

## **Improving the Scale of Marker-Assisted Selection in Virginia-type Peanut**

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While relatively straightforward in theory, marker-assisted selection (MAS) has proven difficult to implement, particularly at a scale equivalent to that of phenotypic selection and in small, public-sector breeding programs. Furthermore, the ability to perform genotyping directly from seed tissue, as opposed to leaf tissue, offers the ability to rapidly accelerate the process while reducing resources committed to greenhouse and field space. Here we described a three step approach tailored to peanut consisting of 1) A novel, high-throughput approach for the non-destructive collection of seed tissue; 2) A rapid, inexpensive crude DNA isolation from that seed tissue and; 3) A custom multiplex approach with integrated data processing to score multiple markers from a single PCR reaction.