EUCALYPTUS

Improving Genetics. Increasing Profits.

RAPID GENOMICS
DNA Genotyping & Genetic Data Analysis
The advent of genome-wide genomic analysis, such as genomic selection or genome-wide association studies, led to a demand for large-scale, high-throughput markers. With the constant decrease in the sequencing cost, one option to genotype a large number of markers distributed throughout the genome is to capture and sequence targeted regions, and detect variants based on the sequencing reads.

Rapid Genomics is a DNA genotyping and genetic data analysis company providing tools for agricultural companies and researchers to quickly breed and grow ideal crops and livestock — resulting in maximum productivity and profits.

**OUR METHODS**

RAPiD-Seq is a method of genotyping by sequencing a reduced representation of genomes, generated by amplifying them by PCR. PCR primers are selected to amplify a defined set of regions equally distributed to ensure suitable coverage and number of targeted loci.

Capture-Seq is a method of genotyping by sequencing specific, target regions of the genome by capturing them. Capture probes are selected and designed to hybridize to unique, specific regions of interest.

**WHAT WE OFFER:**

**DNA GENOTYPING**
Any species and number of loci, fast and flexible, with no minimum number of samples.

**BIOINFORMATICS**
From genome assembly and annotation, to sequence variant detection and transcriptome/methylome profiling.

**GENETIC DATA ANALYSIS**
From QTL analysis to the development of advanced models to predict phenotypes.

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Here, we present a high-throughput genotyping approach for Eucalyptus based on sequence capture. We designed probes to target 40,000 evenly spaced loci of the *E. grandis* genome. These probes were used to capture specific regions of the genome from 700 individuals belonging to a highly heterozygous breeding population made of interspecific hybrids. For each individual, barcoded libraries were prepared and hybridized against the designed probes. The product of the capture reaction was sequenced, sequences were aligned to the *E. grandis* reference genome and SNPs identified in the population.

Using this method, we were able to identify 43,681 polymorphic markers. Moreover, one random sample was repeated 14 times with a genotypic call repeatability of 0.997. The SNPs obtained for the population were used to generate genomic selection prediction models for tree diameter and height and wood specific gravity. The models were developed in a cross-validation design using random regression best linear unbiased predictor (BLUP) and resulted in accuracies ranging from 0.59 to 0.76. These accuracies indicate the feasibility of this genotyping approach to *Eucalyptus* breeding.