

Genomic and computational resources for maize improvement

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Characterizing and understanding genomic contributions to plants are now more tractable due to changes in technology. In this talk I will provide an update on the development of genomic resources for maize, including refinement of assembly and annotation of the B73 reference sequence, updates to characterizing genetic variation in HapMapV2, and preliminary analyses of epigenetic variation in maize. The primary objective of the reference genome assembly was to place genes that are currently missing or incomplete leveraging a whole genome shotgun library was sequenced to 14X coverage using the 454 Titanium methods. Gene-scaffolds were genetically mapped by a previously described genotype by sequencing (GBS) method. Final incorporation of gene-scaffolds into the reference sequence was refined using DNA-based and gene-based synteny to rice and sorghum. Characterizing genetic variation was expanded as part of an international partnership that expanded the breadth and depth of germplasm and the portions of the genome sampled, HapMapV2. In addition to genetic variation, it is also possible to sample epigenetic markers using bisulfite conversion and next generation sequencing. As part of a collaborative project, we have sequenced the methylome of two Maize inbred lines, B73 and Mo17, at 28.7X and 19.7X coverage, respectively. Incorporation of transcription data from RNA-seq experiments, revealed that transcript abundance of genes is related to their DNA methylation profile. Finally, we identified differently methylated regions in B73 and Mo17 genomes. Further BS-seq analysis in several recombinant inbred lines showed good inheritability of methylation patterns in these regions. In the last few moments, I will discuss the development of computational resources to support reference (Gramene) and computational (iPlant) resources, for functional projections and access to computer resources for the community.