Poster Abstract – D.27

## TRANSCRIPTIONAL CHARACTERIZATION OF BERRY DEVELOPMENT, RIPENING AND POST-RIPENING PROCESSES IN *VITIS VINIFERA* (CV CORVINA)

L. MINOIA\*, E. ZAGO\*, A. FERRARINI\*, M. POLESANI\*, G.B. TORNIELLI\*\*, A. ZAMBONI\*, M. DELLEDONNE\*, M. PEZZOTTI\*

\*) Scientific and Technological Department, University of Verona, Strada Le Grazie 15, 37134 Verona, Italy
\*\*) Interuniversity Centre of Viticulture and Enology, Strada Le Grazie 15, 37134 Verona, Italy

grape, ripening, withering, AFLP-TP, differential expression

Grape (*Vitis vinifera*) and its processed products, wine, grape juice, and dried fruit, are economically and culturally important. Grape berry development, ripening and post-ripening processes and the production of those substances deriving from secondary metabolism are of fundamental importance for produced wine quality. The most appreciated wines of the Valpolicella region (near Verona) - Amarone and Recioto - are obtained from grapes which after picking, undergo a period of withering in rooms known as "fruttai". During withering, the grape endures a series of physical, physiological, molecular and biochemical changes; amongst these, the most striking are the berry dehydration and the increase of sugar concentration, allowing the wines to obtain higher alcoholic content and particular flavour properties. Knowledge of numerous grape transformations is of great interest in order to supply useful tools in good management of ripening and withering processes to produce a higher quality wine.

The aim of this work was to analyze, by means of AFLP-TP technique, the transcriptional profile of the grape berry (cv Corvina). We took into consideration eleven different stages (including three stages of "in planta" withering) starting from the early phases of fruit set until the complete withering of the grape. We selected about 2000 fragments pertaining to those genes that showed differential expression in temporal terms. The isolation of the fragments from the gel, their sequencing and the search for sequence homology in the data bank constitute a starting point for a deepened analysis of the complex molecular changes that take part in the grape berry development, ripening and withering processes.