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Detection and genetics of structural diversity in soybean

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We have demonstrated that structural differences such as copy number variation (CNV), presence absence variation (PAV) and more complex rearrangements in the soybean genome underlie multiple important traits in soybean, including Soybean Cyst Nematode and Soybean Aphid resistance. The structures underlying multiple traits, and their common features and differences, were identified using fosmid cloning and other clone-based methods. These were directed at genomic intervals in the hundreds of kilobases defined using fine-mapping techniques. Until very recently, while some structural polymorphisms could be identified using short read sequencing or array hybridization, the unambiguous characterization of structural differences in soybean required the use of these laborious large-insert cloning methods. Recent advances in technology have made the accurate characterization of complex structural polymorphisms possible at the whole-genome scale. Multiple recently developed technologies have been deployed on questions of soybean structural diversity. Each provides important advantages for specific applications. Together these methods have potential for characterizing the genomes of soybean with unprecedented accuracy and resolution.