Abstract: Whole Genome Sequencing of the E. oleifera South-American...

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W488 Whole Genome Sequencing of the E. oleifera South-American Wild Oil Palm

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Oil palm is one of the most important sources of vegetable oil; and, accordingly to FAO, it was responsible for 1/3 of all vegetable oil produced in the World in 2010/11. Recently, Brazil launched two programs to boost the production of oil palm significantly in Brazil - the National Biodiesel Production and Use Program & the Oil Palm Sustainable Production Program. The oil palm production area in Brazil is expected to increase 10 to 15 times in the next decade. Embrapa hosts a breeding program focusing on the development of interspecific hybrids between the African oil palm (*Elaeis guineensis*) and the wild South-American oil palm, known as *Caiaué* (*Elaeis oleifera* Kunt Cortez). Caiaué is a highly important genetic resource for this breeding program, being the source of several important traits, such as: high tolerance to bud rot; reduced annual growth rate of the trunk; and high rate of unsaturated fatty acids. Besides engaging in multinational WGS and transcriptome initiatives in *E. guineensis*, Embrapa also started a WGS initiative specifically to *E. oleifera*. The assembly of a plant genome as big as the oil palm haploid genome is a complex task, and a precise assessment of its genome content is necessary to define the sequencing strategy. Considering that the available estimates are controversial, we revisit the theme and present some new numbers (details in the poster *Revisiting an unfinished business: the genome content of Elaeis guineensis, E. oleifera and its inter-specific hybrid*). Besides that, an initial analysis of sequences (~5X) from three Caiaué genotypes and one oil palm genotype has allowed us to choose the genotype for the WGS initiative, as well as to design a sequencing strategy to obtain the genome draft.

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