

# Genome-wide selection in plant breeding for abiotic stress conditions

**Roberto Fritsche-Neto**

[rfritscheneto@gmail.com](mailto:rfritscheneto@gmail.com)

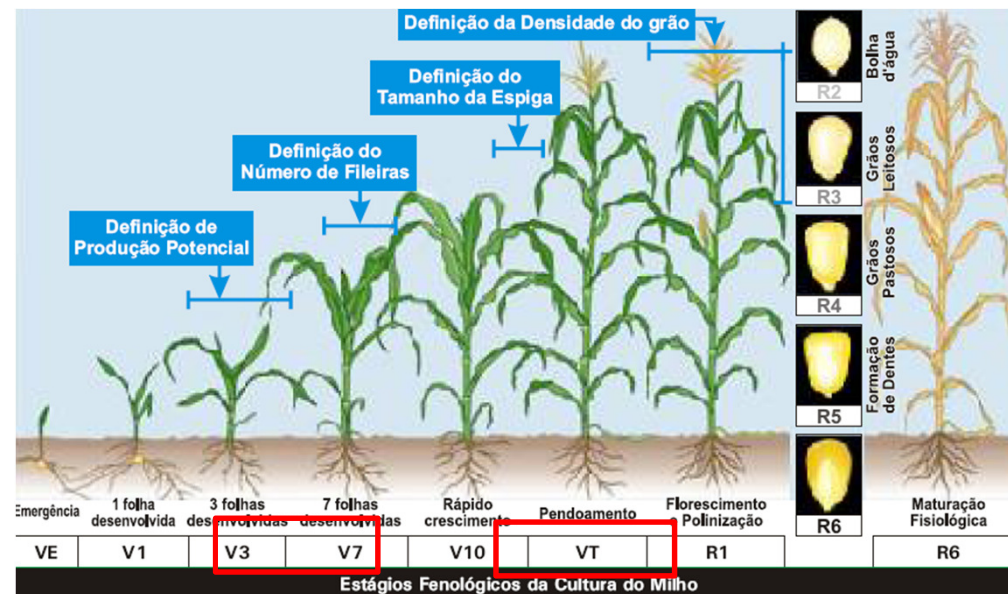
**Campo Grande, June 19, 2013**

# Introduction

- **Objective:** select the most productive genotypes
- **Qualitative traits** - few genes, with high effect each one, low environmental effect and high  $h^2$
- **Quantitative traits** - many genes, small effect each one, with high environmental effect and low  $h^2$
- **How to select for these traits?**
  1. “Traditional” Breeding
  2. Molecular Markers associated with quantitative trait loci (*QTL*)
    - *Marker Assisted Selection (major QTL or QTL of high effect)*
    - *Genome-wide Selection (many QTL of small effects)*

# Selection under abiotic stress conditions

- **Duration:** sufficient to stress coincides with the critical stages of plant
- **Intensity:** severe enough to affect the important characters, but allow identify variability
- **Management:** uniform in time and space - accuracy



# Early selection

## Objective

Reduce the interval between generations

Use characters of easier and cheaper evaluation

Select before flowering

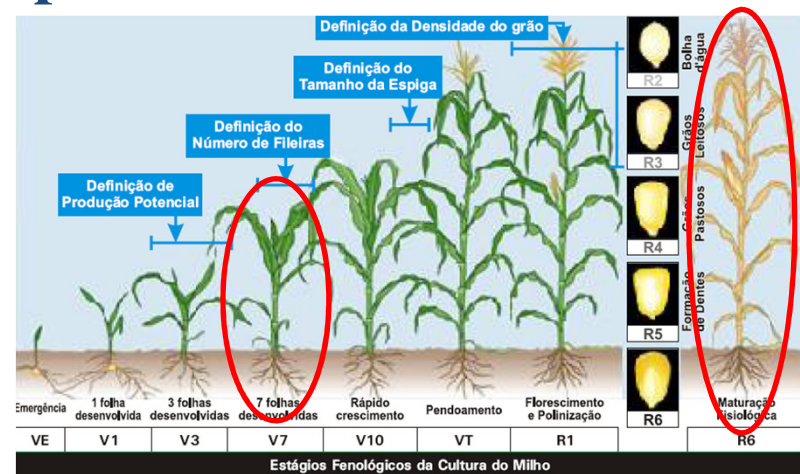
How can the GWS help?

**Problems in abiotic stress**

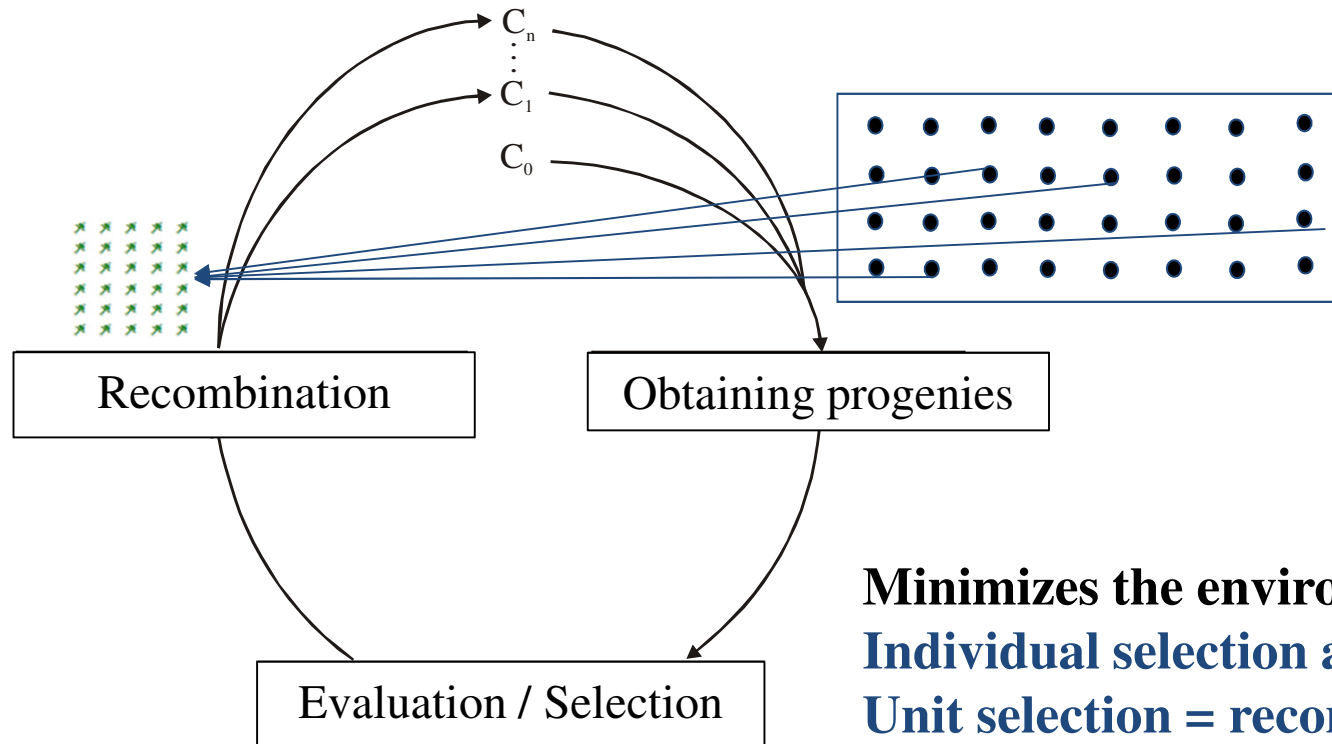
**Negative correlations**

**Phenological stage – genes differentially expressed**

*Exemple: nutrients efficient absorption vs utilization*



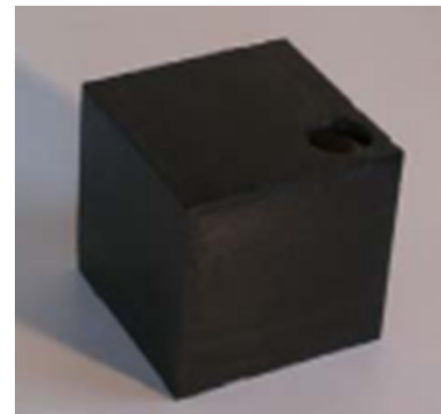
# Genomic Recurrent Selection



- Minimizes the environmental effect**
- Individual selection and in both sexes**
- Unit selection = recombination**
- Early and direct selection**
- Reduce the interval between generations**
- Reduced total cost**
- Anticipated market**

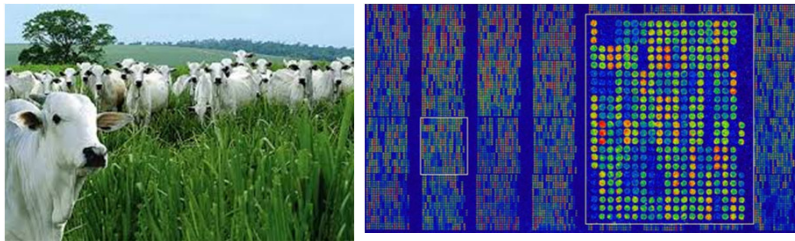
# Genome-wide selection

- **Simultaneous prediction (no significance tests) of the genetic effects of large numbers of markers**
- **Dispersed in wide genome**
- **Capture the effects of all loci (small and large)**
- **Explain much of the genetic variation of a character**
- **Keeps the "black box" about the genetic control**
- **Lower computational requirements**
- **Easy statistically**
- **Minor “aversion” by breeders**



# General procedures of GWS

**Training population**  
*sample from population of selection*  
 Phenotyping and genotyping  
 > 500 individuals



**Application of Recurrent Genome selection**  
 Only genotyping  
 Breeding populations

$$\begin{bmatrix} \mathbf{XX} & \mathbf{XZ} \\ \mathbf{ZX} & \mathbf{ZZ} + \frac{\sigma_e^2}{\sigma_{Am}^2/n} \end{bmatrix} \begin{bmatrix} \hat{\mathbf{b}} \\ \hat{\mathbf{h}} \end{bmatrix} = \begin{bmatrix} \mathbf{Xy} \\ \mathbf{Zy} \end{bmatrix}$$

$$\text{VGG} = \hat{y}_j = \sum_i \mathbf{Z}_i \hat{\mathbf{h}}_i$$

$\mathbf{Y} = \mathbf{Xb} + \mathbf{Zh} + \mathbf{e}$   
 Prediction of markers effects  
 Statistical equations and methods

$$r_{g\hat{g}} = r_{y\hat{y}} / h$$

**Validation of markers**  
 New and independent population or  
 Statistical methods of cross validation

## RR-BLUP

Assumes equal variances among markers (VG / Nm)  
 The characters differ in the number and the markers  
 that maximize accuracy of prediction

**Jackknife method**  
 Number of markers  
**Balance Nm/Ne**

# Balance of $Nm/Ne$

Subgroups of markers formed according to their effects (**module**)

Trait	Estimative	Number of markers considered in the GWS								
		214	150	100	50	25	10	5	2	1
	$r_{\hat{y}\hat{y}}$	0,43	0,47	0,47	0,50	0,42	0,44	0,09	0,20	-0,08
PUtE (LP)	$r_{\hat{g}\hat{g}}$	0,79	0,87	0,88	0,93	0,78	0,82	0,16	0,38	-0,15
	$r_{fen}$	0,20	0,20	0,20	0,20	0,20	0,20	0,20	0,20	0,20
	$\%Vg$	0,63	0,75	0,77	0,87	0,60	0,67	0,03	0,14	0,02

$r_{\hat{g}\hat{g}}$  – accuracy of GWS

$r_{fen}$  - accuracy of Phenotypic Selection

$\%Vg$  – percentage of genetic variance explained

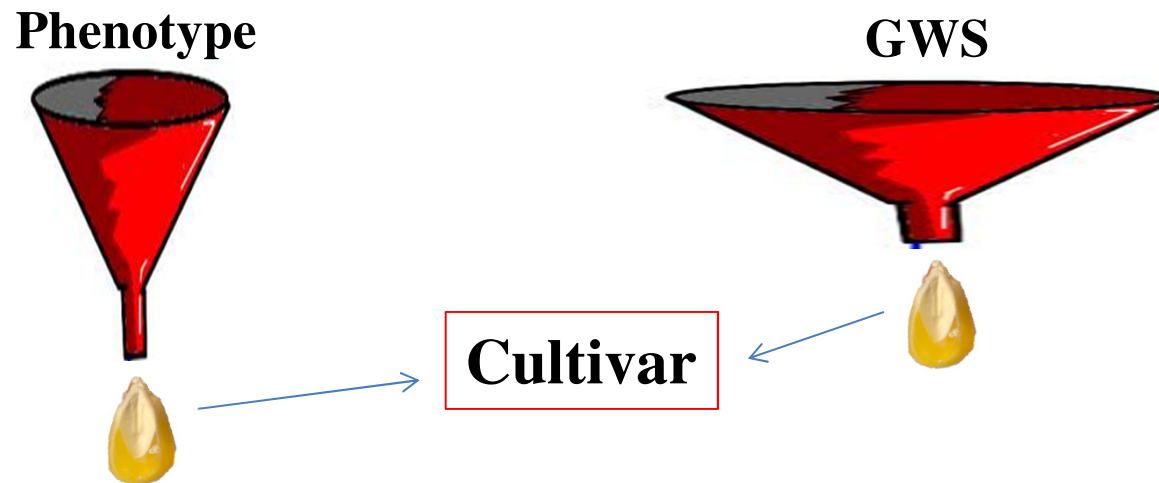


# Important aspects

- What kind of marker? *SNP, GBS, ...*
- Lines *vs* single-crosses
- Should we phenotyping where, how and what plant stage?
- If I have more than one trait of interest, how should I do?
- **Statistical method**
- How many markers and individuals?
  - *Number of genes,  $N_e$ , inbreeding, LD, Balance  $N_m/N_e$*
- How many cycles of GWS can we do?
- And about GxE, dominance and epistasis?
- **Recurrent Selection or Reciprocal Recurrent Selection?**
- **Doubled haploids and Next-generation phenotyping**

# GWS and breeding programs

- **GWS modifies significantly the way to select**



- **Reducing the time to develop cultivars**
- **Increasing the effective size and selection intensity**
- **Increasing the genetic gain per unit time**

**Thank you**