

Integrating model-based environmental characterization in an applied sorghum crop improvement program

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Introduction

Comstock (1977) defined the concept of a target population of environments (TPE) associated with a breeding program as the complete set of "types" of environments in which cultivars can be grown within the geographical area targeted by a breeding program. From the plant breeder's perspective the critical factor that separates one environment type (ET) from another is the degree to which the different ETs cause re-ranking of genotypes within trials (ie genotype x environment interaction).

Breeding programs faced with genotype x environment interaction (GxE) have traditionally used multi-environment trials (METs) in an attempt to representatively sample the TPE. This approach can be used to identify genotypes with general adaptation to most of the "types" of environments within the TPE. Alternatively, if types of environments are sufficiently frequent, breeders may also attempt to exploit specific adaptation.

Once ETs have been defined, breeders are interested in the ETs represented in the current year's trials and the frequency and distribution of those ET in the TPE. Weighting trial results based on their ET frequency in the TPE can lead to improved response to selection (Podlich et al., 1999). In the past, various forms of GxE analyses have been used to group trials into relevant ETs. While this approach has the advantage of being relevant to the breeding program, it requires analysis across seasons to achieve relatively unbiased sampling of the TPE. Leaving aside issues to do with sampling variability, such analyses are complicated as they involve unbalanced sets of genotypes and can be influenced by changes in the genetic composition of breeding populations and changes in management systems. The approach of using environmental data either directly (van Eeuwijk et al, 2005) or in a more integrated fashion via biophysical crop simulation modelling (Chapman et al, 2000) has been demonstrated as a way of effectively characterising breeding environments. While this approach is theoretically attractive and cost effective, care must be taken to ensure it reflects the reality of the TPE.

ET's in water limited environments result from the complex interaction of the genotypes under test with uncontrolled biotic and abiotic factors sampled by the trial. This is further complicated by variation in controlled factors, such as crop management. In such situations particular genotype characteristics (e.g. phenology, tillering) change the pattern of water use over the season so that entries in the same trial may experience different ETs. This may explain some of the differences among genotype rankings across trials. Recently simulation modelling has matured to the point where it may be possible to use modelling to explain components of genetic variation at the individual genotype level, thus generating potential to be exploited to increase response to selection (Cooper and Hammer, 2005; Hammer et al., 2006; Hammer and Jordan, 2007). In this presentation we describe our efforts towards using crop simulation to –

- characterise Australian sorghum production environments,
- validate various characterisation approaches, and
- link with analysis procedures to enhance genetic gain.

Materials and Methods

Environment Characterisation

A set of locations and management systems (population and row spacing) were selected to represent the main sorghum cropping regions in NE Australia. Locations were matched with soil characterisation data and 100 years of climatic data and crop simulation runs were

conducted using the sorghum model in the APSIM cropping system simulation platform (Keating et al., 2003). Twenty five virtual genotypes were created via a factorial combination of 5 rates of phenological development and 5 tillering propensities. A continuous sorghum cropping system was assumed so that each simulated crop-year reflected the sowing of sorghum following a summer crop the previous year. The APSIM sorghum model was used to generate a simulated crop for each year x location x management x genotype combination. This simulated data set was used for a range of purposes in the study.

Field Trials

A set of sorghum field trials consisting of 21 environments over 4 years and containing ~3000 genotypes (~1000 genotypes/year) was used as a source of phenotypic data (yield, phenology, tillering plant height) for GxE analysis. Nine of these breeding trials were characterised (climate, soil water attributes) to the extent that the sorghum model in APSIM could be run as a “virtual entry” in the trial.

Results and Discussion

Results will be presented to show -

- The nature and frequency of representative “crop perceived” seasonal stress patterns for the target population of sorghum production environments in NE Australia.
- Characterisation of the breeding trial sites (soil, climate, crop performance) and generation of “virtual genotypes” as entries for use with actual breeding data.
- Comparison of various methods of clustering simulated seasonal stress patterns to identify representative environment types that best explain the observed GxE
- Simulation of the differing stress patterns associated with specific entries in the breeding trials, allocation of season type to those entries, and investigation of the potential to remove the impact of explainable phenotypic variability in GxE analysis

Discussion will focus on the benefits and costs to the breeding program via the integration of such model-based approaches

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