

## ABSTRACT

*Receptor-Like Protein (RLP)* genes is a gene family encoding proteins associated with plant development and responses to biotic and abiotic stressors. However, among 57 *RLP* genes annotated in the model plant *Arabidopsis thaliana* (*Arabidopsis*), the biological function of only few has been described in detail. Characterization of natural variation in the genomic regions that overlap *RLP* genes might contribute to finding potential functions of RLP proteins as well as discovering new *RLP* alleles.

The recent emerging of long read sequencing methods remarkably enhanced our ability to detect complex genomic rearrangements and to assemble the entire chromosomes and genomes. Accordingly, I hypothesized that by sequencing and assembling the genomes of eight diverse *Arabidopsis* accessions, followed by detailed sequence comparison, I would be able to resolve all types of structural variants affecting *RLP* genes. To achieve this aim, I developed the protocol of high-molecular-weight genomic DNA extraction from leaves, sequenced genomic DNA of selected plants by nanopore technology, and generated de novo genome assemblies. Next, I performed extensive quality evaluation of genomic assemblies in three categories: contiguity, completeness, and correctness. The results indicated that the assemblies had high quality across chromosome arms, but were fragmented at repeat-enriched regions, e.g. centromeres and telomeres. I annotated genes and transposable elements (TEs) and examined variation patterns at *RLP* loci, where I found numerous small- and large-scale variants, including deletions, insertions, and genomic rearrangements associated with TEs. For example, the region spanning genes *RLP47*-*RLP50* genes was found to have an interspersed duplication in one accession, and TE-derived insertion in another accession.

Although *RLPs* are usually not considered as the main source of resistance variation in plants, the findings of this work suggest that many of them display substantial intraspecies diversity. Future extending the description of this diversity to a worldwide *Arabidopsis* population may serve as the foundation for functional studies and contribute to better understanding of plant immune mechanisms.