Gene expression studies on soil fertility and nutritional status in grapevine

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Grapevine is a major fruit crop worldwide that is susceptible to several environmental stresses like diseases and water-nutritional deficiency. Grapevine management involves many agronomic practices and phytochemicals to prevent significant reductions in quality and quantity of production caused by these stresses. Due to the increasing economic and environmental costs associated to these technical inputs, there is an urgent need for developing alternative sustainable protection strategies. This requires innovative and interdisciplinary approaches for a better understanding of grapevine responses to environmental stresses.

AIM

Evaluation of the relationships among grapevine productivity, main soil chemical properties and expression of genes that could be involved in defence mechanism of grapevine to edaphic stresses.

MATERIAL AND METHODS

- Two **vineyards** characterized by high (H) and low productivity (L), both cultivated with cv. Garganega on 1103 Paulsen and located in the North-East of Italy (Fig. 1).
- The main **soil properties** were determined according to the Italian official methods of soil analysis (MiPAF, 1999). **Leaf nutritional status** was evaluated through multielemental analysis (CNS and ICP-OES measurements, Fig. 2).
- Total RNA of grapevine leaves collected on August 2010 was used for **gene expression** analyses by qPCR (Fig 3):
  - ✓ Four selected defence-related genes:
    - phenylalanine ammonia lyase (*PAL*) and stilbene synthase 1 (*VST1*), encoding key enzymes of the phenylpropanoid pathway which leads to the production of various defence-related compounds, like resveratrol;
    - sucrose synthase (*Susy*) encoding an enzyme involved in the metabolism of sucrose;
    - a gene encoding for a WRKY transcription factor, implicated in the regulation of transcriptional reprogramming associated with plant immune responses.
  - ✓ Normalization of expression data with glyceraldehyde-3-phosphate dehydrogenase (GPDH) and actin (ACT) chosen from a set of five commonly used *V. vinifera* reference genes.

Fig. 1. Aerial view of selected vineyards located in North-East of Italy.

CNS ***ICP-OES***

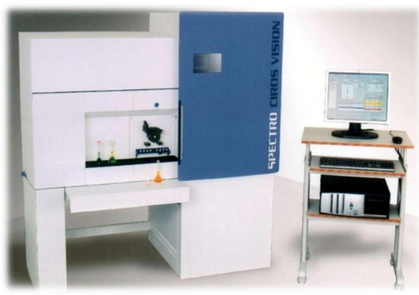

Fig. 2. CNS and ICP-OES instruments used for multielemental analysis.

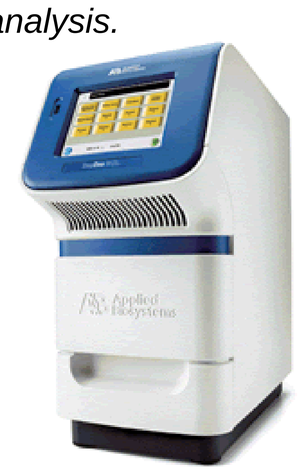

Fig. 3. Real Time PCR used for genetic analysis.

RESULTS AND DISCUSSION

Soil properties

Significant differences ($p<0.001$) between the two vineyards were found:
- the soil of vineyard characterized by high productivity (H) showed neutral pH, good supply of organic matter and appropriate C/N ratio.
- the soil of less productive vineyard (L) was characterized by acid pH, scarce organic matter content, suboptimal C/N ratio and leaves content of nitrogen and sulphur.

Gene expression

All the target genes analyzed showed significant higher relative expression values ($p<0.001$) in plants of low-productive vineyard (L) with respect to those of high-productive vineyard (H) (Fig. 4). These results showed that deficiencies in soil fertility and nutritional status of grapevine lead to the induction of the selected defence-related genes which could be involved in phenotypic adaptation of vine plants to edaphic stress.

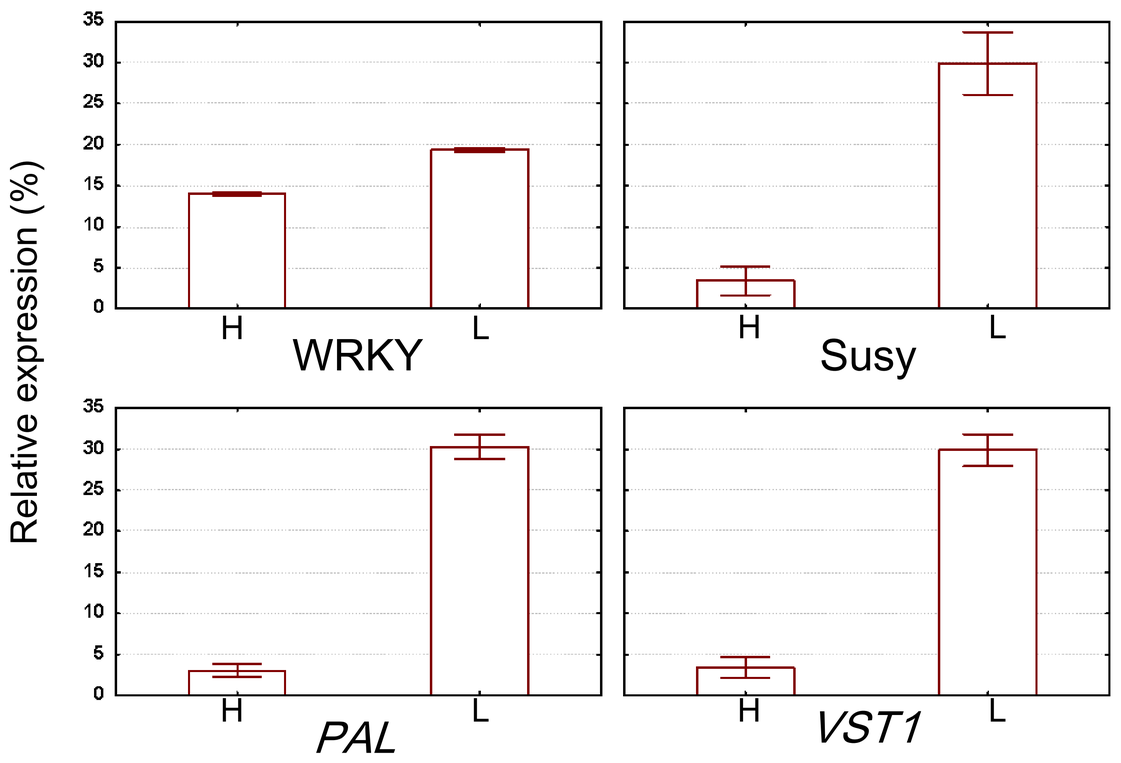

Fig. 4. Relative expression of selected genes (WRKY, Susy, PAL and VST1) in plants of low-productive vineyard (L) with respect to those of high-productive vineyard (H) .

Further qPCR experiments will be carried out for the validation of these patterns of gene expression on nitrogen and sulphur-starved plants grown under controlled conditions (Fig. 5).

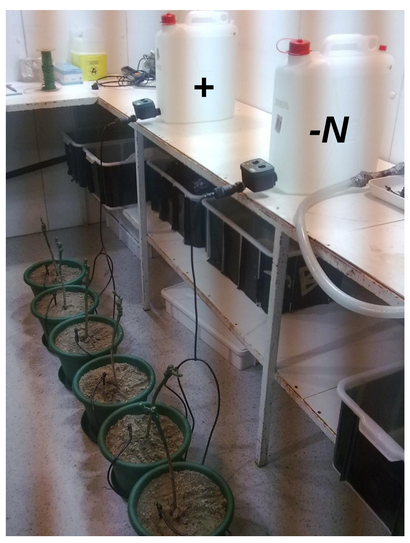

Fig. 5. Plants growing on sand culture irrigated with complete (+) and deprivated (-N) nutrient solution.

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