

Editorial

Genotype × Environment Interactions in Crop Breeding

Catalina Egea-Gilabert ^{1,*}, Mario A. Pagnotta ^{2,*} and Pasquale Tripodi ^{3,*}

¹ Department of Agricultural Engineering, Technical University of Cartagena, Paseo Alfonso XIII, 48, 30203 Cartagena, Spain

² Department of Agriculture and Forest Sciences, Università degli Studi della Tuscia, 01100 Viterbo, Italy

³ Research Centre for Vegetable and Ornamental Crops, Council for Agricultural Research and Agricultural Economy Analysis (CREA), Via Cavaleggeri 25, 84098 Salerno, Italy

* Correspondence: Catalina.Egea@upct.es (C.E.-G.); pagnotta@unitus.it (M.A.P.); pasquale.tripodi@crea.gov.it (P.T.); Tel.: +34-968-325-520 (C.E.-G.); +39-076-135-7423 (M.A.P.); +39-089-368-217 (P.T.)

In the next decades, the agricultural systems will deal with major challenges linked to the expected population growth, climate changes and necessity of sustainable use of resources able to preserve the environment. In this scenario, the development of stable varieties, adapted to various pedoclimatic conditions, marginal habitats and/or low-input farming systems is an imperative target for genetic improvement programs. Plant breeders carefully evaluate their material in multiple locations and over seasons by inferring the phenotypic variation as the sum of interactions affecting performances in the tested genotypes (G) across the different environments (E). The estimation of G, E and G × E interactions (or GEI) ensures valid recommendations of suitable varieties able to overcome the pressure due to variable occurring conditions. The determination of GEI factors helps geneticists in their breeding programs to shift the selection toward varieties suited for wide environments or specific to certain niches.

This Special Issue (SI) has been launched with the intention to collect articles focusing on different aspects of the study of GEI, including the evaluation across multiple trials of a broad range of phenotypic traits, the description of various statistical approaches and prediction models and the integration in trait mapping or genomic selection studies.

The SI consists of 14 original research contributions focusing on diverse crops including cereals (winter wheat, maize, rice and ryegrass) [1–5], legumes (grass pea, soybean, chickpea) [6–8], rapeseed oil [9], eggplant [10], blackgram [11], bambara groundnut [12], strawberry [13] and sugarcane [14]. Investigations combined different types of germplasm, study strategies and application of statistical models.

Approaches of genomic selection and genome-wide association analysis have been applied to investigate the stability of yield and plant architecture in winter wheat and for determining the genomic regions controlling phenotypic stability of these traits [1]. In multi-environment trials and four consecutive seasons, the authors tested a diversity panel of 456 lines adapted to Pacific Northwest growing conditions, for which genotyping was done through the array of 90 K single nucleotide polymorphisms (SNPs) available for wheat. Multiple genomic regions controlling the variation of the considered traits were detected, suggesting pleiotropic effects or tight linkage of loci associated with different aspects of stability and highlighting the possibility of simultaneously selecting for both yield and plant architecture. In addition, the models implemented to estimate G × E and genomic prediction were demonstrated to be suitable for selecting stable and highly performing lines. Another study in winter wheat was carried out in Poland and included the evaluation of grain yield in 29 cultivars grown across 19 experimental sites under both moderate- and high-input management systems, which differed in the doses of fertilizers, growth regulators and fungicides applied [2]. The authors showed how the response to low and high input conditions was cultivar-dependent; furthermore, they confirmed the importance



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of pedoclimatic conditions as essential factors in determining yield. Both water excess and deficit were highlighted as seriously affecting plant performance. From the observation made, it was suggested to address the high variability of soil conditions using cultivars with broad variation in productivity leading to higher adaptation to field conditions.

Similarly, comparisons of crop performance and determination of plant yield and plant yield homeostasis were investigated in maize hybrids under low and normal input conditions across five locations [3]. The study, which aimed at determining hybrid stability in terms of yield loss due to erratic optimum density, highlighted the potentiality of a new statistical model measuring plant yield efficiency by homeostasis over the common parametric and nonparametric stability measures. In addition, the scheme used suggested that at ultra-low-density conditions, the selection of superior genotypes was facilitated since it promoted the phenotypic expression and ensured repeatability across diverse environments.

A differential expression analysis aimed to investigate transcriptional response under different water regimes was performed in rye using susceptible and tolerant drought stress genotypes that allowed the detection of signal transduction in key pathways underlying abiotic responses (e.g., ABA, jasmonic acid) [4]. Several colocalizing differentially expressed genes were associated with regions previously identified to be involved with the drought-yield response, being promising candidate genes for further studies.

Environmental effects on biotic stress resistance due to crown and stem rust were instead determined in 54 ryegrass accessions grown across 34 European locations in three cycles performed in 12 years [5]. Such comprehensive work highlighted the effect of the environment on natural infections and indicated that the tetraploid varieties are better performing than diploid ones; furthermore, it showed how the large number of observations allowed better accuracy in trait performance prediction.

Three studies involving multienvironment evaluations of Leguminosae species are reported. Performances against broomrape infection in grass pea (*Lathyrus sativus*) lines were estimated in 17 Mediterranean environments (locations by years), revealing how mild temperatures, rain and humidity were the factors most influential on broomrape, affecting mostly yield rather than precocity [6]. Results highlighted a better performance of shorter growth cycle cultivars over longer ones in environments with high broomrape incidence, providing a guided cultivar selection to grow in different climates and fields with low/medium/high broomrape incidence. In soybean, models of prediction were applied to determining the effects of $G \times E$ on the time to maturity using multilocation data from 175 experimental lines grown across 67 African sites in eight cropping seasons [7]. Findings revealed that the effect of the environment was 6-fold higher than that of genotype, suggesting a major role of thermal variation rather than photoperiod in determining maturity in tropical areas. In chickpea, Kabuli types were tested for biomass, protein content and seed traits, focusing on the Southern Italian environment [8]. For this crop, the environment exhibited a higher proportion of variance explained in respect to G and $G \times E$, although the level of variation differed among genotypes, thus allowing the selection of the best accession to be grown in the marginal areas.

Multienvironment experiments, involving 25 sites across the southwest Australian grain belt and three consecutive seasons, were conducted to test the impact of fungicide application against *Sclerotinia* disease in canola [9]. Although the authors reported that most of the variation in yield occurred between sites, making challenging the identification of resistant varieties or best practices for disease management, the analysis provided new hints on the response of genotypes related to disease pressure, suggesting traits independent of the response to disease incidence (e.g., sclerotia numbers, lesion length along the stem) to consider as the determinants of variation.

Investigation of $G \times E$ using different experimental mapping populations was also reported. In eggplant, a set of introgression lines of the wild *Solanum incanum* in the genetic background of *S. melongena* were tested in both open field and greenhouse to identify quantitative trait loci (QTLs) and determine their stability across environments [10]. The

authors identified 10 robust QTLs for plant (plant height and stem diameter), flower (peduncle and stigma length, flower calyx prickles), and fruit (fruit pedicel length and fruit weight) traits; the QTLs for fruit traits were syntenic to other ones previously reported in eggplant populations.

In blackgram (*Vigna mungo*), the establishment of a mutant population and the selection of desirable lines for yield-related traits through five M-self cycles were reported [11]. The authors described the development of over 1200 mutants from M₁ to M₃ and the further selection of 36 nonsegregating M₄ progenies that showed desired yield-related traits. The additive main effects and multiplicative interaction (AMMI) model performed in these 36 stable mutants at the M₅ stage was inferred across three environments, demonstrated the opportunities to select elite lines with improved yield and adaptation to diverse environments.

Both the eggplant and the blackgram studies also provided novel materials and potential parental lines to use for breeding programs for the respective crops.

Two F₂ populations were instead used in bambara groundnut (*Vigna subterranea*) to study the variation of main morpho-agronomic traits [12]. Although the target was not the mapping of genes or QTLs, the results provide useful information for establishing structured populations boosting breeding for this crop.

Effect of genotype × environment interactions on strawberry quality was reported by Cervantes et al. [13] in elite varieties across grown across four cropping seasons. The work highlighted how the main organoleptic parameters and bioactive compounds that determine the consumer acceptance of fruits had a contrasting pattern of inter- and intra-annual variation, although the level of stability could change depending on cultivars. Thus, potential candidates are suggested for further quality breeding programs.

The work of Dutra Filho et al. [14] described different models to be applied in sugarcane for selecting genotypes with increased productivity of fiber and sucrose percentage. The application of regression methods, mixed models and multiplicative interaction analysis allowed inferring in a complementary way the classification of sugarcane genotypes for productivity, stability and adaptability, selecting those suitable to be released as commercial cultivars.

By covering a diversified range of crops, traits studied and approaches of investigation, the SI is of interest to a large scientific community including geneticists and breeders, statisticians and agronomists. We wish to thank all the authors for their important contribution to the SI and the staff members at MDPI for their support during the editorial process.

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