

ABSTRACT

Transposable elements, also known as TEs or transposons, are mobile, repetitive, genetic entities that are ubiquitous components of most genomes and one of the major forces of genome evolution. Research has uncovered the vibrant role of TEs in a variety of biological processes, ranging from their effects on altering gene expression, their influences on genome architecture and its epigenetic state, and their capacity to move and replicate DNA (sometimes not just their own). Despite these findings, TEs remain poorly understood, particularly in non-model species like strawberry. Furthermore, a TE's potential to create change is partially a factor of where it is located in the genome, but the analysis of TEs is limited by the availability of computational methods and genomes, as well as our ability to compare and contrast between genomes. I developed TE Density, software that addresses difficulties in quantifying the presence of TEs near genes. The TE Density software introduces a new Python tool that calculates TE presence relative to *all genes* in the genome for *all* TE types and reports this metric over flexible, user-defined distances. I explore the development of this tool as well as the various ways its output data may be used to empower the study of TE-gene relationships. Together, this tool opens up new avenues for studying TE-gene relationships and dissecting the tremendous diversity of the TE world. In plants, TEs have been linked to a variety of traits, such as fruit color, disease resistance, stress response, domestication, and more. However, the role of TEs in the domestication of octoploid strawberry (*Fragaria x ananassa*) remains poorly understood. I leveraged a new, high-quality genome for domesticated strawberry's wild octoploid progenitor *Fragaria chiloensis* and a newly constructed TE-pangenome to examine the influences of TEs on domestication-related phenotypes. Using the TE Density software, I examined gene-centric TE differences, and uncovered large TE differences between wild and domesticated strawberry, despite minimal genome-wide TE differences. Using comparative genomics, I show significant differences in TE content near positionally conserved orthologs, and functional enrichment analyses point to distinct patterns of TE-associated genes between the two genomes, particularly in pathways relevant to strawberry breeding. I identified a number of fruit, defense, transcription factor, and development genes enriched for novel TE presence in domesticated strawberry, demonstrating the potential for TEs to shape phenotypes in domesticated strawberry and laying the groundwork for future functional validation studies.