Title:

What causes peduncle necking in cut *Rosa hybrida*? Transcriptome analysis of rose stem tissue and analysis of microbial load

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Abstract:

Bent-neck or ‘necking’ is a phenomenon often seen in cut roses, whereby the flower head droops due to a bending of the peduncle. Necking is thought to be caused by a blockage of the xylem, either due to an air embolism or an accumulation of microbial populations, limiting water uptake to the flower head and causing the stem to bend. Despite the use of biocides to reduce microbial load, necking still remains an issue for the cut flower sector and roses continue to die prematurely.

As the occurrence of necking varies widely within and between cultivars, a transcriptome analysis of cut *Rosa hybrida* cultivar ‘H30’ has been carried out to investigate the potential responses in the rose tissue and the mechanisms involved. Transcriptomes from peduncle samples at three stages of necking (straight,90°) were sequenced using next generation sequencing to produce over 100 million reads per stage and generating nearly 300, 000 contigs following de novo assembly. Differential expression analysis of the three different stages of necking identified more than 900 genes that changed in transcription during necking (>90°) compared to straight stems. Functional analysis of these differentially expressed genes has revealed multiple pathways that may contribute to the necking response. The variation in microbial loads associated with stem ends has also been analysed and together with the transcriptomics data may help gain a better understanding of the process of necking.

Keywords:

transcriptome, de novo assembly, *Rosa hybrida*, necking, differential expression