

Coefficient of Parentage Users Manual

**Software Development Department
December 15, 1994**



CIMMYT

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Introduction

This document is the Users Manual of the Wheat Coefficient of Parentage System, a system for calculating coefficients of parentage between different wheat cultivars based on their individual pedigrees.

The goal of the Wheat Coefficient of Parentage (WCOP) system is to calculate coefficients of parentage between different cultivars based on their individual pedigrees.

The coefficient of parentage between two genotypes provides an estimate of the genetic relationship between them, based upon analysis of their pedigrees.

WCOP uses information about crosses, pedigrees and selection histories of germplasm used in the CIMMYT Wheat Program, stored in the Wheat Pedigree Management System (WPMS). WPMS keeps track of female and male parents for each cross recorded in the system, which permits the building of the whole cross tree for any genotype (a cross associated to a selection history), up to the landraces, genotypes with unknown parents.

For genotypes existing in WPMS, WCOP will find all their ancestors going back up to the ancestral parents, and will build the corresponding progeny parent trees.

WCOP will write the progeny parent trees data, in formatted files that will be used as input files for the RCL program, which will generate the matrix of coefficients of parentage based on the Rodgers & Cox algorithm.

1. The Menu Interface

This chapter describes the menu interface of the WCOP system and explains the functions associated with the different options.

1.1 Menu General Layout

In all the menus you will find the following elements:

- the label COEFFICIENT OF PARENTAGE SYSTEM.
- the title of the menu within a box.
- another box containing the body of the menu, that may consist of an options menu, or windows to enter, select or review data.
- two lines or more including the function and special keys that can be used in that particular menu, below the menu box(es).
- one message line at the bottom of the menu.

1.2 Function and Special keys

In WCOP the function keys F7, F8 and F9 are used for specific purposes depending on the screen. However, a number of function and special keys are used in the WCOP menus with the same functionality everywhere. Those general function keys are described below:

- F10 — Used to go to the first record in a list of items when displayed in a pick-up or review-data window.
- F12 — Used to go back to the previous option in an option menu, or to the previous field in a list.
- ALT/F4 — Used to go to the last record in a list of items.
- CTRL-Z — Used to return to the previous menu, and to exit the system if used in the Main menu (Figure 1).
- ALT/F6 — Used to trigger a process after reviewing if data entered are correct.
- ENTER — Used to select an option in an option menu, select a field from a list, or after entering data in a data input window.
- TAB — Used to go to the next option in an option menu, or to the next field in a pick-up list.
- PageUp — Used to scroll the active list backwards the number of elements that are visible in the screen.
- PageDown — Used to scroll the active list forwards the number of elements that are visible in the screen.

2. The Main Menu

The main menu of the WCOP system is shown in Figure 1. To invoke it you have to go to the directory [.WCOP_USER] of your own account, and enter the command

\$ @COPSYS

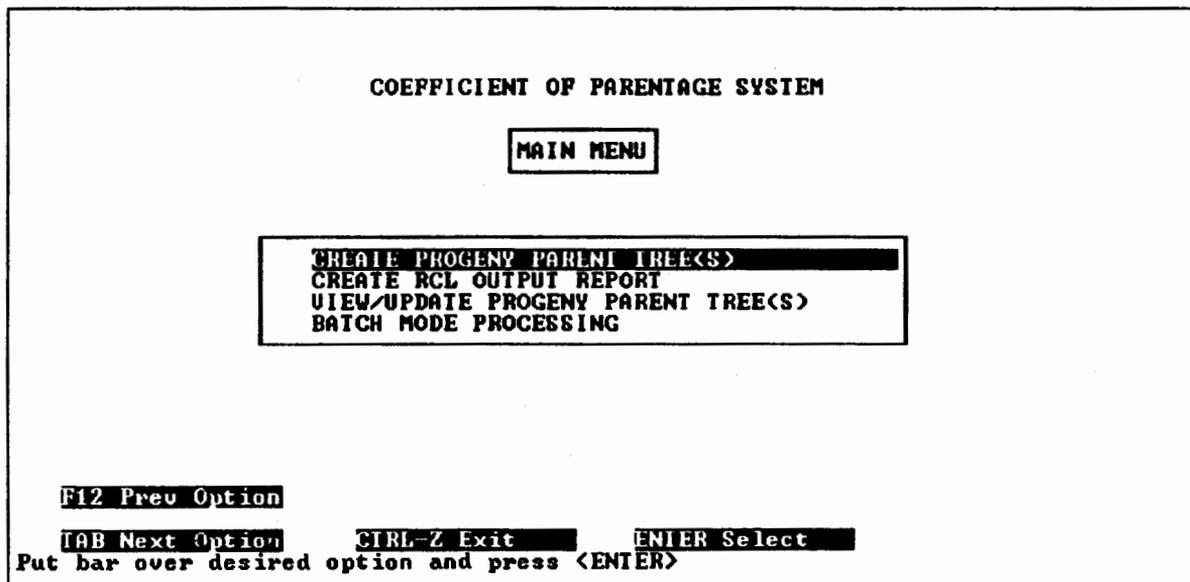


Fig. 1: Main menu

To select an option from the main menu, put bar over desired option and press ENTER. You can use TAB and F12 keys to move the bar to the next and previous option, respectively. To exit from the system press CTRL-Z.

- **CREATE PROGENY PARENT TREE(S)** — To create the progeny parent tree for one or more target genotypes. Also to create a TGF file (Target Genotypes File) with genotypes, that were first checked for existence in WPMS. That TGF file can be used later as input to one of the 4 options of menu BATCH MODE PROCESSING.
- **CREATE RCL OUTPUT REPORT** — To create the RCL output report based on genotypes selected from a list of genotypes for which parent trees have already been generated.
- **VIEW/UPDATE PROGENY PARENT TREE(S)** — To view online the progeny parent tree of a specific genotype, and update its tree interactively if necessary.

- **BATCH MODE PROCESSING** — To execute in batch mode, using as input a TGF file created elsewhere, creation and/or updating of parent trees based on genotypes in a file, with or without RCL output reports.

The following sections will describe in detail the options of the main menu.

2.1 Create Progeny Parent Tree(s)

If you select this option from the Main Menu (Figure 1), the menu shown in Figure 2 will be displayed on the screen.

COEFFICIENT OF PARENTAGE SYSTEM

**CREATE PROGENY
PARENT TREES**

CROSS NAME OR ABBREVIATION

CROSS I.D.: _____
SELECTION I.D.: _____

YOU HAVE SELECTED THE FOLLOWING GENOTYPE(S)

| NAME | CID | SID |
|------|-----|-----|
| | | |

| | | | |
|---------------------|-----------------------|-----------------------------|----------------------------|
| F7 To Scroll | ALT/F6 Execute | ALT/F7 Input by CID | ALT/F9 Recover File |
| ENTER | CTRL-Z Return | ALT/F8 Input By Name | ALT/F10 Save List |

Enter one cross at the time and press <ENTER>, <F7> to scroll list of genotypes

Fig. 2: Create Progeny Parent Tree menu

The menu in Figure 2 shows the name of each selected target genotype, the cross identifier (CID) and the selection identifier (SID) as recorded in WPMS.

You can select the way in which you want to specify the target genotypes for which you want to generate a progeny parent tree. You can either specify the cross name or the cross abbreviation recorded in WPMS, or you can specify the cross and the selection identifiers (CID and SID) assigned to a particular target genotype in WPMS.

When entering the menu the cursor will be in the box with the title **CROSS NAME OR ABBREVIATION**. From here you can directly begin typing a cross name or an abbreviation known to WPMS. When you press **ENTER** the program will search in WPMS to find the name, and if found will add the corresponding CID and SID to the list of genotypes at the right. If the name can't be found in WPMS, the program will display an error message about that.

To switch between entering genotypes by name and by CID and SID, use **ALT/F7** and **ALT/F8**. This will make the cursor jump from one input box to the other.

To enter a genotype based on the CID and SID, press ALT/F7 which will put the cursor in the box with prompts CROSS I.D.: and SELECTION I.D.: Now you must input the CID, press TAB, and then input the SID and press ENTER. If you don't enter both the CID and the SID, the program will display an error message about that.

To enter a genotype based on the Name, press ALT/F8 which will put the cursor in the box with prompt CROSS NAME OR ABBREVIATION. Input the name from PMS either as Cross name or Abbreviation, and then press ENTER.

In both cases the program will search for the genotype in WPMS, and if found add it to the list of target genotypes at the right. If the program doesn't find the genotype specified, the program will display an error message about that. The program will complement the entry in the list with data from WPMS, either putting the name in the list (if a name exists) if you input by CID and SID, or putting CID and SID in the list if you input by Name. If a name doesn't exist for the genotype, the program will put "----".

You may continue entering genotypes, switching freely between entering by name, and by CID and SID. If you press CTRL-Z, you will be returned to the Main menu, and the genotypes in the list will be lost, e.g. entering again the menu of Figure 2 will result in an empty list of genotypes.

To scroll the list of genotypes, press F7, which will put the menu shown in Figure 3. This will put the cursor in the list of target genotypes to the right, and activate a number of new functions:

COEFFICIENT OF PARENTAGE SYSTEM

**CREATE PROGENY
PARENT TREES**

YOU HAVE SELECTED THE FOLLOWING GENOTYPE(S)

| NAME | CID | SID |
|------|-------|-----|
| ---- | 8784 | 2 |
| ---- | 9727 | 1 |
| ---- | 9812 | 1 |
| ---- | 20983 | 2 |
| ---- | 20983 | 4 |
| ---- | 23899 | 34 |
| ---- | 28374 | 3 |
| ---- | 29873 | 1 |
| ---- | 29898 | 1 |
| ---- | 38728 | 1 |

| | | | |
|----------------------|------------------------|------------------------|----------------------------|
| F10 Next Name | F12 Prev. Name | | |
| F10 Top | ALT/F4 Botton | F9 Sort By Name | ALT/F9 Recover File |
| F7 To Input | DELETE Deselect | F8 Sort By CID | ALT/F10 Save List |
| PgDn Screen | PgUp Screen | ALT/F6 Execute | CTRL-Z Return |

<DELETE> to deselect, <ALT/F6> when ready, <F?> to add genotype.

Fig. 3: Scrolling list of genotypes for Create Progeny Parent Trees menu

You may scroll the list of genotypes with the following function keys: PageUp, PageDown, ALT/F4 (go to bottom of the list), F10 (go to top of the list). Besides you

2.2 Create RCL Output Report

The CREATE RCL OUTPUT REPORT option allows you to specify one or more target genotypes for which progeny parent trees are to be combined in a single file (RCL input file), that will be generated writing data in the same format as the format of an input file for the RCL program. Using this input file, RCL program will calculate the coefficients of parentage (COP) and generate the corresponding COP matrix. This means that only existing progeny parent trees can be used in the report. Since the generation of the report will eliminate duplicated CID's and SID's from the list (combining all parents of the chosen tgf's) it can be a time-consuming process. However, the main part is processed in a batch process called OUTPUT_REPORT.

If you select this option in the Main Menu (Figure 1), the menu shown in Figure 6 will be displayed:

COEFFICIENT OF PARENTAGE SYSTEM

CREATE RCL OUTPUT REPORT

ENTER Select/Deselect

F9 Sort By Name

F8 Sort By CID

F10 Top

PageDown Screen

Progeny Parent Trees in the System

| NAME | CID | SID | Sel |
|-------------|-------|-----|-----|
| BR 15 | 7002 | 7 | * |
| VEERY | 7691 | 0 | * |
| PITIC 62 | 6674 | 7 | * |
| CHAPINGO 53 | 6546 | 6 | |
| BR 12 | 7027 | 24 | |
| GABO-AUS | 6538 | 1 | |
| | 34622 | 1 | |
| COOK | 7072 | -1 | * |
| | 7657 | 1 | |
| | 6546 | 5 | |

ALT/F4 Bottom **TAB Next Line** **F12 Prev. Line**

PageUp Screen **PageDown Screen** **F7 Finished** **CTRL-Z Return**

Put bar over genotype. <ENTER> to select/deselect. When ready press <F7>

Fig. 6: Create RCL output report select genotype menu

The list of target genotypes for which the corresponding progeny parent trees have already been generated, will be shown. You may scroll through the list of target genotypes using function keys PageUp, PageDown, TAB, F10, F12, and ALT/F4. To select a specific genotype, put the bar over the desired genotype and press ENTER. That genotype will then be marked as selected with an asterisk "*" in the column with the title "Sel". In Figure 6 you can see that the genotypes BR 15, VEERY, PITIC 62 and COOK have been selected. Pressing ENTER on a genotype works as an on/off toggle of the selection. There is no limit to how many genotypes you can select this way.

Pressing F8 will sort the list of genotypes by CID, and pressing F9 will sort the list of genotypes by NAME. You may press CTRL-Z to cancel this process and go back to the Main Menu (Figure 1), but then you will lose all selections made.

When you are ready processing the selected target genotypes, press key F7. If you press key F7 the system will display the menu in Figure 7:

```

COEFFICIENT OF PARENTAGE SYSTEM

CREATE RCL OUTPUT REPORT

You Have Selected the Following Genotypes

NAME      CID      SID
BR 15    7002     ?
JEERY    7691     0
PITIC 62 6674     ?
COOK     7872    -1

F8 Set Matrix Output  F10 Top      F12 Prev Line  ALT/F4 Botton  TAB Next Line
PgDn Screen          PgUp Screen   ALT/F6 Execute  CTRL-Z Return
Top of the scroll. Confirm selection by pressing <ALT/P6>.<CTRL-Z> to cancel.

```

Fig. 7: Create RCL Output report submit job for selected genotypes menu

The menu in Figure 7 shows the name of each selected target genotype, its cross identifier (CID) and its selection identifier (SID) as recorded in WPMS.

Here you may review the target genotypes previously specified before launching the process to generate the RCL output report with ALT/F6. With CTRL-Z you can go back to the previous menu in Figure 6 to select or deselect more genotypes. Note that returning to the previous menu does not change any of the selections, unless you press CTRL-Z again to return the Main menu in Figure 1. You may scroll through the list in Figure 7 using function keys PageUp, PageDown, TAB, F10, F12, and ALT/F4.

To confirm the selection and trigger the process to generate the RCL output report, press ALT/F6. Then the system will create a file with the CID's and SID's chosen, and submit the batch process OUTPUT_REPORT, which in turn will create the RCL input file, and submit a batch job to create the RCL output report. Once the OUTPUT_REPORT has been submitted (it takes 5-10 seconds in the terminal), you will be returned to the Main Menu (Figure 1). The output report input filename will have the format TEMP_23JUL94_134512.DAT. The RCL input filename will have the format IN_23JUL94_134512.DAT if the user pressed ALT/F6 the 23th of July 1994 at 13 hours with 45 minutes and 12 seconds, e.g. the general format IN_timestamp.DAT. This file contains the COP matrix of ancestral genotypes.

The output filename will have exactly the same timestamp, with the format OUT_timestamp.DAT. As an example, the corresponding output filename of the example would be OUT_23JUL94_134512.DAT. The reason for appending the timestamp to the filenames is to secure the uniqueness so that other processes will not

use the same file, and to secure that you can submit several batch processes simultaneously avoiding that these processes mix their files.

By default, the RCL input file will include only the target genotypes you selected in the COP matrix, therefore, the number of elements in the matrix written in the RCL output report will be equal to the number of target genotypes.

However, if you want to include in the RCL input file the target genotypes and all their progeny parents (this means that the order of the COP matrix will be much higher), you have to press key F8 before starting the process. In that case the following menu will appear, as can be seen in Figure 8:

```

                                COEFFICIENT OF PARENTAGE SYSTEM
                                SET MATRIX OF COP OUTPUT
                                PROGENIES AND TARGET GENOTYPES IN OUTPUT MATRIX ?  Yes No
                                (<'No' Means only target genotypes>)
                                F12 Prev Option
                                TAB Next Option      ENTER Select      CTRL-Z Return
                                Select option by moving bar via TAB key and press ENTER

```

Fig. 8: Set matrix output menu

You can switch between 'Yes' and 'No' with TAB and F12. If you press CTRL-Z you will be returned to Figure 7 without change. You should choose Y (yes) and press ENTER, if you want to include the target genotypes and all their progenies in the RCL input file. If you press TAB to choose N (no) and press ENTER, the RCL input file (if generated) will include only the target genotypes. Then you will be returned to the menu in Figure 7, where the RCL input file only will be generated if pressing ALT/F6 from that menu.

2.3 View/Update Progeny Parent Tree(s)

The VIEW/UPDATE PROGENY PARENT TREE(S) option allows you to review an existing progeny parent tree of a specific target genotype. You can check its particular progeny, identify its ancestral parents, check CID and SID of its parents, etc.

This option allows you also to update interactively an existing progeny parent tree. This is needed if data related to the corresponding target genotype has been changed in WPMS. But it can also be done using the BATCH MODE PROCESSING option from

the main menu if you have an input file with the genotype in question. Preferably View/Update Progeny Parent Tree should only be used to revise the data, not to update it.

If you select this option in the Main Menu (Figure 1), the menu in Figure 9 will be displayed.

COEFFICIENT OF PARENTAGE SYSTEM

VIEW/UPDATE PROGENY PARENT TREE

| NAME | CID | SID | DATE |
|----------|-------|-----|------------|
| BR 15 | 7002 | 7 | 07/22/1994 |
| JEERY | 7691 | 0 | 07/22/1994 |
| PIIIC 62 | 6674 | 7 | 07/22/1994 |
| BR 12 | 7027 | 24 | 07/22/1994 |
| GABO-AUS | 6538 | 1 | 07/22/1994 |
| --- | 34622 | 1 | 07/22/1994 |

F10 Top

F12 Prev Line

ALT/F4 Bottom

PgDn screen

PgUp Screen

TAB Next Line

ENTER Select

CTRL-Z Return

Top of the scroll. Put bar over genotype and press <ENTER>.

Fig. 9: View/update progeny parent tree menu (header part)

The list of target genotypes for which the corresponding progeny parent trees have already been generated, will be shown. Each genotype is represented by its name, CID, SID and the date the progeny parent tree was generated. You may scroll through the list of target genotypes using function keys PageUp, PageDown, TAB, F10, F12, and ALT/F4. Put the bar over one genotype and press ENTER if you want to view or update its progeny parent tree. You may press CTRL-Z to cancel this process and return to the Main Menu (Figure 1).

If you select a target genotype and press ENTER, you will see the menu shown in Figure 10:

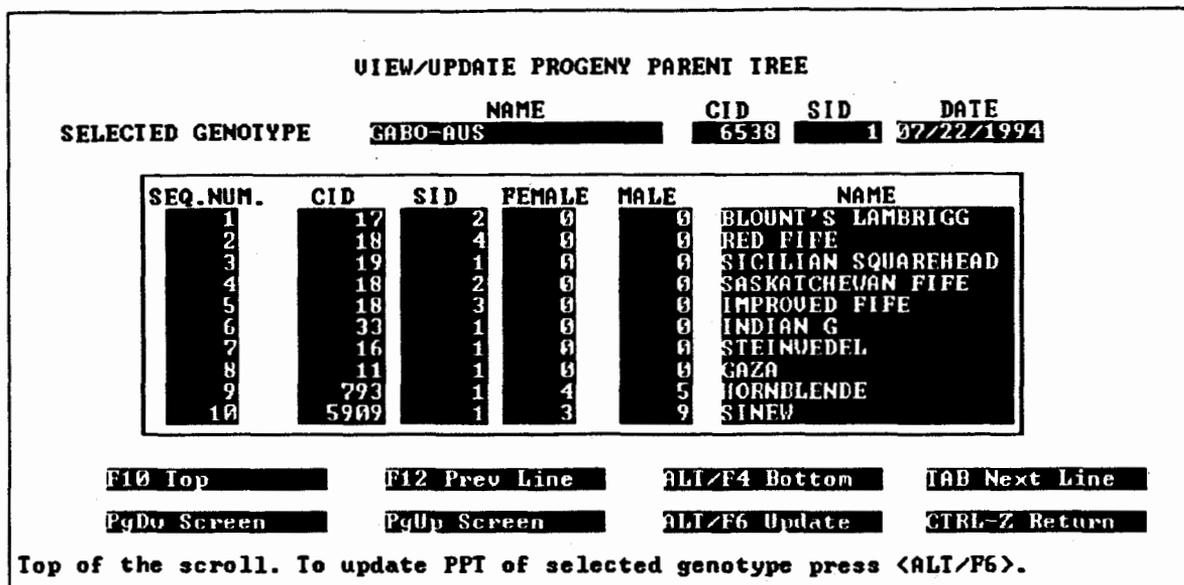


Fig. 10: View/update progeny parent tree menu (tree part)

This menu includes the name, CID and SID of the genotype you have selected as well as the contents of its progeny parent tree for which the following fields are included:

- **SEQ.NUM.** — This is a sequential number to identify each of the ancestor genotypes of the target genotype.
- **CID** — The cross identifier of the genotype, as recorded in WPMS.
- **SID** — The selection identifier of the genotype, as recorded in WPMS.
- **FEMALE** — This field consist of the number that points to the sequential number **SEQ.NUM.** assigned to the female parent of genotype. If this number is 0 (zero) it means that female parent is unknown, therefore the genotype is considered a landrace.
- **MALE** — This field consist of the number that points to the sequential number **SEQ.NUM.** assigned to the male parent of genotype. If this number is 0 (zero) it means that male parent is unknown, therefore the genotype is considered a landrace.
- **NAME** — This is the name associated to the genotype, as recorded in WPMS. Some genotypes have no name assigned, in these cases a long hyphen will be shown in this field.

You may scroll through the list of genotypes using function keys PageUp, PageDown, TAB, F10, F12, and ALT/F4. If you wanted to review only the progeny parent tree, you should press CTRL-Z to return to menu shown in Figure 9. If you want to update the progeny parent tree for the genotype you selected, press ALT/F6. The system will ask you for confirmation, as seen in Figure 11:

```

COEFFICIENT OF PARENTAGE SYSTEM
VIEW/UPDATE PROGENY PARENT TREE

DO YOU REALLY WANT TO UPDATE PROGENY PARENT TREE ?      Yes No

F12 Prev Option
TAB Next Option      ENTER Select      CTRL-Z Return
Select option by moving bar via TAB key and press ENTER

```

Fig. 11: Confirm update progeny parent tree menu

You can switch between 'Yes' and 'No' with TAB and F12. If you press CTRL-Z you will be returned to Figure 10 without change.

Choose Y (yes) or N (no) and press ENTER. If you press TAB to choose Y and then press ENTER, the process to update the progeny tree will start. This might be a very time consuming process, especially if there are many ancestral parents for the genotype, and in that period of time the screen will be frozen. When it is finished the following message will appear.

PROGENY PARENT TREE FOR GENOTYPE (*name, cid, sid*) HAS BEEN UPDATED.

Where *name*, *cid* and *sid* represent the corresponding cross name, cross identifier and selection identifier of the selected genotype. After processing you will be returned to the Main menu shown in Figure 1.

2.4 Batch Mode Processing

The BATCH MODE PROCESSING option allows you to perform creation and/or update of the genotypes which are present in an input file previously generated. This means that you start the process from your terminal, but your terminal is freed as soon as the process is submitted (the process is executed in the background), so you may continue using the WCOP menu system, or leave the menus to use your terminal for other purposes.

One of the features of batch mode processing is that instead of reading data directly from the screen (as the interactive mode does), it reads data from a file. This means that you will tell the system the name of the file that contains the data needed to

perform the requested tasks, we will refer to this file as the Target Genotypes File (TGF). Usually it will be the file you have saved with ALT/F10 from the menu in Figure 5, after entering genotypes from the menu CREATE PROGENY PARENT TREE(S) of the main menu. We will talk more about this TGF later in this section.

If you select this option in the Main Menu (Figure 1) you will see the Batch Mode Processing Menu shown in Figure 12:

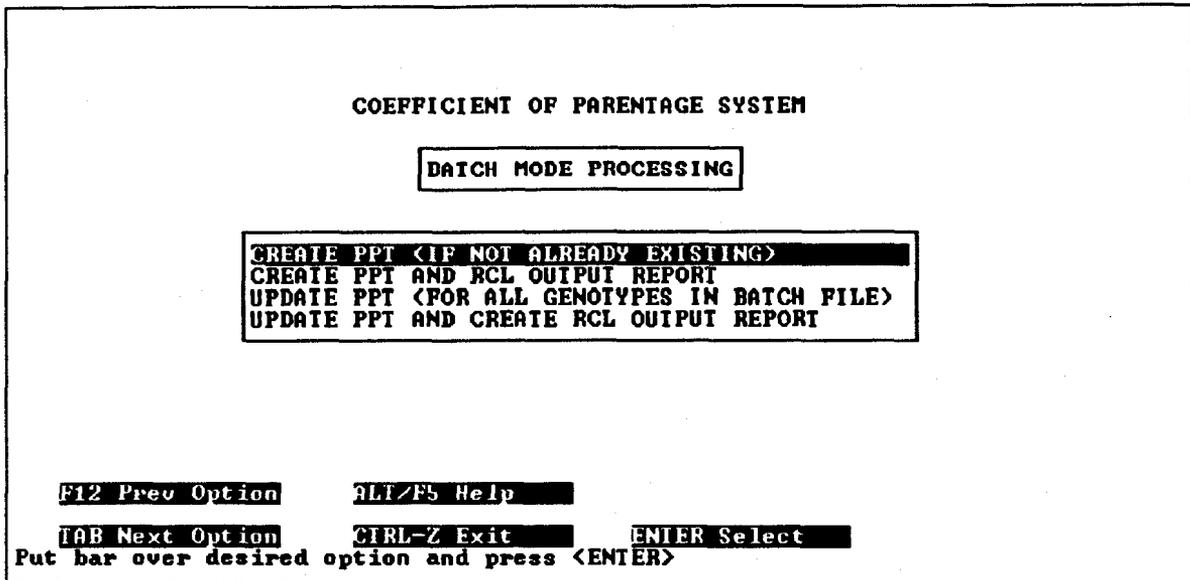


Fig. 12: Batch mode processing menu

You may press CTRL-Z to go back to the Main Menu (Figure 1). If you press ALT/F5 you will get the help screen corresponding to the option the cursor is on, e.g. the Figures 16, 18, 20 or 22. From these help screens you must press CTRL-Z to return to the menu in Figure 12.

The options available in this menu allow you to perform the following tasks:

- **CREATE PPT (IF NOT ALREADY EXISTING)** — This option will create the progeny parent tree for genotypes included in the TGF, but not existing before in WCOP. This option should be used to create new progeny trees, leaving the existing ones unchanged.
- **CREATE PPT AND RCL OUTPUT REPORT** — This option will perform as the previous one, but after generating the progeny parent trees will also create the file to be used as input file for the RCL program. This RCL input file will contain the progenies of all target genotypes included in the TGF. Then the RCL output report will be generated.
- **UPDATE PPT FOR ALL GENOTYPES IN BATCH FILE** — This option will create or update the progeny parent tree for all target genotypes included in the TGF.

- **UPDATE PPT AND CREATE RCL OUTPUT REPORT** — This option will perform as the previous one, but after updating the progeny parent trees will also create the file to be used as input file for the RCL program. This RCL input file will contain the progenies of all target genotypes included in the TGF. Then the RCL output report will be generated.

To select an option from this menu, put bar over the desired option and press ENTER. You can use TAB and F12 keys to move bar to the next and previous option, respectively. After pressing ENTER the system will ask you for the name of the target genotypes file, as shown in the menu in Figure 13:

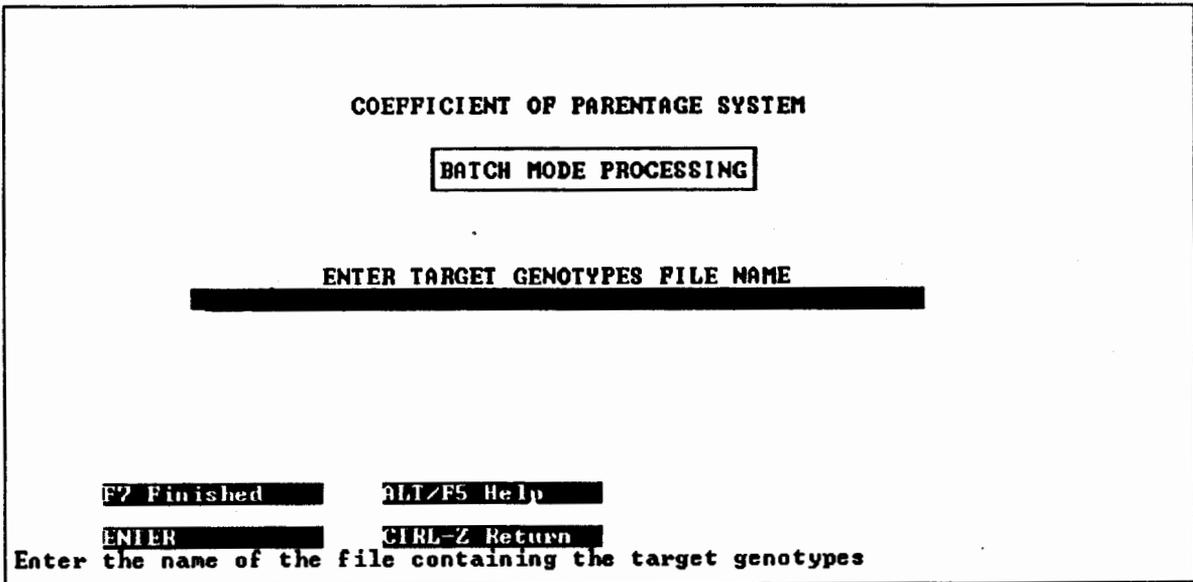


Fig. 13: Batch mode processing input file menu

You should enter the name of the file with the target genotypes and press ENTER or F7, which have the same functionality. You may press CTRL-Z to go back to the menu shown in Figure 12. If you press ALT/F5 you will get the help screen in Figure 14:

COEFFICIENT OF PARENTAGE SYSTEM

HELP INFORMATION

You are requested to enter a name for a file with target genotypes. It should be a text file containing the cross and selection identifiers (CID/SID) of genotypes. The CID and SID of each genotype should contain 6 characters. The file should look like:

006517000001
007027000023

Preferably this file should be produced using CREATE PROGENY PARENT TREE(S), using ALT/F10 to save the file, although it could also be made with a text editor.

F10 Top

ALT/F4 Botton

TAB Next Line

F12 Prev Line

PgDn Screen

PgUp Screen

CTRL-Z Return

View help information. When ready press <CTRL-Z>

Fig. 14: Help for Batch mode processing input file menu

When you are ready after scrolling and reading the help screen, press CTRL-Z to return to the menu in Figure 13.

If you specified a filename in Figure 13 and pressed ENTER, the system will verify if the file exists and if it has the correct format to be processed (described later), then one of the four confirmation menus in Figures 15, 17, 19 or 21 (depending on the option you selected), will be shown, asking you to confirm your selection and start the execution of the process.

COEFFICIENT OF PARENTAGE SYSTEM

You selected CREATE PPT <IF NOT ALREADY EXISTING> option

Target genotypes in file will be used to create its progeny parent tree but only if this tree does not already exist.

Processing can take a long time depending on the number of progeny trees that will be created and on the number of UAX users.

ALT/F6 Execute

CTRL-Z Cancel

Confirm batch process by pressing <ALT/F6>. <CTRL-Z> to return

Fig. 15: Confirmation menu for CREATE PPT (IF NOT ALREADY EXISTING)

COEFFICIENT OF PARENTAGE SYSTEM

HELP INFORMATION

CREATE PPT <IF NOT ALREADY EXISTING>.

You will be asked to enter a file name with target genotypes (see for format of the file the help when the file name is requested).
For each target genotype in the file a progeny parent tree (PPT) will be created unless that tree already exists in the system.
The job of producing the PPT's will be put in a queue and the system returns to the main menu.

F10 Top

ALT/F4 Bottom

TAB Next Line

F12 Prev Line

PgDn Screen

PgUp Screen

CTRL-Z Return

View help information. When ready press <CTRL-Z>

Fig. 16: Help screen for CREATE PPT (IF NOT ALREADY EXISTING)

COEFFICIENT OF PARENTAGE SYSTEM

You selected CREATE PPT AND RCL OUTPUT REPORT option.
Target genotypes in file will be used to create its progeny parent tree but only if this tree does not already exist.
Then the RCL input file will be produced including all target genotypes, and the output report generated.
Processing can take a long time depending on the number of progeny trees to create and target genotypes in file and on the number of UAX users

ALT/F6 Execute

CTRL-Z Cancel

Confirm batch process by pressing <ALT/F6>. <CTRL-Z> to return

Fig. 17: Confirmation menu for CREATE PPT AND RCL OUTPUT REPORT

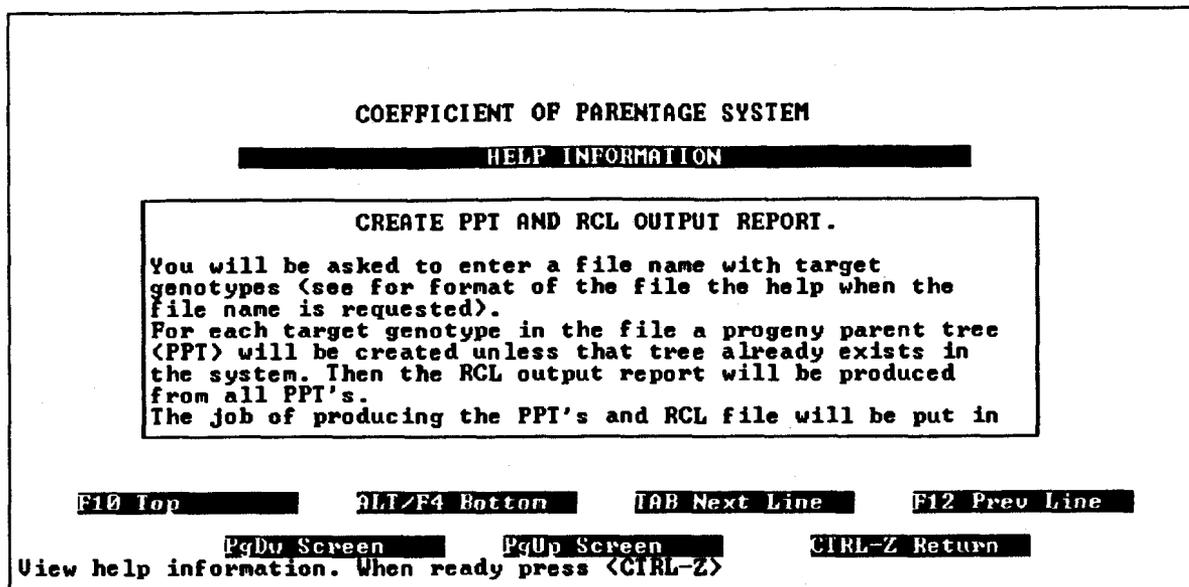


Fig. 18: Help screen for CREATE PPT AND RCL OUTPUT REPORT

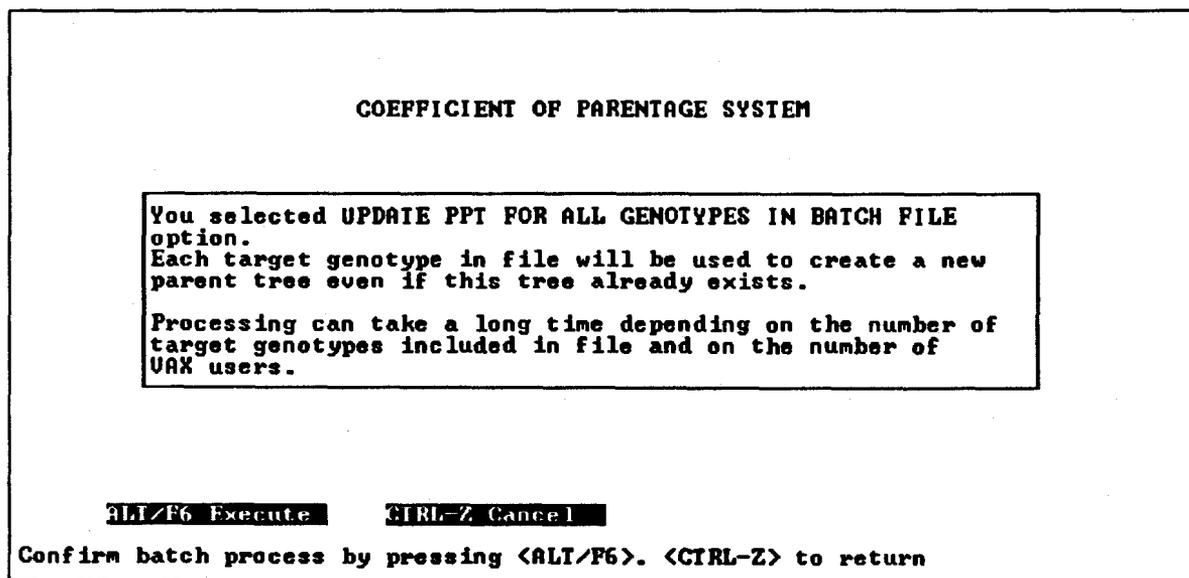


Fig. 19: Confirmation menu for UPDATE PPT FOR ALL GENOTYPES IN BATCH MODE

COEFFICIENT OF PARENTAGE SYSTEM

HELP INFORMATION

UPDATE PPT FOR ALL GENOTYPES IN BATCH FILE

You will be asked to enter a file name with target genotypes (see for format of the file the help when the file name is requested).
For each target genotype in the file a new progeny parent tree (PPT) will be created. If a tree already existed in the system it will be replaced with the newly created one. The job of updating the PPT's will be put in a queue and the system returns to the main menu.

F10 Top

ALT/F4 Bottom

TAB Next Line

F12 Prev Line

PgDn Screen

PgUp Screen

CTRL-Z Return

View help information. When ready press <CTRL-Z>

Fig. 20: Help screen for UPDATE PPT FOR ALL GENOTYPES IN BATCH MODE

COEFFICIENT OF PARENTAGE SYSTEM

You selected UPDATE PPT AND CREATE RCL OUTPUT REPORT option. Each target genotype in file will be used to create a new parent tree even if this tree already exists. Then the RCL input file will be produced including all target genotypes, and the output report generated.

Processing can take a long time depending on the number of target genotypes in file and on the number of UAX users

ALT/F6 Execute

CTRL-Z Cancel

Confirm batch process by pressing <ALT/F6>. <CTRL-Z> to return

Fig. 21: Confirmation menu for UPDATE PPT AND CREATE RCL OUTPUT REPORT

COEFFICIENT OF PARENTAGE SYSTEM

HELP INFORMATION

UPDATE PPT AND CREATE RCL OUTPUT REPORT.

You will be asked to enter a file name with target genotypes (see for format of the file the help when the file name is requested).
For each target genotype in the file a new progeny parent tree (PPT) will be created. If a tree already existed in the system it will be replaced with the newly created one. Then the RCL output report will be produced from all PPT's. The job of updating the PPT's and RCL output report will be

F10 Top

ALT/F4 Bottom

TAB Next Line

F12 Prev Line

PGDN Screen

PGUP Screen

CTRL-Z Return

View help information. When ready press <CTRL-Z>

Fig. 22: Help screen for UPDATE PPT AND CREATE RCL OUTPUT REPORT

In any of the Figures 15, 17, 19 or 21 you may press ALT/F6 to execute the batch process, or press CTRL-Z to return to the Batch Mode Processing menu shown in Figure 12.

The target genotypes file (TGF) is used to execute WCOP processes in batch mode. The TGF file must be a text file where each line will specify the CID and SID of a genotype as it is registered in WPMS. It should be created using the menus in Figure 2 (Create Progeny Parent Tree) of WCOP rather than using a text editor, to avoid problems of typing mistakes, nonexistent CID, nonexistent SID etc. The general format for each line is: CID will be written right justified in the first six columns of each line, and SID will be written right justified in the following six columns.

3. Running RCL Output Report interactively

The previous version of the WCOP system was not generating the RCL output report automatically as it does now, it was only creating the TGF target genotypes file to use later in an interactive run of generating the RCL Output report. As of now you don't need this interactive way of generating the RCL output report, because when submitting batch processes or when generating the report in option 2 of the Main menu (Figure 1), the report is generated automatically. However, if you find it convenient to use the interactive way, you can still do so. This chapter explains how. This will only serve you if you have once before generated the output report, then deleted it, but you still have the input file (which is much smaller) intact. Then you can run it again, to produce the same output. The next chapter explains how to submit the output report using any TGF target genotypes file with CID's and SID's, to produce a complete new report.

First you have to determine which file you want to use as input. You would probably be using one of the IN_timestamp.DAT files generated by the system as explained in section 2.2. Then you should invoke the RUN_RCL.COM with the command

```
@RUN_RCL
```

and the batch file will prompt you for the name of the input file (for example IN_timestamp.dat) and the output report file name. This is a typical dialog when running RUN_RCL, with the above files:

```
Type filename of input file   : in_23aug94_153612.dat
Type filename of input file   : out.dat
FORTRAN STOP
```

Now the RCL output report has been generated to the file OUT.DAT.

4. Submitting the Output Report with input file

To generate an output report with an existing TGF target genotypes file you can submit the file OUTPUT_REPORT.COM directly, instead of doing the selection from the screen (see section 2.2). This is especially useful if you want to use a previously generated TGF target genotypes file, removing a couple of entries and adding a few others (in a text editor). However, it should be pointed out that the target genotype (the CID and SID) in each line must be generated previously in the system, or it will not be included in the report at all. The process of generating the output report will continue without notifying the user.

To check that all target genotypes in the file are in the WCOP system, you could go to Create Progeny Parent Trees in option 1 of the Main Menu (Figure 1), and here recover the file you want to use as input to OUTPUT_REPORT, and read it in with ALT/F9. If there are target genotypes that are reported as not existing in PMS, those should be corrected. If some of the target genotypes are added to the list, it means that they have not yet been generated to WCOP, and would not be included in the report, using the input file. They should be generated first using e.g. the Batch Mode Processing (see section 2.4). If none of the target genotypes in the input file are reported as not existing in PMS, and all are reported as already existing, you are ready to use the file as input to submit the RCL Output report.

When submitting the report, at least the input filename should be given as a parameter. As the second parameter can be given if you want full generation of both the target genotypes and their progenies (See section 2.2 about this) with the keyword "full", or the small generation with only the target genotypes with the keyword "small". The default if you don't specify the second parameter is "small", e.g. the report without the progenies.

With only filename as parameter (here shown with bold) specified, submit like this:

```
$ submit/notify/noprint/que=large_jobs/par=cop_user:example_tgf.txt output_report
```

With both filename and parameter "full" for including progenies specified, submit like this:

```
$ submit/notify/noprint/que=large_jobs -  
/par=("cop_user:example_tgf.txt","full") output_report
```

If you are logged on to nodes ALPHAC or SYRIUS, you should use the batch que SYRIUS_LARGE_JOBS instead.

Here the file example_tgf.txt should be in the general format where each line contains: CID is written right justified in the first six columns of each line, and SID is written right justified in the following six columns. And each target genotype in each line should be in WCOP, or else it won't be included in the report.

5. Multi-user Restrictions

The WCOP system has been made so that several users can simultaneously access the system, submit batch jobs, revise records interactively etc. However since the unit of update is not a single record in a database, but rather a whole chain of records in one update pass (the parent tree), a few restrictions have been imposed on the users:

- Each user and each batch job submitted will work on their own temporary files, which are created in SCRATCH_AREA in a sub directory which is unique to any other user or batch process. The general format of the temporary sub directory is SCRATCH_AREA:COP_processid.DIR, e.g. SCRATCH_AREA:COP_538968404.DIR. Here the three temporary files PARENT2.DMS, PARENT3.DMS and IPPS2.DMS are created, and possibly also a number of IN.DAT processing files. When a user session of WCOP is ended, or a batch job finishes, all these temporary files are deleted.
- When entering one of the WCOP menus, other processes might add data to the list of progeny parent trees you are currently reviewing.
- The lists of SELECTED genotypes which is created dynamically in the menus of Figure 3 and 7, will never be affected by another user, because it resides in the temporary datasets for the current session, but the list of already generated genotype in Figure 6 you are selecting FROM, may be updated during the interactive session.
- Submitting several batch jobs at the same time might give problems if the file MPPSUBMIT.LOG in the users root directory has version_limit 1 or 4. The VAX command SET FILE /VERSION_LIMIT=15 MPPSUBMIT.LOG could avoid those problems.
- The main datasets are never deleted, and are present in the logical name COP_DATA with the filenames PARENT.DMS and IPPS.DMS
- Each user is granted access to the main datasets by an SCS process. If new users should be added to the system, the access list must be updated, and the process of changing the privileges for that user must be run. If you don't have access, invoking @COPSYS will give an error message about the lacking privileges to access the two datasets PARENT and IPPS. In that case you should contact SCS to be granted full access. If you don't have full access to the datasets, you can still enter the menus and revise the data which have been generated, but you can't perform any updates on the data, e.g. all the batch jobs you send will fail, and pressing ALT/F6 to update data in a menu will also fail.
- Both batch process updates and interactive user updates will be lined in queue so that the first access will be given total control of the datasets PARENT and IPPS in the time it takes to update, in which all other processes will have to wait until the particular update is processed. However, each process will release the datasets between each generation of a parent tree, thus granting access to other processes to continue while the process itself is building another genotype parent tree.

- Each genotype generated by mean of WCOP system does not have duplicate leafs in their genetic tree, so when you select different genotypes for creating the RCL input file the system has to process all of them to generate one genetic tree without duplicate leafs. When WCOP has generated the genetic tree, it dumps the information into a file that will serve as an input information source for the RCL program. This file contains the number of genetic lines that are common for the original genotypes, and with no duplicates of ancestral parents. Each of these genetic lines represents an entry in the genetic matrix of parentage, so the number of lines is equivalent to the size of the matrix. The RCL program actually has a limit of 2300 by 2300 in matrix size. For this reason the RCL program will abort if there are more than 2300 genetic lines in the input file. Since this number of lines is not easily deducted from the number of progeny parents chosen by the user originally, it is difficult to detect this problem before the RCL program actually aborts. If the process does not generate the output RCL file please verify the number of genetic lines that has been written in your input file.

It has been established that some parameters of the user profile often have to be changed in order to be able to run the programs of WCOP. Specifically it is noted that the AST quota and the Enqueue quota have to be changed. However, since it is not sure which parameters are obligatory to change and which not, here is a list of a user profile which has been proven to work (you can obtain a similar report with the command SHOW PROCESS /ALL):

```

5-AUG-1994 14:12:11.41   User: XXXXXXXXXX          Process ID: 20800523
                          Node: SATURN              Process name:
"XXXXXXXXXX"

Terminal:                 LTA5338: (LAT_AA0004005205)
User Identifier:         [XX,XX]
Base priority:          4
Default file spec:     USER7:[XXXXXXXXXX]

Devices allocated:     SATURN$LTA5338:

Process Quotas:
Account name: XXXXX
CPU limit:              Infinite   Direct I/O limit:      4096
Buffered I/O byte count quota: 32672   Buffered I/O limit:    100
Timer queue entry quota: 20         Open file quota:       254
Paging file quota:     63002   Subprocess quota:      6
Default page fault cluster: 16         AST quota:             4094
Enqueue quota:         2000     Shared file limit:     0
Max detached processes: 0         Max active jobs:       0

```

6. The RCL output report

This chapter will describe the output report generated either in CREATE RCL OUTPUT REPORT from the main menu (Figure 1), or option 2 or 4 of the BATCH MODE PROCESSING menu (Figure 12).

The first part of the report is a matrix of the genotypes which were selected, where each number with coordinates (x,y) for genotype x and genotype y will be the value of the coefficient of parentage for the two genotypes. The value for (x,y) will always be the same as the value for (y,x). Each genotype is represented in the matrix with a consecutive number VAR, the CID and the SID. The first value in the first line of values in the matrix below says 1.000 because x is (253,20983,1) and so is y, e.g. coefficient of parentage is 100% for itself. The next value in the line is 0.095 meaning that the coefficient of parentage of y (253,20983,1) with x (277,23899,34) is 9.5%.

| VAR | CID | SID | 1 | 2 | 3 | 4 | 5 | 6 | 7 | 8 | 9 | 10 |
|-----|-------|-----|-------|-------|-------|-------|-------|-------|-------|-------|-------|----|
| 253 | 20983 | 1 | 1.000 | 0.095 | 0.079 | 0.118 | 0.129 | 0.170 | 0.086 | 0.104 | 0.034 | |
| 277 | 23899 | 34 | 0.095 | 1.000 | 0.047 | 0.102 | 0.130 | 0.119 | 0.140 | 0.080 | 0.028 | |
| 366 | 28374 | 3 | 0.079 | 0.047 | 1.000 | 0.035 | 0.057 | 0.052 | 0.043 | 0.042 | 0.012 | |
| 372 | 8784 | 2 | 0.118 | 0.102 | 0.035 | 1.000 | 0.100 | 0.156 | 0.149 | 0.064 | 0.021 | |
| 397 | 29898 | 1 | 0.129 | 0.130 | 0.057 | 0.100 | 1.000 | 0.169 | 0.120 | 0.140 | 0.048 | |
| 481 | 38728 | 1 | 0.170 | 0.119 | 0.052 | 0.156 | 0.169 | 1.000 | 0.113 | 0.094 | 0.031 | |
| 517 | 29873 | 1 | 0.086 | 0.140 | 0.043 | 0.149 | 0.120 | 0.113 | 1.000 | 0.079 | 0.028 | |
| 552 | 9812 | 1 | 0.104 | 0.080 | 0.042 | 0.064 | 0.140 | 0.094 | 0.079 | 1.000 | 0.046 | |
| 557 | 9727 | 1 | 0.034 | 0.028 | 0.012 | 0.021 | 0.048 | 0.031 | 0.028 | 0.046 | 1.000 | |

The second part of the output report is a list of the varieties with cross name, exactly in the order that it was present in the input file, e.g. sorted by the field NP:

| LIST OF VARIETIES WITH CROSS NAME | | | | |
|-----------------------------------|-----|-------|-----|------------|
| NP | VAR | CID | SID | CROSS NAME |
| 1 | 253 | 20983 | 1 | ---- |
| 2 | 277 | 23899 | 34 | ---- |
| 3 | 366 | 28374 | 3 | ---- |
| 4 | 372 | 8784 | 2 | ---- |
| 5 | 397 | 29898 | 1 | ---- |
| 6 | 481 | 38728 | 1 | ---- |
| 7 | 517 | 29873 | 1 | ---- |
| 8 | 552 | 9812 | 1 | ---- |
| 9 | 557 | 9727 | 1 | ---- |

The third part of the output report, with the header DENDROGRAPH DATA, includes data to be used for generating the dendrograph. If the list ends with the line "LDIF = 0" then the generation of the report went well, else an error occurred.

DENDROGRAPH DATA

| VAR | CID | SID | CROSS NAME | | NP |
|-----|-------|-----|------------|--------|-----|
| | | | WGR | BGR | ORD |
| 253 | 20983 | 1 | ---- | | 1 |
| | | | 0.0000 | 0.0000 | 1 |
| 481 | 38728 | 1 | ---- | | 6 |
| | | | 0.0000 | 0.0000 | 2 |
| 397 | 29898 | 1 | ---- | | 5 |
| | | | 0.8647 | 0.8853 | 4 |
| 277 | 23899 | 34 | ---- | | 2 |
| | | | 0.0000 | 0.0000 | 5 |
| 372 | 8784 | 2 | ---- | | 4 |
| | | | 0.0000 | 0.0000 | 3 |
| 517 | 29873 | 1 | ---- | | 7 |
| | | | 0.0000 | 0.0000 | 6 |
| 552 | 9812 | 1 | ---- | | 8 |
| | | | 0.8995 | 0.9492 | 7 |
| 366 | 28374 | 3 | ---- | | 3 |
| | | | 0.9150 | 0.9690 | 8 |
| 557 | 9727 | 1 | ---- | | 9 |

.....

```

1  0.0000
6  0.0000
5  0.8647
2  0.0000
4  0.0000
7  0.0000
8  0.8995
3  0.9150
9

```

LDIF= 0

