

W493 Multi-Parent QTL/Gene Mapping, Novel Field Trial Systems and Intra-Gene Markers: A Key Method for Marker-Assisted Selection in Oil Palm (*Elaeis guineensis* Jacq.)

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Norbert Billotte , CIRAD, Montpellier Cedex 5, France
 Franc-Christophe Baurens , CIRAD, Montpellier Cedex 5, France
 Benoit Cochard , CIRAD, Montpellier Cedex 5, France
 Brigitte Courtois , CIRAD, Montpellier Cedex 5, France
 Teresa Cuellar , CIRAD, Montpellier Cedex 5, France
 Sandra Espeout-Fois , CIRAD, Montpellier Cedex 5, France
 Albert Flori , CIRAD, Montpellier Cedex 5, France
 Ange-Marie Risterucci , CIRAD, Montpellier Cedex 5, France
 Manuel Ruiz , CIRAD, Montpellier Cedex 5, France
 Philippe Amblard , PalmElit SA, Montferrier/Lez, France
 Hubert de Franqueville , PalmElit SA, Montferrier/Lez, France
 Claude Louise , PalmElit SA, Montferrier/Lez, France
 Bruno Nouy , PalmElit SA, Montferrier/Lez, France
 Tristan Durand-Gasselín , PalmElit SA, Montferrier/Lez, France
 Angélique D'Hont , CIRAD, Montpellier Cedex 5, France
 Brigitte Mangin , INRA (UR875 BIA), Castanet-Tolosan cedex, France
 Claire Lanaud , CIRAD, Montpellier Cedex 5, France

CIRAD (www.cirad.fr) and PalmElit SA (www.palmelit.com) are implementing a Marker-Assisted Selection (MAS) of the oil palm through a long-term multi-stage project in order to make optimum use of its existing network of field experiments while capitalising upon recent advances in molecular marker technology. Biotechnology projects, performed in both *E. guineensis* and *E. oleifera* species, combine genetics, structural genomics, functional genomics and whole genome sequence information. A QTL (Quantitative Trait Locus) analysis designed for multi-parent populations was designed for crosses between heterozygous parents and tested in oil palm (*Elaeis guineensis* Jacq.), which is a diploid cross-fertilizing perennial species with small family sizes tested in breeding trials. The algorithm, MCQTL *OutBred* available for any allogamous species, an extension of MCQTL (INRA, <http://carlit.toulouse.inra.fr/MCQTL/>), a software application to handle multiallelic QTL detection in multicross design, was used to compare two types of QTL search for small size families, within-family analysis and across-family analysis. Results showed that the across-family analysis proved to be efficient due to the interconnected families, but the small family size issue is just partially solved. A conclusion is that a "real-time" MAS of the oil palm perennial crop can be performed, apart a genome wide methodology, by generalising a multi-parent QTL/Gene detection approach through adapted classical genetic trials, novel Field Methodological Systems and Multi-parent QTL/Gene mapping methods and extensive catalogues of expressed *Elaeis* genes for intra-gene markers, all information analyses being supported by the South Green Bioinformatics Platform (SGBP) applied by CIRAD to the genomic resource analysis of southern and mediterranean plants. Therefore, our presentation focuses on how our current biotechnology researches are integrated into the genetic improvement plan for optimizing the MAS creation of new high yielding commercial varieties in the context of a more sustainable oil palm agro-industry.

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