

Helping Wild *Arachis* Taxonomy and Introgression Using SNP Markers

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Wild *Arachis* species are being universally reported as source of traits to beat the challenges of the food production in a world climate changing context. Wild species identification is currently done solely using morphological traits, which is not an easy task. Few taxonomists are able to positively identify *Arachis* species. Accession identification adds a new whole layer of complexity. The accurate identification of wild *Arachis* species and accessions is an important issue for introgressions. Due to plasticity in phenetic characters the identification based on morphological features has been exclusively performed by botanists. In order to help identification of species/accessions a set of 696 wild *Arachis* accessions and 378 *A. hypogaea* lines were analyzed using the 48K 'Axiom_*Arachis2*' SNP array. A filtering process resulted in about 100 SNP distinguishing *A. hypogaea* vs non-*A. hypogaea* species/accessions. Based on the results, a set of Single Nucleotide Polymorphism (SNP) markers were designed which were used to successfully differentiate *A. hypogaea* from non-*A. hypogaea* (wild) genotypes. The development of this set of SNP markers is the first step for the assembly of a toolbox to help speed the introgression of wild desirable genes into peanut elite lines to obtain new peanut varieties with resistance traits.