**WORKSHOP ON: FROM QUANTITATIVE GENETICS TO GENOMIC PREDICTION IN PLANT BREEDING**

**Venue**

Nelson Mandela African Institution of Science and Technology

**Dates and Course Time**

1 week

Back to back with the annual meeting of Breeding Better Bananas (26-30 April 2018)

Days 1 and 2 /whole) + Day 5 (9:00AM – 12:00AM) Theory and Results from real data applications

Days 3 and 4 (whole) + Day 5 (2:00PM-5:00PM) Practices – hands on for running R codes fitting a variety of models using the BGLR package

**Guest Lecturers**

Dr. Jose Crossa (Biometrics and Statistics Unit, Centro Internacional de Mejoramiento de Maíz y Trigo – CIMMYT – Mexico) and Dr. Paulino Pérez-Rodríguez (Colegio de Postgraduados, Mexico)

**Co-Coordinators**

Professor Rodomiro Ortiz (Swedish University of Agricultural Sciences – SLU), rodomiro.ortiz@slu.se + Dr. Allan Brown (IITA) A.Brown@cgiar.org

Logistics: Ms. Scola Ponera (IITA) S. Ponera@cgiar.org

**History**

Previously in SLU Sweden and ICARDA Marocco

**General themes**

* Quantitative genetics in plant breeding.
* Concept on genotype-by-environment interaction (G×E) and methods for its analysis.
* Genetic models and their use in plant breeding.
* Basic concepts of association genetics and genomic-enabled prediction.

**Objectives**

* To provide some basic quantitative genetic concepts to be applied in plant breeding.
* To provide some basic statistical models and methods for genetic and genomic analyses.
* To detect and measure the genotype-by-environment interaction.
* To show practical results of association genetics and genomic prediction in a breeding context.
* To demonstrate implementations of various genetic analyses using R-packages.

**Learning outcomes**

* Refreshing some basic ideas of quantitative genetics applied to plant breeding.
* Dissecting the genotype-by-environment interaction and estimating stability of genotypes.
* Understanding the conceptual framework of selection in plant breeding.
* Learning results that clearly show how biometrical genetics, association genetics genomic-estimated prediction of breeding values WORK!
* Knowing how to run some R codes for biometrical genetics, association genetics. and genomic-estimated prediction of breeding values involving different statistical models.

**Day 1: Thursday 26th April 2018 (José Crossa)**

**Morning 9:00 -12:30 [coffee break: 10:30–11:00]**

**CONCEPTS IN QUANTITATIVE GENETICS**

* Basics of quantitative genetics. Genotypic and phenotypic values.
* Breeding value (additivity), dominance [and epitasis].
* The basic genetic model and genotypic effects among single cross.
* Phenotypic and genetic variances. Additive and dominance variances. Genetic variance from a factorial model.
* Covariance between relatives.
* Why to estimate genetic variances? Heritability concepts and use.

**BREEDER’S EQUATION**

* The breeder’s equation. Response to selection. Theoretical equations. How to improve response to selection?.

**Further Reading:**

Bruce Walsh (2001) Quantitative genetics in the age of genomics. Theor. Pop. Biol. 59:175–184

William G. Hill (2012) Quantitative genetics in the genomics era. Current Genomics 13:196–206

**Afternoon 14:00-17:00 [coffee break: 15:15–15:30]**

**GENOME WIDE ASSOCIATION ANALYSIS (GWAS) AND GENOMIC PREDICTION (GS)**

* Introduction and concepts of GWAS and GS.
* Single-marker regression.
* Single-marker regression, accounting for population stratification and relatedness.
* Models for variable selection.
* Principles of genomic prediction and selection (GS) as a tool to accelerate genetic gains. What genomic selection does?
* The complexity of GS data, the curse of dimensionality.

* Genomic-enabled prediction models (Ridge Regression BLUP and GBLUP).
* How GS can be implemented in plant breeding programs.

**Further Reading**:

José Crossa et al. (2007) Association analysis of historical bread wheat germplasm using additive genetic covariance of relatives and population structure. Genetics

Zeratsion Abera Desta, and Rodomiro Ortiz (2014) Genomic selection: genome-wide prediction in plant improvement. Trends Plant Sci. 19:592–601

H. P. Piepho, J. Möhring, A.E. Melchinger, and A. Büchse (2008) BLUP for phenotypic selection in plant breeding and variety testing. Euphytica 161:209–228

**Day 2: Friday 27th April 2018 (José Crossa)**

**Morning 9:00 -12:30 [coffee break: 10:30–11:00]**

**MULTI-ENVIRONMENT TRIALS AND G**×**E**

* Why Multi-Environment Trials in Plant Breeding?
* What is G×E?
* Dealing with G×E: Ignore it? Reduce it? Exploit it! How G×E can be study and quantified?
* Error variance, G×E variance and number of environments and number of replicates.
* Components of G×E and its influence in heritability and genetic gains.

**STATISTICAL METHODS FOR STUDYING G**×**E**

* Methods for assessing G×E.
* Simple Linear regression – regression on the site mean.
* Advantages and disadvantages of simple linear regression.
* Introduction to multivariate methods for assessing G×E.

**Further Reading:**

J.C. Bowman (1972) Genotype × environment interactions. Ann. Génet. Sél. Anim. 4:117–122

Walter T. Federer, and José Crossa (2012) I.4 screening experimental designs for quantitative trait loci, association mapping, genotype-by environment interaction, and other investigations. Front. Physiol. 3:156 doi: 10.3389/fphys.2012.00156

**Afternoon 14:00-17:00**

**STATISTICAL METHODS FOR STUDYING G**×**E**

* Family of Linear-Bilinear models for assessing G×E.
* Site Regression Model (SREG).
* Random effects SREG with Factorial Regression and pedigree.
* Random effects SREG with Factorial Regression and molecular markers.
* Additive Main Effects and Multiplicative interaction Model (AMMI).
* Partial Least Squares and Factorial Regression for incorporating environmental co-variables for understanding G×E.

**Further Reading:**

Juan Burgueño et al. (2008) Using factor analytic models for joining environments and genotypes without crossover genotype × environment interaction. Crop Sci. 48:1291–1305

Hugh G. Gauch, Jr. (2006) Winning the accuracy game. Amer. Scientist 94:134–143

Rodomiro Ortiz et al. (2007) Studying the effect of environmental variables on the genotype × environment interaction of tomato. Euphytica 153:119–134

Alison B. Smith et al. (2015) Factor analytic mixed models for the provision of grower information from national crop variety testing programs. Theor. Appl. Genet. 128:55–72

**Day 3: Saturday 28th April 2018 (Paulino Pérez)**

**Morning 9:00 -12:00 [coffee break: 10:30–11:00]**

* Introduction to R and fundamentals of R programming.
* Introduction and use of META-R for the basic analysis of multi-environment trials.

**Further Reading:**

Heather Merk (n/a) Introduction to R stat software application to plant breeding. <http://www.extension.org/pages/60427>

**Afternoon 14:00-17:00 [coffee break: 15:15–15:30]**

* Introduction and use of META-R for the basic analysis of multi-environment trials.
* Introduction and use of AGE-R for studying G×E.

**Day 4: Sunday 29th April 2018 (Paulino Pérez)**

**Morning 9:00 -12:00 [coffee break: 10:30–11:00]**

* Introduction and use of AGE-R for studying G×E.
* Use of AGD-R Software for genetic analyses, diallel analysis, and line x tester analysis.

**Afternoon 14:00-17:00 [coffee break: 15:15–15:30]**

* Software for GWAS and intro to genomic prediction

**Day 5: Monday 30th April 2018 (morning: José Crossa + afternoon: Paulino Pérez)**

**Morning 9:00 -12:00 [coffee break: 10:30–11:00]**

**GENOMIC SELECTION**

* Short introduction to GBLUP.
* How to integrate G×E into Genomics.
* Statistical models for incorporating G×E into genomic prediction.
* The Reaction Norm model for incorporating G×E.
* The Marker × Environment Model – Main effect of markers and specific effects of markers.
* Practical examples and results for models with genomic G×E.

**Afternoon 14:00-17:00 [coffee break: 15:15–15:30]**

* R for GBLUP and Ridge Regression BLUP.
* Closing

**Further Reading:**

Filippo Bassi et al. (2015) Breeding schemes for the implementation of genomic selection in wheat (*Triticum* spp.). Plant Sci. <http://dx.doi.org/10.1016/j.plantsci.2015.08.021>

Yoseph Beyene et al. (2015) Genetic gains in grain yield through genomic selection in eight bi-parental maize populations under drought stress

Shizhong Xu et al. (2014) Predicting hybrid performance in rice using genomic best linear unbiased prediction. Proc. Natl. Acad. Sci. (USA) www.pnas.org/cgi/doi/10.1073/pnas.1413750111