshchar Mizrachi

Functional analysis of secondary cell wall-associated *Eucalyptus* transcription factors. What are the functions of *Eucalyptus* transcription factors that have been implicated in secondary cell wall regulation? This functional genomics project uses *Populus* trees as a woody model to study the phenotypic and transcriptome-wide effects of overexpression and dominant repression of *Eucalyptus* transcription factors implicated in wood formation. Growth monitoring, microscopy analysis, cell wall chemistry and RNA-seq analysis of transgenic lines will be conducted to characterise several *Eucalyptus* transcription factor candidates. The work is supported by the forestry industry and government. Main supervisor: Dr Steven Hussey

Systems genetics in a *Eucalyptus grandis* x *Eucalyptus urophylla* backcross population to uncover genes and markers linked to disease resistance. The aim of this project is to dissect defence mechanisms and identify markers linked to resistance against the stem canker pathogen *Chrysoporthe austroafricana* in a hybrid backcross population. Genetic loci (QTLs) and genes involved in resistance will be identified using the *Eucalyptus* SNP Chip (GeneSeek). Disease resistance will be further dissected at the gene level by performing transcriptome-wide profiling of infected tissues for each of 100-200 F2 progeny and mapping expression QTLs (eQTLs) for genes linked to disease resistance. Main supervisor: Dr Sanushka Naidoo

Positions in FMG are supported by bursary additions from industry and THRIP (in addition to NRF and other bursaries). For more information or to submit an application, please contact the FMG Project Coordinator, Mrs Marja O'Neill, at rmarja.oneill@up.ac.za

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