**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). Other biological functions reported for mobile mRNAs are 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).

**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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