

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

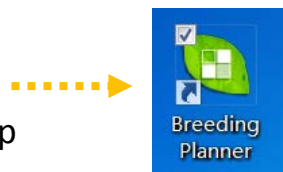
August 2013



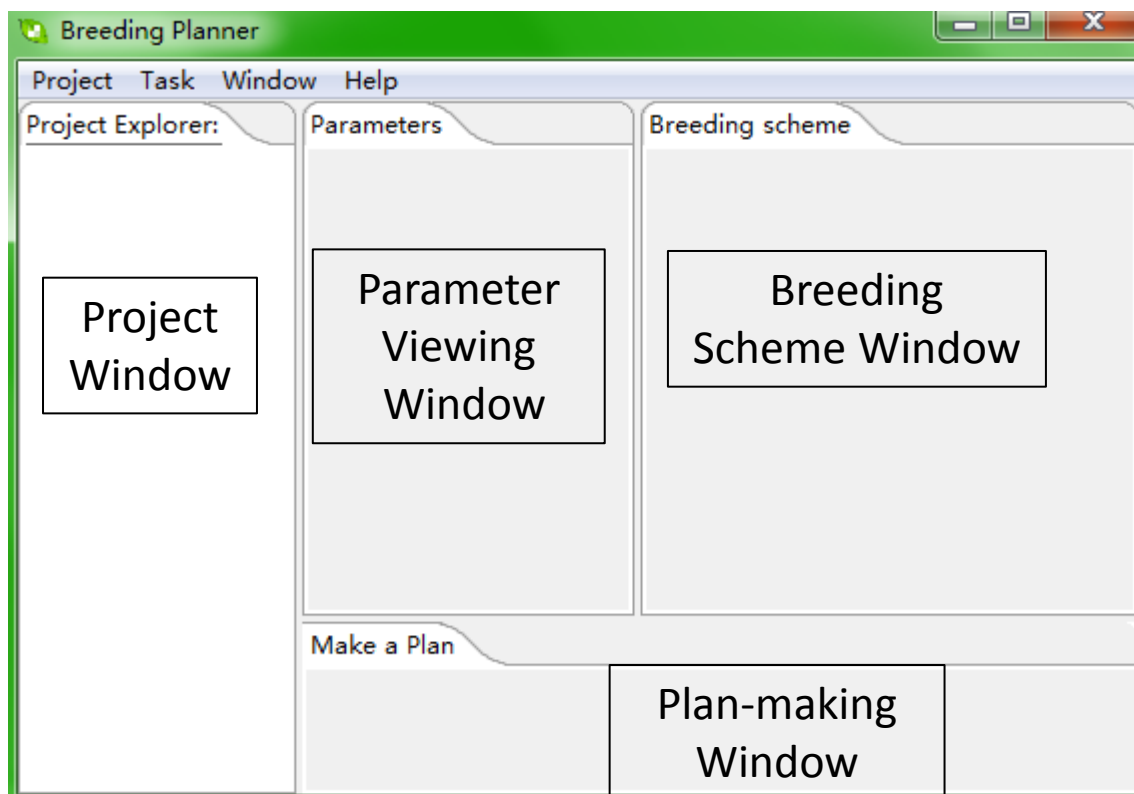
Please make sure you have installed Java jdk 1.6 or 1.7 in your computer!

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



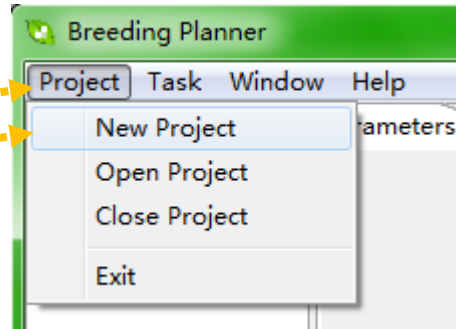
2. **Overview of the software.** The screen is split into four window.
 - **Project Window:** List all molecular breeding programs you have planned. Three distinct breeding programs can be considered: MARS, MABC and MAS.
 - **Parameter Viewing Window:** You can view your breeding parameters in this window.
 - **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.



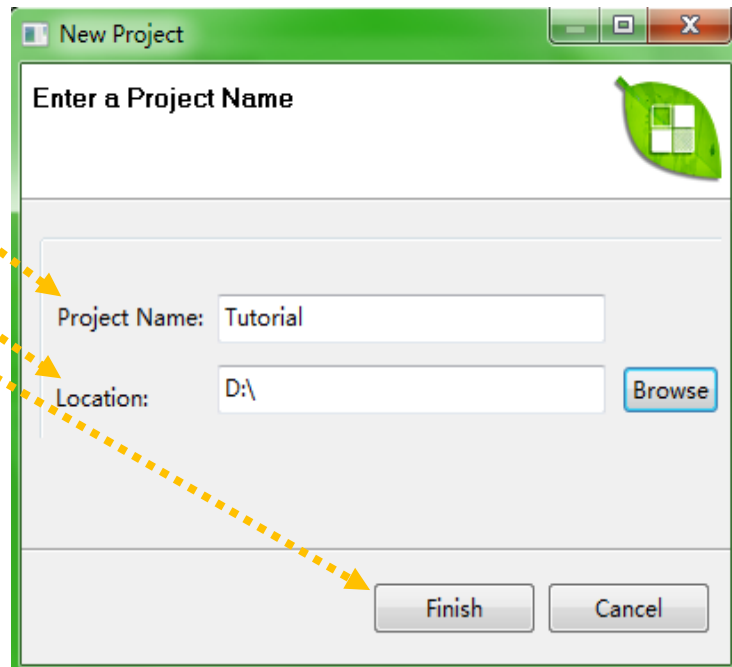
Build a new project

3. Build a new project

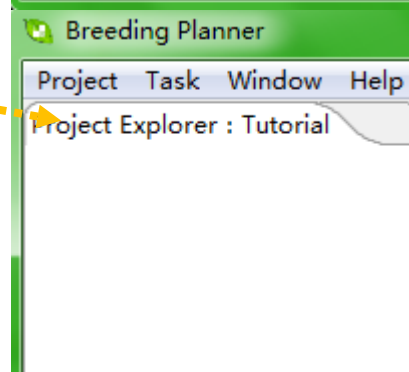
- Click **Project** menu
- Choose **New Project**



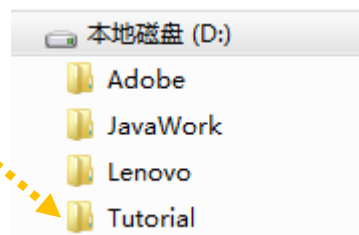
- Specify Project Name (Tutorial for example) and Project Path (D:\ for example)
- Click **Finish** to complete



New project is displayed in the **Project Window**



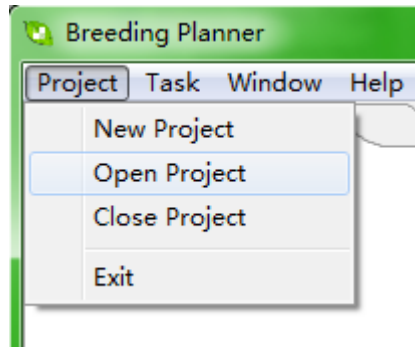
All inputs and outputs will be automatically saved in path of the project (**D:\Tutorial\...** for example)



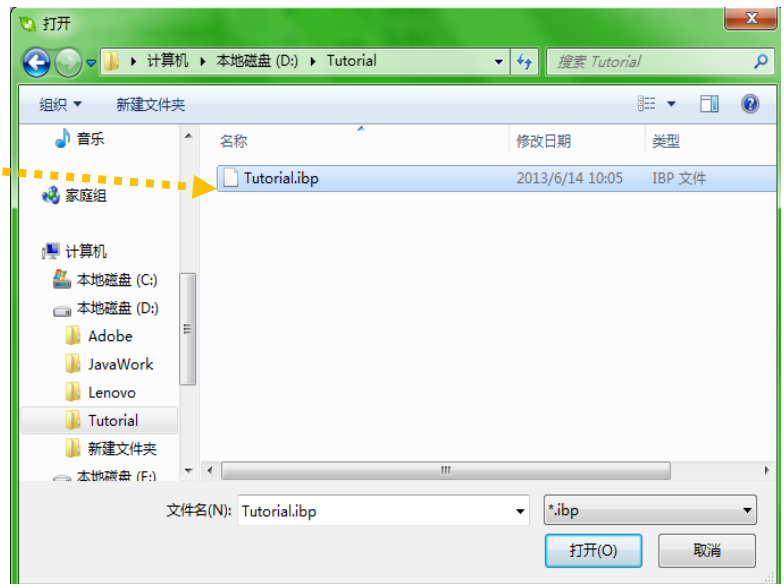
Open an existing project

4. Open an existing project

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



- Choose an existing project in your computer →

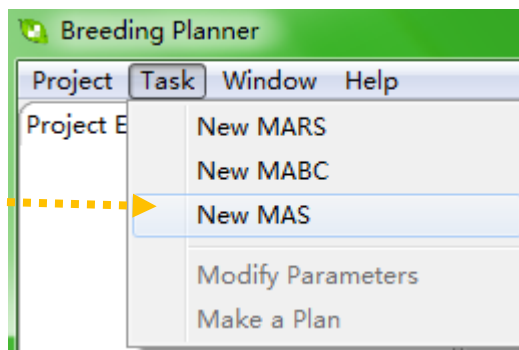


- **Please note:** The BP system is project-based. When you first use the system, you need to build a new project first. Then you can make various breeding programs. When you leave the system, the system automatically save the jobs you have done. The next time, you can start from a new project, or from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

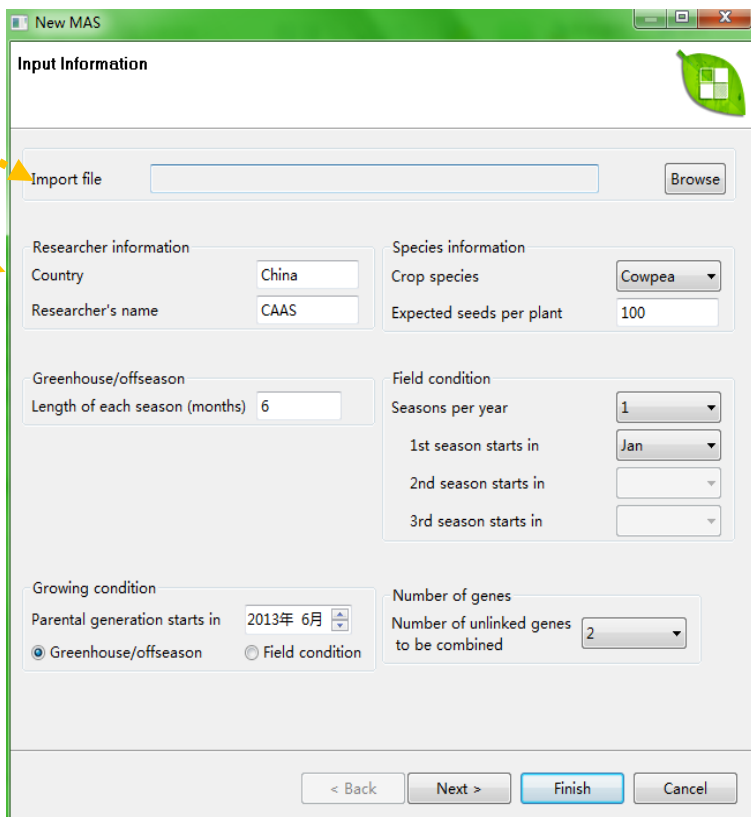
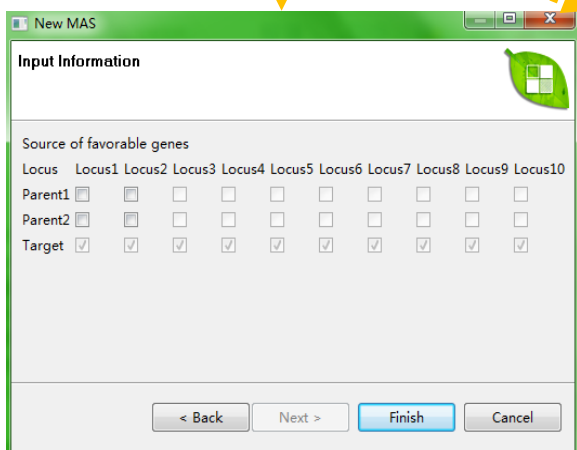
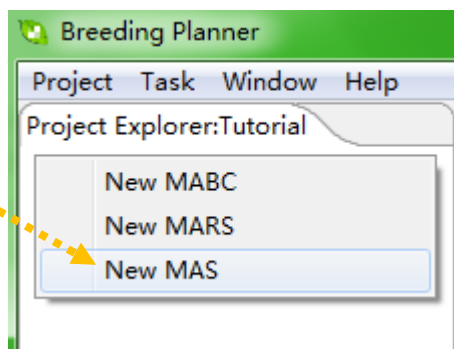
PMAS Tutorial: Start a new MAS breeding program

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 MABC scheme can be 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:

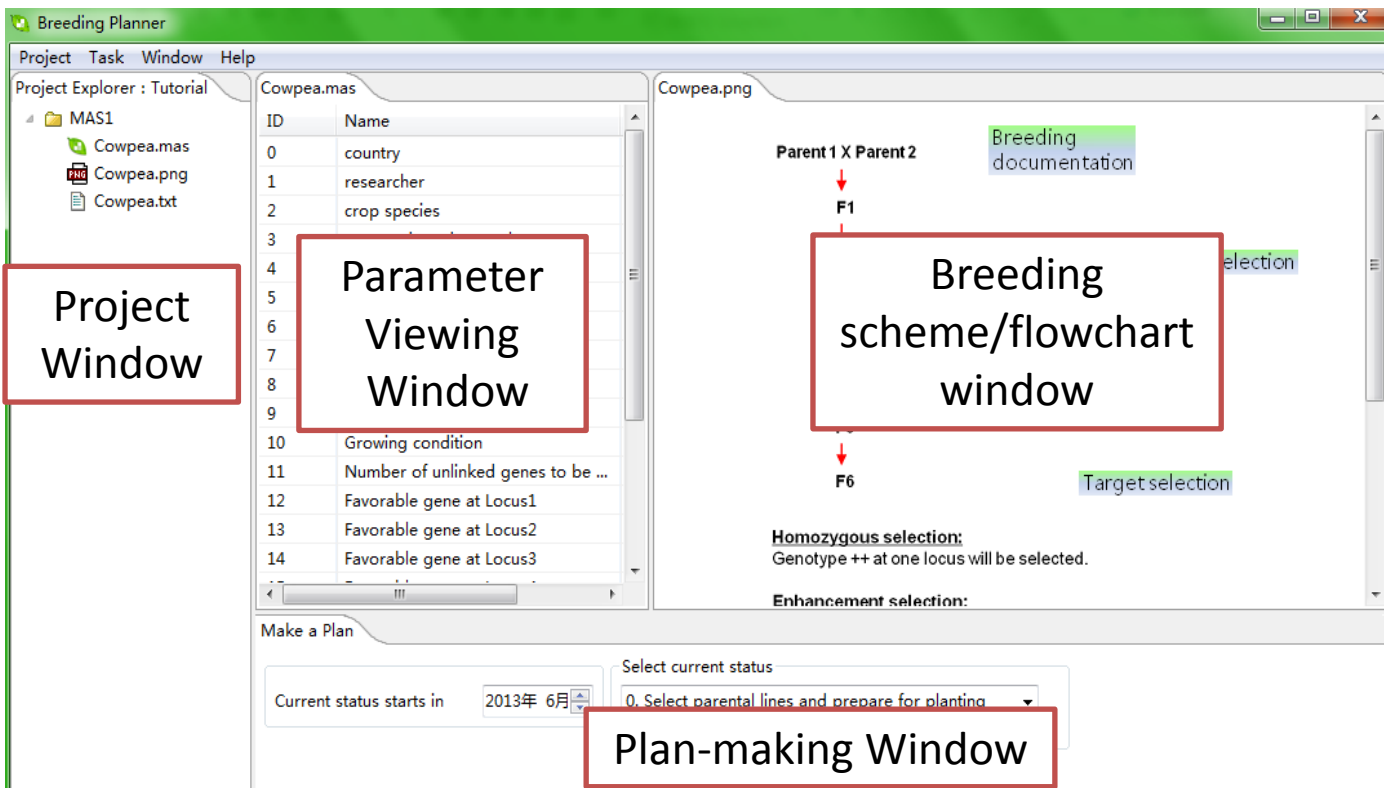
- Expected seeds per plant in Breeding Planner will be used to calculate if there are enough seeds for phenotyping. If not, additional seed increase (by selfing) will be requested.
- The user input must fall into the min-max range for the selected crop! Otherwise, when the input number is smaller than 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 MARS 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.

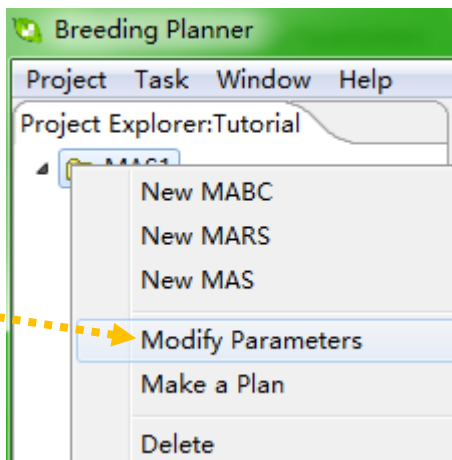
When the required parameters are set in the Parameter setting/viewing Window, the defined MARS breeding program is graphed in the Breeding Scheme/flowchart Window. A set of output files are listed in the Project Window.



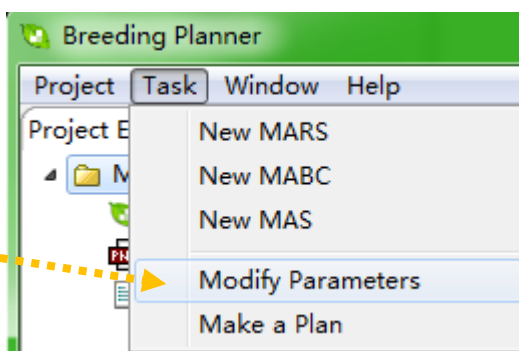
PMAS Tutorial: Modify your parameters

7. Modify Parameters

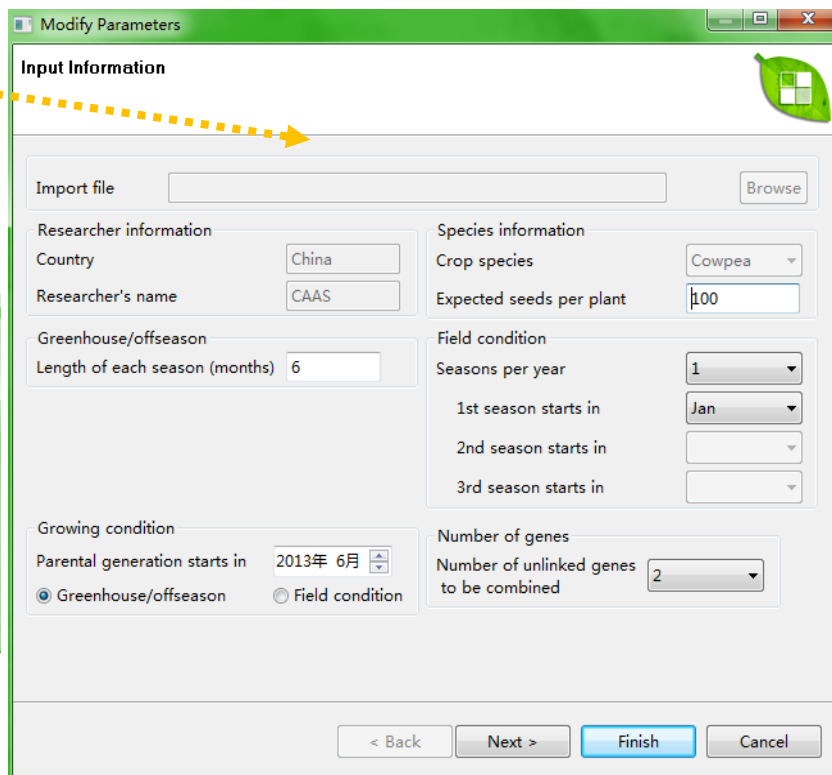
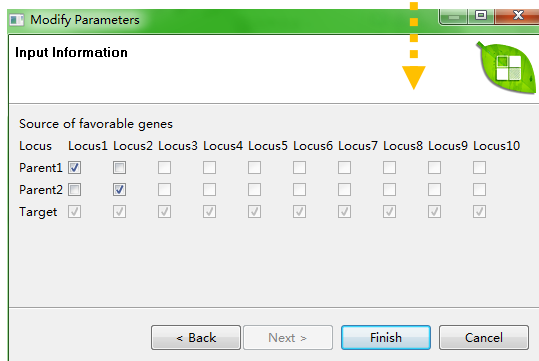
- Right click the MAS1 folder, then choose **Modify Parameters**



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



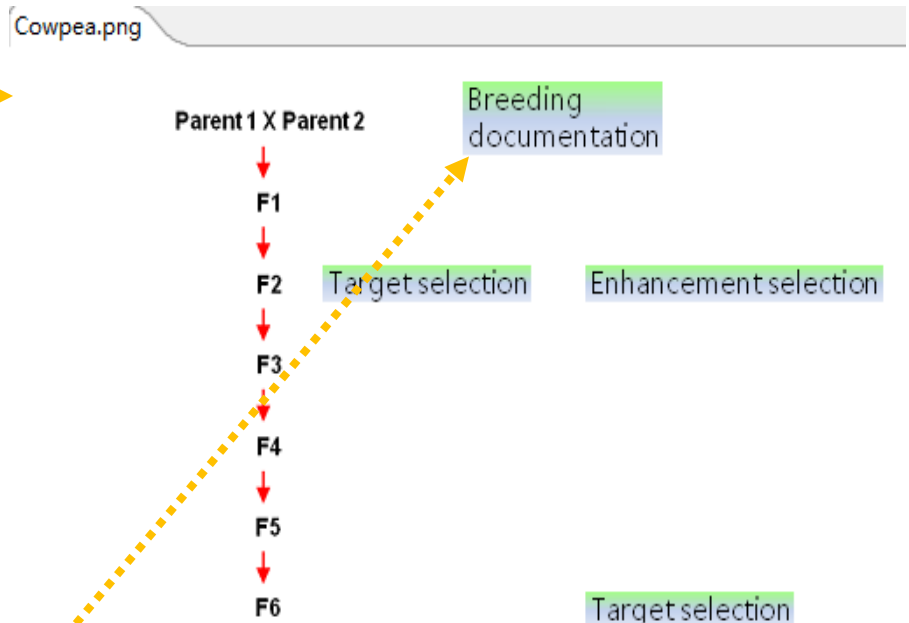
- You may modify the parameters in the Dialog Window, and then click Finish button to save your modifications. The breeding scheme will be automatically modified.



PMAS Tutorial: The breeding scheme and documentation

8. View the flowchart

- It is in the right window



9. View breeding documentation

- Click the **Breeding Documentation** button

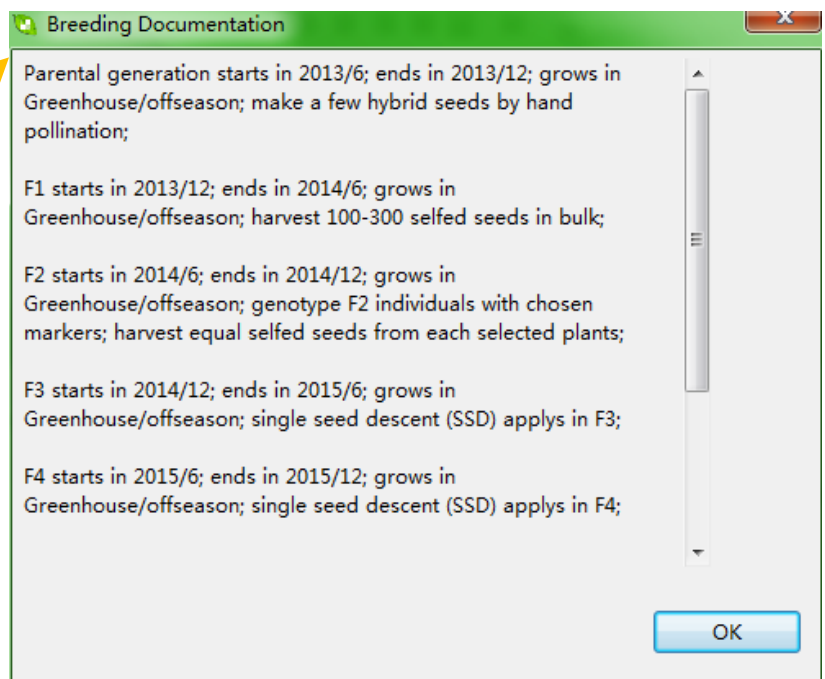
Homozygous selection:

Genotype ++ at one locus will be selected.

Enhancement selection:

Genotype ++ and +- at one locus will be selected.

- The **Breeding Documentation** is in the pure text describing the whole flow of the MAS program.



PMAS Tutorial: Additional information

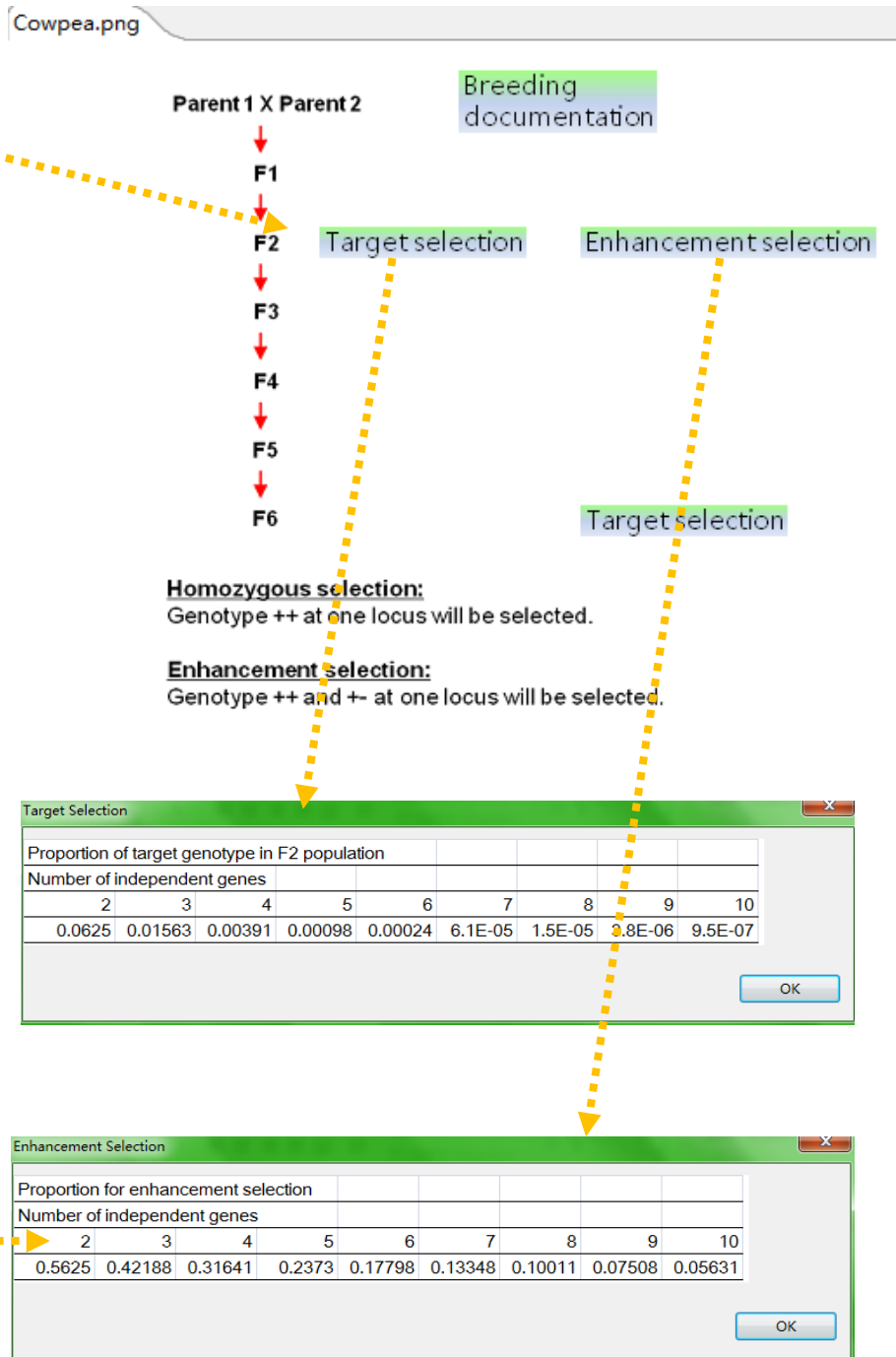
10. Additional information on the flowchart

- Click **Target selection**

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

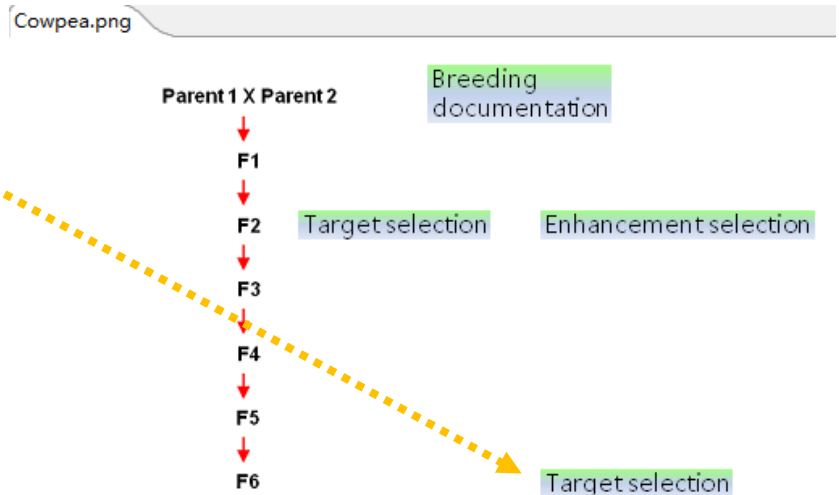
- Click **Enhancement selection**

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



PMAS Tutorial: Additional information

- Click **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

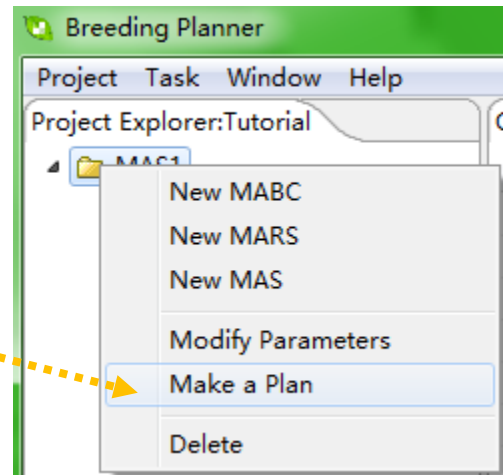
Proportion of target genotype when enhancement selection is applied in F2									
Number of independent genes									
2	3	4	5	6	7	8	9	10	
0.44444	0.2963	0.19753	0.13169	0.08779	0.05853	0.03902	0.02601	0.01734	

OK

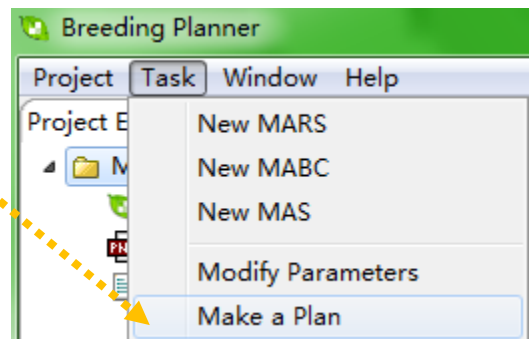
PMAS Tutorial: Make a plan from wherever you are

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

Select current status
0. Select parental lines and prepare for planting

Make a Plan

PMAS Tutorial: Tell the system where you are

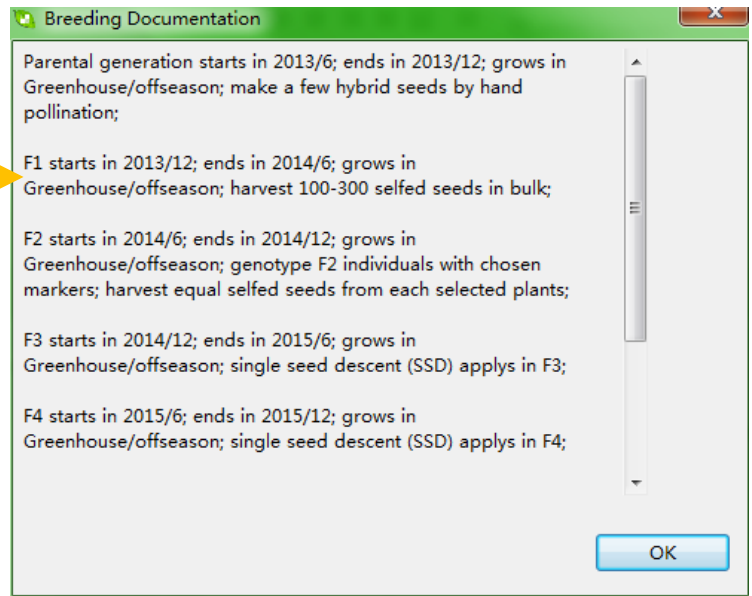
- Tell the system when the current season starts. The system will know the current season is grown in Greenhouse or in Field from the breeding parameters you specified.
- Tell the system where you are by selecting:
 0. Select parental lines and prepare for planting
 1. Parental lines is growing
 2. F1 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

The screenshot shows the 'Make a Plan' interface. It features a grey header bar with the text 'Make a Plan' on the left. Below the header, there are two input fields. The first field is labeled 'Current status starts in' and contains a date selector showing '2013年 6月'. The second field is labeled 'Select current status' and contains a dropdown menu with the selected option '0. Select parental lines and prepare for planting'. A 'Make a Plan' button is located below these fields. Two yellow dashed arrows point from the text above to the 'Make a Plan' header and the 'Select current status' dropdown. A third yellow dashed arrow points from the 'Make a Plan' button to the text below.

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

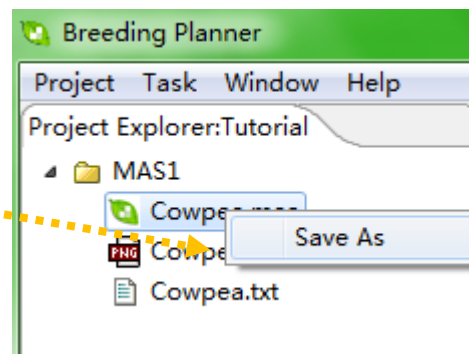
PMAS Tutorial: See the breeding plan the system makes

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

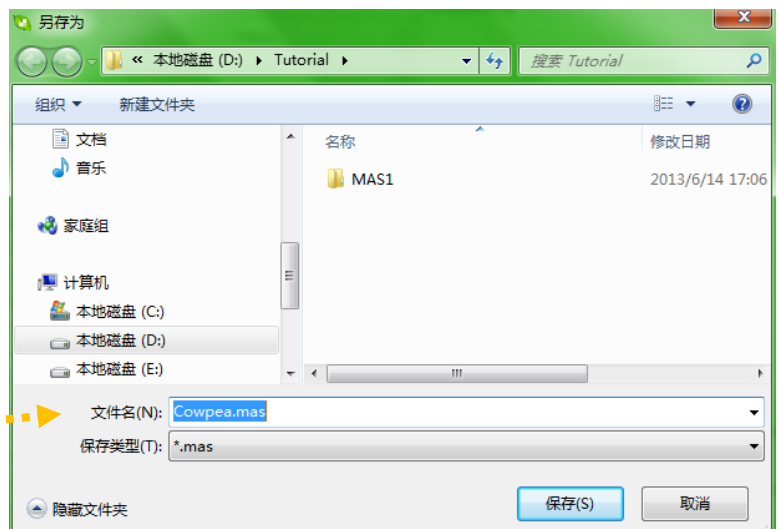


12. Save the result files

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



- Specify the path and rename of the output file



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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