

Discovery of a Resistance Gene Cluster Associated with Smut Resistance in Peanut

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Peanut smut, caused by *Thecaphora frezzii* Carranza & J.C. Lindq., is an emerging threat for the global peanut industry. The disease's destructive potential can be exemplified by pod incidence values as high as 70% and yield losses reaching 30%. Because fungicides have shown moderate but highly variable levels of control, development and deployment of smut resistant cultivars are the best strategies for disease management. Screening for smut-resistant germplasm requires years of field trials and is currently the only option for breeders because genetic markers for resistance have not yet been developed. The objectives of this study were to perform whole genome sequencing (WGS) on a recombinant inbred line (RIL) population developed for smut resistance mapping and subsequently fine map discovered QTL associated with smut resistance. An expedited strategy was employed by phenotyping in the F₅ generation. We phenotyped 200 families with 3 plants per family for smut resistance in infested fields during the 2019/2020 season in General Deheza (32°45'23"S 63°47'20"W), Argentina. Each individual was sequenced using iGenomX RipTide library preparation and Illumina NovaSeq sequencing to yield approximately 1 times genome coverage. Analysis of the phenotype and genotype data using Khufu resulted in the identification of a single major smut resistance QTL on chromosome 12 (B02). Chromosome level genome sequences were assembled for the resistant parent (Ascasubi) and susceptible parent (10_2870) using PacBio HiFi sequencing. Analysis of the QTL region identified a resistance gene cluster where the resistant lineage retained certain R genes that were lost in the susceptible lineage. The structural variation represents strong functional variation controlling smut resistance. A validation population was sequenced using Khufu to validate the QTL region and analysis confirmed the major locus on chromosome 12. The identified variation will be used to develop smut resistant varieties quickly using molecular assisted breeding strategies.