

Sharing Insights from Recent Plant Breeding Training

Delgado Munoz, Luis Fernando

luis.delgado@cgiar.org

Palmira, July 2022



Summer Institute in Plant Breeding

3–7 July 2023

Ghent, Belgium

Sponsored by the

Plant Breeding Center at the University of Minnesota

VIB | International Plant Biotechnology Outreach at Ghent University

The entire training was divided into two modules:

- Genomewide Markers in Plant Breeding (Dr. Rex Bernardo).
 - Monday to Wednesday noon:
- Data Bootcamp for Genomic Prediction in Plant Breeding (Dr. Aaron Lorenz).
 - Wednesday afternoon to Friday afternoon



International Plant
Biotechnology Outreach

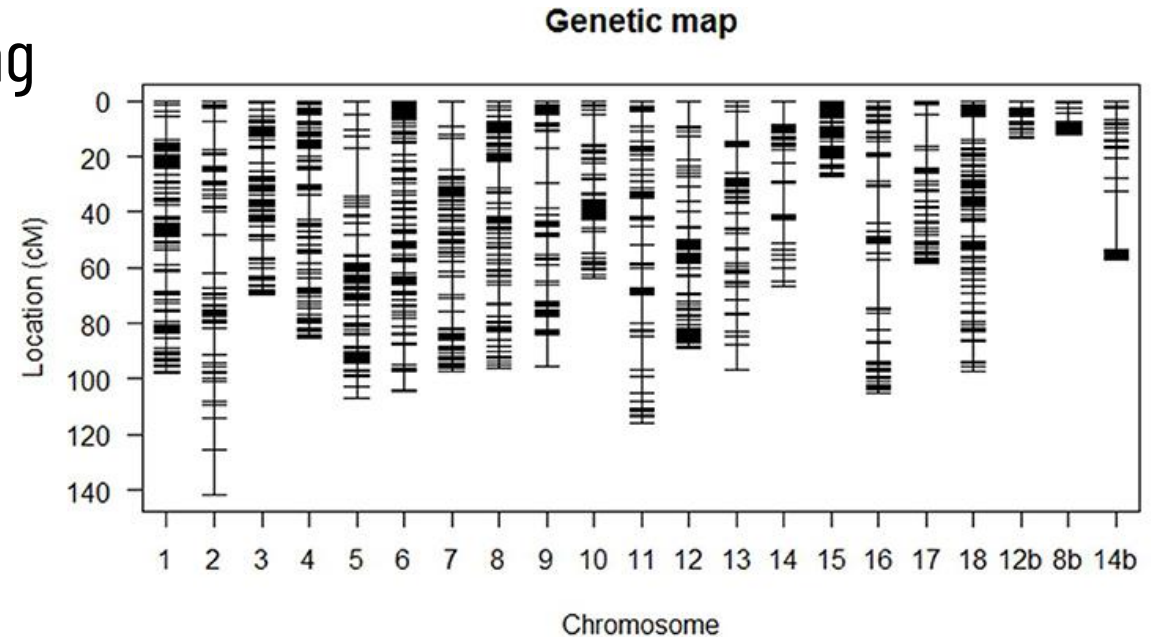


Genomewide Markers in Plant Breeding

(Dr. Rex Bernardo)



- Concepts in trait variation and QTL mapping
- What do we do with QTL we've detected.
- Linkage and association mapping
- Introduction to genomewide prediction
- RR-BLUP and GBLUP
- Genomewide recurrent selection.



High-density genetic linkage map based on SNP markers.

<https://doi.org/10.3389/fpls.2017.01168>

REX BERNARDO

Breeding for Quantitative Traits in Plants

Third Edition



Leveraging cassava QTL mapping capabilities

- Identification of QTLs associated with important traits:
 - Yield, starch content, and resistance to pests and diseases.
 - Developing of markers for marker-assisted selection (MAS) to improve the efficiency of breeding programs (Ceballos et al., 2015; Whankaew et al., 2011).
- Development of genomic selection models:
 - This can help breeders to select the best parents for crossing and to predict the performance of their progenies (Inosters Nzuki et al., 2017)
- Accelerating the breeding cycle:
 - QTL mapping can help to accelerate the breeding cycle by reducing the time and resources required to develop new cassava varieties.

Data Bootcamp for Genomic Prediction in Plant Breeding (Dr. Aaron Lorenz).

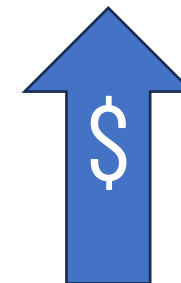
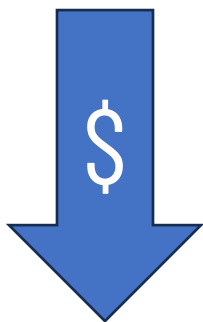
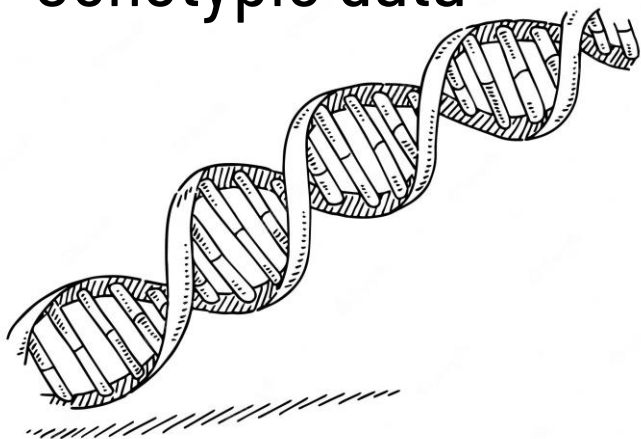


- Formatting and quality control of genotype/phenotype data for genomic prediction.
- Model implementation and exploration of various types of models. Techniques in cross validation for assessing prediction accuracy, training population optimization, multi-trait prediction.
- Genomic prediction for GxE, predictions of all possible crosses (genomic mating). Other special topics in genomic prediction, tour of available tools for implementing genomic prediction.

Plant breeding in the 21st century

Two important trends

Genotypic data



Phenotypic data



Measuring branching height, one of the cassava standard descriptors (photo: H. Ceballos)

Genomic prediction and genomic selection

- Genomic prediction: The prediction of an individual's genetic value using genome-wide markers.
- Genomic selection: Selection of individuals based on their genomic prediction value(s).

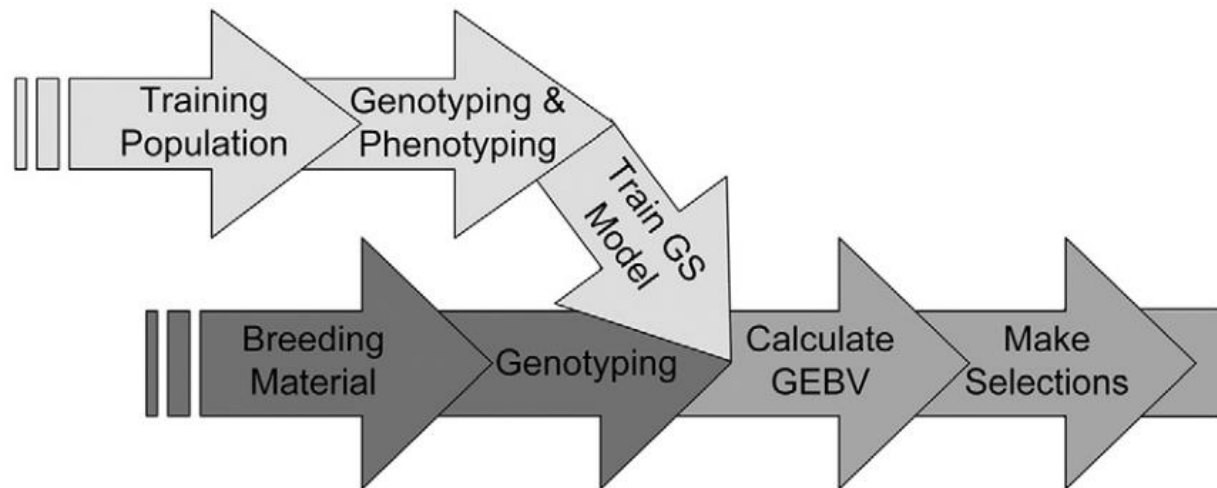
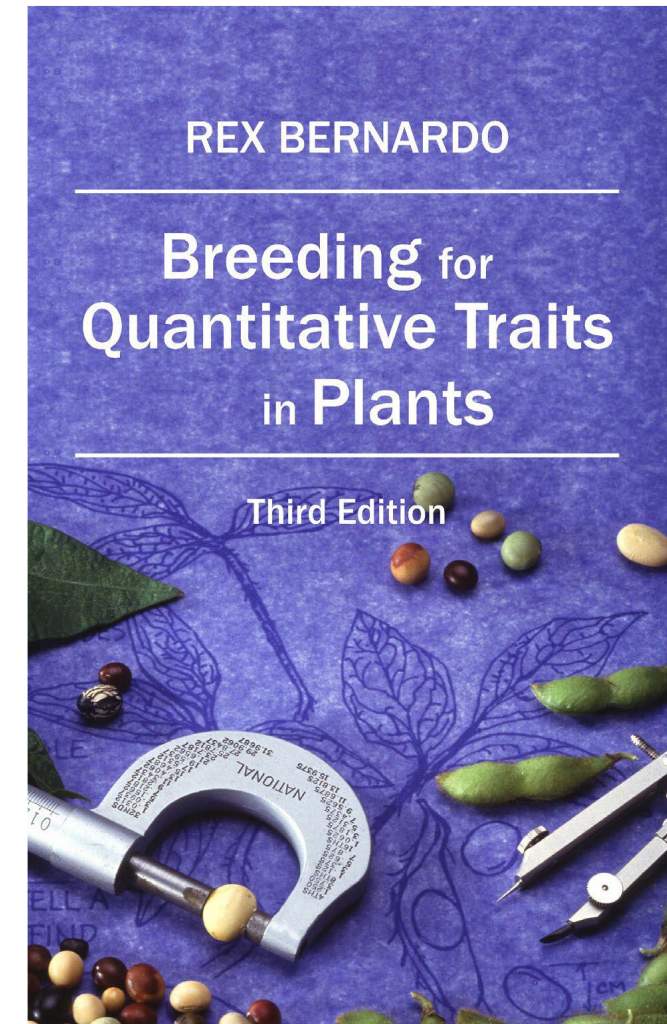


Figure from Heffner et al. (2009)

When to use genomic predictions and selection

- When phenotypic selection is ineffective
- To increase gain per unit time
- For traits that are difficult to measure
- For other target populations of environments
- To reduce phenotyping
- When there are too many candidates to phenotype
- When seed amounts are insufficient



Conventional breeding, marker-assisted selection, genomic selection and inbreeding in clonally propagated crops: a case study for cassava

Hernán Ceballos¹ · Robert S. Kawuki² · Vernon E. Gracen³ · G. Craig Yencho⁴ · Clair H. Hershey¹

Received: 12 April 2015 / Accepted: 5 June 2015 / Published online: 21 June 2015
© The Author(s) 2015. This article is published with open access at Springerlink.com

Abstract

Key message Consolidates relevant molecular and phenotypic information on cassava to demonstrate relevance of heterosis, and alternatives to exploit it by integrating different tools. Ideas are useful to other asexually reproduced crops.

Abstract Asexually propagated crops offer the advantage that all genetic effects can be exploited in farmers' production fields. However, non-additive effects complicate selection because, while influencing the performance of the materials under evaluation, they cannot be transmitted efficiently to the following cycle of selection. Cassava can be used as a model crop for asexually propagated crops because of its diploid nature and the absence of (known) incompatibility effects. New technologies such as genomic selection (GS), use of inbred progenitors based on doubled haploids and induction of flowering can be employed for accelerating genetic gains in cassava. Available information suggests that heterosis, non-additive genetic effects and within-family variation are relatively large for complex traits such as fresh root yield, moderate for dry matter or

starch content in the roots, and low for defensive traits (pest and disease resistance) and plant architecture. The present article considers the potential impact of different technologies for maximizing gains for key traits in cassava, and highlights the advantages of integrating them. Exploiting heterosis would be optimized through the implementation of reciprocal recurrent selection. The advantages of using inbred progenitors would allow shifting the current cassava phenotypic recurrent selection method into line improvement, which in turn would allow designing outstanding hybrids rather than finding them by trial and error.

Introduction

Cassava (*Manihot esculenta* Crantz) is a perennial shrub originated in the neotropics. Its most important product is the starchy roots used as a source of caloric energy by millions of people, particularly in Sub-Saharan Africa. It is also a competitive source of starch; cassava is the second most important source of starch worldwide, after maize (Stapleton 2012; Norton 2014), and is the starch most traded internationally. Dried cassava root chips are also used at industrial levels for animal feeding and ethanol production. Cassava is typically propagated through the use of stem cuttings. Since nearly all known landraces and bred varieties are directly derived from a cross between two heterozygous parents, the plants that farmers grow are clonally propagated hybrids. As such, cassava can be used as a model for clonal crops with the advantage that it is grown annually and does not have the complication of polyploidy that several other clonally propagated species have, e.g., potato, sweetpotato, yam and banana. Although Magoon et al. suggested in 1969 that certain portions of the genome may be duplicated; cassava should be considered as a

Communicated by R. K. Varshney

✉ Hernán Ceballos
h.cebillos@cgiar.org

- ¹ International Center for Tropical Agriculture (CIAT), Apartado Aéreo, 6713 Cali, Colombia
- ² National Crops Resources Research Institute (NaCRRI), Kampala, Uganda
- ³ West African Center for Crop Improvement (WACCI), Cornell University, Accra, Ghana
- ⁴ Department of Horticultural Science, North Carolina State University, Raleigh, USA

The 2023 *Summer Institute in Plant Breeding*



Any questions, want to discuss?



Thanks!