Table 2 Comprehensive comparative genomics analysis of *E. ulmoides* with relevant references

Aspect	Description	References
Genome Sequencing	High-quality genome sequencing using PacBio and Hi-C technologies has enabled the construction of a haploid chromosome-scale genome assembly for *E. ulmoides*, providing detailed insights into its genetic makeup.	Li et al., 2020
Genome-Wide Association Studies (GWAS)	GWAS has identified genetic loci associated with the biosynthesis of key metabolites in *E. ulmoides* leaves, enhancing the understanding of the genetic basis of its medicinal properties.	Liu et al., 2021
Genetic Linkage Mapping	Genetic linkage maps have been constructed to identify quantitative trait loci (QTL) affecting growth-related traits, aiding in marker-assisted selection and genome studies.	Li et al., 2014; Jin et al., 2020
Transcriptome Analysis	Transcriptome analyses have identified genes related to floral development and rubber biosynthesis pathways, contributing to the understanding of the species' reproductive biology and rubber production.	Liu et al., 2016
Comparative Genomic Visualization	Tools like Genomicus facilitate the visualization of gene organization and evolutionary relationships across eukaryote genomes, revealing gene loss/gain, segmental duplications, and homology relationships.	Louis et al., 2012
Evolutionary Insights	Comparative genomics provides insights into the evolutionary history, sex differentiation, and adaptation mechanisms of *E. ulmoides*, highlighting the evolutionary processes shaping its genome.	Qing et al., 2022
Secondary Metabolite Biosynthesis	Studies have focused on the biosynthesis of secondary metabolites such as aucubin, chlorogenic acid, and polyphenols, which are crucial for the medicinal properties of *E. ulmoides*.	Ye et al., 2019; Du et al., 2023
Selection of Comparative Species	The choice of species for comparative analysis is guided by research questions, phylogenetic relationships, and the availability of genomic data, enhancing the understanding of functional genomic elements and evolutionary patterns.	Cordone et al., 2021
Applications of Comparative Genomics	Comparative genomics aids in identifying conserved protein functions, adaptation mechanisms, and evolutionary history, providing a comprehensive framework for the conservation and improvement of *Eu. ulmoides* for industrial and medicinal uses.	Filipski and Kumar, 2005; Li et al., 2020