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TRANSCRIPTOME PROFILING OF SENSITIVE AND RESISTANT APPLE FRUIT RESPONSE TO NEOFABRAEA VAGABUNDA INFECTION

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Apple (*Malus x domestica* Borkh.) is one of the most consumed fruit in the world. After harvesting, apple fruits can be stored at 4 °C and conserved for months. During this period, several events can occur decreasing fruit quality and marketability, going from physiological disorders such as scald or bitter pit to different types of rots, usually caused by fungi. One of these rot is known as bull's eye rot, and is caused by *Neofabraea vagabunda* . This pathogen infects apples in the orchard, and remains quiescent for months before its symptoms are visible. In order to better understand the molecular mechanisms occurring in the apple fruits during *N. vagabunda* infection, we performed a RNA-Seq transcriptome study comparing infected fruits of the sensitive 'Roho' cultivar to uninfected ones during a 4 months storage period. The cultivar 'Ariane' was used as resistant control. Our results showed the modulation of several genes after 4 months of storage, and differences in transcriptomic profiles between infected and uninfected fruits were highlighted. In particular, stress-responsive genes were highly modulated in the infected 'Roho' apples when compared to uninfected fruits of the same cultivar. Moreover, several putative susceptibility genes (S-genes) belonging to the *DMR6* and *MLO* family were shown to be differentially regulated not only between the susceptible and resistant cultivars, but also between infected and uninfected 'Roho'. The putative role of the differentially regulated genes in apple fruit during *N. vagabunda* infection is discussed.