Clone Selector 3.0

IPBO Summer Course 2012: Modern Breeding Techniques for Improvement of Sweetpotato

Raúl Eyzaguirre / Luka Wanjohi

International Potato Center
CIP

August 27, 2012

Outline

1. Clone Selector characteristics
2. Clone Selector installation
3. Statistical designs
    - Randomized Complete Block Design
    - Augmented Block Design
    - Alpha(0,1) Design
4. Examples and exercises

What is Clone Selector?

Clone Selector is an Excel based data management tool. It aims to:

- Create fieldbooks for several statistical designs.
- Define a standard way for data recording.
- Provide some options for statistical analysis.

How does Clone Selector work?

Behind the scenes it has:

- A set of Visual Basic macros. They provide different options through a typical Excel menu to interact with Clone Selector.
- The addin RExcel for Microsoft Excel. RExcel allows access to R from within Excel.
- R is a free software environment for statistical computing and graphics (`http://www.r-project.org/`).

Statistical designs included

Up to now, there are three statistical designs included in Clone Selector:

- Randomized complete block design (RCBD).
- Augmented block design (ABD).
- Alpha(0,1) design (A01).

In addition, there is an implementation for GxE analysis.

Installation steps

- If you have a previous installation, remove previous versions of R, RExcel and statconnDCOM. You should do it through Add or Remove Programs at Control Panel.
- Install R 2.15.1.
- Install R libraries: agricolae, lme4, rcom, rscproxy.
- Register rcom and rscproxy.
- Install statconnDCOM and RExcel.
- Install Clone Selector 3.0.

Randomized Complete Block Design

The statistical model is

$$y_{ij} = \mu + \tau_i + \beta_j + \epsilon_{ij}$$

where:

- y_{ij} is the response variable for treatment (genotype) i and block j,
- μ is the overall mean,
- τ_i is the effect of treatment i,
- β_j is the effect of block j,
- ϵ_{ij} is the error term with normal distribution (i.e. $\epsilon_{ij} \sim N(0, \sigma^2)$).

Randomized Complete Block Design

- It is not completely randomized because treatments are randomized independently inside each block (it implies a restriction to randomization).
- The idea is to remove the variability due to blocks, so it doesn't interfere with the differences between genotypes.
- Blocks are complete because all the treatments are present in each block.
- It is advisable to have the block size not too large. Since the blocks are complete, the number of treatments should not be too large.

Randomized Complete Block Design

Example: Suppose you want to test 5 genotypes with 3 blocks. The 5 genotypes must be randomized inside each block. The experimental layout could be like this:

Block	Genotypes				
1	g4	g3	g1	g2	g5
2	g3	g5	g2	g4	g1
3	g1	g2	g5	g3	g4

Augmented Block Design

- This is a block design where some treatments (checks) are present in all the blocks, and some others (new) are present in only one block.
- The check treatments are disposed in a randomized complete block design layout. Each block is augmented with some different treatments.
- The checks are used to estimate the error mean square and the block effect. The block effect is estimated from the check means and then removed from the means of the new treatments.

Augmented Block Design

Example: Suppose you want to test 10 new genotypes (g1, g2, . . . , g10) with 3 common checks (c1, c2, c3) in each block, with 4 blocks. Treatments are randomized in each block.

Block	Treatments					
1	g4	g8	g10	c2	c3	c1
2	g7	c2	g5	c3	c1	g9
3	c3	c1	c2	g1	g6	
4	c1	c2	g2	c3	g3	

Alpha(0,1) Design

- It is a design useful for large number of treatments.
- Each complete replication (with all the treatments) is divided into incomplete blocks.
- The number of concurrences of each pair of treatments in the same block is 0 or 1 (hence the name Alpha(0,1)).
- Let r be the number of replications, s the number of blocks in each replication, and k the size of the blocks. Then the number of treatments t must be $k \times s$. Clone Selector creates experimental layouts for the following conditions:
    1. $r = 2$, $k \leq s$.
    2. $r = 3$, s odd, $k \leq s$.
    3. $r = 3$, s even, $k \leq s - 1$.
    4. $r = 4$, s odd but not a multiple of 3, $k \leq s$.

Alpha(0,1) Design

Example: Suppose you want to test 12 genotypes (1, 2, . . . , 12) with 3 complete replications divided in blocks of size 3. Hence $t = 12$, $r = 3$, $k = 3$, and $s = 4$.

Rep	Block 1			Block 2			Block 3			Block 4		
1	4	12	10	2	11	9	3	7	1	6	5	8
2	9	6	4	10	2	3	11	5	7	1	12	8
3	3	9	12	5	4	2	1	11	6	7	10	8

Create fieldbook for the Randomized Complete Block Design

Steps:

1. Go to **CloneSelector** > **List of Germplasm** > **New**.
   Define the **Season**(e.g. 2012A). This will be the folder name.
   Define the **List ID** (e.g. LGOF12A). This will be the file name.
2. Type the list of germplasm under column **Name**, correlative numbers under column **Entry**, and the number of vines under column **Vines/plot**.
3. Go to **List of Germplasm** > **Create Design**.
   Choose **RCBD**, type the **# Reps**, and click on **OK**.
4. Save and close your list of germplasm.
   Go to **CloneSelector** > **Trials** > **New**.
   Type a name in **Trial Series Name** (e.g. OFMZ12A).
   Select the **Season** and **List ID** to import the design.

Exercise: Create the appropriate fieldbook for a RCBD to test 10 genotypes with 3 blocks.

Create fieldbook for the Augmented Block Design

Steps:

1. Go to **CloneSelector** > **List of Germplasm** > **New**.
   Define the **Season**(e.g. 2012B). This will be the folder name.
   Define the **List ID** (e.g. LGOF12B). This will be the file name.
2. Type the list of germplasm under column **Name**, correlative numbers under column **Entry**, the number of vines under column **Vines/plot**, and type 1 for check clones and 2 for experimental clones on column **Type**.
3. Go to **List of Germplasm** > **Create Design**.
   Choose **ABD**, type the **# Reps**, and click on **OK**.
4. Save and close your list of germplasm.
   Go to **CloneSelector** > **Trials** > **New**.
   Type a name in **Trial Series Name** (e.g. OFMZ12B).
   Select the **Season** and **List ID** to import the design.

Exercise: Create the appropriate fieldbook for a ABD to test 30 genotypes with 3 blocks and 4 common checks.

Create fieldbook for the Alpha(0,1) Design

Steps:

1. Go to **CloneSelector** > **List of Germplasm** > **New**.
   Define the **Season**(e.g. 2012C). This will be the folder name.
   Define the **List ID** (e.g. LGOF12C). This will be the file name.
2. Type the list of germplasm under column **Name**, correlative numbers under column **Entry**, and the number of vines under column **Vines/plot**.
3. Go to **List of Germplasm** > **Create Design**.
   Choose **Alpha(0,1)**, type the **# Reps**, **# Blocks** and the **# Plots per block** and click on **OK**.
4. Save and close your list of germplasm.
   Go to **CloneSelector** > **Trials** > **New**.
   Type a name in **Trial Series Name** (e.g. OFMZ12C).
   Select the **Season** and **List ID** to import the design.

Exercise: Create the appropriate fieldbook for an Alpha(0,1) design to test 50 genotypes with 2 replications and 10 blocks per replication

Data analysis for the Augmented Block Design

Open the ABD_OFMZ12B1.xls file and run the analysis for traits BC and VW. To do that you need to go through the following steps:

1. Go to **CloneSelector** > **Augmented Block Design Analysis** > **Open ABD** and choose the file ABD_OFMZ12B1.xls.
2. Click on any cell of the column with the trait you want to analyze and go to **CloneSelector** > **Augmented Block Design Analysis** > **New data sheet for selected trait**.
3. Make sure you are in the new data sheet for the selected trait. Then go to **CloneSelector** > **Augmented Block Design Analysis** > **ABD Analysis**.

Data analysis for the Alpha(0,1) Design

Open the A01_OFMZ12C1.xls file and run the analysis for traits CRW and BY. To do that you need to go through the following steps:

1. Go to **CloneSelector** > **Alpha(0,1) Design Analysis** > **Open A01** and choose the file A01_OFMZ12C1.xls.
2. Click on any cell of the column with the trait you want to analyze and go to **CloneSelector** > **Alpha(0,1) Design Analysis** > **New data sheet for selected trait**.
3. Make sure you are in the new data sheet for the selected trait. Then go to **CloneSelector** > **Alpha(0,1) Design Analysis** > **A01 Analysis**.