

VARIABILITY IN LTR-RETROTRANSPOSON REDUNDANCY AND PROXIMITY TO GENES BETWEEN SUNFLOWER CULTIVARS AND WILD ACCESSIONS

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The sunflower (*Helianthus annuus*) genome contains a very large proportion of transposable elements, especially long-terminal-repeat retrotransposons. Being knowledge on the retrotransposon-related variability within this species still limited, we performed a quantitative and qualitative survey of intraspecific variation of LTR-retrotransposon fraction of the genome across different genotypes of *H. annuus*, using next generation sequencing technologies. First, we characterized the repetitive component of a sunflower homozygous experimental line, using 454 reads, and prepared a library of retrotransposon-related sequences. Then, we analysed the LTR-retrotransposon fraction of 7 wild accessions and 8 cultivars of sunflower by mapping Illumina reads of the 15 genotypes onto the library. We observed large variations in redundancy among genotypes, at both superfamily and family levels. In another analysis, we mapped Illumina paired reads of the 15 genotypes onto two sets of sequences, i.e. retrotransposons and protein-encoding sequences, and evaluated the extent of retrotransposon proximity to genes in the 15 genomes by counting the number of paired reads of which one mapped onto a retrotransposon and the other onto a gene. Large variability among genotypes was ascertained also for retrotransposon proximity to genes. Both retrotransposon redundancy and proximity to genes showed different behaviour among retrotransposon families and also between cultivated and wild genotypes, indicating a possible involvement in sunflower domestication.