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Development of sequencing for genotyping within soybean breeding programs

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Genomic selection requires a cheap molecular marker system to be effectively deployed in a breeding program. Current marker array and GBS technologies used in soybean research can genotype 6,000 to 50,000 markers for a cost ranging from \$8 to \$100. For a breeding program to deploy genomic selection, cheaper methods are needed to genotype breeding population parents at a higher SNP density and more importantly, an ultra-cheap method is needed to genotype 200-1000 markers on early generation breeding lines. Using low pass sequencing and imputation, we are developing methods to effectively genotype parental lines at an ultra-high density number of SNPs for similar cost of 50k array chips. In addition, we are developing targeted enrichment genotyping-by-sequencing methods, which are capable of genotyping 200-4000 markers on samples for a lower cost than current array genotyping technologies. Combination of these two technologies will enable genomic selection to be deployed within breeding programs helping to accelerate the genetic gain of yield within soybean.