**Introduction**

Grafting is an old technique that has been used for the production of individuals with higher resistance to stresses, precocious flowering plants, controlling of plant architecture, and or …. (Kondhare et al., 2021; Yang et al., 2015). Potato/tomato heterografting, watermelon/bottle gourd, or fruit grafting are some examples that heterografting helped plants to survive under stresses or have better growth in different situations (Wang et al., 2020; Zhang et al., 2022). Grafting causes changes in the heterograft traits but the molecular mechanisms behind that had been unknown for decades (Kondhare et al., 2021). There must exist a communication system between different compartments within cells, adjacent cells, and different organs that could transport the environmental or developmental signals that also transport back and forward signals among rootstock and scion in heterografts (Spiegelman et al., 2013; Turnbull & Lopez‐Cobollo, 2013; Xia & Zhang, 2020). Long-distance transportation occurs in the vasculature system transporting different molecules, including sugars, hormones, proteins, amino acids, and RNAs (Turgeon & Wolf, 2009). Unlike other long-distance transport molecules, the biological functions of mobile RNAs have not been completely identified (Xia & Zhang, 2020). The signaling role of RNAs was firstly reported in virus-infected plants, moving virus RNAs through plasmodesmata in plants (Petty et al., 1990; Ryabov et al., 1999). In Arabidopsis, some mobile mRNAs transport from leaf to the floral meristem to regulate the reproductive functions responding to environmental cues (Corbesier et al., 2007; Yoo et al., 2013). Various physiological processes reported having association with mobile mRNAs, such as the regulation of potato tuberization (Ghate et al., 2017; Hannapel & Banerjee, 2017), lateral root formation in parasitic plants (Yoshida et al., 2016), leaf morphology changes in tomato (Haywood et al., 2005), and or floral initiation in Arabidopsis (Huang et al., 2012).

Different methods have been utilized to detect the mobile RNAs (small RNAs or mRNAs), however, transcriptome profiling of scions and rootstocks has efficiently appeared (Li et al., 2022). To choose the species for mobile mRNA detection, the species that are used for heterografting must be compatible for heterografting but with genome sequences distant enough to be unambiguously able to detect mobile mRNAs (Xia & Zhang, 2020). According to the distance between genome sequences, different strategies might be utilized for RNA-seq analysis to detect mobile mRNAs; for those which are not so different such as different genotypes of one species, SNPs could help to identify transcripts from different genotypes. In fact, first SNPs will be identified by mapping the raw reads to the same reference genome, then the transmitted mRNAs are defined if their corresponding reads from one genotype were detected in the other genotype in the heterografts (Wang et al., 2020; Yang et al., 2015). However, for heterografts composed from two distant genome sequences, RNA-seq reads will be mapped against two reference genomes and those reads present in one species that are aligned to the other species but not to the corresponding species’ reference genome will be identified as transmitted mRNAs (Notaguchi et al., 2015; Xia et al., 2018). Indeed in both strategies some criteria must be considered to detect more reliable mobile mRNAs.

Transcriptome assessment of heterografting has become an interesting tool to detect mobile RNAs as long-distance signals in plants (Kondhare et al., 2021).

The genus *Flaveria* contained more than 20 species representing the evolution of C4 photosynthesis (Powell, 1978).

**Material and method**

De novo assembly

Before running analysis on the raw sequence data, the quality control of samples were checked for adaptor pollination and the law quality bases using FastQC package. Afterwards, trimming of the raw sequences were conducted using Trimmomatic with parameters: SLIDINGWINDOW:4:15, CROP:50, and HEADCROP:10.

To have an assembly for SNP calling and RNAsrq analysis, we created two assemblies, one using only homograft samples from both root and shoot, and another from all samples of root and shoot.

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