

## Poster Abstracts

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### **#24: Atlas of Almond Nucleotide-Binding Leucine-Rich Repeat (NLR) Proteins**

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Nucleotide-binding leucine-rich repeat (NLR) proteins represent one of the principal families involved in diseases resistance in plants. They are on the front-line of the defense mechanisms with their abilities to recognize effectors from all kinds of pathogens and triggering defense response and are particularly important for almond breeders to obtain disease-resistant Almond cultivars. NLR is also one of the largest protein family in the plant genomes with highly conserved and repeat domain that represent a real challenge for the gene annotation algorithms. In order to provide a high-quality index of NLR gene and proteins structure for almond we performed a manual curation of the family using data from two automatic annotation pipelines, cross species comparison, available expression data and long read sequencing in several tissues. The whole almond genome was also scanned with HMM for all the TIR, LLR and NBS domains detected in the annotated genes. The outputs of these different tools were integrated for the manual review for gene curation. NLR were classified according to the presence of TIR LRR and NBS motif into 3 families each containing subgroup with specific domain. Performances of the annotation algorithm were dependent of the complexity of the coded protein with LRR only family showing lowest proportion of curated models while for the TIR-NBS-LRR, automatic annotation failed half of the time. Structural annotation was improved for a third of the 1125 identified genes compared to the initial annotation delivered with the genome. We also created an expression atlas through the almond tissues (bud, roots, flower, stem, leave, shoot tip) to help identifying NLR location and possible correlations with a disease.

Keywords: Genome, Disease Resistance, Annotation, Tissue Gene Expression, Phylogeny, Molecular Markers

### **#73: Inheritance estimates of some almond kernel physical traits**

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