

Next Generation Sequencing (NGS) Applications in Crop Breeding

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ArrayXpress has developed advanced genomics processes using NGS to increase the performance and cost effectiveness of genetic studies in Plant Sciences. Applications of our expertise and techniques utilized specifically for Crop Breeding are highlighted below.

Establishment of valuable genomics resources

Sequencing genomic DNA, mRNA (cDNA) and/or microRNAs from your reference production genotypes, using NGS technology, provides genomic resources that will have a direct impact on understanding: the overall biology of your production genotypes, gene regulation (e.g., the role of non-coding regulatory RNA elements in gene expression and protein activity), and genome structure and dynamics (e.g., alternative splicing events). These types of data and analysis can have a direct impact on understanding the genome architecture for applications in crop genetics.

Marker development, QTL mapping, wide crosses and alien gene introgression

Genotyping parental lines of mapping/production populations and/or of wild relatives to accelerate the discovery of molecular markers (e.g., SSRs-simple sequence repeats and/or SNPs-single nucleotide polymorphism markers). Such markers can be used to construct genetic maps, identify QTLs, and monitor alien genome introgression (wide crosses). The QTL-associated markers for a particular trait of interest can then be used in selecting progenies carrying favorable alleles via marker-assisted selection (MAS, see below).

Quantitative expression analysis using RNA-seq and the development of functional or perfect gene-based markers

RNA-seq of contrasting genotypes for traits of interest (e.g., yield, seed quality, resistance to pests and diseases, nutrient efficiency, drought and coldtolerance) can identify candidate genes involved in or associated with that particular trait. The comprehensive, quantitative expression mapping of these candidate genes, together with the phenotyping of segregating populations developed from the contrasting genotypes, provides valuable expression QTLs (eQTLs). The eQTL-associated markers can serve as perfect markers for MAS in crop breeding programs.

Association genetics, population biology and marker assisted selection (MAS)

Single or pooled genomes (whole or partial), including candidate regions, can be (re-)sequenced for all the individuals in a population using both amplification- and capture-based methods. The sequence data obtained can then be used to identify markers or haplotypes across genes or genomes for association genetics and breeding programs.

Contact the Experts

Our experienced scientific team can assist you in selecting, designing and developing a customized genomics pipeline to your target species, in a cost-effective manner and with the highest quality standards to accelerate your crop breeding and genetic improvement programs.