Simulation and analysis of realistic GxE using a crop growth model with physiological parameters without GxE

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Abstract

A different response of genotypes across environments is frequent in multi-location trials and is known as genotype by environment interaction (GxE). The study and understanding of these interactions is a major challenge for breeders and agronomic researchers.

In this paper we use an adaptation of the LINTUL (light interception and utilization simulator) crop growth model (Spitters, 1990) with 6 physiological parameters, to simulate two-way phenotypic data tables. Each of these 6 parameters was obtained based on *a prior* knowledge regarding the characteristics of the studied crop. Considering θ the vector of the 6 parameters and $f(.)$ a nonlinear function, the phenotypic realisations (e.g. yield for genotype i and environment j) can be written as

$$Phe_{i,j} = f(\theta)_i + \varepsilon_{i,j}. \tag{1}$$

Standard tools such as AMMI (additive main effect and multiplicative interaction) (Gauch, 1992) and linear mixed models (van Eeuwijk, 1995; Basford et al. 2004) are used to analyse the GxE presented in the simulated data. A case study for yield of sweet pepper (*Capsicum annuum* L.) is presented.

Keywords

Genotype by environment interaction, Crop growth model, Linear mixed models, AMMI models, Simulation, Pepper.

References

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