

FABI TEAMWORK: ALMOST 1500 GENES ANNOTATED IN 5 HOURS!

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FABI is well known for using “the power of many” to get certain tasks done faster, more effectively and with more enjoyment. The team spirit and enthusiasm of the students far overshadow the pressures involved in many research projects and other crucial tasks in and around the institute. On 4 April, FABI students and staff again demonstrated this team spirit during a jamboree to curate more than 1400 genes of the tree pathogen, *Ceratocystis albifundus*. This fungus is an important pathogen of native trees (including several *Protea* spp.) and the commercially important *Acacia mearnsii*. The whole genome of the fungus was recently sequenced as part of a larger project where genomes of 20 *Ceratocystis* spp. were sequenced. The jamboree was organized with two goals in mind. Firstly, to train the gene annotation pipeline MAKER using *C. albifundus* as model. The trained program will be of benefit to many students working on various aspects of the *Ceratocystis* genomes in the foreseeable future. The second purpose was to provide hands-on experience to staff and students in gene annotation and using MAKER. Twenty-one FABIans volunteered to take part in the jamboree and aimed to curate 1000 genes over two days. Because of the eagerness, fervour and commitment of all the participants, 1458 genes were curated in 5 hours, making it unnecessary to return the following day. Now that is team work!



The FABI students and staff who volunteered to take part in the genome jamboree