Development and Utilization of InDel Markers to Identify Peanut (*Arachis hypogaea* L.) Disease Resistance.

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Peanut diseases, such as leaf spot and spotted wilt caused by Tomato Spotted Wilt Virus, can significantly reduce yield and quality. Application of marker assisted plant breeding requires the development and validation of different types of DNA molecular markers. Nearly 10,000 SSR- based molecular markers have been identified by various research groups around the world, but less than 14.5% showed polymorphism in peanut and only 6.4% have been mapped. Low levels of polymorphism limit the application of marker assisted selection (MAS) in peanut breeding programs. Insertion/deletion (InDel) markers have been reported to be more polymorphic than SSRs in some crops. The goals of this study were to identify novel InDel markers and to evaluate the potential use in peanut breeding. Forty-eight InDel markers were developed from conserved sequences of functional genes and tested in a diverse panel of 118 accessions covering six botanical types of cultivated peanut, of which 104 were from the U.S. mini-core. Results showed that 16 InDel markers were polymorphic with polymorphic information content (PIC) among InDels ranged from 0.017 to 0.660. With respect to botanical types, PICs varied from 0.176 for *fastigiata* var., 0.181 for *hypogaea* var., 0.306 for *vulgaris* var., 0.534 for *aequatoriana* var., 0.556 for *peruviana* var., to 0.660 for *hirsuta* var., implying that *aequatoriana* var., *peruviana* var., and *hirsuta* var. have higher genetic diversity than the other types and provide a basis for gene functional studies. Single marker analysis was conducted to associate specific marker to disease resistant traits. Five InDels from functional genes were identified to be significantly correlated to tomato spotted wilt virus (TSWV) infection and leaf spot, and these novel markers will be utilized to identify disease resistant genotype in breeding populations.