Oral Communication Abstract – 7.08

MULTIVARIATE GENOMIC PREDICTION FOR AGRONOMIC TRAITS IN DURUM WHEAT UNDER TWO FIELD MANAGEMENTS

VITALE P.************, LAIDÒ G.*, DONO G.***, PECORELLA I.*, RAMASUBRAMANIAN V.****, LORENZ A.****, DE VITA P.*, PECCHIONI N.*

*) Research Centre for Cereal and Industrial Crops (CREA-CI), CREA—Council for Agricultural Research and Economics, 71122 Foggia, Italy
**) Department of Agriculture, Food, Natural Science, Engineering, University of Foggia, Via Napoli 25, 71122 Foggia, Italy
***) Charles Darwin Department of Biology and Biotechnologies, University of Rome, La Sapienza, viale dell'Università 32, 00185 Rome, Italy
****) Department of Agronomy and Plant Genetics, University of Minnesota, 1991 Upper Buford Circle, Saint Paul, MN 55108, USA

genomic prediction, multivariate analysis, durum wheat, agronomic traits

Genomic prediction (GP) was implemented successfully in durum wheat breeding programs for several years. Though, for some traits, prediction accuracy (PA) doesn't satisfy the breeder's needs. Multivariate analysis has recently attracted much attention cause it can offer significant improvements in PA. In this study, we evaluated PA for several agronomic traits and derived an index using a univariate model in a panel of durum wheat, subsequently, different multivariate genomic prediction models were performed in order to increase PA. The panel was phenotyped for 10 agronomic traits for two consecutive crop seasons in two different field management: high nitrogen and water (HNW) input and low nitrogen and water (LNW) input. Consequently, seven indexes were calculated starting from the agronomic traits. The same panel was genotyped using the "Axiom TaBW420" SNP array. Univariate GBLUP was performed for all traits, afterwards, five multivariate models (GBLUP, BRR, RKHS, SpikeSlab, Random Forest) were trained using each trait in both field management by applying two cross-validation methods: predicting new genotypes with genotypic information only (CV1), and predicting using both genotypic and phenotypic information from the same trait in the other field management (CV2). We observed PA for all traits in HNW was higher than LNW for the same trait except for the

yellow index. PA in univariate GLUP ranged from 0.24 (difference of days between maturity and anthesis in LNW, Δ mat-anth) to 0.74 (test weight in HNW). Performing the multivariate GP with the CV1 method, we didn't detect relevant improvements in PA compared with univariate analysis for most of the traits, except for the trait NDVI in LNW and the index Δ mat-anth in HNW which showed an increase of 12.14 and 11.94% respectively. On the other hand, we observed significant gains in terms of PA implementing the multivariate analysis using the CV2 method, up to 56% (thousand kernel weight in LNW). In this work, we showed the potential of employing a multivariate approach in a genomic prediction pathway. The multivariate analysis with CV1 methods did not prove useful for most of the traits, on the contrary, the CV2 method always outperformed the univariate model. Therefore, the resulting information from this work can be useful for durum wheat breeding programs based on GP.