

Molecular and Agronomic Evaluation for Genetic Background Recovery of Introgression Lines of *AhFad2* Mutations

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High oleic acid composition is imperative for the quality of peanut seed in regard to both its nutritional benefit for human health and prolonged shelf-life for peanut products. Fatty acid desaturase (FAD2) is a key enzyme that catalyzes the conversion of oleic acid to linoleic acid. For the tetraploid cultivated peanut, the *AhFad2A* and *AhFad2B* genes function independently on the A and B subgenomes, respectively. High oleic acid phenotype in peanut is caused by loss of function of *AhFad2A* and *AhFad2B*, and thus mutations in these genes can be used as functional markers for trait introgression in high oleic acid peanut breeding. In the present study, four peanut varieties of different market types popular in the main peanut production regions of China, namely YH 15, YZ 9102, YH 9326, and YH 9327, were selected to cross with high oleic acid donors and backcrossed for four generations as recurrent parents. Twelve high oleic acid lines with morphological features and agronomic traits similar to those of the recurrent parents were obtained by *Fad2* marker-assisted backcross selection (MABC). The results demonstrate that the genetic background recovery rates of BC₃F₂ and BC₄F₂ were apparently higher than that of BC₂F₂. The genetic backgrounds of BC₄F₂ were closer to the recurrent parents than those of BC₃F₂ and BC₂F₂ families. To our knowledge, this is also the first application of single nucleotide polymorphism (SNP) markers based on the high-throughput and cost-effective Kompetitive Allele Specific PCR (KASP) technology for genetic background evaluation in peanuts.