

7th World Summit on

PLANT GENOMICS

July 03-05, 2017 Bangkok, Thailand



Parwinder Kaur

University of Western Australia, Australia

Advanced reference genome of *Trifolium subterraneum* L. reveals loci governing important agronomic traits for biotechnological improvement of forage legumes

Subterranean clover is an important annual forage legume, whose diploidy and inbreeding nature make it an ideal model for genomic analysis in *Trifolium*. We reported a draft genome assembly of the subterranean clover TSUd_r1.1. Here we evaluate genome mapping on nano channel arrays and generation of a transcriptome atlas across tissues to advance the assembly and gene annotation. Using a BioNano-based assembly spanning 512 Mb (93% genome coverage), we validated the draft assembly, anchored unplaced contigs and resolved misassemblies. Multiple contigs (264) from the draft assembly coalesced into 97 super-scaffolds (43% of genome). Sequences longer than >1 Mb increased from 40 to 189 Mb giving 1.4-fold increase in N50 with total genome in pseudomolecules improved from 73 to 80%. The advanced assembly was re-annotated using transcriptome atlas data to contain 31,272 protein-coding genes capturing >96% of the gene content. Functional characterization and GO enrichment confirmed gene expression for response to water deprivation, flavonoid biosynthesis, and embryo development ending in seed dormancy, reflecting adaptation to the harsh Mediterranean environment. Comparative analyses across Papilionoideae identified 24,893 *Trifolium*-specific and 6,325 subterranean-clover-specific genes that could be mined further for traits such as geocarpy and grazing tolerance. Eight key traits, including persistence, improved livestock health by isoflavonoid production in addition to important agro-morphological traits, were fine-mapped on the high density SNP linkage map anchored to the assembly. This new genomic information is crucial to identify loci governing traits allowing marker-assisted breeding, comparative mapping and identification of tissue-specific gene promoters for biotechnological improvement of forage legumes.

Biography

Parwinder Kaur is working as a Research Scientist with a focus on the plant molecular genetics and genomics at the Centre for Plant Genetics and Breeding (PGB), University of Western Australia. She has received the Science and Innovation Award for Young People in Agriculture, Fisheries and Forestry in 2013 and has produced the world's first genome scaffold for subterranean clover using the *de-novo* sequencing pipelines anchored to a high resolution genetic map and BioNano optical maps for trait mapping. She has been working with a team of researchers across various disciplines to develop methodologies to enable breeders to identify environmentally friendly pasture legume to tackle future challenges for Australian livestock industries.

parwinder.kaur@uwa.edu.au

Notes: