[Workshop 2] Crop Production under Heat Stress Simulating Breeding Systems for Climate Change

S.C. Chapman (1), K. Chenu (2), G. McLean (2), G.L. Hammer (3), M. Dieters (3), J. Wang (4)

(1) CSIRO Plant Industry, Australia, (2) APSRU/QDPI&F, Australia,

(3) The University of Queensland, Australia, (4) CIMMYT/CAAS, China

(scott.chapman@csiro.au / Fax: +61-7-32142920 / Phone: +61-7-32142254)

In most crop breeding programs, the time between the making of a cross and the release of a new variety from a cross is between 5 and 10 years. Given current climate change scenarios, there are only two to three cycles of breeding between the present and the time of major impacts of heat stress on agriculture. Hence there is an urgency to review the diversity of germplasm for performance in 'future' climates and to determine how to utilize this diversity. With the increased availability of molecular marker and gene sequence information, a major challenge for plant breeders is how to incorporate this information to increase genetic gain through improvements in both crossing and selection decisions. Simulation of breeding programs allows testing and development of new methods now, i.e. before breeding programs have the data needed to apply such methods in practice.

In response to climate change, breeders may have to utilize different combinations of traits to identify useful adaptations. Using climate predictions of future weather patterns, researchers have begun to use crop simulation models to try to determine what combinations of traits may be most suitable for 'future' climates, i.e. how much 'phenotypic' diversity will we need in our parental lines to maintain or increase yields. However, there are many options in determining how to rapidly move breeding programs toward such new targets for adaptation, i.e. what are the best design breeding systems that will efficiently combine traits based on both molecular and phenotypic selection indices.

This paper outlines software applications that have been built around the QU-Gene genetic simulation platform (http://www.uq.edu.au/lcafs/qugene/) with an example to simulate selection for the response of maize leaf and silk growth to drought and temperature. To use this system we provide information on the genetic control of different traits (e.g. from QTL experiments) and generate new genotypes using any breeding and crossing system. The phenotypes are estimated by a crop simulation model (APSIM) and can be selected using either phenotypic or molecular-markers. The recent development of the system has integrated genetic and biophysical simulations in high-throughput computer 'grids' (>4000 PCs). This allows us to compare breeding strategies for current vs future climates for many combinations of traits, genetic models of trait effects and selection methodologies.