

## Genetic determinism of grain yield and its related traits in bread wheat (*Triticum aestivum* L.) crosses under semi-arid environment.

**Z.E.A. Fellahi**<sup>1</sup>, A. Hannachi<sup>2</sup>, H. Bouzerzour<sup>3</sup>.

1-Département d'Agronomie, Fac. Sci. Nat. & Vie, Université Ferhat Abbas Sétif 1, Algérie.

2-Institut National de la Recherche Agronomique d'Algérie, Unité de recherché de Sétif, Algérie.

3-Département d'écologie et Biologie végétale, Fac. Sci. Nat. & Vie, Lab. VRBN, Université Ferhat Abbas Sétif 1, Algérie.

Four generations (P<sub>1</sub>, P<sub>2</sub>, F<sub>1</sub> and F<sub>2</sub>) were raised and subjected to generation mean analysis for detecting the nature of gene effects responsible for inheritance of chlorophyll content, plant height, spike length, thousand-kernel weight and grain yield in two bread wheat crosses (Acsad<sub>1135</sub> × Hidhab and Ain Abid × Rmada).

Highly significant genotypic variability was observed within and among the studied generations for various studied parameters. Results revealed that heterosis values were positive and significant relative to mid-parent in the two crosses for most of the studied traits. Inbreeding depression values were recorded for plant height, thousand kernel weight and grain yield in both crosses and for chlorophyll content in the second cross. F<sub>2</sub> broad sense heritability estimates were higher for chlorophyll content, plant height, spike length and thousand-kernel weight indicating better chance for improvement following selection procedure in these traits.

Low heritability along with a large number of effective genes, involved in the genetic control of grain yield imply more complex nature of inheritance and/or influence of the environment on the expression of this trait. Potence ratio indicated over-dominance for all studied traits in the two crosses except for plant height in Ain Abid × Rmada cross combination, suggesting that delayed selection would be better to practice. Altogether, the obtained results indicated that the two crosses understudy would be of interest in the breeding program and selection in segregating generation could be effective to produce lines that have high yielding ability under semi-arid environment.

**Key-words:** gene action, heritability, hybrid vigor, selection, yield.

---

## Label-free proteomic analysis of soybean seeds during germination under salt stress.

**A. Fercha**<sup>1</sup>, G. Caruso<sup>2</sup>, A. Lagana<sup>2</sup>, A. Laabassi<sup>1</sup>, H. Gherroucha<sup>3</sup>, M. Baka<sup>3</sup>.

1-Department of Biology, University of Abbes Laghrour Khenchela, 40000 Khenchela, Algeria.

2-Department of Chemistry, Sapienza Università di Roma, Piazzale Aldo Moro 5, 00185 Rome, Italy.

3-Department of Plant Biology and Ecology, University of Mentouri Constantine, 25000 Constantine, Algeria.

Salinity is one of the main abiotic stresses that threaten worldwide crop production. Seed imbibition and radicle emergence are generally less affected by salinity in soybean than in other crop plants. Towards unraveling the mechanisms underlying salt tolerance in soybean comprehensive quantitative proteomic analyses of proteins from soybean embryonic axes during *germination sensu stricto* (GSS) under saline conditions were performed. As revealed by nano-liquid chromatography-tandem mass spectrometry, the application of 100 and 200 mmol L<sup>-1</sup> NaCl at GSS was significantly accompanied by the change in abundance (>2-fold) of 97 and 75 proteins, respectively.

Most of these proteins were involved in three major functions, namely stress response and defense, protein turnover and protection and primary metabolism. Overall, our results suggest that the protection of proteins against osmotic-, ROS- and aldehydes-induced damages is essential to withstand the salt stress.

**Key-words:** *Glycine max* (L.) Merrill, embryonic axis, salt tolerance, gel-free proteomics, label-free quantification, biomarkers.