

## **COMPARATIVE PROTEOMIC ANALYSIS OF HEAT STRESS ON THE METABOLIC SEED PROTEIN FRACTION IN THE WIDELY GROWN ITALIAN DURUM WHEAT CULTIVAR SVEVO**

LAINO P.\*\*\*, SHELTON D.\*\*, FINNIE C.\*\*, DE LEONARDIS A.M.\*\*\*,  
MASTRANGELO A.M.\*\*\*, SVENSSON B.\*\*, LAFIANDRA D.\*, MASCI S.\*

\*) Department of Agrobiology and Agrochemistry, University of Tuscia, 01100 Viterbo (Italy)

\*\*) Enzyme and Protein Chemistry BioSys-DTU, Technical University of Denmark, Lyngby (Denmark)

\*\*\*) C.R.A.-Experimental Institute for Cereal Research of Foggia, 71100 Foggia (Italy)

*durum wheat, heat stress, albumins and gGlobulins, Mass spectrometry*

Durum wheat is mostly grown and represents one of the most important crops in Central and Southern Italy and the grain filling occurs between April and May, when sudden increases in temperature may take place. High temperature during grain filling has already been recognized to cause a deviation of expected properties and quality characteristics of bread wheat doughs. This is a consequence of differential accumulation of gluten proteins that resulted in an alteration of their ratios that, in turn, modify technological properties of doughs.

Wheat grain proteins are typically classified according to their solubility properties into albumins (water soluble), globulins (salt soluble) and prolamins (gliadins and glutenins). These latter make up the gluten, and are mostly responsible for rheological properties of wheat doughs. Non-prolamin fractions include proteins with metabolic activity or structural function. Many of these proteins may generate allergies or intolerance in sensitive individuals.

In order to verify the consequences of heat stress on endosperm protein accumulation in durum wheat, we submitted the widely grown cultivar Svevo (5 D.P.A) to two thermal regimes (heat: 37/17°C day/night for five days and control 20/17°C), by producing four biological replicas for each treatment.

Two-dimensional electrophoresis (IEF/SDS-PAGE) was carried out on the metabolic (non-prolamin) fraction. IPG strips (18 cm long) in the pH range 3-10 were used to perform three different technical replicas for each biological replica. Spots were revealed with Coomassie Brilliant Blue (CBB) and analyzed with Progenesis SameSpots (Nonlinear Dynamics, UK), in order to identify differentially expressed polypeptides between heat stressed and control plants.

The gel analysis revealed 132 differentially expressed polypeptides. These polypeptides were collected and their identification performed by MALDI TOF and MALDI-TOF-TOF.

Forty seven spots differentially regulated (15% down-regulated and 85% up-regulated) were identified by NCBI Inr and TIGR Wheat protein database search. The identified proteins are functionally diverse and include: Heat Shock Proteins (HSP70), proteins related to ATP synthesis, proteins involved in glycolysis, carbohydrate metabolism, and stress defensive related proteins.

Differences found between bread and durum wheat are discussed.