



W336

Interspecific Introgression and Trait Dissection In Peanut (*Arachis hypogaea*)

Date: Monday, January 14, 2013

Time: 12:55 PM

Room: Royal Palm Salon 4,5,6

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Cultivated peanut is originating from South-America and has become very important for many economies and populations in Asia and Africa. It emerged from a single event of allotetraploidization that gave rise to a limited diversity at the DNA level. Peanut wild relatives represent an important source of novel alleles that could be used to broaden the genetic basis of the cultigen. Using a synthetic amphidiploid as donor parent new interspecific populations have been developed with an improved variety cultivated in Senegal. An advanced backcross (AB-QTL) population was first used to conduct a QTL study for several traits involved in peanut productivity and adaptation. A total of 95 QTLs were detected, about half of them showing positive effects associated with the wild allele. We then produced a set of 122 Chromosome Segment Substitution Lines (CSSL) that globally incorporate the whole genome of the wild donor as overlapping segments introgressed in the recipient cultivar. As a demonstration of the utility of these lines, four morphological traits were evaluated on a subset of 80 CSSLs. A detailed analysis of one of these traits, plant growth habit, showed that it is complex and governed by several QTLs with various effects. The comparison of the number of QTLs mapped for growth habit between CSSLs and AB-QTL showed the higher efficiency of the CSSL population and its interest for QTLs validation, breeding and gene discovery.