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# *USER GUIDE* for the



(Tree Genotype Decision Support System)

A DECISION SUPPORT SYSTEM INFERRING THE GENOTYPES  
OF SEED TREES FROM OPEN POLLINATED PROGENIES  
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## INSTALLATION AND EXECUTION

The program is directly executable. Just copy the folder TGDSS from the CD to the hard disk and double click on the icon TGDSS to execute. The system runs in Win XP, Win 2000 or Win 98 environment.

## INTERACTING WITH THE SYSTEM

The system is easy to follow and it uses a friendly user interface. Initially the user is prompted to input the number of trees under examination. Seed samples have been collected from these trees.

### Screen 1: Input of the number of trees

**INPUT DATA - QUALITATIVE TEST**

Please input the number of Trees to be examined and then press the Button "Number of Trees"

2 Number of Trees

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Please input the Maximum Number of Alliles found in the sample and then press Allile Number

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Input the Number of cases of each alternative Genotype in the seed sample of the tree and Press Input

$\alpha/\alpha$	11	22	33	12	13	23
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The system understands the number of trees to be examined and appears a proper message. It also requires the number of Alliles found in the seed sample.

Screen 2: Input the number of Alliles found in the seed sample.

The screenshot shows a software window titled "INPUT DATA - QUALITATIVE TEST". The window contains the following elements:

- A title bar with standard window controls (minimize, maximize, close).
- A header instruction: "Please input the number of Trees to be examined and then press the Button 'Number of Trees'".
- An input field labeled "Number of Trees" containing the value "2".
- A feedback message: "We have 2 Trees to examine".
- A second header instruction: "Please input the Maximum Number of Alliles found in the sample and then press Allile Number".
- A dropdown menu for "Allile Number" with options 1, 2, and 3. Option 1 is selected.
- A button labeled "Allile Number".
- A table with the following data:

	11	22	33	12	13	23
$\alpha/\alpha$						
- A large empty text area below the table.
- Buttons for "File Construction" and "Exit" at the bottom.

The user is prompted to input the cases from the alternative possible Genotypes found. The TGDSS determines the possible Genotypes according to the Alliles found in the sample.

### Screen 3: Input the cases from the Genotypes found in the seed analysis

**INPUT DATA - QUALITATIVE TEST**

Please input the number of Trees to be examined and then press the Button "Number of Trees"

Number of Trees: We have 2 Trees to examine

Please input the Maximum Number of Alliles found in the sample and then press Allele Number

Allele Number: We have 2 Alliles and 3 alternative Genotypes

Input the Number of cases of each alternative Genotype in the seed sample of the tree and Press Input

$\alpha/\alpha$	11	22	33	12	13	23
1	2	3		0		

Input

File Construction Exit

The TGDSS shows the results of the Qualitative test. It show not only the final decisions but also the possible Genotypes it has determined.

#### Screen 4: Results of the Qualitative test

**INPUT DATA - QUALITATIVE TEST**

Please input the number of Trees to be examined and then press the Button "Number of Trees"

Number of Trees: We have 2 Trees to examine

Please input the Maximum Number of Alleles found in the sample and then press Allele Number

Allele Number: We have 2 Alleles and 3 alternative Genotypes

Input the Number of cases of each alternative Genotype in the seed sample of the tree and Press Input

Please Press here to show the results of the Qualitative test

The tree number 1 is heterozygous with Genotype D12

Please Press here to show the results of the first Quantitative test

Screen 5: A new input of data for three (3) different trees

INPUT DATA - QUALITATIVE TEST

Please input the number of Trees to be examined and then press the Button "Number of Trees"

Number of Trees We have 3 Trees to examine

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Please input the Maximum Number of Alliles found in the sample and then press Allile Number

Allile Number We have 3 Alliles and 6 alternative Genotypes

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Input the Number of cases of each alternative Genotype in the seed sample of the tree and Press Input

$\alpha/\alpha$	11	22	33	12	13	23	
1	10	0	17	0	24	0	Input

## Screen 6: Determined and Possible Genotypes appear in the Qualitative test results

**INPUT DATA - QUALITATIVE TEST**

Please input the number of Trees to be examined and then press the Button "Number of Trees"

Number of Trees We have 3 Trees to examine

Please input the Maximum Number of Alliles found in the sample and then press Allile Number

Allile Number We have 3 Alliles and 6 alternative Genotypes

Input the Number of cases of each alternative Genotype in the seed sample of the tree and Press Input

Please Press here to show the results of the Qualitative test

The tree number 1 might have Genotype  $\Delta 33$  or  $\Delta 13$   
The tree number 2 is heterozygous with Genotype D13  
The tree number 3 is heterozygous with Genotype D13

Please Press here to show the results of the first Quantitative test

File Construction Exit

## Screen 7: Results of the first Quantitative test

**INPUT DATA - QUALITATIVE TEST**

Please input the number of Trees to be examined and then press the Button "Number of Trees"

We have 3 Trees to examine

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Please input the Maximum Number of Alliles found in the sample and then press Allile Number

We have 3 Alliles and 6 alternative Genotypes

---

**Input the Number of cases of each alternative Genotype in the seed sample of the tree and Press Input**

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The tree number 1 might have Genotype  $\Delta 33$  or  $\Delta 13$   
The tree number 2 is heterozygous with Genotype D13  
The tree number 3 is heterozygous with Genotype D13

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The tree number 1 might have Genotype  $\Delta 33$  ή  $\Delta 13$

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## Screen 8: Results of the second Quantitative test

Allfile Number We have 3 Allfiles and 6 alternative Genotypes

**Input the Number of cases of each alternative Genotype in the seed sample of the tree and Press Input**

Please Press here to show the results of the Qualitative test

The tree number 1 might have Genotype  $\Delta 33$  or  $\Delta 13$   
The tree number 2 is heterozygous with Genotype D13  
The tree number 3 is heterozygous with Genotype D13

Please Press here to show the results of the first Quantitative test

The tree number 1 might have Genotype  $\Delta 33$   $\hat{r}$   $\Delta 13$

Please Press here to show the results of the second Quantitative test

The tree number 1 is homozygous  $\Delta 33$   
The testing has finished for all of the trees  
Press 'File construction' in order to store the results,  
or 'EXIT' to terminate the program

File Construction Exit

The user presses the File Construction Command Button to store case data and the results in a text file.

The Exit button is used to stop execution of the system.