**P.4.33**

## TITLE: PHENOTYPIC AND GENOTYPIC DIVERSITY IN AN ARGENTINIAN DURUM WHEAT (TRITICUM TURGIDUM L. VAR DURUM) PANEL

Achilli Ana Laura[1], Roncallo Pablo Federico[1], Larsen Adelina Olga[2], González Lisardo[3], Miranda Rubén[4], Dreisigacker Susanne[5], Echenique Viviana[1]

*1) Centro de Recursos Naturales Renovables de la Zona Semiárida (CERZOS), Departamento de Agronomía, Universidad Nacional del Sur (UNS)-CONICET, Bahía Blanca, Argentina;*
*2) INTA CEI Barrow, Tres Arroyos;*
*3) Buck Semillas, Necochea;*
*4) Asociación de Cooperativas Argentinas (ACA), Bahía Blanca;*
*5) International Maize and Wheat Improvement Center (CIMMYT), D.F., México*

Durum wheat (Triticum turgidum L. var. durum) is the quintessential raw material needed to produce pasta, an important component of human diet. Argentina is one of main producers of pasta in the world, taking the eighth place. The aim of this work was to evaluate the genotypic and phenotypic variability of 61 Argentinean cultivars and breeding lines. Three experiments were performed in contrasting environments across the durum wheat production area. The analysis of the genetic diversity and the population structure was performed using 1,000 selected SNPs from the Axion 35K array in low linkage disequilibrium (r<0.5). Yield (kg/ha) and 19 yield-related traits were evaluated from either 4.2-5.5m2 plots. The effect of SNP markers on major genes (Rht-B1, Ppd-A1 and Vrn-A1) was evaluated in the collection. Cultivars carrying Rht-B1b showed the highest yield associated with increased spike fertility, harvest index, grain number and grain weight per plant. Cultivars with the allele Vrn-A1b exhibited lower yields related to a lower harvest index and spike fertility while Ppd-A1a was associated with higher yields and grain numbers. The analysis of population structure showed two main groups (K=2), one consisting of old cultivars carrying the wild type allele Rht-B1a and the other of the modern cultivars. Cluster analysis (UPGMA) clearly differentiated one winter cultivar and one cultivar with partial cold requirement from the others. In addition, the genotypes from each breeding program were mainly clustered together. Phenotypic analysis showed significant differences between genotypes for all of the evaluated traits. Moreover, in the case of yield highly significant differences between environments and genotype by environment interactions were detected. Harvest index, spike fertility and grain number per spike showed positive high and highly significant correlations with yield. Harvest index showed the highest correlation coefficients with values over 0.65 for two of the locations considered.

**ABSTRACT**