Grapevine is an ancient culture that constitutes one of the most economically important fruit species worldwide. The production can be qualitatively and quantitatively different depending where the plants are grown. Soil conditions and rootstocks are among the main causes that can influence quality and wine production. In this work was analyzed the transcriptome responses of the grapevine variety Pinot noir (clone 115) to different soils and to different rootstocks. The grapevine plants were grown in three different soils: sand, turf and a typical vineyard soil from the Asti DOC region. The plants were grafted on February 2005 on two rootstocks with contrasting features: 101/14 a “weak” rootstock and 1103 Paulsen a “vigorous” one. Leaf samples were collected on September 2006 taking three replicates for each condition/treatment.

The total RNA of the eighteen samples were extracted, subjected to quality control and afterward the corresponding c-RNA were synthesized and labelled. The c-RNA samples were then subjected to array analysis with the Vitis vinifera GeneChip® array from Affymetrix carrying about 17,000 probe sets from grape genes. The poster will present the preliminary data on genes and pathways up or down regulated in the samples grown under different grafting and soil conditions.