

CloneSelector Users guide - Potato

14 April 2011, Jens Riis-Jacobsen, Rumbidzai Matemba-Mutasa, and Anne Forbes

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1. Introduction to the CloneSelector Users Guide

CloneSelector is a tool developed to **help plant breeder carry out field trials**. In version 1.1 the functionality is focused on the process of carrying out a trial to test a list of germplasm, and it may help you in the following task:

- 1) Elaborate list of germplasm to test
- 2) Design of field trial with one or more experiments
- 3) Generation of a field book for each experiment
- 4) Register metadata for each experiment
- 5) Data collection in field and post harvest for each entry
- 6) Enter collected data into electronic field book
- 7) Calculation of derived variables (yield/ha etc)
- 8) Statistical analysis of trial
- 9) Elaboration of consolidated result table for each trial

The **CloneSelector is based on the Maize Fieldbook** developed by CIMMYT, and this tool has many additional functions especially related to seed management. For clonally propagated crops this functionality is not adequate and it has been eliminated in CloneSelector, however, for seed based crops it might be better to use the original Maize Fieldbook, which is available at CIMMYT. The current version of CloneSelector is targeted at sweetpotato, but it can be used for any crop as long as the trial template is adapted to include the relevant traits.

The **CloneSelector for Potato is based the *Procedures for standard evaluation trials of advanced potato clones. An International Cooperators' Guide, CIP (2007) (ICG)***, and as such **it is a practical tool that aims to help the potato breeders put these standardized methods into practice, and by doing that it aims to improve the efficiency and effectiveness of the breeding effort**. The Procedures have been incorporated into the user's guide in order to facilitate the learning and adoption of both tools. Furthermore, the process of operationalizing the procedures in a specific tool has lead to some minor adjustments on how the information is structured or presented, and the User Guide presents these changed data formats. Also in order to keep CloneSelector relatively simple to use, it only includes the most common traits used for potato breeding, and not the full range covered in the ICG.

For the **installation** of CloneSelector see Chapter 5.

2. How to use CloneSelector in a potato trial

This section describes how to use CloneSelector as an integrated tool in the process of carrying out a potato trial in accordance with the general protocol described in the CIP manual for procedures for standard evaluation for advanced potato clones. The information is organized in the sequence of the general steps for carrying out a trial, and the user should consult the relevant section as the trial is carried out.

When CloneSelector is first installed the templates are in a generic format. In order to work more efficiently and not have to tweak for example the fieldbooks every time, the user may modify the templates to be more suitable for the local conditions, however, for the first trials it is recommend to use the standard templates in order to gain a better understanding before the templates are modified. The process for modifying the templates is described in a subsequent section.

Some general advice on using CloneSelector for trials

1. **Save your data frequently** as errors may happen and you may lose the work you have done
2. **Backup you data files frequently.**
3. **For the first trials follow the instructions in this guide as closely as possible.** Once you know the general working of CloneSelector you can start adapting it to your more specific needs.
4. **Experiment with CloneSelector before you using it in a real trial.** You can for example try to do all the steps in the guide with a trial from last season.
5. The fieldbook in CloneSelector as you will see below is made up of several sheets and these are linked in different manners. If you want **to make changes outside what is described in the following steps only do so on a copy, not in the original.** Changes may prevent CloneSelector from working, and you will probably not be able undo the changes.
6. Remember, in the worst case your data is in Excel, and if CloneSelector fails to do exactly what you need, **you can always do your calculations or analysis as a normal Excel sheet or exporting the data to a statistical package of your choice.**

If you invest a little time on learning CloneSelector this will make you a more efficient breeder, and you will spend more time drawing the right conclusions from your trial, and less time on repetitive steps.

2.1 How to start CloneSelector?

CloneSelector is an 'Add-in' to Microsoft Excel, and to use it you must open it as any other Excel file¹. After opening, Excel 2007 will have an additional menu in the Add-in section and in Excel 2003 the menu is added directly in the primary menu bar of the application.

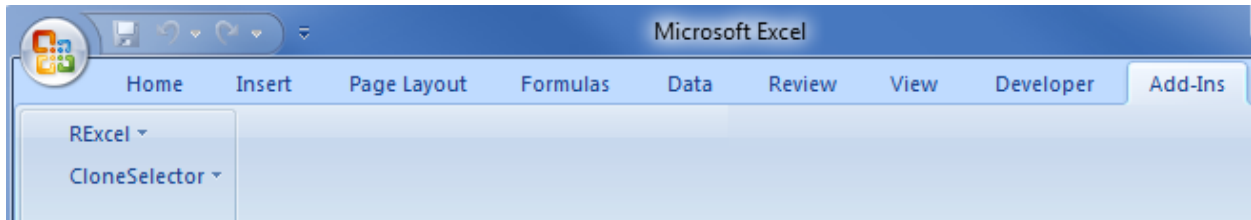


Figure 1 CloneSelector Add-in menu in Excel 2007

When you click on the CloneSelector menu it opens up. Initially, only the List of Germplasm, Trial and Options menus are available. **The rest of the menus will become available once you open or create a List of Germplasm or a Trial.** If you cannot access a menu it is because you are not in the right type of workbook, or you are not on the correct sheet.



Warning: CloneSelector use the name of the sheet to activate the relevant menus. **Do not change the names of the Fieldbook, Results and Master sheets** as the menus will not work properly.

CloneSelector is based on Excel, and apart from the tools in the system, you also have access to all the normal Excel functions. You must however, **be careful not to change the structure of the CloneSelector sheets as these will most likely not work correctly afterwards.** The safest solution is to insert a new sheet or use the space below the tables generated by CloneSelector. Similarly, it is preferable to **hide columns or rows, rather than deleting them** as this may cause problems.

If you have changed the structure of a worksheet and this is not working properly or if you have data in a normal Excel sheet that you want to analyze in CloneSelector the best solution is to create a new List of Germplasm or Trial sheet in CloneSelector and **copy the information over using Paste Special and only paste Values.** Doing this will not change your data and will maintain all the functionality and formatting in CloneSelector.

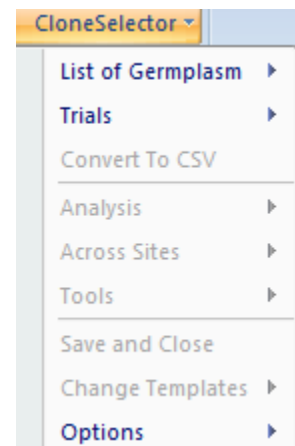


Figure 2 CloneSelector menus

¹ On Windows XP it is possible to add the CloneSelector to the XLSTART folder and it will start automatically when Excel is initiated, however, the security of Windows Vista and Windows 7 does not allow this approach.

2.2 Elaboration of list of germplasm to test

A trial in CloneSelector is conceptually a method for evaluating a list of germplasm with regard to certain traits. To some extent all the tools in CloneSelector are focused on manipulating the List of Germplasm and the first step in a trial is to prepare a List of Germplasm:

CloneSelector -> List of Germplasm -> New

In the dialog that opens **enter or select the Season**. The recommendation is to indicate **Year** either as e.g. **2010** or **10** and **A, B, C** for the **Season**. The Season you enter will be the

name of the folder where the file is stored. You must also enter a **List ID**, which will become the name of the file. It is recommend that you use a code such as **LG** for **List of Germplasm**, and **AT** (Advanced Trial) for **type of trial**, and then the **season** e.g LGAT10B.

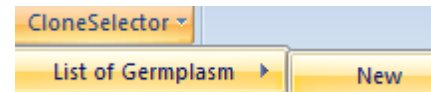


Figure 3 Makin a new List of Germplasm

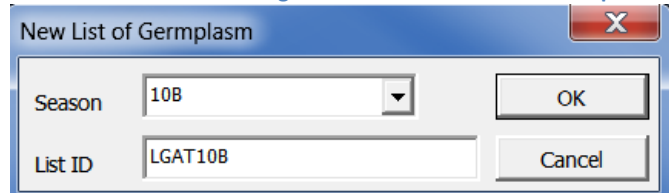
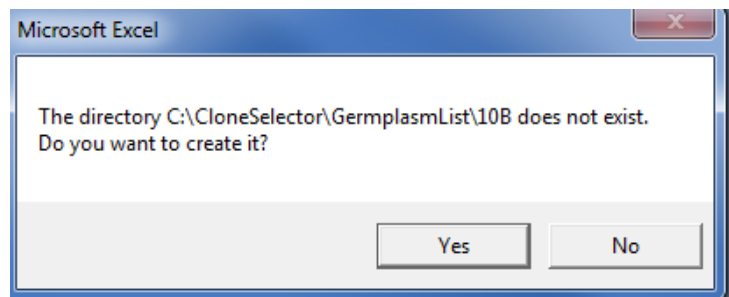


Figure 4 List of Germplasm dialog



Warning: Do not use spaces in the name, as this will cause problems when trying to generate the field book.

Click OK once you have entered the Season and List ID. If it is the first List of Germplasm in a season, a dialog will appear asking if you want to create a new directory, **click Yes**². After this a **List of Germplasm file will open with the name you indicated as List ID**.



Two fields must be filled in the List of Germplasm: **Entry** number and **# Tubers/Plot**.

Entry number must be a consecutive list of numbers starting with 1, such as 1,2,3,4, you cannot leave gaps in numbers such as 1, 2, 5, 6 or start at a different number 100, 101 etc. Use "Fill down" in Excel to generate list.

Tubers/plot is the number of tubers to be planted in each plot and must be a positive integer number such as 5 or 10.

Once you have established the List of Germplasm click **Save** as you would any other

Season: 10B				
Exp: POTATO2				
Entry	Stock ID	Name	Pedigree	Tubers /plot
1		PUKARA-INIA		40
2		DESIREE		40
3		YAGANA-INIA		40
4		PEHUENCHE-INIA		40
5		KARU-INIA		40
6		PUREN-INIA		40

Figure 5 Example of germplasm list

² If you click No CloneSelector cannot create the Germplasm list and you will get an error. In that case try again.

Excel file.

Note: **CloneSelector organizes the lists of germplasm in a separate folder and inside this it creates a folder for each season.** It is **important that you accept the default locations** assigned when saving files in CloneSelector. If you use Save As and saves a file outside the default structure CloneSelector cannot locate the file for example when it is need for generating a fieldbook for your trial. When CloneSelector creates a list of germplasm or fieldbook it is automatically stored in the correct folder, and as long as you do not change it, it will work fine.

The List of Germplasm workbook has three sheets:

- **GermplasmList** contains a list of the entries to be tested in the experiment and the quantities of tubers or seed required for each plot
- **Design** is where the experimental design is stored once it has been generated as will be shown in the next section
- **SeedLabels** contains the labels for the planting material for each plot

2.2.1. Open List of Germplasm

CloneSelector automatically organizes the List of Germplasm in a separate folder for each year which helps keeping in order all the files related to a breeding program. You can open the files as normal Excel files, but this may implicate some clicking to arrive at the right folder, unless of course the file is still in the list of most recent files used in Excel in which case you just click on it to open it. In order to ensure that the file organization of CloneSelector works well it is, however, preferable to use the Open command:

CloneSelector -> List of Germplas -> Open

This will open the Open Germplasm List dialog. The drop down list for Season will have a list of all the seasons for which you have created a list of germplasm. **Select the season** in which you want to locate the list. After selecting the season the List ID drop down will now have a list of all the lists of germplasm generated in that season. **Select the List ID and click OK to open the List of Germplasm.**

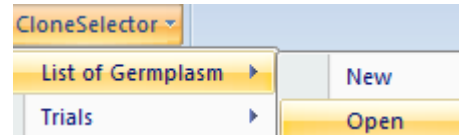


Figure 6 Open List of Germplasm menu

In Excel 2007 you may get a message from the Microsoft Office Excel – Compatibility Checker, which is a product of the changes made in the different versions of Excel. If this message appears you must **clear the check box for Check compatibility when saving this workbook** or this message will appear all the time.

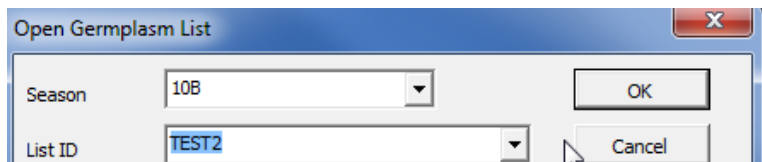


Figure 8 Open List of Germplasm dialog

Unfortunately in Excel 2007 it is not possible to completely disable the annoying feature.

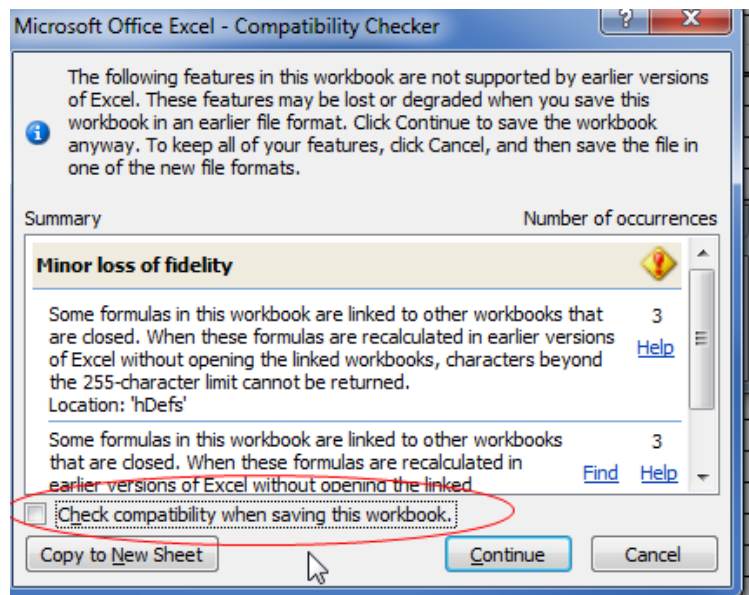


Figure 7 Excel 2007 Compatibility Checker problem

2.3 Design of field trial with one or more experiments

Next step is to create a design. To do this the List of germplasm must be open and if that is not the case, see the previous section on how to open it.

CloneSelector -> List of Germplasm -> Create Design

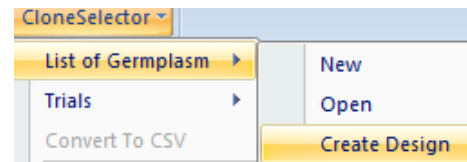


Figure 9 Create Design menu

Note: Your germplasm list must be open and the **GermplasmList sheet must be the active sheet**, else the Create Design menu is disabled.

In the dialog **Create Design**:

Note: The Create design will automatically detect the # entries, and you should not change this. If the number is incorrect, you may not have used a consecutive list of numbers starting with 1.

The design options are divided between **unreplicated** and replicated designs. Among the former you may choose **No randomization**, which means the design is simply a copy of the list of germplasm

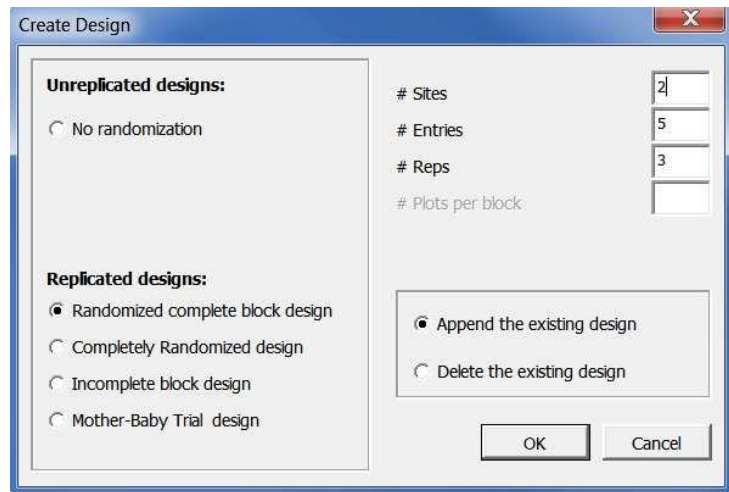


Figure 10 Create Design dialog

for each site. “When some treatments (checks) are replicated r times and other treatments (new treatments) are replicated less than r times, an **augmented design** may be used. These designs may be minimum variance designs for estimating contrasts of check effects, of new variety effects, of new variety versus checks, or of all check and new varieties simultaneously”.³ For an Unreplicated design designs you must indicate the **# of sites** or if you have more than one experiment at a site indicate in the total number of experiments. The # of sites determines the number of field books that will be generated in a subsequent step.

For Replicated designs you can choose **Randomized Complete Block** design (RCBD), Completely Randomized design (CRD), Incomplete block design⁴, or Mother-Baby trials⁵. For RCBD and CRD indicate the **# of sites** and **# replications per site**. To create a Split plot design you have to use the RCBD and create one experiment for each treatment at each site e.g. 3 treatments at 2 sites, you should make the design for 6 sites, and once you have made the fieldbooks you can assign the treatments.

³ On Augmented Designs, W. T. Federer and D. Raghavarao, Biometrics, Vol. 31, No. 1 (Mar., 1975), pp. 29-35, Published by: International Biometric Society, <http://www.jstor.org/stable/2529707?seq=1>

⁴ See for example: <https://docs.google.com/viewer?url=http://www.designcomputing.net/pdf/federer.pdf>

⁵ See for example: <http://www.cazs.bangor.ac.uk/ccstudio/Library/publications/ReviewPapers/mother.pdf>

If you have already created a previous design and want to change it you may use the option Delete the existing design. Note if you have not made a design yet, or if you just opened the file this option may not be available. In the latter case you may have to create a design twice to be able to delete properly the previous version.

Click OK to generate design.

A Dialog will appear as if you want to create labels, see below for that option.

Once the design has been generated you must **click on the Design tab**, and **verify that the design** that was generated has the correct number of sites, number of reps, etc. You must also manually define Blocks if that is relevant. It is important to ensure that the design is correct before you generate field books, as the design in the field book is not updated if you change it later on.

Exp	Rep	Block	Plot	Entry	SeedsPerF
1	1	1	1	3	12
1	1	1	2	6	12
1	1	1	3	5	12
1	1	1	4	2	12
1	1	1	5	1	12
1	1	1	6	4	12
1	2	1	7	4	12
1	2	1	8	3	12
1	2	1	9	1	12
1	2	1	10	2	12
1	2	1	11	6	12
1	2	1	12	5	12

Figure 11 Example of design of experiment

In the example you can see how the first column in the design indicates the Experiment number, the second column the Replication within the experiment, the third indicates the Block (must be entered by user as CloneSelector cannot know what blocks are relevant to your field), the fourth is the consecutive list of plot numbers, and the fifth is the Entry numbers from the list of germplasm, and these will be randomized if that is part of the chosen design.

If you want to use CloneSelector to analyze an existing trial, you must first enter the list of germplasm as described above and then generate the design. **If the trial was made with a randomized design you should copy the original trial design and overwrite the design that was generated.** You can for example do this by sorting your original design by Experiment, Replication and Plot and then copy the Entry numbers into the design or manually enter the Entry numbers. If you do this your fieldbooks will subsequently have the same layout as your trial, and it will be much easier to enter the data.

2.3.1. Make labels for planting material

CloneSelector -> List of Germplasm -> Seed Labels

In the Labels: **Choose Sites dialog**, you must **choose for which sites you want to create labels**, typically you want to choose **Select All**.

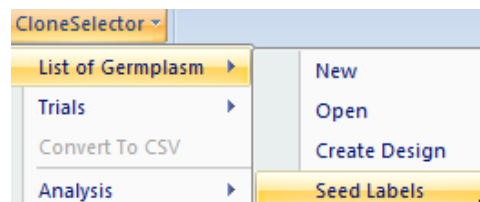


Figure 12 Seed Labels menu

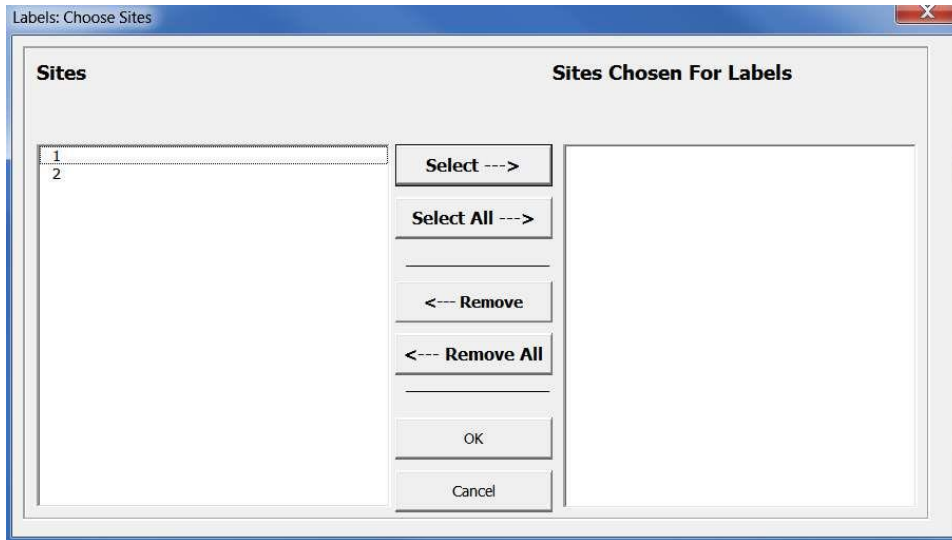


Figure 13 Choose Sites for generating labels dialog

Click OK to define the sites.

In **Make Seed Label** select the **# of labels in a row** on your paper. If for example you have labels on an A4 sized sheet you may have 3 labels in each row.

Click OK to generate labels.

The labels generated may not have the exact size of your labels, and you may have to adjust the size. **Print a small test sample before trying to print all labels**, in order to be able to adjust the print size to your labels.

Save the List of Germplasm and **Close it**.

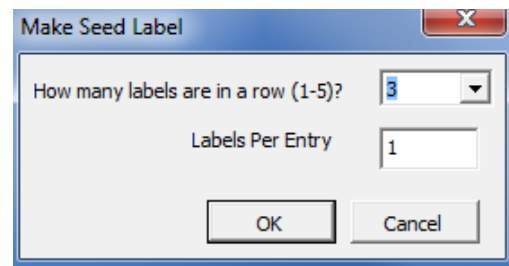


Figure 14 Layout of seed labels dialog

2.4 Generation of a field book for each experiment

Make sure **your List of Germplasm is closed** before you start making field books. If this is not the case you may get an error as CloneSelector will attempt to open the file again.

This step will generate one fieldbook in a separate Excel file for each experiment defined in the design of the germplasm list. For example if you entered 3 sites in the Create Design dialog, then CloneSelector will generate 3 fieldbooks. What happens behind the scene is that CloneSelector takes the information from the List of Germplasm and inserts it in all the right places in a fieldbook template. The first time you may find the process a bit confusing, but soon you will appreciate the work saved in this step.

CloneSelector -> Trials -> New

In **New Trial Series Dialog**.

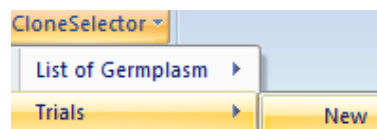


Figure 15 New trial menu

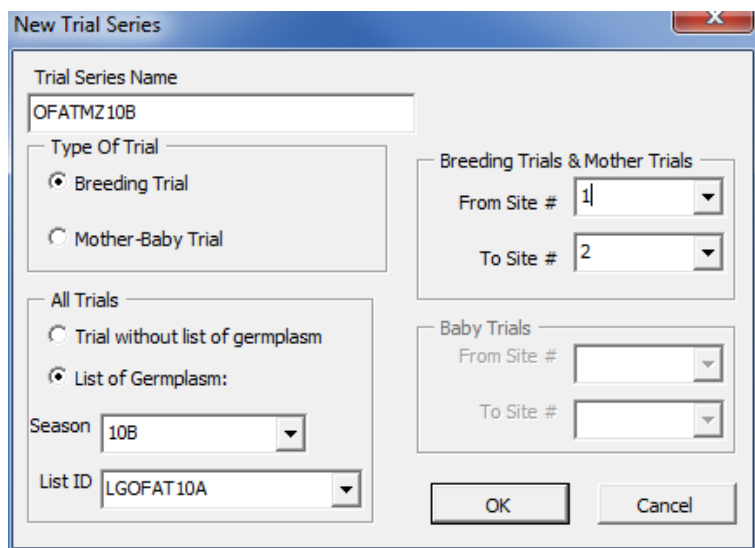
A screenshot of the 'New Trial Series' dialog box. The 'Trial Series Name' field contains 'OFATMZ10B'. Under 'Type Of Trial', 'Breeding Trial' is selected. The 'Breeding Trials & Mother Trials' section has 'From Site #' set to 1 and 'To Site #' set to 2. Under 'All Trials', 'List of Germplasm:' is selected. The 'Season' dropdown is set to '10B' and the 'List ID' dropdown is set to 'LGOFAT10A'. 'OK' and 'Cancel' buttons are at the bottom.

Figure 16 New Trial Series dialog

1. **Enter a name for the trial series. Names should not include spaces.** The name entered will be the name of the Fieldbook files and for each site a number will be added such as for example ATYLMZ10B1, ATYLMZ10B2 etc.
2. Leave **Type of Trial** as **Evaluation Trial** (unless of course it is a Mother Baby trial)
3. In drop down list **Select the Season** in which you put the Germplasm List, typically this should be 10B or something similar.
4. **Select the List ID** that is the name you assigned to the List of Germplasm. Note: If you have not made a Design in the List of Germplasm, you will get a message, in that case click Cancel and open List of Germplasm to create design before proceeding.

- The **system will automatically detect the number of Sites in the From Site # to Site #**, and if that is not correct you have a problem with the design in your List of Germplasm. Cancel and fix before proceeding.

Click OK to start process of fieldbook generation

Note: If it is a large germplasm list this may take time, **wait**, do not click or close.

If it is the first Fieldbook in the season Excel will ask if you want to create a new directory. Click **Yes**. If you click No the process will be canceled, and you may get an error if you Click OK again. In that case close Click Cancel in New Trial Series and start again.

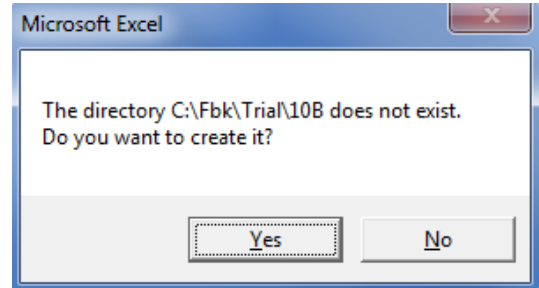


Figure 17 Create directory for trials in new season dialog

Important in Excel 2007: Excel will open a **Dialog Compatibility Checker**. Make sure to **Uncheck** the box Check Compatibility When Saving this book, before clicking **Continue**. If you do not uncheck the option you may have to wait for some time. Note: The **Dialog will appear once for each field book**, and if you have for example 4 sites it will appear 4 times.

CloneSelector generates automatically a new field book for each experiment, but they are closed.

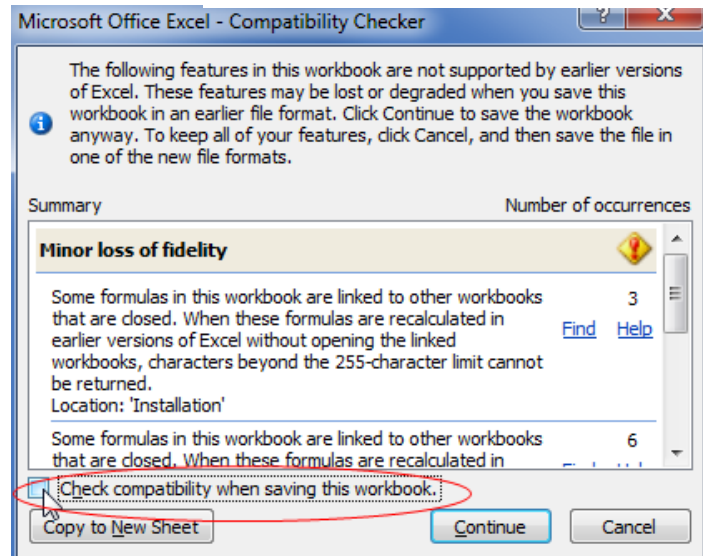


Figure 18 Excel 2007 Compatibility checker problem

2.4.1. How to open a field book

To verify the new field books click **Trial -> Open**.

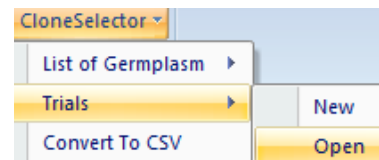


Figure 19 Trial Open menu

Select **Season** and **Trial name** in the dialog. The files will have the Name of the Trial series plus a consecutive number.

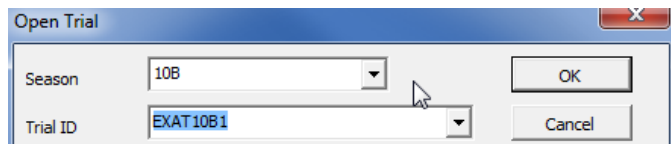


Figure 20 Open Trial dialog

Each Excel workbook has a number of sheets: **Fieldbook**, **Results**, and **Master** are all related to the data being recollected on each entry and the analysis of this information. **General**, **Installation**, **Field**, **Climate_data**, and **Crop_management** are all related to the general information on the setup of the experiment. The use of these will be explained in the subsequent steps.

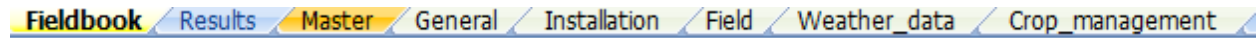


Figure 21 Sheets in a CloneSelector fieldbook

Open the **field books and verify that they are correct**. In particular verify the germplasm list and design of the trial on the Fieldbook sheet. If you identify a problem you must correct it in the List of Germplasm and generate the field books again.

The field books are stored in **C:\CloneSelector\Trial\Season**, where the season is for example 10B.

2.5 Register metadata for each experiment

The interpretation of an experiment is not only based on the specific observations, but also on the context under which they were observed such as for example where was the experiment undertaken, by whom, with what purpose, what was the management, the soil and the weather like? This information can be considered metadata i.e. data about data. In CloneSelector you can register a wide range of metadata and each Fieldbook has five sheets for documenting the experiment:

- **General** with general information on the trial
- **Installation** which is the specific setup. You must add the **Plot size**
- **Field** is soil type and previous management
- **Weather data**
- **Crop management**

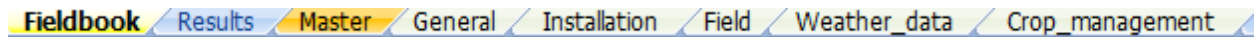


Figure 22 Meta data sheets in Fieldbook

You should not change or delete the standard fields, but if you do not need a field you can leave it blank and consider hiding the row. Below the table of standard fields you can add new fields (rows) if needed.

2.5.1. General information

This form contains general background information on the trial, and includes information on who carried it out, where it was done, and finally it contains the Dublin Core standard information.

Table 1 General information

Factor	Value
Trial Name	
Institution	
Short name or Title: *	
Begin(mm/dd/yyyy): *	
End(mm/dd/yyyy):	
Leader : *	
SubLeader :	
Assistant:	
Creator	
Country: *	
Department	
Province	
Distritc	
Locality :	
Crop: *	
Altitude (masl) *	

Latitude *	
Longitude *	
Type Content:	
Advance%:	
Type of Trial :	
Description: *	
Objetives:	
Comments:	
Year *	
Version	
Contributor	
Owner	
Subject	
Description	
Publisher	
Date	
Type	
Format	
Identifier	
Source	
Language	
Relation	
Rights	
Rightsholder	
License	
Audience	
Provenance	
Embargo till	
Status	
Data	
Project Name and Code:	

2.5.2. Installation information

The installation form contains the information related to establishing the trial in the field. In particular it is important to indicate the **Density (plants/ha)** as this is used in many calculations such as the conversion of the yield into t/ha.

Table 2 Installation information

Factor	Value
Trial design *	
No. of entries *	
No. of replications *	
No. plants per plot *	
No. rows per plot *	

No. plants per row	
Plot size (m ²)	
Distance between plants (m) *	
Distance between rows (m) *	
Density (plants/ha)	
Date of planting (Date)	
Date of vine cutting / killing (Date)	
Date of harvest (Date)	
Measurement date late blight 1	
Measurement date late blight 2	
Measurement date late blight 3	
Measurement date late blight 4	
Measurement date late blight 5	
Measurement date late blight 6	
Measurement date late blight 7	
Measurement date late blight 8	
Measurement date late blight 9	
Measurement date late blight 10	
Measurement date late blight 11	
Measurement date late blight 12	
Interval in days, Late Blight 1 -2	
Interval in days, Late Blight 2 -3	
Interval in days, Late Blight 3 -4	
Interval in days, Late Blight 4 -5	
Interval in days, Late Blight 5 -6	
Interval in days, Late Blight 6 -7	
Interval in days, Late Blight 7 -8	
Interval in days, Late Blight 8 -9	
Interval in days, Late Blight 9 -10	
Interval in days, Late Blight 10 -11	
Interval in days, Late Blight 11 -12	
Late Blight Control cultivar	
Late Blight control AUDPC observed	
Late Blight control scale value	

2.5.3. Field information

The field information is related to soil characteristics and prior use of the field.

Table 3 Field information

Factor	Value
Predominant Soil Texture *	
Organic matter (%) *	
Ph. (0 - 14) *	
Crop 1	
Crop 2	

Crop 3	
--------	--

2.5.4. Weather data

The weather data contains monthly average data for the weather in the trial period.

Table 4 Weather data

Values	Month	Avg. precipitation (mm)	Average temperature (°C)	Avg. min. temperature (°C)	Avg. max. temperature (°C)	Avg. day/night temp. fluctuation	Relative humidity (%)	Radiation level
1	Jan-10							
2	Feb-10							
3	Mar-10							
4	Apr-10							
5	May-10							
6	Jun-10							
7	Jul-10							
8	Aug-10							
9	Sep-10							
10	Oct-10							
11	Nov-10							
12	Dec-10							

2.5.5. Crop management

Crop management indicates how the trial was managed.

Table 5 Crop management

Intervention category	Intervention type	Date of intervention	Name of product *	Product concentration	Dose of application	Observations
Fertilizing						
Weed control						
Pest control						
Disease control						
Irrigation						

2.6 Field and post harvest data collection in for each entry

2.6.1. Introduction to potato traits⁶

[Note: While under some circumstances, there are different meanings of the words “variable, trait and attribute,” for our purposes we use these words synonymously.] In experiments, we distinguish between **classification variables**, and **response variables which have to be analyzed**. Classification variables help us to identify plots and how experimental factors and factor levels are applied to plots (e.g., year, location, genotype, genotype name, and replication). The classification variables can be comparable to our home address by which we can identify who is living where (country, town, street, name). Classification variables allow us to identify a plot, its location, which genotype was planted in it, and how the plot was treated. Moreover, classification variables are needed to provide statistical program packages with information about how the data were organized (e.g. data records are sorted by locations, within locations by genotypes and within genotypes by replications) and they are used to inform statistical procedures about how to analyze the data records. In CloneSelector **the classification variables are mainly entered in the List of Germplasm** and automatically transferred when the fieldbooks are generated, **and the trial metadata are entered as** described in the previous section. **This section is focused on how to collect the response variables data.**

Variables which have to be analyzed can be distinguished:

- (i) **Parametric variables:** Real numbers following an approximately normal distribution (e.g., storage root yield, upper biomass yield, storage root dry matter, etc.).
- (ii) **Non-parametric variables:** Real numbers which show strong deviations from a normal distribution (e.g., disease damage).
- (iii) **Rank variables** (e.g., scores with a scale of 1 to 9 for plant uniformity or scores with a scale of 1 to 7 for flowering degree, or scores from 1 to 5 corresponding to chipping color).

It should be noted that the analysis of variance (ANOVA) procedure is relatively robust to deviations from the normal distribution, so that even symmetrically distributed rank scores from 1 to 9 can be analyzed by an ANOVA. However, the ANOVA is very sensitive to deviations due to variance in homogeneity of the error [this is the case when a genotype obtains a common score value across replications (e.g., 1 for tuber uniformity = very heterogeneous), while other genotypes obtain different scores (e.g. 6 to 9 for tuber uniformity = very uniform)]. No variation among replications results in variance in homogeneity, and the requirements of an ANOVA are not fulfilled! Rank variables with scores from 1 to 3 should never be analyzed by an ANOVA; however, the frequency means provide useful information. Rank variables with scores from 1 to 3 have to be analyzed by rank statistics and for these, significance tests and multiple comparison procedures (procedures to compare each clone with a check or among all other clones in the trials) are available.

⁶ This introduction builds mainly on Chapter 3: Description of Data Collection Forms in Procedures for the Evaluation and Analysis of Sweetpotato Trials, Gruneberg et al, 2010.

Note: in some places, established breeding programs may have already developed different rating scales (e.g. 1 to 5, or 1 to 7 or 1 to 9). It is our hope that all of our partners in this collaborative potato breeding effort will be willing to adopt and use the scales given below, so that all may benefit from the power of the information provided from comparative analysis of our combined results.

The following presents the standardized traits recommended for potato⁷. The traits are grouped according to the different stages in an experiment or the method used for measurement:

- Pre-harvest data
- Late blight data
- Harvest data
- Post harvest data

In the fieldbook each group of traits have been coded with a color in order to easily be able to identify them. **Below is a description of the traits in each group, and how they should be measured or assessed.** It is very important that all breeders use the same definition of traits and methods of measurement in order to be able to analyze data from different breeding programs jointly.

Initially you should use the fieldbooks without modifications, but **after a while you will have identified which traits are relevant for your work**, and at that point **you should modify the trial template in accordance with your own needs**. This way you will avoid having to add the same information every time or hide the same columns. However, in order to know what to modify it is preferable to acquire some experience before doing the modifications.

In the fieldbook you should hide the traits you are not going to measure. Do not delete any columns as this may create errors and you may not be able to analyze the data. If you need to measure traits that are not in the standard list each group have two or three traits available where breeding programs can define additional traits relevant for their local area.

2.6.1.2 Pre-harvest data

In the Fieldbook tab the traits with a light green header color are the ones collected before the harvest

Plants Planted	Plants Emerged	Plant Uniformity	Plant Growth habit	Plant Vigor	Flowering Degree	Senescence	Trait1	Trait2	Trait3
----------------	----------------	------------------	--------------------	-------------	------------------	------------	--------	--------	--------

Figure 23 Pre-harvest traits

Plants Planted = number of plants (tubers) planted per plot.

Plants Emerged = number of plants (tubers) emerged per plot to be determined 3 weeks after planting.

Plant Uniformity = uniformity of plants per plot to be determined 4 weeks after planting and recorded on a scale of 1 to 5 where:

⁷ Based on *Procedures for standard evaluation trials of advanced potato clones. An International Cooperators' Guide, CIP (2007)*

- 1 = very heterogeneous
- 3 = heterogeneous
- 5 = intermediate
- 7 = Uniform
- 9 = very uniform

Plant Growth Habit = growth habit of plants in each plot to be determined 30-45 days after planting and recorded on a scale of 1 to 6 where:

- 1 = erect
- 2 = semi-erect
- 3 = decumbent
- 4 = prostrate
- 5 = semi-rosette
- 6 = rosette

Plant Vigor = Vigor of the plants to be determined 45 days after planting; recorded in scores from 1 to 9, where:

- 1 = very weak
- 3 = weak, 5 = medium
- 7 = vigorous
- 9 = very vigorous

Flowering Degree 0-7 = flowering density to be determined at flowering and recorded in scores from 0 to 7, where:

- 0 = no buds
- 1 = bud abortion
- 3 = scarce flowering
- 5 = moderate flowering
- 7 = profuse flowering

Senescence = Plant maturity to be determined before harvest and recorded in scores from 1 to 9, where:

- 1 = very late
- 3 = late
- 5 = medium
- 7 = early
- 9 = very early

2.6.1.3 Late Blight Data

Late Blight 1	Late Blight 2	Late Blight 3	Late Blight 4	Late Blight 5	Late Blight 6	Late Blight 7	Late Blight 8	Late Blight 9	Late Blight 10	Late Blight 11	Late Blight 12	Trait4	Trait
---------------	---------------	---------------	---------------	---------------	---------------	---------------	---------------	---------------	----------------	----------------	----------------	--------	-------

A maximum of 12 readings of late blight damages should be taken. The percentage of leaf infection is recorded throughout the season and the date of each reading is carefully noted. The first reading is taken 30 to 40 days after planting and 10 days after the last fungicide application. It is important to begin readings as soon as symptoms appear, so the field should be carefully observed to detect the initiation of disease.

Percentage of foliage affected by Late Blight 1 – 12 is the percentage of leaf area affected by late blight as observed on the date of reading. On the Installation sheet you must enter the date of the reading, in Measurement date late blight 1.

CloneSelector will calculate the intervals between the readings in days, and will use this to calculate the AUDPC.

Measurement date late blight 1	2/1/2011	
Measurement date late blight 2	2/8/2011	
Measurement date late blight 3	2/15/2011	
Measurement date late blight 4	2/22/2011	
Measurement date late blight 5	3/1/2011	
Measurement date late blight 6	3/8/2011	
Measurement date late blight 7	3/15/2011	
Measurement date late blight 8	3/22/2011	
Measurement date late blight 9	3/29/2011	
Measurement date late blight 10	4/5/2011	
Measurement date late blight 11	4/12/2011	
Measurement date late blight 12	4/19/2011	
Interval in days, Late Blight 1 -2	7	
Interval in days, Late Blight 2 -3	7	
Interval in days, Late Blight 3 -4	7	
Interval in days, Late Blight 4 -5	7	
Interval in days, Late Blight 5 -6	7	
Interval in days, Late Blight 6 -7	7	
Interval in days, Late Blight 7 -8	7	
Interval in days, Late Blight 8 -9	7	
Interval in days, Late Blight 9 -10	7	
Interval in days, Late Blight 10 -11	7	
Interval in days, Late Blight 11 -12	7	

Fieldbook Results Master General Installation

Trait1, Trait2, Trait3...Trait 14 There are 14 columns available to take data on additional traits if required. Indicate the trait being evaluated in rows 23 and 24 on the Fieldbook sheet. Use a 1 to 9 scale if making a rating, and provide the description of the trait on the Installation sheet. The user can change for example the label Trait1 in row 23 and 24 on the Fieldbook sheet, and also in row 20 and 21 on the

Results sheet. There are also 10 notes fields which may be used if desired. Note: For CloneSelector to work, no changes should be made in row 1 on any of the sheets as this will most likely cause problems. Nor should the order of columns be changed.

2.6.1.4 *Potato harvest data*

The following are the traits to be collected at the potato harvest

Plants Harvested	# Mark. Tub Cat I	Mark. Tub Cat I Weight	# Mark. Tub Cat II	Mark. Tub Cat II Weight	Non-Mark. Tub. Num	Non-Mark. Tub. Weight		
Tuber Appearance	Tuber Uniformity	Tuber Size	Size Stolons	Selected Clon	Trait6	Trait7	Trait8	

Figure 24 Harvest traits

Plants Harvested = Number of plants harvested.

Mark. Tub Cat I = Number of marketable tubers in Category I (tubers measuring > 60mm)

Mark. Tub Cat I Weight = Weight of marketable tubers in Category I

Mark. Tub Cat II = Number of marketable tubers in Category I (tubers measuring 30mm to 60mm)

Mark. Tub Cat II Weight = Weight of marketable tubers in Category II

Non-Mark. Tub Num = Number of non-marketable tubers (tubers measuring < 30mm)

Non-Mark. Tub Weight = Weight of non-marketable tubers

Tuber Appearance = Appearance of the tubers to be determined on 5 tubers per plot as per the requirements in the ICG.

Tuber size = Size of tubers. Overall assessment of tuber size based on inspection of the harvested tubers using a 1 to 9 scale, where:

- 1 = very small (< 2cm)
- 3 = small (2-4 cm)
- 5 = medium (4-6 cm)
- 7 = big (6-9 cm)
- 9 = very big (> 9cm)

Tuber Uniformity = Uniformity of tubers. Overall assessment of tuber uniformity is based on the inspection of the harvested tubers using a 1 to 9 scale, where:

- 1 = very heterogeneous
- 3 = heterogeneous
- 5 = intermediate

7 = uniform
 9 = very uniform

Size of stolons = Overall assessment of the length of the stolons based on inspection of the stolons using a 1 to 9 scale, where:

1 = very short (< 8 cm)
 3 = short
 5 = medium
 7 = long
 9 = very long

Selected Clones = Clones selected during the evaluation:

S = selected
 NS = Not selected

Trait6, Trait7, and Trait8 See note with respect to Trait 1, Trait 2, and Trait 3 above. If the number of traits recorded exceeds the 3 available here, additional Trait columns may be used from elsewhere in the fieldbook.

2.6.1.1 Post-harvest data (Dry matter and Specific Gravity)

150	150	25	25		2	0
200	200	60	60		4	0
F. Weight Tub. Samp	F. Weight Tub. Samp	D. Weight Tub. Samp	D. Weight Tub. Samp 2	Trait 9	Tub. Weight Air	Tub. Weight Water

Figure 25: Dry matter and specific gravity measurements

F. Weight Tub. Sample 1 = Fresh weight of tubers in sample 1

F. Weight Tub. Sample 2 = Fresh weight of tubers in sample 2

D. Weight Tub. Sample 1 = Dry weight of tubers in sample 1

D. Weight Tub. Sample 2 = Dry weight of tubers in sample 2

Tub. Weight Air = Weight of tubers in air

Tub. Weight Water = Weight of tubers in water

2.6.1.1 Post-harvest data (Oil absorption and French-frying quality)

The following traits are used to assess the quality of the potato tubers. Note in PTs only the top fraction of clones (15 to 25% of all PT clones) needs to be determined, whereas in ATs all clones have to be determined. Note also, that an alternative is to use near-infrared reflectance spectroscopy methods to assess the quality, and the traits used for this are described under NIRS quality data.

Initial Weight	Initial Weight	Final Weight	Final Weight	Trait12	External	External	Internal	Texture	Texture	Trait13
Sample 1	Sample 2	Sample 1	Sample 2		Appearance	Color	Color	Outside	Inside	

Figure 26 French-frying measurements

Initial Weight Sample 1 = initial weight of tubers in sample 1

Initial Weight Sample 2 = initial weight of tubers in sample 2

Final Weight Sample 1 = final weight of tubers in sample 1

Final Weight Sample 2 = final weight of tubers in sample 2

External Appearance = External appearance of French-fries assessed using a scale of 4-20, where 4 = poor, 8 = fair, 12 = good, 16 = very good, and 20 = excellent

External Color = External color of French-fries assessed using a scale of 2-10, where 2 = dark, 4 = slightly brown, 6 = Golden, 8 = light golden, and 10 = light whitish.

Internal Color = Internal appearance of French-fries assessed using a scale of 4-20, where 4 = dark grey, 8 = grayish, 12 = off-white or opaque, 16 = bright white, and 20 = crystalline.

Texture Outside = External appearance of French-fries assessed using a scale of 4-20, where 4 = soggy, 8 = moderately soggy, 12 = slightly crispy/soggy, 16 = moderately crispy, and 20 = crispy.

Texture Inside = External appearance of French-fries assessed using a scale of 6-30, where 6 = very soggy, 12 = soggy, 18 = slightly mealy/soggy, 16 = moderately mealy/soggy, and 30 = mealy.

2.6.1.1 Post-harvest data (Cooking quality)

10	10	0	0	5	0	0	0
30	30	10	10	40	20	10	10
Cook time	Cook time	Appearance	Appearance	Texture	Off-flavor	Sloughing	Discoloration
Sample 1	Sample 2	Whole tuber	mashed sample	Mashed sample	mashed sample	Whole tuber	

Cooking time sample 1 = Time to cooking for the first sample of tubers, assessed according to procedures by E. Mihovilovich.

Cooking time sample 2 = Time to cooking for the second sample of tubers, assessed according to procedures by E. Mihovilovich.

Appearance Whole tuber = Appearance on cooked tubers assessed using a scale of 0-10, where 0 = poor, 2.5 = fair, 5 = good, 7.5 = very good, and 10 = excellent.

Appearance mashed sample = Appearance on the mashed sample of tubers assessed using a scale of 0-10, where 0 = poor, 2.5 = fair, 5 = good, 7.5 = very good, and 10 = excellent.

Texture = Texture of cooked tubers assessed using a scale of 5-40, where 5 = very soggy, 10 = soggy, 15 = moderately soggy, 22.5 = slightly mealy/soggy, 30 = moderately mealy, 35 = very mealy, and 40 = extremely mealy.

Off-flavor Mashed sample = Off-flavor on mashed sample of cooked tubers assessed using a scale of 0-20, where 0 = extreme, 5 = much, 10 = moderate, 15 = slight, and 20 = none.

Sloughing Mashed sample = Sloughing on mashed sample of cooked tubers assessed using a scale of 0-10, where 0 = extreme, 2.5 = much, 5 = moderate, 7.5 = slight, and 10 = none.

Discoloration Whole tuber, = Discoloration on cooked whole tubers assessed using a scale of 0-10, where 0 = extreme, 2.5 = much, 5 = moderate, 7.5 = slight, and 10 = none.

2.6.2. Printing the fieldbook sheet

In order to collect data in the field you can print the Fieldbook sheet, however, before doing so you must do some preparations such as adding header information to the fieldbook sheet and hiding the traits that will not be scored in this particular experiment.

2.6.2.1 Adding fieldbook headers

When working in the field it is necessary to be able to identify well which fieldbook to use for which experiment and this can be done automatically if you have filled in the relevant metadata as described above.

The fieldbook header includes the following information:

- Name of experiment (the same as the name of the file)
- Site name or location
- Agroecology
- Planting date
- Harvest date
- Plot size
- Collaborator
- Institution

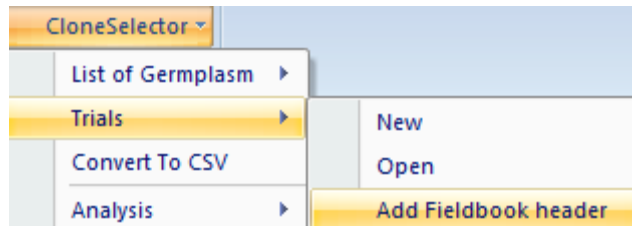


Figure 27 Add Fieldbook header menu

This information should be added in to the metadata (see above) before inserting the fieldbook header

CloneSelector -> Trials -> Add Fieldbook header

After inserting the header you may have to move it or adjust the size of the box or the rows for it to be properly positioned.

2.6.2.2 Hide traits that will not be measured and set print area

The fieldbook include many traits and you may not measure all of them in the particular trial, and before printing you should **hide the traits that will not be used**. Note: **Do not delete columns** as this may cause problems when trying to analyze the data.

Before Printing fieldbooks

1. **Hide the columns** you do not wish to collect. **Do not delete columns**, only hide.
2. **Define the Print Area** as in any Excel sheet
3. **Use Print Preview** and **Set Print Area** as you would in any other Excel sheet.

Once you have configured the print setup **print the fieldbook as any other Excel sheet.**

Note: If you have problems with printing a fieldbook, you may consider copying the relevant headers and germplasm list into a temporary Excel file, but do only use this for printing.

Note: In some cases you may have problems if you try to hide too many columns, and in that case use printing via a temporary sheet.

Save the fieldbook once the printing has been set up correctly.

2.7 Enter collected data into electronic field book

Once **data has been collected in the field it must be entered in the fieldbook sheet**. The data is entered as in any normal Excel sheet.

When data is entered **missing values should be entered as a point or dot i.e. "."**. This is very important as **Excel in some cases considers an empty cell as zero and this may lead to errors in your data analysis**.

2.7.1.1 Checking data quality of the fieldbook data

CloneSelector include tools to **verify that the data are on a valid scale** and it will also **flag outliers in relation to a normal distribution**, however, these tools will only detect the obvious errors and **it is very important that you take precautions to ensure the data is transcribed without errors**.

After data Entry you must check the data quality of the fieldbook. To do this it is useful to have a paper copy of the data present so that the problems identified can be corrected immediately.

CloneSelector -> Analysis -> 1. Check Field Data

A **Dialog Correct Errors/Outliers** will appear in the upper left corner if problems are encountered.

If you are not able to enter the correct data **you must enter a point i.e. "." as a missing value**. If you leave the cell blank then this may cause problems when calculating the derived values in the Master sheet as **Excel considers an empty cell as zero, and instead of a missing value the calculation may return a zero, and you would end up with a difficult to detect error in the results sheet**.

In the Correct Errors Dialog the first line indicates the type of error or problem for example in this case a 10 is an invalid data as the scale is only 1-9, and CloneSelector propose to change this to a "." i.e. a missing value.

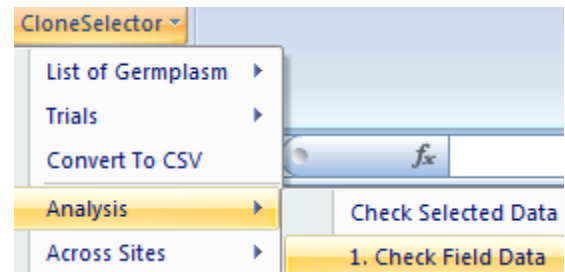


Figure 28 Check Field Data function

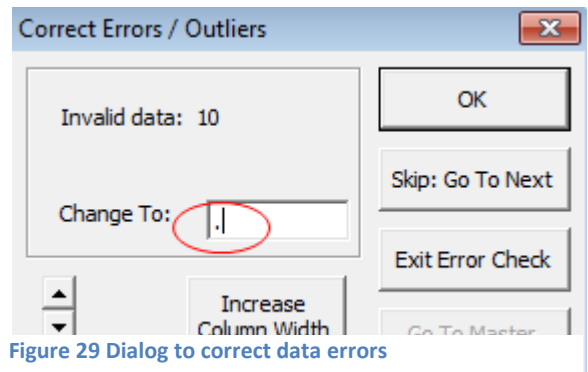


Figure 29 Dialog to correct data errors

The data check is both for false values such as letters in a numeric columns or outliers. The latter is values that are more than two standard deviations away from the normal distribution of the other values observed. In columns with very homogenous results, this may well flag correct values, and the check is only meant for you to ensure that the value is not an entry error.

In the Dialog **you may enter a new value** if you discover a mistake, or **accept the automatic proposal** by clicking **OK**. When clicking Ok the **value of the Cell is changed**, and it is **colored yellow** to flag that a change was made to the data.

The Option **Skip, Go to Next** will leave the value unchanged, but will color the cell red so that you can check it later.

The check is finished with a **Dialog Data Change Completed**.

Check all the cells in red before proceeding with the data analysis. If you subsequently change a data value you will have to redo the other steps, so **it is important to complete one step fully before moving on to the next.**

Save the Fieldbook after data check of field data.

2.8 Calculation of derived variables

Several of the traits observed in the field may need to be converted in order to be more easily interpreted or be comparable with results from other trials. For example the yield per plot should be converted to yield per hectare. The following table includes some of the most commonly derived variables used in potato breeding.

Table 6 Calculated fields for potato

Measurement	Calculation
Percentage plants emerged	$(\text{Number of plants emerged} \times 100) / (\text{Number of plants Planted})$
AUDPC	$\frac{1}{2}(Y_i + Y_{i+1}) \times (t_{i+1} - t_i)$
rAUDPC	$\text{AUDPC Observed} / ((\text{last reading} - \text{first reading}) \times 100)$
Scale(AUDPC)	$\text{Scale control Genotype} \times (\text{AUDPC genotype observed} / \text{AUDPC control})$
Percentage plants harvested	$(\text{Number of plants harvested} \times 100) / \text{Number of plants Planted}$
Total number of tubers per plot	$(\text{Number of marketable tubers category I} + \text{Number of marketable tubers category II} + \text{Number of Non marketable tubers})$
Total tuber weight per plot	$(\text{Marketable tuber weight category I} + \text{Marketable tuber weight category II} + \text{Non-marketable tuber weight})$
Total tuber yield per plant	$(\text{Total Tuber Weight} / \text{Number plants harvested})$
Total tuber yield (no adjusted)	$(\text{Total tuber yield kg plant} \times \text{Density plant/ha}) / 1000$
Total tuber yield adjusted	$(\text{Total tuber yield kg plant} \times \text{Density plant/ha}) / 1000 \times (\text{Plants harvest percent} / 100)$
Marketable tuber yield per plant	$(\text{Marketable tuber weight category I} + \text{Marketable tuber weight category II}) / \text{Number plants harvested}$
Marketable tuber yield per ha	$(\text{Marketable Tuber Yield kg plant} \times \text{Density plant/ha}) / 1000$
Total number of tubers per plant	$\text{Total Number Tuber} / \text{Number plants harvested}$
Number of marketable tubers per plant	$(\text{Number marketable tubers category I} + \text{Number marketable tubers category II}) / \text{Number plants harvested}$
Average weight of a tuber	$(\text{Total Tuber Weight} / \text{Total Number Tuber}) \times 1000$
Percentage dry matter content for sample 1	$(\text{Dry weight of tuber sample 1} / \text{Fresh weight of tuber sample 1}) \times 100$
Percentage dry matter content for sample 2	$(\text{Dry weight of tuber sample 2} / \text{Fresh weight of tuber sample 2}) \times 100$
Average percentage dry matter	$\text{Average}(\text{DryMatterContentSample1_Per}; \text{DryMatterContentSample2_Per})$
Specific gravity	$\text{Tuber weight in air} / (\text{Tuber weight in air} - \text{Tuber weight in water})$
Percentage oil content for sample 1	$(\text{Final weight sample 1} / \text{initial weight sample 1}) \times 100$
Percentage oil content for sample 2	$(\text{Final weight sample 2} / \text{initial weight sample 2}) \times 100$
Average percentage of oil content	$\text{Average}(\text{OilContentSample1_Per}; \text{OilContentSample2_Per})$
Average cooking time	$(\text{Cooking time of Tuber sample 1} + \text{Cooking time of Tuber sample 2}) / 2$

¹The formula given for AUDPC in the table above is where t is the time of each reading, y is the percent of affected foliage at each reading, and n is the number of readings. The variable t can represent Julian days ,days after planting or days after emergence.

In CloneSelector this conversion or calculation is done in the **Master sheet where the first line contains the formulas for calculating the variable**. You can click at the formulas in the first data row and you will see that the formulas are simple Excel formulas that take the data from the Fieldbook sheet and calculate the relevant variables.

2.8.1.1 Calculating variable in CloneSelector

The variables are calculated almost automatically, however, for the best result you must do some preparations:

1. **Finish the Check Fieldbook data quality** as described in the previous step and ensure that all data is valid or if it is missing a “.” has been inserted.
2. **Make sure that the Density (plants/ha) has been entered on the Installation sheet**. This value is used in all conversions to hectares.
3. Note: **Do not hide or unhide columns in the Master sheet** as this may cause problems when running the statistical analysis.
4. On the Master sheet check in the first second row the formulas that calculate the values. Especially the values #Div/0 . Delete the formula if the problem is that you are not collecting the data in this experiment.

Once you have done the preparations and checked the formulas you are ready to do the calculation:

CloneSelector -> Analysis -> 2. Fill in Master sheet

This should copy the formulas down to fill in all the rows in trial.

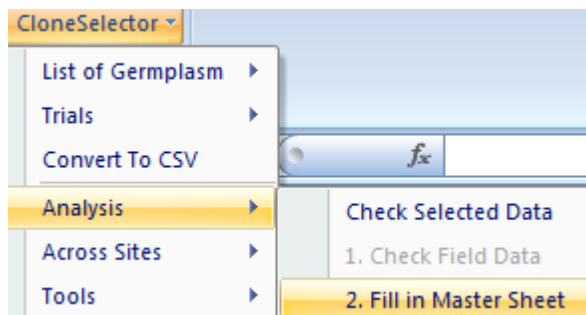


Figure 30 Fill in Master sheet

Next step is to check the Master data for errors and particularly to solve issues with missing data:

CloneSelector -> Analysis -> 3. Check Master Data

The two most common error in the Master data are generated by

1. An empty value in the fieldbook is indicated as “.” but in the Master sheet it must be an empty cell for R to analyze the data correctly.

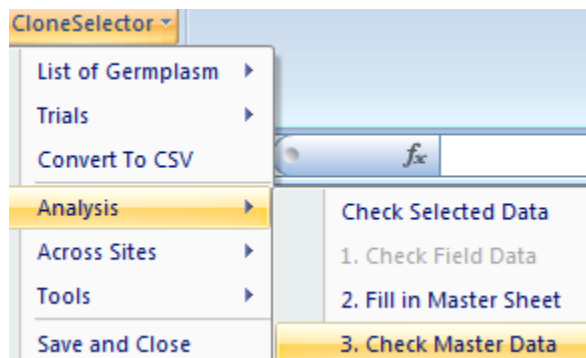


Figure 31 Check Master Data

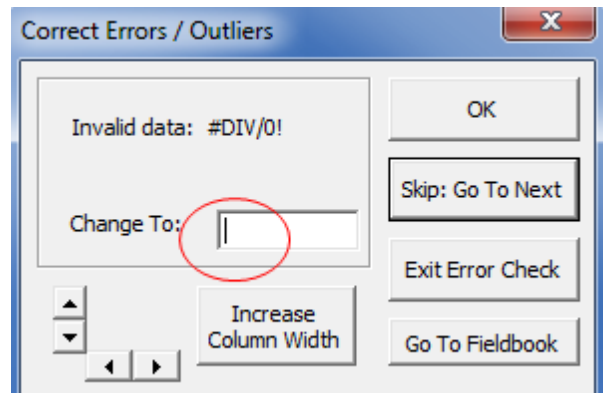
2. If the "." In Fieldbook is used in a formula in the Master it will generate an error indicated as #VALUE!

In both cases **Check Master Data** will automatically change the value in the cell to empty and the color to yellow to indicate the change.

A **Dialog Correct Errors/Outliers** will appear in the upper left corner if other problems than the two previously mentioned are encountered.

If you are not able to enter the correct data **you must leave the cell blank for a missing value.** RExcel which is used for the analysis will give an error if you enter a "." Or anything else that a blank cell for missing values.

In the Correct Errors Dialog the first line indicates the type of error or problem for example in this case a missing value that creates a "division by zero error", and CloneSelector propose to change this to a blank cell i.e. a missing value.



In the Dialog **you may enter a new value** if you discover a mistake, or **accept the automatic proposal** by clicking **OK**. When clicking Ok the **value of the Cell is changed**, and it is **colored yellow** to flag that a change was made to the data.

The Option **Skip, Go to Next** will leave the value unchanged, but will **color the cell red** so that you can check it later.

The check is finished with a **Dialog Data Change Completed**.

Check all the cells in red before proceeding with the data analysis. If you subsequently change a data value you will have to redo the other steps, so it is important to complete one step fully before moving on to the next.

Save the Fieldbook after the master data has been checked

2.9 Statistical analysis of trial

CloneSelector include an option for analyzing a trial in a randomized complete block design with a standardized method that generates 2 outputs

1. A table with the mean value across the replications of each trait for each entry
2. A table with statistical information for each trait
 - a. Mean value of the observations of the trait
 - b. Minimum value
 - c. Maximum value

- d. LSD of the genotype
- e. LSD of block
- f. P-value of genotype
- g. P-value of block
- h. Coefficient of variation
- i. Variance estimation for genotypes
- j. Variance estimation for blocks
- k. Residual variance estimation

The statistical variables can only be calculated if the trait has some variation within, and are not calculated for values that are the same in all plots such as for example Number of tubers planted.

Before doing the Statistical analysis you must Check the Master data as described in the previous step.

Make sure your data is Saved before attempting the analysis.

Note: The statistical analysis **requires RExcel to be installed**, and CloneSelector must have the correct Reference to this. RExcel must also be correctly Referenced which is done in the VBA Editor under Tools -> Reference, where there should be a reference to RExcelVBA Lib. This is a different library in Excel 2003 and 2007. In some cases it may have a reference such as for example Missing RExcelVBA LIB 2007 in Office 2003, in that case just remove the reference, and make the correct one. **If this has not been done, you probably need help from an IT person to do this.** We will be working on a more user-friendly installer, but for now you may need expert help.

To do the analysis:

CloneSelector -> Analysis -> 4. Analyze Master Data

This takes time so **WAIT**, it may take several minutes, depending on the size of your trial and your computer. **When it is finished it will automatically show the Results sheet.**

Note: This step implies sending data to a statistical program, and many things can go wrong, so error may occur, and it is important to save before running the analysis.

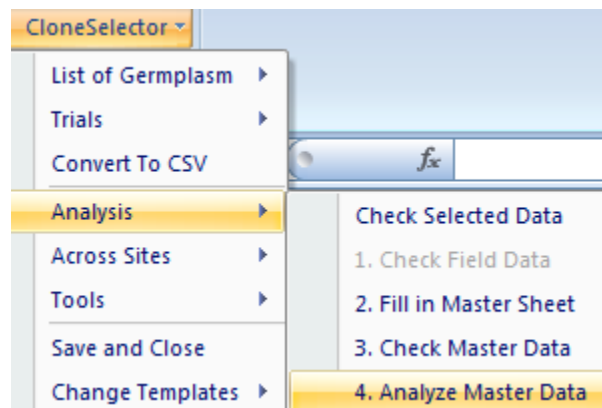


Figure 32 Analyze master data

Check that the Result columns are correctly aligned with the labels on the Result table. The Row just above the first Entry has the name of the column in the Master Sheet, and this should correspond to the column in the Result table. If they do not coincide you have probably hidden/unhidden columns in the Master sheet. To correct it you can either try to revert the Master sheet back to the original state, or manually move the content of the result table. We are working on making this more robust. This will be the case for the calculation of the AUDPC which is illustrated in section 1.8, page 31 of this manual.

2.9.1. Analysis of scale(AUDPC)

The scale(AUDPC) represent a special case in that you need to first calculate the AUDPC in order to obtain the observed AUDPC for the reference clone, and then you must enter that value and rerun the analysis in order to obtain the scale(AUDPC). If your analysis includes the scale (AUDPC) you must perform the following steps after running the first analysis.

Step 1: After the analysis has finished, observe on the **Result sheet** the AUDPC of the reference clone, such as for example 3670.3 for PUREN-INIA.

Entry	Name	AUDPC
		Units
		mAUDPC
1	PUKARA-INIA	3434.7
2	DESIREE	3710.0
3	YAGANA-INIA	3503.5
4	PEHUENCHE-INIA	3410.2
5	KARU-INIA	3763.7
6	PUREN-INIA	3670.3

Figure 33 Observe AUDPC of reference clone

Step 2: Enter the **AUPC value of the reference clone** and the **standard scale value** for it on the **Installation sheet**.

Late Blight Control cultivar	PUREN-INA
Late Blight control AUDPC observed	3670.3
Late Blight control scale value	8

Figure 34 Enter observed AUDPC on Installation sheet

Step 3: Go to **Master Sheet and Click Analyze Master Data** to rerun the analysis with the Scale AUDPC. When the analysis is finished you the values will be shown on the Results sheet.

Note: The analysis is done by sending the data to R and it is not like in Excel where you get an automatic recalculation. You must click Analyze Master Data to get the scale(AUDPC)

Entry	Name	AUDPC	rAUDPC	scale (AUDPC)
		Units	Units	Units
		mAUDPC	mrAUDPC	m-scaleAUDPC
1	PUKARA-INIA	3434.7	0.28	7.5
2	DESIREE	3710.0	0.30	8.1
3	YAGANA-INIA	3503.5	0.28	7.6
4	PEHUENCHE-INIA	3410.2	0.28	7.4
5	KARU-INIA	3763.7	0.30	8.2
6	PUREN-INIA	3670.3	0.30	8.0

Figure 35 Rerun analysis from Master sheet to obtain scale(AUDPC)

2.10 Elaboration of consolidated result table for each trial

After running Analyze Master Data in the previous step the Result sheet should have two tables:

1. A table with the mean value across the replications of each trait for each entry
2. A table with statistical information for each trait

- a. Mean value of the observations of the trait
- b. Minimum value
- c. Maximum value
- d. LSD of the genotype
- e. LSD of block
- f. P-value of genotype
- g. P-value of block
- h. Coefficient of variation
- i. Variance estimation for genotypes
- j. Variance estimation for blocks
- k. Residual variance estimation

The final step in the analysis is to check that the Result data are within the range defined for each trait.

On the **Result Sheet**, below the **Statistical data** you will see two rows, **Lower and Upper Limit**, and in these you can define **the range that is valid for each trait**. In the initial use of CloneSelector you may change the values directly in the Result Sheet, but in order not to do this every time you may also consider changing it in the Trial Template as described in another section.

Lower Limit			0.00	1	0.0		1.0	1.0
Upper Limit			50.00		100.0		5.0	9.0

Figure 36 Lower and Upper limits for results

Once you have defined the valid ranges or simply accepting the default values, you should check the result data:

CloneSelector -> Analysis -> Check Result Data

CloneSelector will now apply a yellow color to all results that are outside the defined range for the trait. It will also check the Min and Max value for each trait, so that if you have many entries you only have to revise the Min and Max to see if there is a problem in a trait.

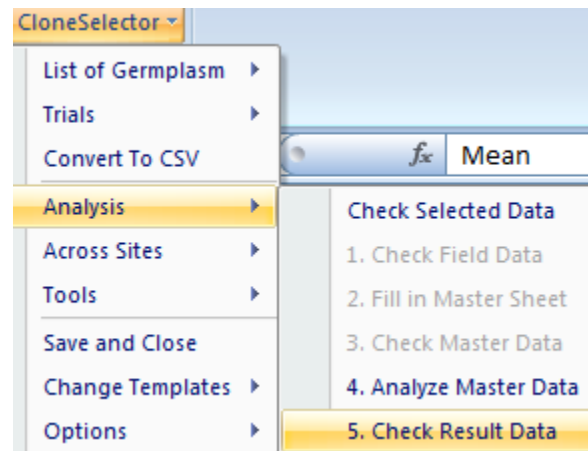


Figure 37 Check result menu

That a result is **out of bounds** may have different explanations:

- It could be a **problem with the data on the Fieldbook sheet**, but this is not so likely if you checked the Fieldbook data and corrected any problem found there. If you find that you have a problem on the Fieldbook sheet, you should verify that the Upper and Lower limits are the same for the trait on the Fieldbook and Results sheets. If you correct data in the Fieldbook sheet you must rerun the whole analytical process, from Check Fieldbook data and all subsequent steps.

- You may also have a **problem with formula on the Master sheet**, particularly, a problem of the data not being converted to the correct scale, and for example your data range may be defined considering results in gram, but the actual data has been calculated in kg. In this case you can
 - Change the Upper and Lower limits to reflect the used unit
 - Or change the formula used in the first line on the Master Sheet, and you must then rerun the analysis from Calculate derived fields above i.e. initiate with Fill in Master Sheet, and then redo the subsequent steps.
- Or you may find that your **Upper or Lower Limits are not correctly defined on Result sheet**, in which case you should correct them and rerun Check Result data. Or you may accept that in this particular case the result is acceptable.

What is important to understand is that **when you change data in the Fieldbook, formulas on the Master sheet or limits on the result sheet you must rerun the analytical process from the relevant step.**

3. Other functions in CloneSelector

The previous section of the CloneSelector outlines the uses related to carrying out a trial which is the main workflow at this point in time. This section explains some additional functionality which may more occasionally be useful such as for example sorting the fieldbook observations or the result sheet.

3.1 Tools for sorting data and results

The Fieldbook and result sheets in CloneSelector have quite a complicated structure and if you need to sort them according to a certain column you have to be careful not to accidentally mix up your data. To avoid problems it is therefore recommend using the sorting tools presented in this section.

3.1.1. Sorting Fieldbook according to entry number

Sorting the fieldbook according to entry number will order the fieldbook so that all the plots for one entry can be observed easily. To sort by entry the Fieldbook must be the active sheet or the menu will not be available.

CloneSelector -> Tools ->Fieldbook -> Sort by Entry

After this you can observe in the Entry column how the fieldbook has been ordered i.e. it starts with all the replicates of entry number one, followed by entry number two etc.

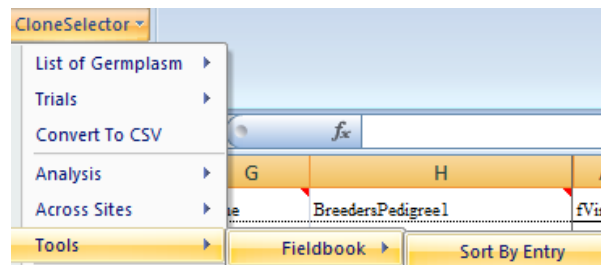


Figure 38 Sort fieldbook by entry menu

3.1.2. Sorting Fieldbook according to plot number

Sorting the fieldbook according to plot number is the default situation and it will bring the fieldbook back to its original order, which means for example the entries will be show the way they were randomized. To sort by plot the Fieldbook must be the active sheet or the menu will not be available.

CloneSelector -> Tools ->Fieldbook -> Sort by Plot

After this you can observe in the Plot column how the fieldbook has been ordered i.e. it starts with plot one, followed by plot two etc.

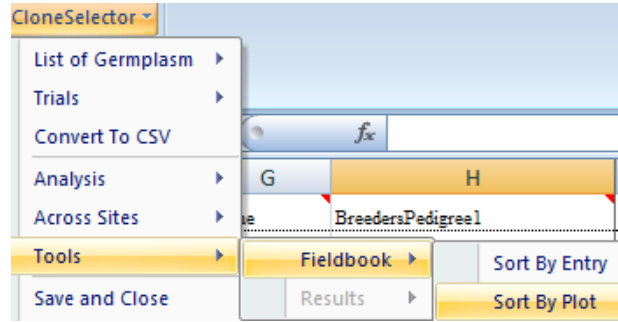


Figure 39 Sort fieldbook by plot menu

3.1.3. Sorting Result table according to user selected column

As part of the analysis of the results it can be useful to sort the Results table according to a column such as for example Total Root Yield. To do this the Results sheet must be active.

CloneSelector -> Tools -> Results -> Sort by Column

After clicking the menu a Sort dialog appears where you must **enter the column which will determine the sort order** and you can also **chose if it should be ascending or descending**. Once you have entered

the information **click OK** to do the sorting. After sorting by yield you can for example easily fill in the Yield Rank column.

The default sort order in results is according to Entry, and to return to the original table, you can enter B as the Sort by Column and Sort Ascending which will then return the results to the original order.

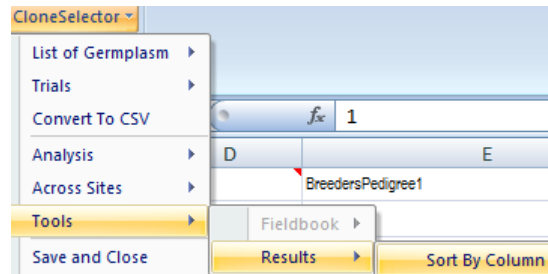


Figure 40 Sort results by column menu

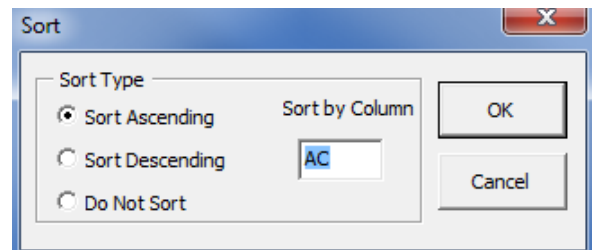


Figure 41 Sort results dialog

3.2 Copy existing data set into a CloneSelector Fieldbook

You may have a trial you already carried out or are in the process of carrying out, and you would like to enter the data in CloneSelector, so that you can verify the data and analyze the data. To do this you must first create a Fieldbook with the same design as your original design, and subsequently copy over the data.

3.2.1. How to create a CloneSelector Fieldbook based on an existing design

It is assumed that you already know how to create a germplasm list with a design, and how to generate a Fieldbook from this. If that is not the case then consult the relevant sections in chapter 2. **The critical issue is in Step 3 where you must ensure you use the same randomization as in your original trial**, as that is the only way to copy over the data with a limited effort.

Step 1: Generate a Germplasm List and enter the list of germplasm from your original trial (see also 2.2 Elaboration of list of germplasm to test). Note: CloneSelector requires Entry numbers to be a

consecutive list of numbers starting with 1, and if that is not the case in your original experiment, you must assign new Entry numbers.

Step 2: Generate a Design of a field trial with the same number of sites and repetitions as you have in your historical data for example 2 sites with 3 reps (see 2.3 Design of Field Trial with one or more experiments)

Step 3: From your original trial you must enter the randomization of the entries into the Entry column on the Design sheet in the Germplasm list. This is very important as this will help you copy/paste or enter your data into the Fieldbook. (see 2.3 Design of Field Trial with one or more experiments)

If your data is in Excel, you should make sure the data is sorted according to Rep before you copy the Randomization over.

After you have modified the randomization to match the original trial **Save the Germplasm list.**

Exp	Rep	Block	Plot	Entry	SeedsPerPac
1	1	1	1	1	4
1	1	1	1	2	5
1	1	1	1	3	1
1	1	1	1	4	3
1	1	1	1	5	2
1	1	1	1	6	6
1	2	1	1	7	5
1	2	1	1	8	6
1	2	1	1	9	1
1	2	1	1	10	4
1	2	1	1	11	3
1	2	1	1	12	2
1	3	1	1	13	2
1	3	1	1	14	1
1	3	1	1	15	3
1	3	1	1	16	5
1	3	1	1	17	4
1	3	1	1	18	6

Step 4: Generate the CloneSelector Fieldbooks using the Germplasm list you created in the previous steps. Note: It is critical you have entered the original randomization in the Design before you generate the fieldbooks. (See 2.4 Generation of a fieldbook for each experiment)

3.2.2. Enter or copy your existing data into the CloneSelector Fieldbook

Before you do this you must as described in the previous section Generate a Fieldbook in CloneSelector with the same design as your original data.

Step 1: If your data is on paper you will have to transcribe them into Excel. If you already have the data in Excel you can obviously omit this step.

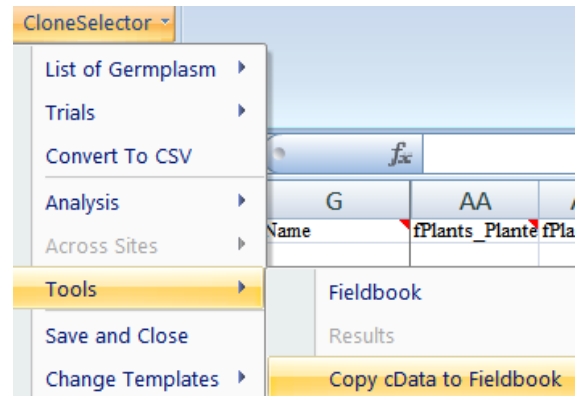
Step2: Copy your data into the cData sheet and insert **below** each column the official abbreviation for each trait. The abbreviations are listed on the Fieldbook Sheet in the second row. Note the abbreviations must be below and not

	A	B	C	D	E	F	G
1	32	32	5	2	8	1	
2	32	30	3	1	6	3	
3	32	32	4	3	5	2	
4	32	32	7	2	4	2	
5	32	31	8	1	5	1	
6	32	32	5	3	3	3	
7	32	30	8	2	5	4	
8	32	30	6	1	8	4	
9	32	30	5	3	6	2	
10	32	31	4	2	3	1	
11	32	30	5	2	4	1	
12	32	27	3	1	5	2	
13	32	30	5	3	5	1	
14	32	31	8	4	3	3	
15	32	30	6	4	4	2	
16	32	31	3	2	7	1	
17	32	32	4	1	8	3	
18	32	32	5	1	5	2	
19	NOPS	NOPE	PUNI	PGH	PVIG	FLOD	

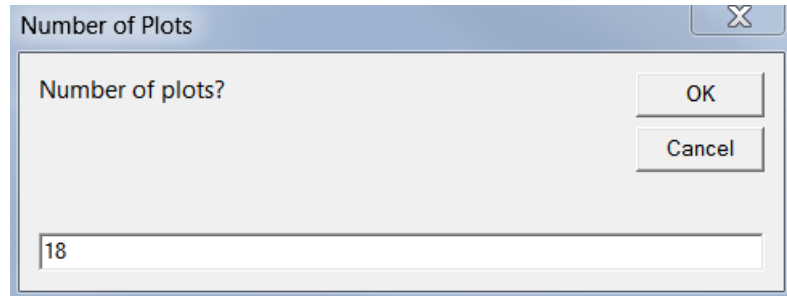
above the columns with data. The order of the columns on the cData is not important as long as you have the correct abbreviation in each one. When the data is copied to the Fieldbook sheet, they will be reordered according by matching the abbreviations.

Step 3: On the Fieldbook or cData sheet select:

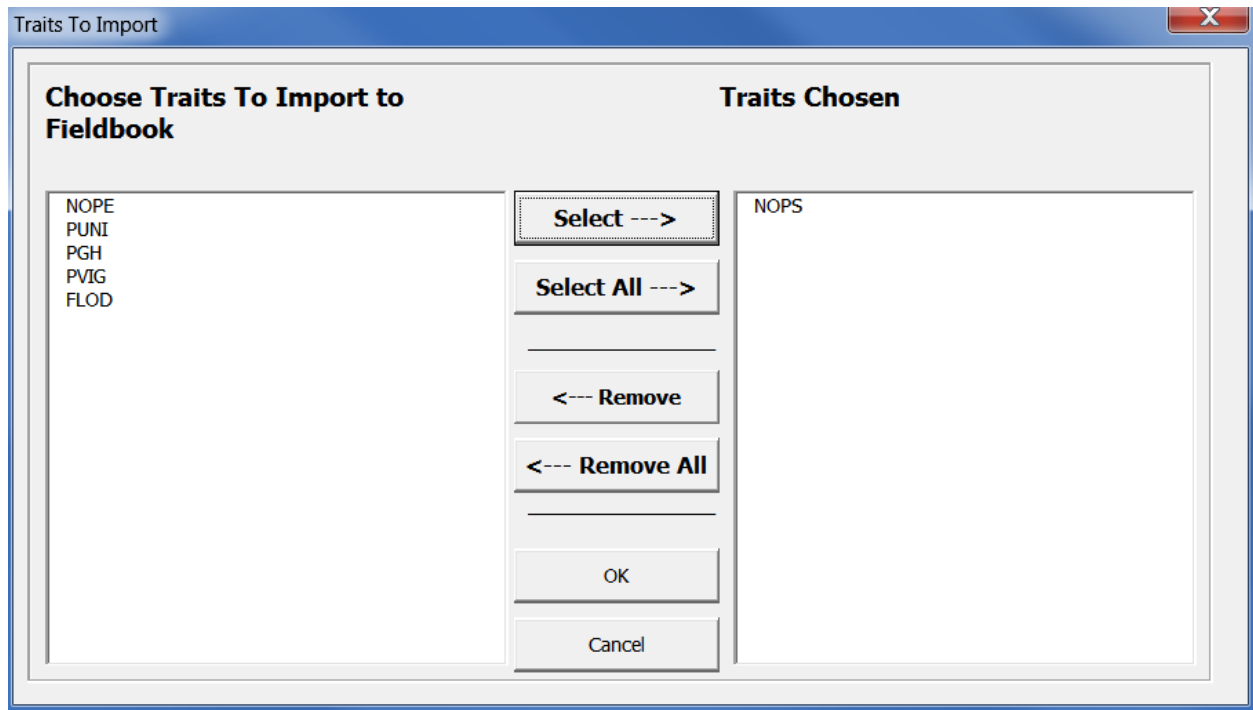
CloneSelector -> Tools -> Copy cData to Fieldbook



Step 4: Confirm the number of plots by clicking **OK in the Number of plots dialog**. If the number of plots in your data is not equal to the number of plots in your Fieldbook, the automatic import may not work. Though, in some cases you may have data with fewer repetitions.



Step 5: Choose the traits to import to the Fieldbook from cData by selecting traits and **clicking Select or clicking Select All**. The traits in the list Traits chosen will be imported. Remember you must put the trait abbreviations below the data in each column in the cData sheet. When you have selected the traits you want to import **click OK**.



Step 6: On the Fieldbook **verify** that your data was imported correctly, and **Save** the work sheet.

3.3 Saving files in CloneSelector

CloneSelector files are generally just normal Excel spreadsheets and you can save and close them as any other spreadsheet. However, CloneSelector also include a menu that will save and close the current sheet with just one click.

CloneSelector -> Save and Close

The outcome of doing it this way is no different from just using Excel menus.

CloneSelector automatically stores the Germplasm lists and trials in a folder structure order by seasons, and assigning standardized names to the files. This will help you organize your work, and at the same time ensure the good functionality of CloneSelector, so it is recommend to use the default options with regard to naming and storage locations.

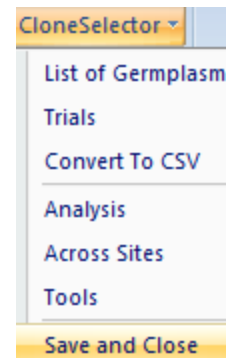


Figure 42 Save and Close menu.

3.4 Convert Fieldbook to CSV

CSV is an abbreviation for comma separated value file and is a standard format for data exchange of information presented in tables. Converting fieldbooks to CSV is relevant for using CloneSelector with FieldLog, which is an application for logging trial data on a hand held computer, a PocketPC. At this stage the functionality has not been tested, however, **it is expected that over the next year we will do some testing of the use of hand held computers for data logging.** More complete information will be included in this section once the testing has been done.

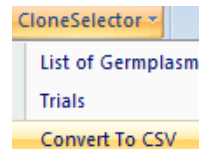


Figure 43 Convert to CSV menu

CloneSelector -> Convert To CSV

In practice you will want to for example convert all your fieldbooks from one season and store them on the hand held computer and the conversion is therefore set up for bulk conversion so that you select all the

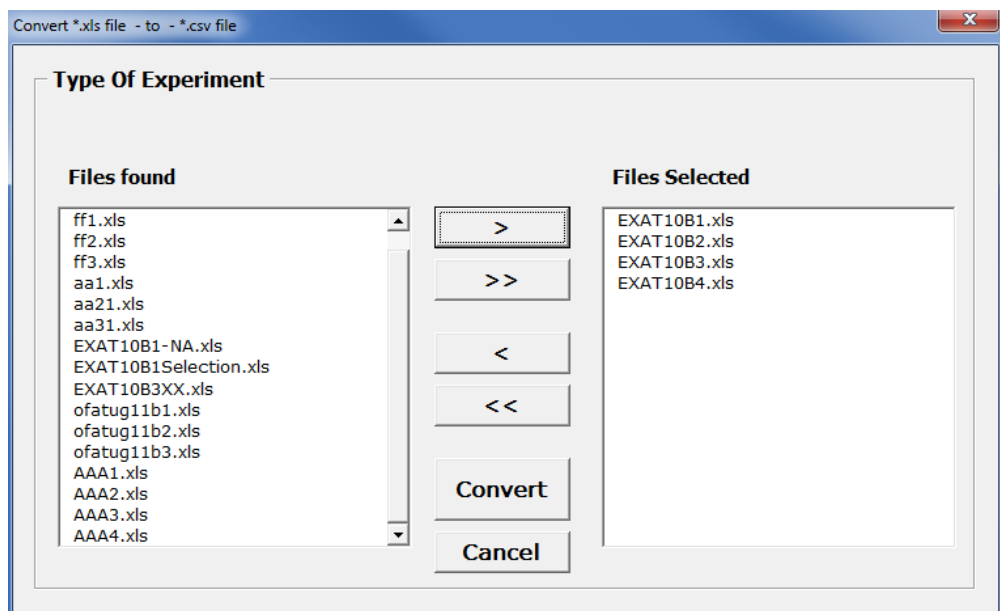


Figure 44 Convert to CSV dialog

files you want to convert and it is all done in one operation.

To select one or more files click on them and then click > to move over to selected or use < to move a file back if a mistake was made.

Once you have selected the files to be converted click **Convert** to do the conversion.

The CSV files will be saved in the Trial and season folder with the name CSV + current time. Inside the folder you will find the fieldbooks of all the selected files converted to CSV format.

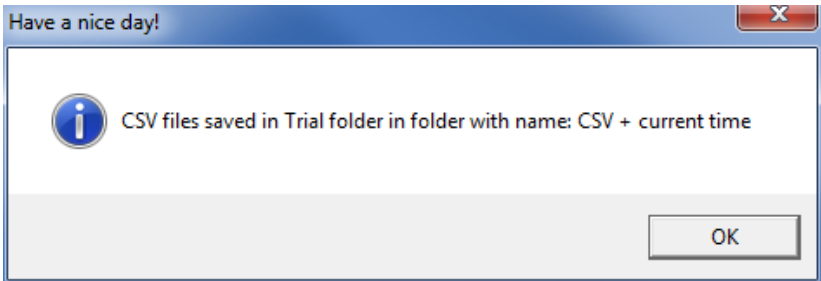


Figure 45 Dialog advising that CSV conversion has finished.

Computer ▶ OS (C:) ▶ CloneSelector ▶ Trial ▶ 10B ▶ CSV_20100901_14.9

Figure 46 Example of name and location of CSV file.

4. Customizing CloneSelector to your needs

The potato version of CloneSelector is developed in accordance with the established protocol for potato breeding and as such it should be generally applicable for most potato breeders, however, you may still have to do some modification to work as efficiently as possible.

1. If you have not placed the CloneSelector folder in the default location directly on the C disk, then you will have to adjust the file locations in the options menu as explained below
2. Once you have acquired some experience with CloneSelector you may decide to modify the trial template in order not to have to repeat the same modifications for each trial. This does however, require some general understanding of the different elements of CloneSelector and it is recommended to carry out a few trials before this is attempted. For the specific instructions see below.

However, before you start out modifying CloneSelector you should understand the basic structure of the files and folders used as is described in the following section.

4.1 CloneSelector file structure

The CloneSelector folder contains a number of folders and files.

The Excel file CloneSelector is the file you must open to start CloneSelector.

Note: with time the CloneSelector file may get corrupted and will not work properly. It is therefore recommend that you maintain a backup of CloneSelector, and if you experience problems, you can simply copy the backup version into the CloneSelector folder. To do so make sure that Excel is closed.

The **fieldbook.R** document is an R script used for analyzing the CloneSelector data with R. With time we hope to include more analytical options.

The **tpFbk** folder is where the templates are stored. Everytime CloneSelector generates a new Germplasm List or Trial it is based on a template, and these are stored in **tpFbk/Potato**. The modification of the templates is described below.

The **GermplasmList** and **Trial** folders are for storing user data. A new Germplasm List is sorted in GermplasmList/Season and a trial in Trial/Season where Season is folders named for example 10A and 10B for the two seasons in 2010. CloneSelector automatically stores the information in these folders, however, for this to work well the user should adopt naming conventions of both seasons and trial series.

BackupCopy contains a backup of the CloneSelector application and the templates in case any of them get corrupted. Should that happen simply copy the relevant files into the original place and restart CloneSelector by closing down Excel and reopening CloneSelector.

Summary is currently not used, but the intention is to be able to generate season summaries in this folder.

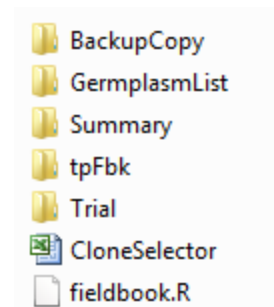


Figure 47 CloneSelector file structure

4.2 Setting up the location of the CloneSelector files and templates

CloneSelector aims to help automate and organize certain parts of the trial process. To do this it needs to be able to find the templates used for example for generating a trial or for storing the fieldbooks. CloneSelector is made to be installed by default directly in on the C drive i.e. in C:\CloneSelector. If you install it in another place you will need to adjust the File Locations.

CloneSelector -> Options -> File Locations



This will open the File Locations dialog. To change the locations you must click **Browse for CloneSelector Folder** and **Browse For tpFbk Folder**.

If you click one of the **Browse For** buttons that will open the **Browse for Folder dialog**, and you must here locate the relevant folder. For **CloneSelector folder you must locate a folder named CloneSelector** and **for the templates the folder must be named tpFbk** or they will not be accepted. When you have selected the relevant folder click OK to confirm the selection. To close the File Locations dialog and save your selection click OK again.

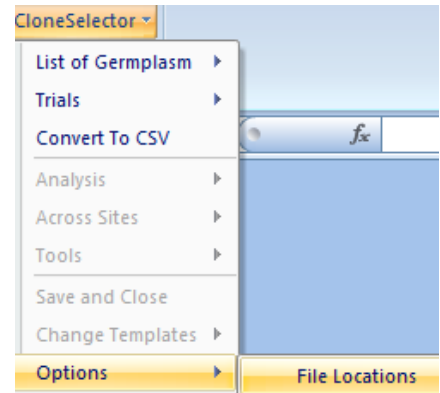


Figure 48 File Locations menu

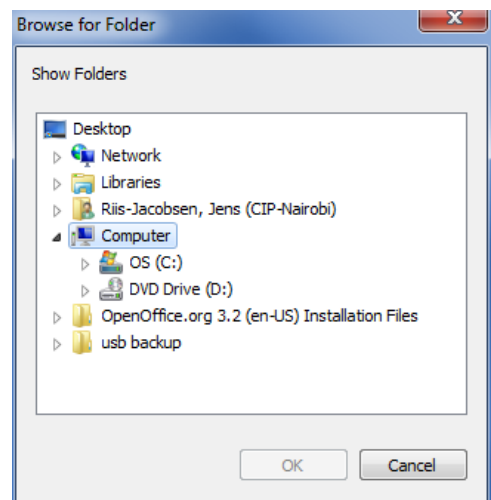


Figure 49 File Locations dialog

Note: At this point in time the Language option is not activated and CloneSelector only works in English, though it is hoped at a later stage that we will at least also have templates in other languages.

4.3 Customizing the trial template to your own needs

The Trial template is what CloneSelector uses to generate fieldbooks for your trials. When you customize the template, the changes will be reflected in all the new fieldbooks you generate, but existing fieldbooks will be left unchanged. The benefits of changes may include:

1. You may **hide the traits that are not relevant for your work**, and that way your future fieldbooks will only show what is relevant for you.
2. You can **add meta data** such as Country, project leader and other **information that is the same in all or most trials** you generate, so that you only enter it once.
3. You can use the place holders Trait1, Trait2 etc to **insert new traits** that are not included as standard traits.
4. You can **modify the formula for calculating derived variables** e.g. if you want to use plot size instead of plant density to calculate yield per hectare, then you will need to change the formula in the master sheet.

4.3.2. Steps to changing the Trial Template

Changing the template is a delicate procedure and it is recommended you make a backup of the template folder before you do any modifications. You should also close all open trial files or similar to avoid problems.

Note: **You should not delete Rows or Columns in the Trial Template**, and also be very careful with moving information around. If you do this CloneSelector may not work properly, or you may have made your data incompatible with other breeders data. **You should use “Hide” instead of “Delete”**, if you do not want information to be shown.

Step 1: Make a backup of the folder C:\CloneSelector\tpFbk , which is the folder with all the templates. If you have put the CloneSelector in another location the route is different, but should include CloneSelector\tpFbk.

Step 2: Select **CloneSelector -> Change Templates -> Change**

Step 3: Select **MSTRIAL** as **Template to modify** and

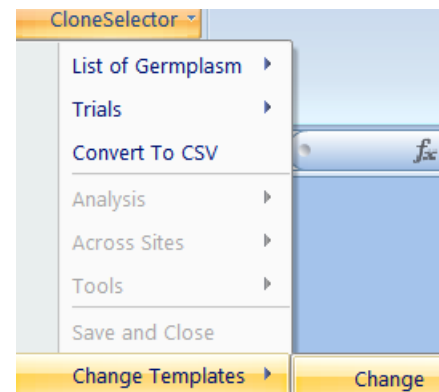


Figure 50 Change Template menu

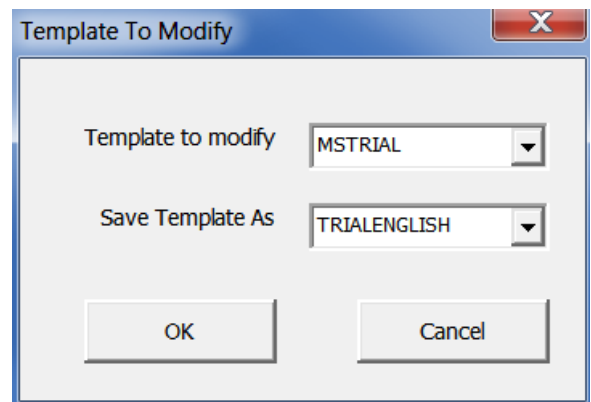
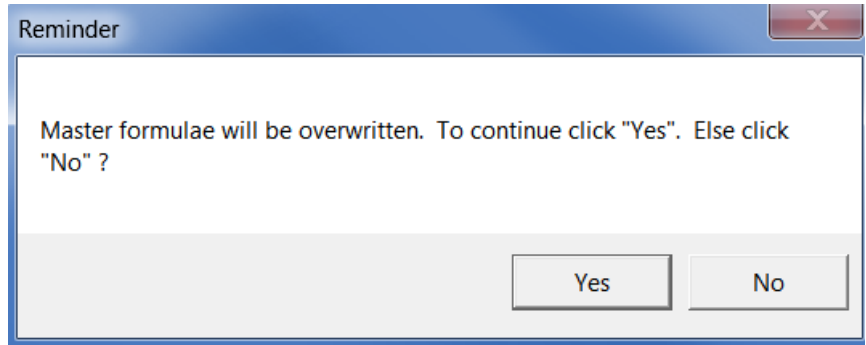


Figure 51 Select template to modify

TRIALENGLISH as Save Template As.

Note: We hope to be able to work with templates in different languages, but in this version you have to use the English one.

Step 4: You will be asked if you want to overwrite the Master formulae. If you click Yes, your formulas will be set to the default



CloneSelector calculations. If you answer No, the formulas will remain unchanged. The latter is useful if you have entered your own formulas.

4.3.2.1 Changing the Fieldbook sheet

Typical changes to the Fieldbook sheet include: Setting upper and lower limits to control range of valid values, modify labels of traits or inserting new traits on placeholders (Trait1, Trait2 etc).

To modify the Fieldbook sheet **click on the tab tpFieldbook.**

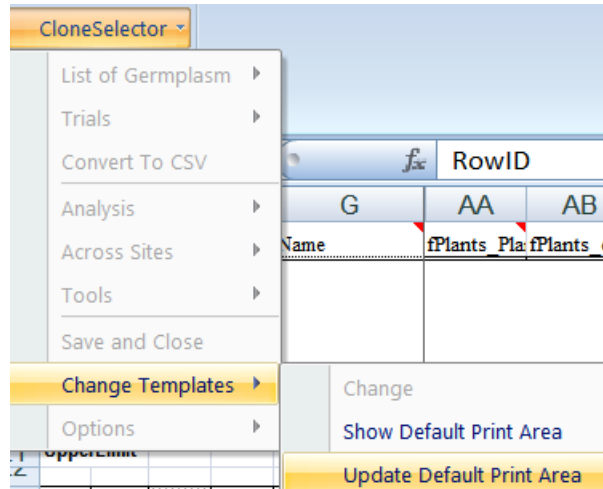
Hide traits that are not measured or observed

You are unlikely to routinely use all traits in the Fieldbook, and you should hide the traits you never or rarely use, so that you only see what you need.

Step 1: Hide all the columns you do not want to use in your Fieldbook

Step 2: Select **CloneSelector -> Change Templates -> Update Default Print Area**

Note: If you have already modified the template before you can click **Show Default Print Area**, and this will hide/show all the columns from the previous modifications.



Modify range of valid observations

The lower and upper limits of each trait in the Fieldbook are defined in rows 20 and 21, and to modify the range you simply change the existing values. If you leave a cell blank, not check will be undertaken.

20	LowerLimit					0	0	1
21	UpperLimit					40	40	9
23	Rep	Bloc	Plot	Entry	Name	Plants	Plants	Plant
24						Planted	Emerged	Uniformity

Figure 52 Setting lower and upper limits in Fieldbook

Insert a new trait to be measured or observed

To insert a new Trait you simply modify the text in row 23 and 24 where it says Trait1, Trait2,.....Trait14. If you want the trait included in the Result sheet either directly or in a calculated form you should also change the label on the tpResult, and insert the formula on the tpMaster sheet. For example if we want to include a trait: Insect Damage on a scale of 1-9

Step one: On **tpFieldbook** in row **23** and **25**, modify the Trait2 to Insect Damage and in row **20** and **21** set the lower and upper limits to 1 and 9 respectively.

20	LowerLimit						1	
21	UpperLimit						9	
22								
23	Rep	Bloc	Plot	Entry	Name	Trait1	Insect Damage	Trait3
24								

Figure 53 Modify a placeholder on tpFieldbook e.g. Trait2

Step two: On **tpResults** in row **20** and **21**, modify Trait 2 to Insect Damage

Step three: On **tpMaster**, enter the formula for the trait under **mTrait2**. In our case it is simply =tpFieldbook!A125 , which means the value is simply copied over. If you want to

=tpFieldbook!A125				
D	E	F	R	S
Entry	Row	Col	mTrait1	mTrait2
				0.00

Figure 54 Insert formula in Master sheet

make more complicated calculations look at the other formulas on the Master sheet, and you can probably find one that shows you how to do it. Note, if you use a value such as Plant Density or Plot size from the Installation sheet, you typically want to make it as a fixed reference (by adding \$ in front of the row and column reference e.g. \$A\$1), so that when it is copied down in the Master sheet you maintain the correct reference. Again, you may need help from an Excel expert. If you have problems with the formula get help from someone with good knowledge of Excel formulas.

Note: It is important that you insert the formula in exactly the same placeholder trait on the Master and the Result sheets, e.g. use mTrait2 and Trait2, as the analysis automatically put the Results in the same order as on the Master sheet. But the relation to the Fieldbook sheet is only via the formula on the master sheet. You can for example

Insert a new trait to be calculated without new observations

To insert a new calculated trait you simply insert the trait on the tpResult and tpMaster as described in step 2 and 3 above. You do not need to insert it on the tpFieldbook unless you also have something to observe or measure in each plot.

4.3.2.2 Changing the Result and Master sheet

The Result and Master sheets are linked by the analysis, and it is crucial that the order of the columns is exactly the same on both sheets, which means if you change something on the Result sheet, you will probably also have to change the same column in the Master sheet.

Step One: On **tpResults** in row **20** and **21** modify the placeholder e.g. Trait 2 is modified to Insect Damage

Step two: On **tpMaster** the formula is entered for the trait in the same placeholder, e.g. **mTrait2**.

See also above example on modifying Fieldbook for full example.

4.3.2.3 *Changing the General, Installation, Field, Weather_data, and Crop_Management sheets*

On these sheets you should enter any variable that does only change infrequently within your breeding program. Especially on the General and Installation sheets you may identify variable that are the same in all your trials such as: Institution, Leader, and Country.

If you do not need some of the variables you can hide the rows, but should not delete them. If you need to add new variables you can do so below the existing ones.

4.3.3. Steps to saving changes to trial template

Once you have done the desired modifications to the Trial Template you must save the changes, and to do this **you must use Update Template Settings**. If you simply click Save, this will not work.

The update process involves a series of steps and allows you to do additional changes. In the beginning it is probably a bit confusing, but you can **simply click OK or Yes** to go to the next step, and not do any additional changes.

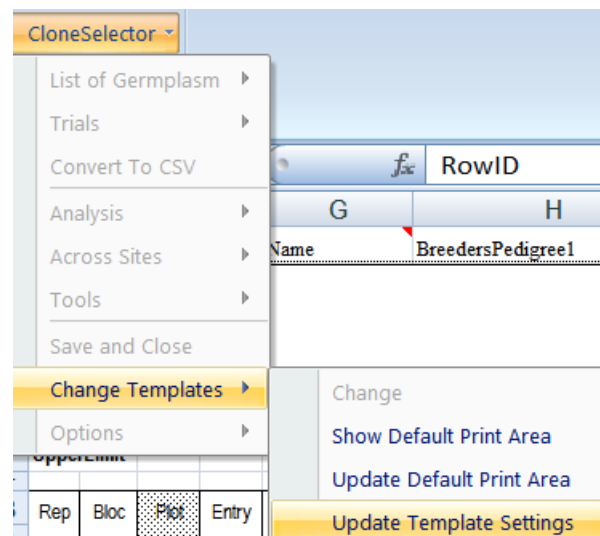
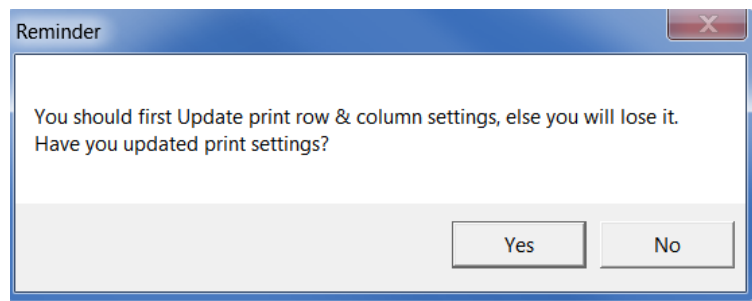


Figure 55 Use Update Template Settings to save changes

First you get a reminder that you must Click Update Default Print Area if you have changed which columns are visible. **Click Yes**, and you can move on.



Next dialog is **Trial Options**. You can here change the position of the data on the Fieldbook and Results sheets. **You should NOT make any changes on this form. Click OK to move on.**

In the **Trait Limits dialog** you can set the **Lower** and **Upper** values that are acceptable on the **Result sheet**. You can scroll down to see more traits. When you are satisfied with the ranges **click OK** and **wait**.

Your trial template is now being updated and it will close once the update is finished. **Wait until the template closes by itself.**

Test the modification of the trial template by creating a new trial.

5. Installation of CloneSelector

Note: We hope to be able in the future to provide an automated install for both RExcel and CloneSelector, but at the moment it is a bit complicated, especially if you do not have Internet.

5.1 Installing RExcel

CloneSelector requires RExcel to be installed, and you cannot run the statistical analysis if that is not the case.

5.1.1. Good Internet or copy of RandFriends and some Internet available: Easiest option is using RandFriends

Note: This is a download of 280 Mb, and may take a long time.

Note also: **The computer must have Internet connection** when doing the install or else the install will fail.

Go to:

<http://rcom.univie.ac.at/download.html#RAndFriends>

and click on Download **RAndFriendsSetup2122V3.1-13-1-64inc** . Note the version number may have changed a little.

Simply follow default installation.

5.1.2. No Internet: Install R, required components, and RExcel individually, but it is a bit complicated

To do this you must obtain a copy of all the R and RExcel files e.g. on USB stick, CD, or similar. The files required are:

1. R-2.12.2-win.exe
2. statconnDCOM.latest.exe
3. rcom_2.2-3.1.zip
4. rscproxy_1.3-1.zip
5. RExcelInst.latest.exe

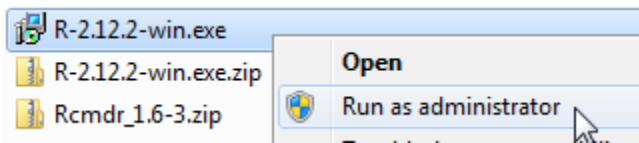
Note: You may need help from your IT support to do this manual install.

Note 2: You will need the Administrative privileges to your computer to do this process. Ask your IT support.

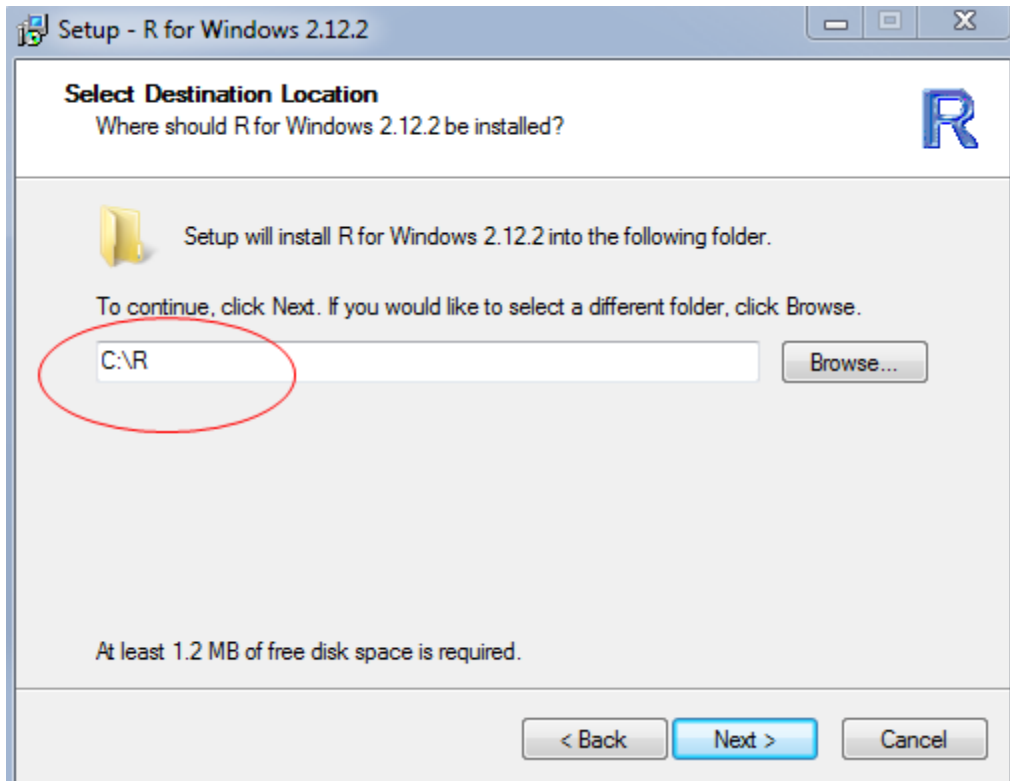
5.1.2.1 Step 1 Install R

1. Unzip **R-2.12.2-win.exe.zip**

2. Run **R-2.12.2-win.exe** as Administrator (You right-click on file and choose Run as Administrator)



3. Accept the default installation options until the **Select Destination Location**, here you must change the location to **C:\R** . This is important as Windows security will prevent you from installing other components if you leave it in Program Files



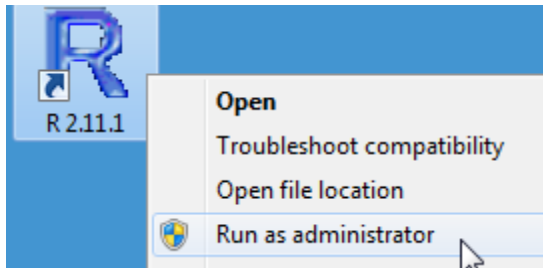
4. Accept the default for the rest of the installation

5.1.2.2 Step 2: Install rscproxy and rcom

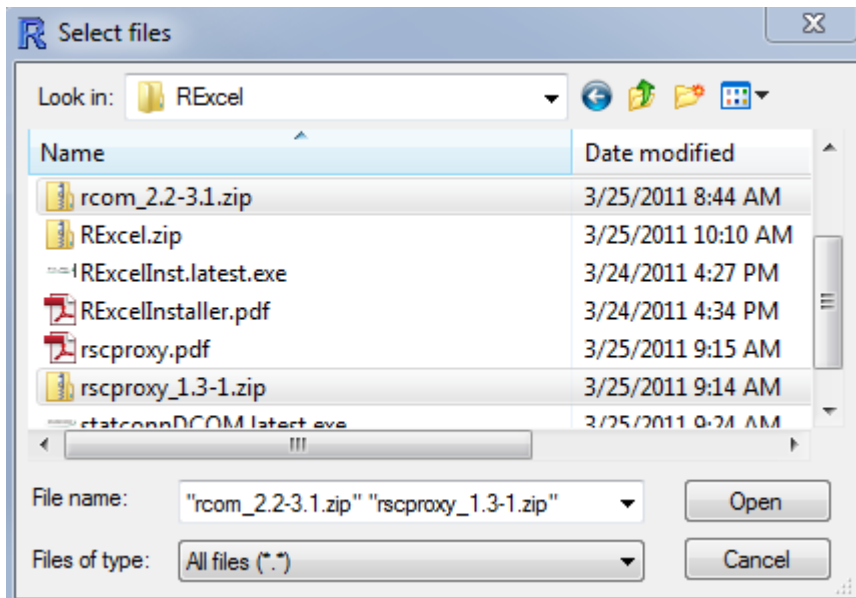
To do this step you must **Run R as Administrator**. See step 1 for running as Administrator. Verify that R has not been installed inside Program files in step 1 as this may cause problems.

1. Download from the SweetpotatoKnowledge portal the **RExcel.zip** file, and unzip this on your computer.

2. **Right-click on the R icon** on the desktop and choose **Run as Administrator** . You will be asked to give permission for program to make changes, Click **Yes**.



3. In the R window Click Packages menu, and select the menu Install package(s) from local zip files....
4. In the **Select files dialog** navigate to the location where you **unzipped RExcel folder**, and select the zip files **rcom_2.2-3.1.zip** and **rscproxy_1.3-1.zip** (use Ctrl+click for the second file). With both files selected Click **Open**



5. In the R Console you should see the messages: Package: 'rcom' successfully unpacked.... And package 'rscproxy' successfully unpacked.... If you get a warning, you are probably not running R as administrator or you have installed it in Program Files and windows may have blocked the install.
6. You must now Register the rcom in Windows: to do this enter in the R Console the commands and press Enter after each command:

```
library(rcom)
comRegisterServer()
comRegisterRegistry()
```

7. **Exit RGui**, and Click **No** when asked to Save workspace image

5.1.2.3 Step 3: Install statsconnDCOM

1. In Windows Explorer **double-click on statsconnDCOM.latest.exe** (you may not see the exe extension)
2. **Click Yes** to allow to make changes
3. **Accept License agreement**
4. In **Select Destination Location** make sure to change the Program Files to R i.e. location should be **C:\R\statsconn\DCOM**
5. Accept default installation in next dialogs, and in Ready to install **Click Install**
6. You should end up with a dialog **Completing the statsconnDCOM Setup Wizard**, and **Click Finish**

5.1.2.4 Step 4: Install RExcel

1. In Windows Explorer **double-click on RExcelInst.latest.exe** (you may not see the exe extension)
2. **Click Yes** to allow changes
3. **Accept License agreement**
4. In **Select Destination Location** make sure to change the Program Files to R i.e. location should be **C:\R\RExcel**
5. Accept default installation in next dialogs, and in Ready to install **Click Install**
6. You may now get a dialog about R version, **Click OK**
7. You will also get a dialog about Excel being hidden during install, **Click OK**
8. And you will get a dialog about multiple users of Excel, **Click OK**
9. And you will get a dialog about Help in RExcel, **Click OK**
10. You should end up with a dialog **Completing the RExcel Setup Wizard**, and **Click Finish**

5.1.2.5 Step 5: Check RExcel working

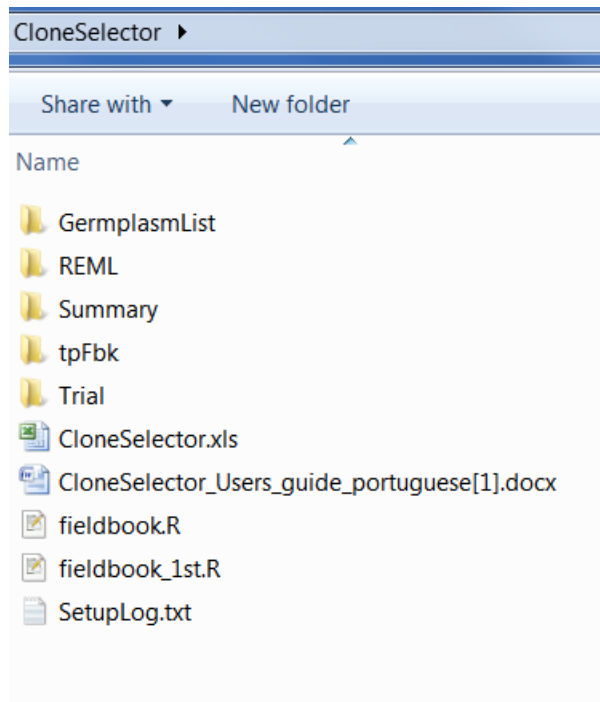
1. Start **Excel**
2. **Click on Add-Ins** (Excel 2007). In Excel 2003 you have a separate RExcel menu
3. **Click RExcel** drop down
4. **Click Start R**
5. After a while click RExcel again and you should now **see almost all menus active**

You are now ready to run your analysis in CloneSelector

5.2 Installing CloneSelector

CloneSelector is a collection of Excel sheets and templates, and does not require an install as such, you can simply copy it on to your computer.

1. Download the CloneSelector.zip, and unzip the folder, you should now have a folder called CloneSelector with some archives and subfolders similar to:

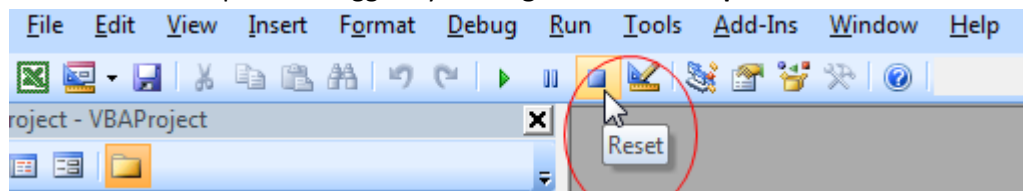


2. **Copy the CloneSelector folder to C:**, so that the direction of the folder is C:\CloneSelector . You may want to put it e.g. on the D drive, or similar, but in that case consult section “Setting up the location of CloneSelector files and templates” in this guide.
3. **Double click on CloneSelector.xls inside the folder C:\CloneSelector** to open the applications. If you get an error message regarding a missing reference see below how to solve it.

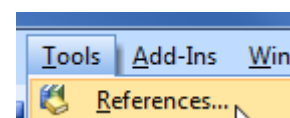
5.2.2. Solving Reference Error problem in Excel 2007 or 2003

RExcel for Office 2003 is different from RExcel in Office 2007, and this may cause a Reference problem when trying to start CloneSelector. The solution is to remove the RExcel 2003 reference and put the correct office 2007 or vice versa:

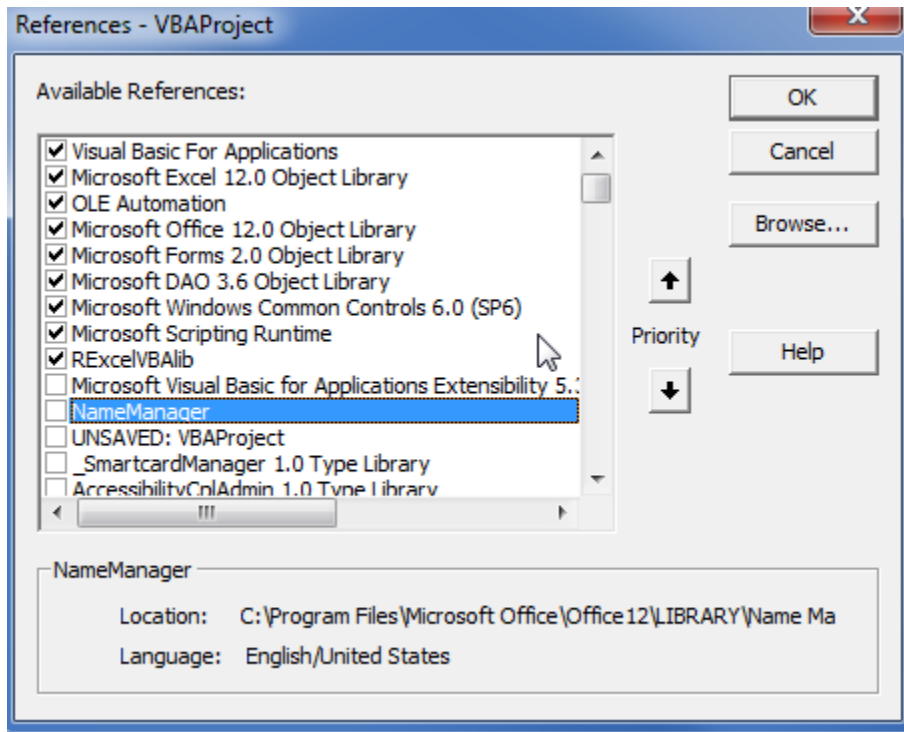
1. When you receive a **message that some library or reference** is missing, say **Yes** to start **debugger**.
2. You must then stop the debugger by **clicking on the Reset square in the toolbar**.



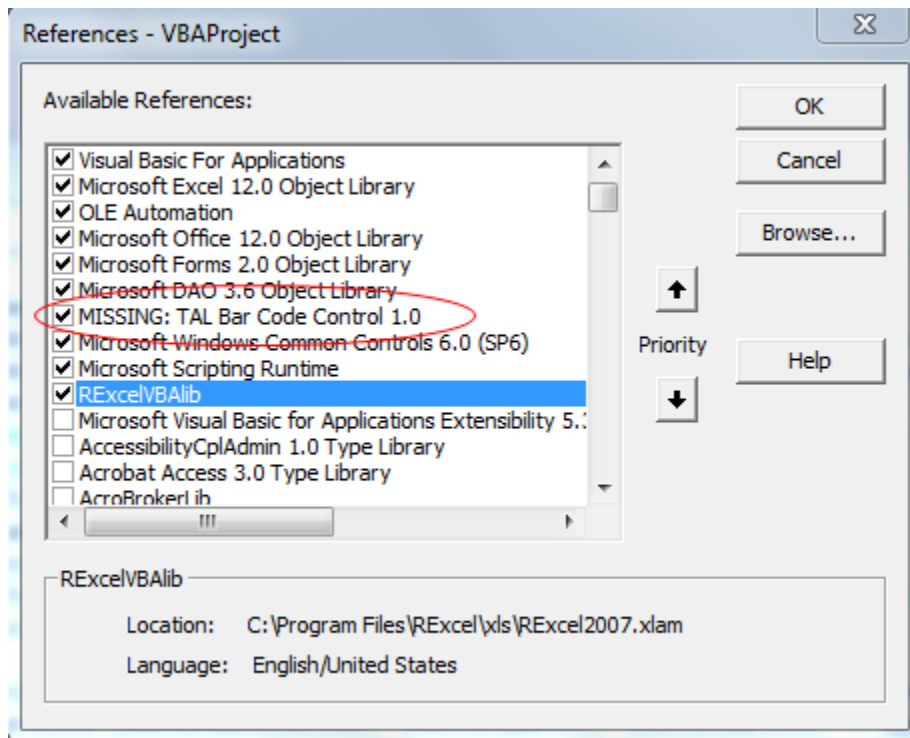
3. Then click **Tools -> References**



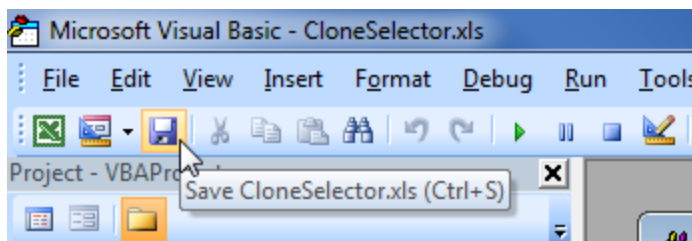
4. Your References on Office 2007 should look like:



5. **RExcelVBAlib** is called something else on Office 2003, and you may have to **'untick'** the REExcel reference that is **MISSING** and **tick the correct REExcelVBAlib**. Or as the Example below you have a missing TAL Barc Code Control, which you should 'untick'.



6. Once done click **OK** to close Reference dialog
7. **Save CloneSelector** in the VBA window



8. **Close Excel**
9. **Open Excel**
10. **Open CloneSelector**, as indicated in the section “How to start CloneSelector” and now you should not get the reference error.

6. Annex A: Abbreviations for Potato Fieldbook

Trait in Fieldbook	Abbreviation	Trait in Fieldbook	Abbreviation
Plants Planted	NOPS	F. Weight Tub. Samp 1	FWS1
Plants Emerged	NOPE	F. Weight Tub. Samp 2	FWS2
Plant Uniformity	PUNI	D. Weight Tub. Samp 1	DWS1
Plant Growth habit	PGH	D. Weight Tub. Samp 2	DWS2
Plant Vigor	PVIG	Trait 9	T9
Flowering Degree	FLOD	Tub. Weight Air	TWA
Senescence	SEN	Tub. Weight Water	TWW
Trait1	T1	Trait10	T10
Trait2	T2	Chipping Color	CHCO
Trait3	T3	Trait11	T11
Late Blight 1	LB1	Initial Weight Sample 1	IWS1
Late Blight 2	LB2	Initial Weight Sample 2	IWS2
Late Blight 3	LB3	Final Weight Sample 1	FWS1
Late Blight 4	LB4	Final Weight Sample 2	FWS2
Late Blight 5	LB5	Trait12	T12
Late Blight 6	LB6	External Appearance	EXAP
Late Blight 7	LB7	External Color	EXCO
Late Blight 8	LB8	Internal Color	INCO
Late Blight 9	LB9	Texture Outside	TXOU
Late Blight 10	LB10	Texture Inside	TXIN
Late Blight 11	LB11	Trait13	T13
Late Blight 12	LB12	Cook time Sample 1	COT1
Trait4	T4	Cook time Sample 2	COT2
Trait5	T5	Appearance Whole tuber	APWT
Plants Harvested	PH	Appearance Mashed sample	APMS
# Mark. Tub Cat I	MTIN	Texture	TX
Mark. Tub Cat I Weight	MTIW	Off-flavor Mashed sample	OFMS
# Mark. Tub Cat II	MTIIN	Sloughing Mashed sample	SLMS
Mark. Tub Cat II Weight	MTIIW	Discoloration Whole tuber	DCWT
Non-Mark. Tub. Num	NMTN	Trait 14	T14
Non-Mark. Tub. Weight	NMTW	Notes1	N1
Tuber Appearance	TUBA	Notes2	N2
Tuber Uniformity	TUBU	Notes3	N3
Tuber Size	TUBS	Notes4	N4
Size Stolons	STOL	Notes5	N5
Selected Clones	SECL	Notes6	N6
Trait6	T6	Notes7	N7
Trait7	T7	Notes8	N8
Trait8	T8	Notes9	N9
		Notes10	N10
		Other	O1