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Exploring American Oil Palm (*Elaeis oleifera*) Genetic Resources in Brazil through a Combination of Genetic and Genomic Approaches

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The Oil Palm expansion areas in Brazil coincide with the area of occurrence of bud rot, a major threat to the crop. Because of that breeders are now using *E. oleifera* germplasm in Oil Palm breeding programs, generating inter-specific hybrids. The species, however, lack the genomic resources currently available for Oil Palm. Therefore, we started a project to explore American Oil Palm genetic resources through a combination of genetic and genomic approaches. We've obtained so far, using the DArTSeq platform, over 7.000 silico-DArTs markers and 5.500 high-quality SNP loci, that were first used to evaluate the extent and organization of the genetic diversity of the collection of *E. oleifera* maintained by Embrapa. In parallel we started the whole-genome sequencing of the *E. oleifera* using a low cost hybrid-strategy. In phase 1 we sequenced and assembled (N50 ~2Kbp) three *E. oleifera* genotypes (each on 1 Illumina HiSeq 2000 lane). From phase II onwards, we concentrated our efforts in sequencing one genotype (from Manicoré, Brazil), using libraries with different insertion sizes in the Illumina platform (180 and 800bp PE and 3, 5 and 10Kbp MP libraries). The phase 2 assembly showed a N50 of ~27Kbp, with >90% of filtered reads included into contigs. Despite the high coverage we obtained with the small reads (~100x), we decided to improve the scaffolding by sequencing large inserts (8 and 20Kbp) using the Roche 454 technology (Phase 3). We are currently working on a hybrid assembly strategy to use all the data we have in hands.

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