

**W196****Associating Phenotype to Genotype in Lettuce Using NGS, *in silico* Analyses, High Resolution Genetic Maps and Targeted Fine Mapping**

Date: Tuesday, January 13, 2015

Time: 1:50 PM

Room: Pacific Salon 4-5 (2nd Floor)

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The genome of cultivated lettuce (*L. sativa* cv. Salinas) has been sequenced in collaboration with BGI and a consortium of ten breeding companies. The assembly currently consists of 21,500 scaffolds totaling 2.38 Gb and representing 88% of the 2.7 Gb lettuce genome. Annotation of the reference genome of *L. sativa* now contains 39,000 high confidence gene models based on an overlapping weighted evidence gene model scoring method (OWEG score) that combines transcriptomic and prediction evidence. More than 12 million high quality SNPs were identified between *L. sativa* cv. Salinas and *L. serriola* acc. US96UC23 and used to construct an ultra-dense genetic map using a RIL population derived from *L. sativa* x *L. serriola*. Segregation analysis of scaffold haplotypes assigned over 96% of the assembled genome to genetic bins ordered along the nine chromosomal linkage groups. Additional sequencing has provided six new *de novo* genome assemblies of *L. sativa* (Valmaine, La Brillante, Diana, Greenlake, PI251246, and Iceberg) as well as low-pass sequencing of 16 additional genotypes (*L. sativa* and *L. serriola*). The ultra-dense map has facilitated genetic dissection and mapping of domestication and agriculturally important loci. QTLs are being fine mapped using RILs containing residual heterozygosity at QTL regions. Recombinants at these QTL regions are being characterized using next-gen sequencing to identify candidate genes.

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## Meeting Information

**When:**

January 10 - 14, 2015

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