# Tutorial of the Breeding Planner (BP) for Marker Assisted Selection for pyramiding multiple genes (MAS)

BP system consists of three tools relevant to molecular breeding.

- MARS: Marker Assisted Recurrent Selection
- MABC: Marker Assisted Backcrossing
- MAS: Marker Assisted Selection for pyramiding multiple genes
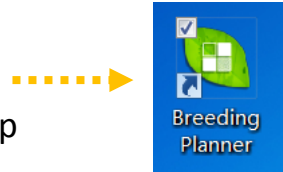
- This tutorial is designed for MAS
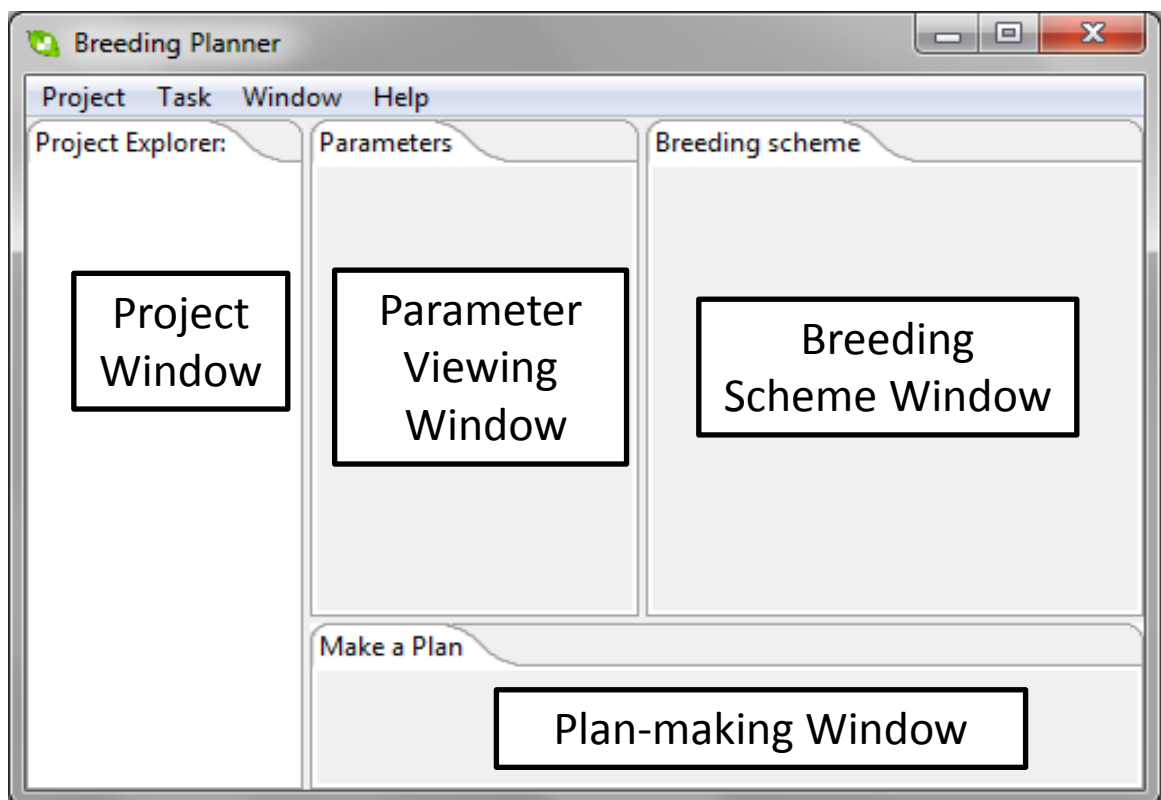
November  2013

# Open the Breeder Planner (BP) software

1. **Open the software:** The BP software can be open by double click the **software icon** in your computer desktop

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   Breeding Planner

2. **Overview of the software.**
   The screen is split into four windows.
   - **Project Window:** List all molecular breeding programs you have planned. Three distinct breeding programs can be considered: MARS, MABC and MAS.
   - **Parameter Viewing Window:** You can view your breeding parameters in this window.
   - **Breeding Scheme Window:** Once the breeding parameters are specified, a breeding flowchart will be demonstrated in this window.
   - **Plan-making Window:** You can select the current stage/generation of your breeding programs in this window. A detailed plan for the near future will be made by the BP system.

   **Breeding Planner**

   Project   Task   Window   Help

   | Project Explorer: | Parameters | Breeding scheme |
   |---|---|---|
   | Project Window | Parameter Viewing Window | Breeding Scheme Window |

   Make a Plan

   Plan-making Window
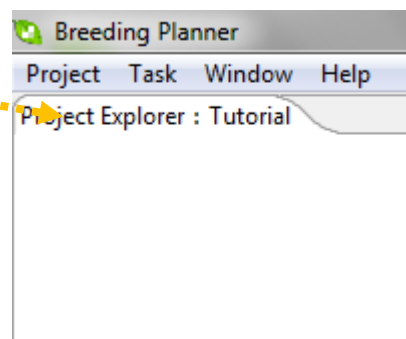
# Build a new project

### 3. Build a new project
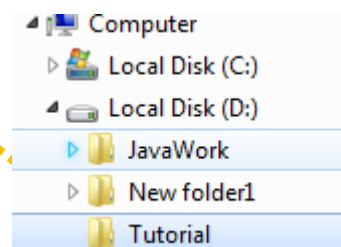- Click **Project** menu
- Choose **New Project**
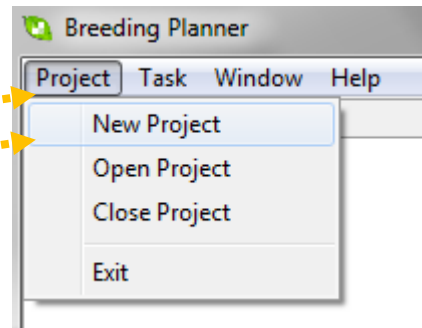
- Specify Project Name (Tutorial for example) and Project Path (D:\ for example)
- Click **Finish** to complete
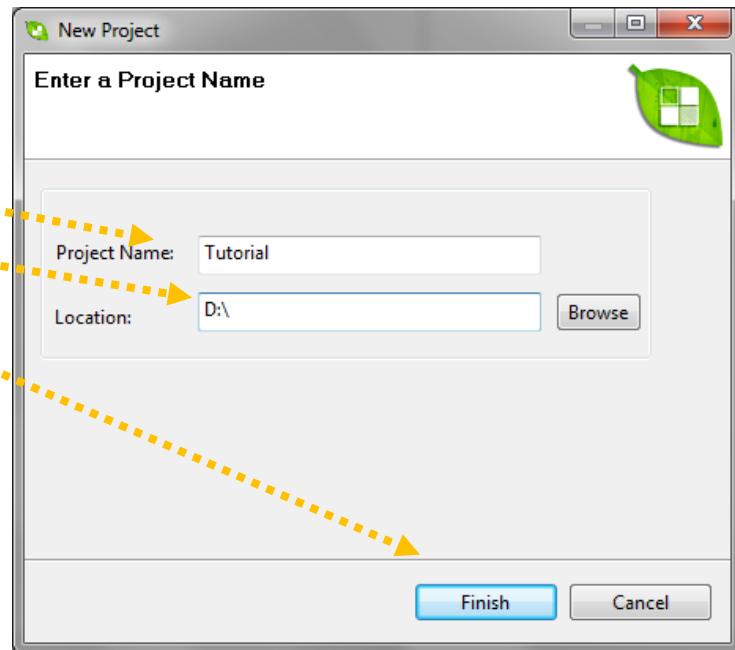
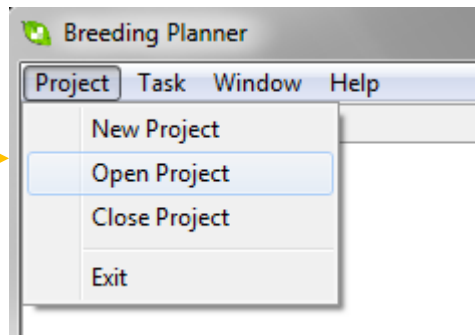New project is displayed in the **Project Window**

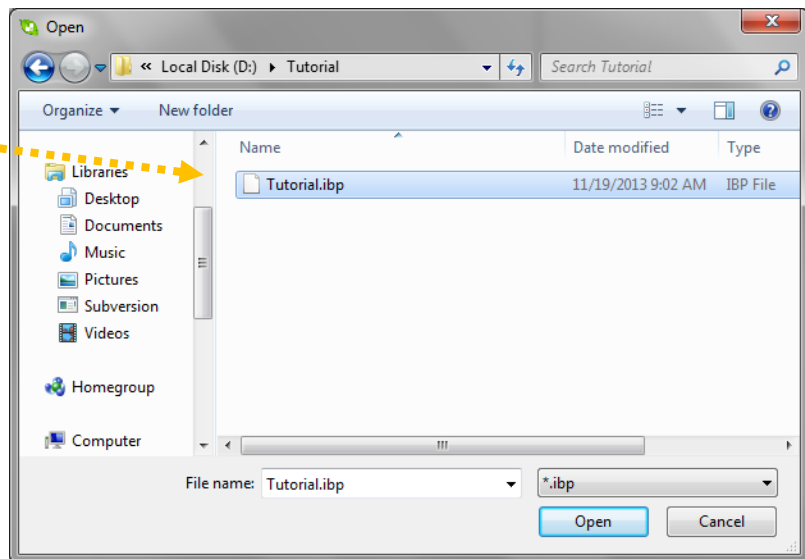All inputs and outputs will be automatically saved in path of the project **(D:\Tutorial\... for example)**

# Open an existing project

**4. Open an existing project**

- Click **Project** menu
- Choose **Open Project**



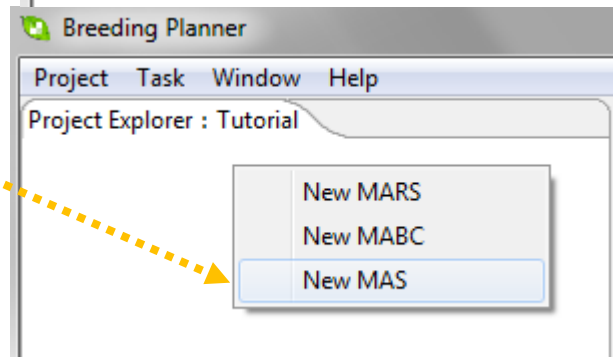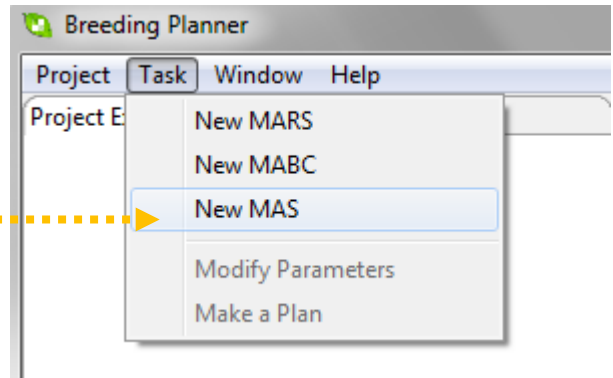- Choose an existing project in your computer



- **Please Note:** The BP system is project-based. When you first use the system, you need to build a new project first. Then you can make various breeding programs. When you leave the system, the system automatically save the jobs you have done. The next time, you can start from a new project, or from an existing project.

# PMAS Tutorial: Start a new MAS breeding program

## 5. Make a new MAS program to the newly-built project

- Click **Task-> New MAS**
- Or right click in the blank area of project explorer, then choose **New MAS**

- You can use either way to make a MAS program
    - Import parameters from an external file
    - Or specify the initial parameters by hand

- There are two pages of input parameters.

- **Note:** two alleles at each locus must be present in both parent. Otherwise, this locus is irrelevant to breeding.

# PMAS Tutorial: Parameters required to define a MAS program

Users have to specify a set of parameters before a MAS scheme can given by the system. Below are more details on the required parameters.

**1. Researcher information**
> Country;
> Researcher's name;

**2. Species information**
> Crop species: Select one crop species from Cowpea, Rice, Wheat, Maize, Groundnuts, and Cassava
> Expected seeds per plant (or propagation rate) **(more on the next page)**

**3. Greenhouse/offseason**
> Length of each season (months).
> **Note:** We assume the crop can be grown across the whole year under the Greenhouse condition. That is, the next season can start in the same month when the previous season is harvested. So the planting time for each season is not needed.

**4. Field condition**
> Seasons per year: the number of seasons per year, select from 1-3
> 1st season starts in: select a month
> 2nd season starts in: select a month, after the end of the 1st season
> 3rd season starts in: select a month, after the end of the 2nd season
> **Note:** The crop cannot be grown across the whole year under the Field condition. So if multiple seasons are possible, the system asks for the planting time for each season.

**5. Growing condition**
> Parental generation starts in: select the start time of the parental generation
> Early generation growing condition: select one case "Greenhouse/offseason" or "Field condition"

**6. Number of genes**
> Number of unlinked genes to be combined: 2-10

**7. Source of favorable genes:** select the favorable genes in the two parents

## Minimum and maximum numbers of seeds per plant for each crop under optimum or normal conditions

| Crop | Minimum number | Maximum number | Median (used as default in Breeding Planner) |
| --- | --- | --- | --- |
| Cowpea | 10 | 300 | 50 |
| Rice | 50 | 300 | 200 |
| Wheat | 50 | 250 | 150 |
| Maize | 50 | 500 | 200 |
| Groundnuts | 30 | 200 | 80 |
| Cassava | 10 | 100 | 50 |

**Notes**:

- Expected seeds per plant in Breeding Planner will be used to calculate if there are enough seeds for phenotyping. If not, additional seed increase (by selfing) will be requested.

- The user input must fall into the min-max range for the selected crop! Otherwise, when the input number is smaller than the minimum number, the minimum number will be assumed. When the input number is greater than the maximum number, the maximum number will be assumed.

- The number of seeds required is calculated from settings for "Multi-locational phenotyping". Say, when genotyping is conducted in F2, multi-locational phenotyping is only possible when each F2 plant can give enough seeds. Otherwise, phenotyping will be delayed until the required seeds are produced.

# PMAS Tutorial: The interface

## 6. Overview of the MAS functionality:

There are four windows in MAS functionality

- **Project Window:** List all molecular breeding programs you have planned. Three distinct MB programs can be considered: MARS, MABC and MAS.
- **Parameter Viewing Window:** You can view your breeding parameters in this window.
- **Breeding Scheme Window:** Once the breeding parameters are specified, a breeding flowchart will be demonstrated in this window.
- **Plan-making Window:** You can select the current stage/generation of your breeding programs in this window. A detailed plan for the near future will be made by the BP system.

When the required parameters are set in the Parameter setting/viewing Window, the defined MAS breeding program is graphed in the Breeding Scheme/flowchart Window. A set of output files are listed in the Project Window.

# PMAS Tutorial: Modify your parameters

## 7. Modify Parameters

- Right click the MAS1 folder, then choose **Modify Parameters**
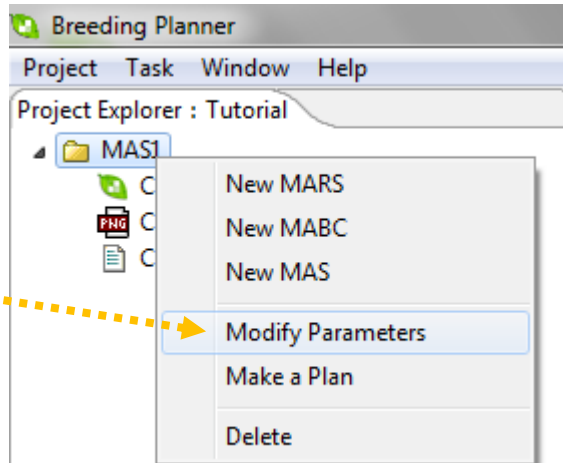


- Or click **Task-> Modify Parameters**



- You may modify the parameters in the Dialog Window, and then click Finish button to save your modifications. The breeding scheme will be automatically modified.

# PMAS Tutorial: The breeding scheme and documentation

## 8. View the flowchart
- It is in the right window  ┄┄┄┄▶
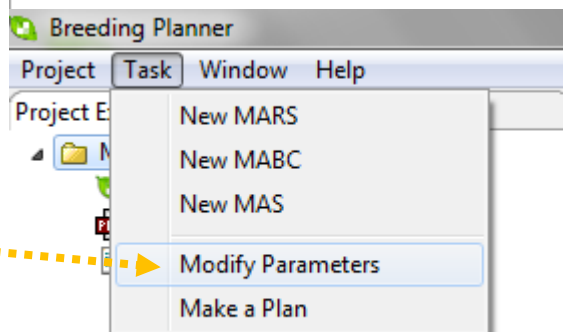
**Cowpea.png**

Parent 1 X Parent 2

Breeding documentation

F1

F2  Target selection   Enhancement selection

F3

F4

F5

F6   Target selection

**Homozygous selection:**
Genotype ++ at one locus will be selected.

**Enhancement selection:**
Genotype ++ and +- at one locus will be selected.
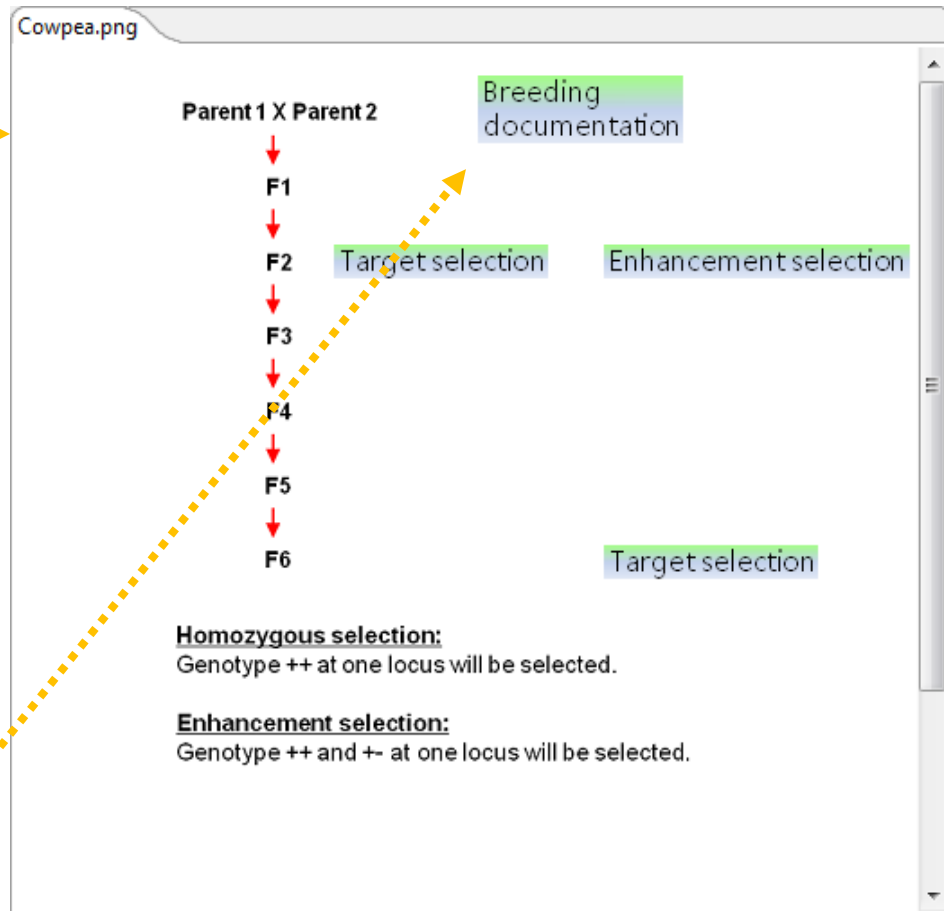
## 9. View breeding documentation
- Click the **Breeding Documentation** button
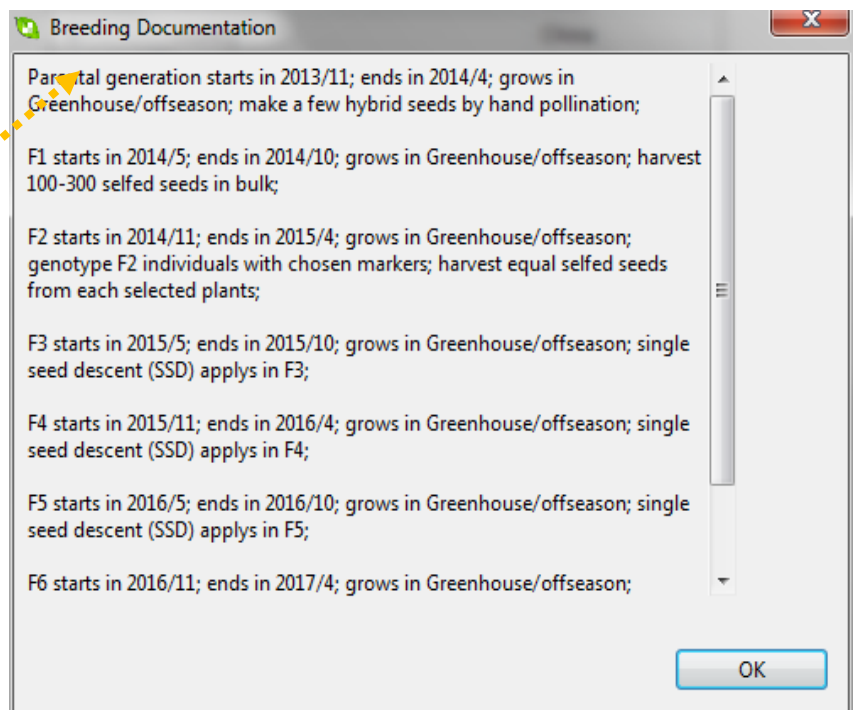
- **The Breeding Documentation** is in the pure text describing the whole flow of the MAS program.

**Breeding Documentation**

Parental generation starts in 2013/11; ends in 2014/4; grows in Greenhouse/offseason; make a few hybrid seeds by hand pollination;

F1 starts in 2014/5; ends in 2014/10; grows in Greenhouse/offseason; harvest 100-300 selfed seeds in bulk;

F2 starts in 2014/11; ends in 2015/4; grows in Greenhouse/offseason; genotype F2 individuals with chosen markers; harvest equal selfed seeds from each selected plants;

F3 starts in 2015/5; ends in 2015/10; grows in Greenhouse/offseason; single seed descent (SSD) applys in F3;

F4 starts in 2015/11; ends in 2016/4; grows in Greenhouse/offseason; single seed descent (SSD) applys in F4;

F5 starts in 2016/5; ends in 2016/10; grows in Greenhouse/offseason; single seed descent (SSD) applys in F5;

F6 starts in 2016/11; ends in 2017/4; grows in Greenhouse/offseason;

OK

# PMAS Tutorial: Additional information

**10. Additional information on the flowchart**

- Click **Target selection**

- The table for **Target selection** will be popped up to show the proportion of target genotype in F2 population



### Cowpea.png

Parent 1 X Parent 2

Breeding documentation

F1

F2 — Target selection — Enhancement selection

F3

F4

F5

F6 — Target selection

**Homozygous selection:**
Genotype ++ at one locus will be selected.

**Enhancement selection:**
Genotype ++ and +- at one locus will be selected.
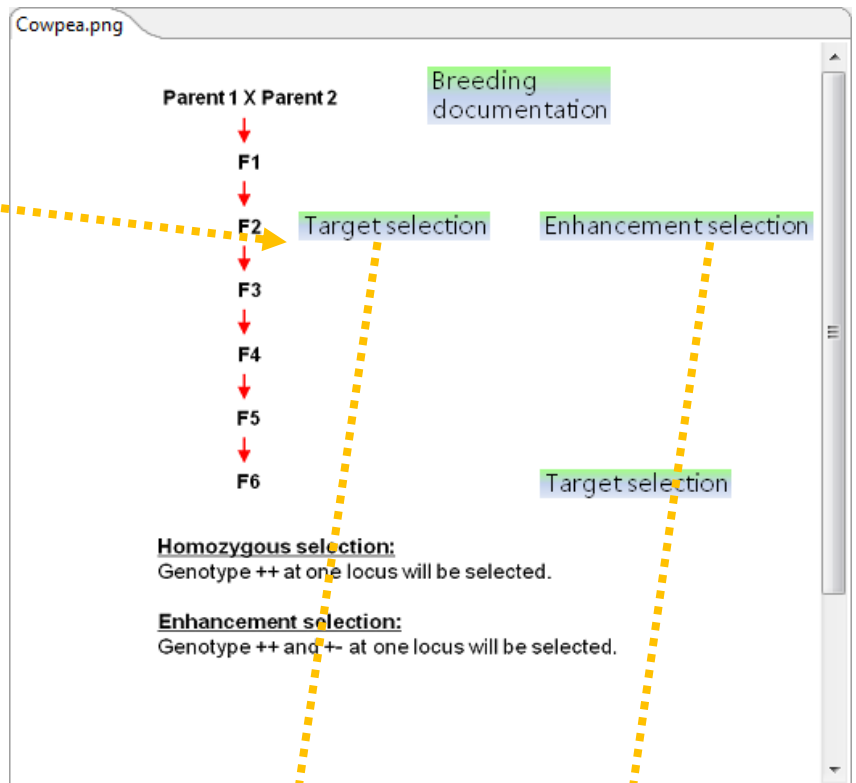
### Target Selection

| Proportion of target genotype in F2 population | | | | | | | | |
|---|---|---|---|---|---|---|---|---|
| Number of independent genes | | | | | | | | |
| 2 | 3 | 4 | 5 | 6 | 7 | 8 | 9 | 10 |
| 0.0625 | 0.01563 | 0.00391 | 0.00098 | 0.00024 | 6.1E-05 | 1.5E-05 | 3.8E-06 | 9.5E-07 |

- Click **Enhancement selection**

- The table for **Enhancement selection** will be popped up to show the proportion for enhancement selection

### Enhancement Selection

| Proportion for enhancement selection | | | | | | | | |
|---|---|---|---|---|---|---|---|---|
| Number of independent genes | | | | | | | | |
| 2 | 3 | 4 | 5 | 6 | 7 | 8 | 9 | 10 |
| 0.5625 | 0.42188 | 0.31641 | 0.2373 | 0.17798 | 0.13348 | 0.10011 | 0.07508 | 0.05631 |

# PMAS Tutorial: Additional information

- Click **Target selection**
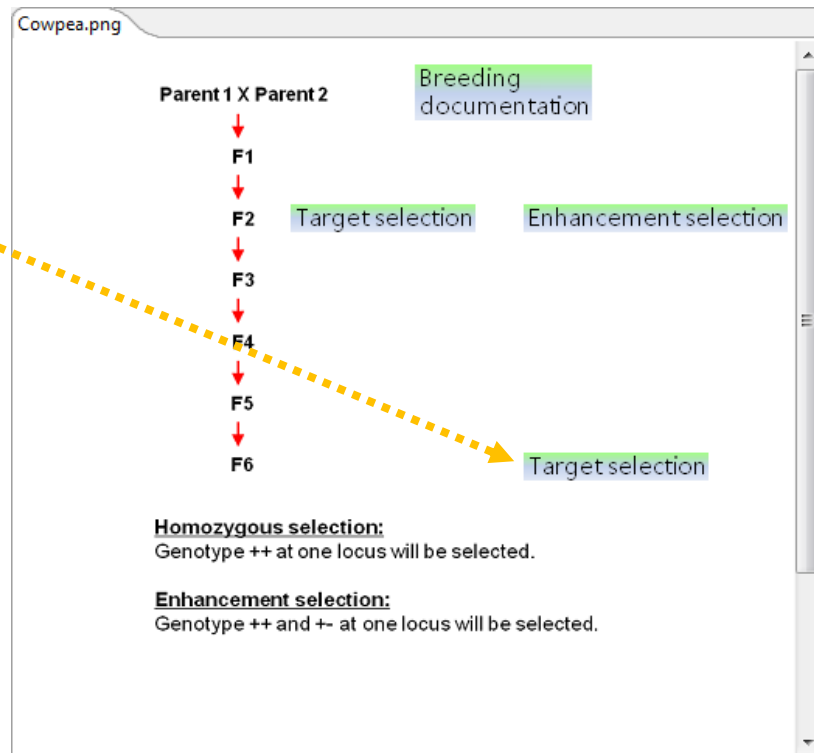


Cowpea.png

Parent 1 X Parent 2
F1
F2   Target selection   Enhancement selection
F3
F4
F5
F6   Target selection

**Homozygous selection:**
Genotype ++ at one locus will be selected.

**Enhancement selection:**
Genotype ++ and +- at one locus will be selected.

- The table for **Target selection** will be popped up to show the proportion of target genotype when enhancement selection is applied in F2 population.



Target Selection2

| Proportion of target genotype when enhancement selection is applied in F2 | | | | | | | | |
|---|---|---|---|---|---|---|---|---|
| Number of independent genes | | | | | | | | |
| 2 | 3 | 4 | 5 | 6 | 7 | 8 | 9 | 10 |
| 0.44444 | 0.2963 | 0.19753 | 0.13169 | 0.08779 | 0.05853 | 0.03902 | 0.02601 | 0.01734 |

OK

## 11. Make a plan

- Right click the **MAS** folder in the **Project Window**, then choose **Make a Plan**
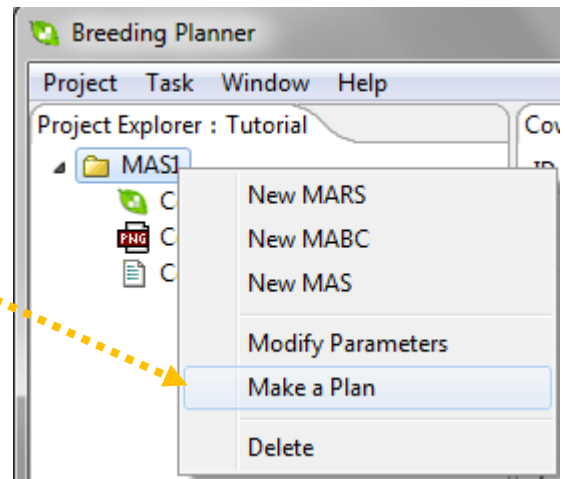
- Or click **Task-> Make a Plan**

- The window for making a plan will be initialized. Some dialog information will appear in the Plan-making Window.

**Make a Plan**

| Current status starts in | November, 2013 ⬍ | Select current status |
|---|---|---|
| | | 0. Select parental lines and prepare for planting ▾ |
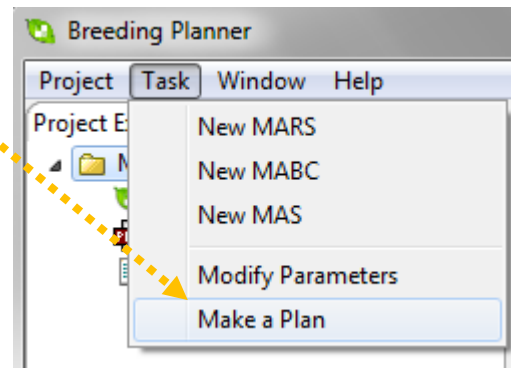
Make a Plan

# PMAS Tutorial: Tell the system where you are

- Tell the system when the current season starts. The system will know the current season is grown in Greenhouse or in Field from the breeding parameters you specified.

- Tell the system where you are by selecting:
  0. Select parental lines and prepare for planting
  1. Parental lines is growing
  2. F1 generation is growing
  3. F2 generation is growing
  4. F3 generation is growing
  5. F4 generation is growing
  6. F5 generation is growing
  7. F6 generation is growing

Make a Plan

Current status starts in     November, 2013

Select current status

0. Select parental lines and prepare for planting

Make a Plan

- Click the **Make a Plan** button to complete the on-going MAS breeding program.

- New window will show the breeding documentation for the remaining status, and the time to complete the MAS breeding program

> **Breeding Documentation**
>
> F1 starts in 2013/12; ends in 2014/5; grows in Greenhouse/offseason; harvest 100-300 selfed seeds in bulk;
>
> F2 starts in 2014/6; ends in 2014/11; grows in Greenhouse/offseason; genotype F2 individuals with chosen markers; harvest equal selfed seeds from each selected plants;
>
> F3 starts in 2014/12; ends in 2015/5; grows in Greenhouse/offseason; single seed descent (SSD) applys in F3;
>
> F4 starts in 2015/6; ends in 2015/11; grows in Greenhouse/offseason; single seed descent (SSD) applys in F4;
>
> F5 starts in 2015/12; ends in 2016/5; grows in Greenhouse/offseason; single seed descent (SSD) applys in F5;
>
> F6 starts in 2016/6; ends in 2016/11; grows in Greenhouse/offseason; genotype each family with chosen markers;
>
> The MAS scheme takes 3 years and 0 months.
>
> OK

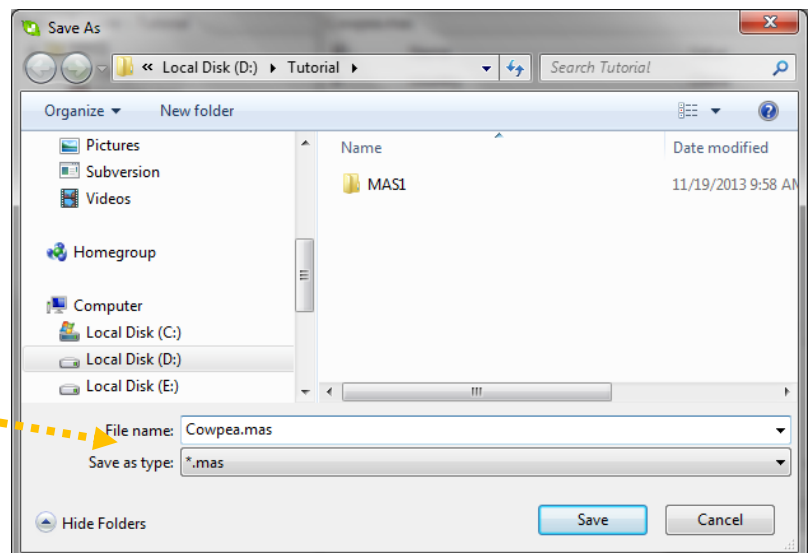## 12. Save the result files

- Right click the file name, and then select **Save As** to save the breeding documentation on your computer

> **Breeding Planner**
>
> Project   Task   Window   Help
>
> Project Explorer : Tutorial
>
> ▲ 📁 MAS1
>    - 🐸 Cowpea.m...          Save As
>    - PNG Cowpea.png
>    - 📄 Cowpea.txt
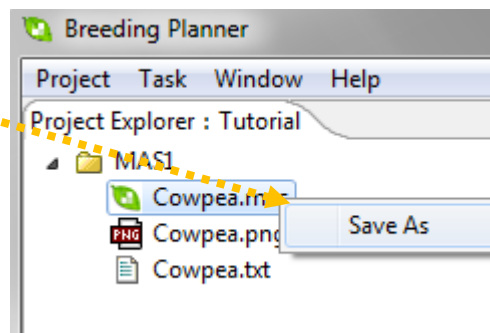
- Specify the path and rename of the output file

> **Save As**
>
> « Local Disk (D:) ▶ Tutorial ▶
>
> Organize ▼   New folder
>
> Pictures
> Subversion
> Videos
>
> Homegroup
>
> Computer
> Local Disk (C:)
> Local Disk (D:)
> Local Disk (E:)
>
> Name: MAS1   Date modified: 11/19/2013 9:58 AM
>
> File name: Cowpea.mas
>
> Save as type: *.mas
>
> Hide Folders   Save   Cancel

# BP-MAS Tutorial: The contact information

- Any comments or suggestions? You may contact any one on the BP development team
    - Dr. Jiankang Wang, CIMMYT China and CAAS, wangjiankang@caas.cn or jkwang@cgiar.org
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