Crop Variety Trials: Data Management and Analysis


Crop improvement has three main components: (i) germplasm enhancement (pre-breeding), (ii) development of new crop cultivars (breeding), and (iii) cultivar performance trials (post-breeding). Crop breeders and agronomists invest 3 to 5 yr in pre-breeding, 7 to 10 yr in the second component and 2 to 4 yr in the third component. With the advent of molecular techniques, i.e., use of molecular markers and marker-aided selection (MAS), the time required to develop/release a cultivar may be shortened. Nevertheless, the process of cultivar development and release is expensive and time-consuming. Huge amounts of monetary and personnel resources are needed for crop cultivar development and testing.

Whether cultivars are developed via conventional breeding methods or via MAS, all cultivars must still be field-tested in multi-environment trials (METs). Selection of appropriate experimental designs and statistical analyses is extremely important. How cultivars perform in farmers’ fields is the ultimate test of their success. There are consequences, for growers, of researchers’ commission of statistical errors (Type 1 and Type 2). Thus, cultivar testing assumes considerable importance. The METs are essential from the standpoint of identifying adapted cultivars for a given area.

In Chapter 2, variety trial data and data analysis are discussed. Decision making based on multiple traits is also covered. In Chapter 3, biplot analysis is introduced, and ‘inner product property’ of a biplot and ‘singular value decomposition’ are explained. In Chapter 4, types of data centering, evaluation of genotypes and environments via biplots, and quantitative trait loci (QTL) interaction are described. Chapter 5 covers data scaling methods in GGE biplot analysis and factor-analytic-based GGE biplot. Chapter 6 is devoted to ‘frequently asked questions about GGE biplot analysis’; many ‘what if’ scenarios are presented. The GGE biplot method is compared with additive main effects and multiplicative interaction (AMMI) analysis. The author mentions common mistakes that users make in interpreting biplots. Chapter 7 covers case studies regarding spatial analysis to correct field trends and variation. It also informs the reader that the purpose of single-trial analysis is to assess data quality, details genotype × location analysis, mega-environment analysis, evaluation of test locations and genotypes, and identification of specifically adapted genotypes. The number of test locations required for cultivar testing is also discussed.

Various aspects of genotype × trait data analysis are covered in Chapter 9, which includes genotype on the basis of multiple traits. Independent culling, followed by index selection, is promoted as a useful strategy.