

PedigreeMaster

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Pedigree Master Software Manual

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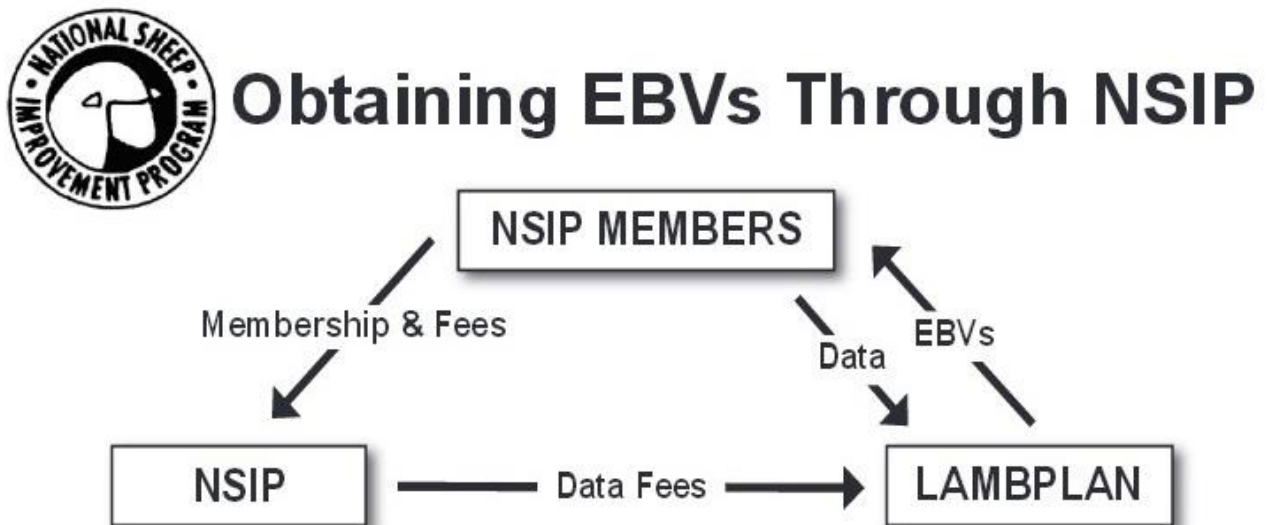
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Chapter 1 -- Introduction

Congratulations on enrolling in the National Sheep Improvement Program (NSIP). By enrolling in the program you have made a major step forward toward the genetic improvement of your flock. The technology utilized in this program is identical to that which is highly successful in also improving the genetics of cattle and swine. It is a powerful tool that can produce great results. Computers are, of course, needed to successfully submit data, receive the results and utilize the selection aids that this technology produces. The purpose of this manual is to help you more smoothly interact with the software and be able to fully utilize all of the technology that is available to you.

First, though, it is important to realize how NSIP, its members and Lambplan, which processes the data, all interact with each other and how the process works. The chart below shows the overall view of this interaction.



Graphic courtesy of Katahdin Hair Sheep International

Basically, NSIP is an administrative body that administers the program in the United States and works with breeders and Lambplan to encourage growth and successful use of the program. NSIP is also responsible for improvements in the program. The NSIP office is located at PO Box 244, Harlan, IA 51537. Mary Sorensen is in charge of the office. Her telephone number is 712-579-6376 and her email is office@nsip.org. As shown in the diagram, NSIP sends the fees for data processing to Lambplan, located in Australia.

Lambplan is an Australian organization that has a long and proven history of successfully processing data for thousands of sheep flocks in Australia. NSIP members submit their data to Lambplan and in turn receive Estimated Breeding Values (EBVs) from Lambplan. Data is accepted twice monthly by Lambplan and a calendar of submittal dates is online at the NSIP website: <http://nsip.org>. As your NSIP fees are on an annual basis, you may submit data on any of the submittal dates.

Information can be submitted on a wide variety of traits. Currently, traits which are analyzed are number of lambs born, number of lambs weaned, birth weight, weaning weight, maternal weaning weight, postweaning weight, fleece weight, fiber diameter, staple length, standard deviation of fiber diameter, yearling weight, hogget weight, postweaning scrotal circumference, yearling scrotal circumference, ultrasound fat and loin muscle depth and fecal egg count. Additional traits may be available in the future. A listing of the abbreviations of these traits, and explanations of them, are included in Appendix A.

There are two software programs that producers can choose to work with – Pedigree Wizard and Pedigree Master. Pedigree Wizard was the first software to be developed and works only on 32-bit machines. Assistance for this program is available at:

<http://katnsip.com/nsip-help-documents.html>

<http://kidplan.mla.com.au/pedigreewizard/index.htm>

and instructional videos from Lambplan at:

<http://www.sheepgenetics.org.au/Resources/Software-for-managing-data/Pedigree-Wizard-Help>

Pedigree Master was introduced late in 2012 and works on both 32- and 64-bit machines. This manual is a guide to help producers better utilize the Pedigree Master software.

Chapter 2 -- Downloading, Installing and Customizing Machine Usage

PedigreeMaster (PM) software may be used in either 32- or 64-bit machines. The alternative software is PedigreeWizard which can only be used on 32-bit machines. As of this writing (April 2015), ways are being researched to make PM easier to use on Apple computers. Currently, Apple users must have software such as BootCamp, VirtualMachine or another type of program that is capable of running PC programs. A program called Parallels has been used successfully by recent users. Appendix B gives additional information on using PM with a Mac.

Downloading and Installing

The latest PM software can be downloaded at:

<http://kidplan.mla.com.au/pedigreemaster/index.htm>

This site should be checked at least twice per year for new versions of the software that may include new features, be more efficient, or resolve problems encountered in previous versions.

The screenshot shows the Pedigree Master website's download page. The browser window title is "Pedigree Master - Mozilla Firefox". The address bar shows "kidplan.mla.com.au/PedigreeMaster/". The page has a navigation menu on the left with links like "Help Topics...", "Pedigree Display's", "Importing", "Backups", "Update Pedigree", "Logo Image", "Reports", "Browse Screens", "Import data", "Add&Change screen", "Setup options", "Misc", "Links...", "SheepGenetics", and "Results Downloads". The main content area is titled "Download" and features a green warning: "Please .. always create a backup before installing new or updated version of PedigreeMaster". Below this, a list of versions is shown, with the most recent at the top: "Version 1.38 - 26 Nov 2013" with a "Download" link. The changes for version 1.38 include "Added Auto RFID reading" and "Modifications to RFID reader (compatibility)". Other versions listed include 1.37, 1.36, 1.35, 1.34, 1.33, and 1.32, each with a brief description of updates.

The newest version is near the top of the page in the large rectangle with **Download** next to the version title. You will be asked to save the file so you should know where you would like to store the download, or where your computer normally stores downloads, before you click on it. Once a site such as the desktop has been decided on, click on the **Download** link to the newest software version and store it. Note: In some systems, a problem may occur with Norton Security if your setting is high. In these cases you will be asked if the file is alright to process.

The file name is typically PM-Y-XX, where Y is a one-digit number and XX is some two-digit number. If this is the file Norton is evaluating, it is alright to process.

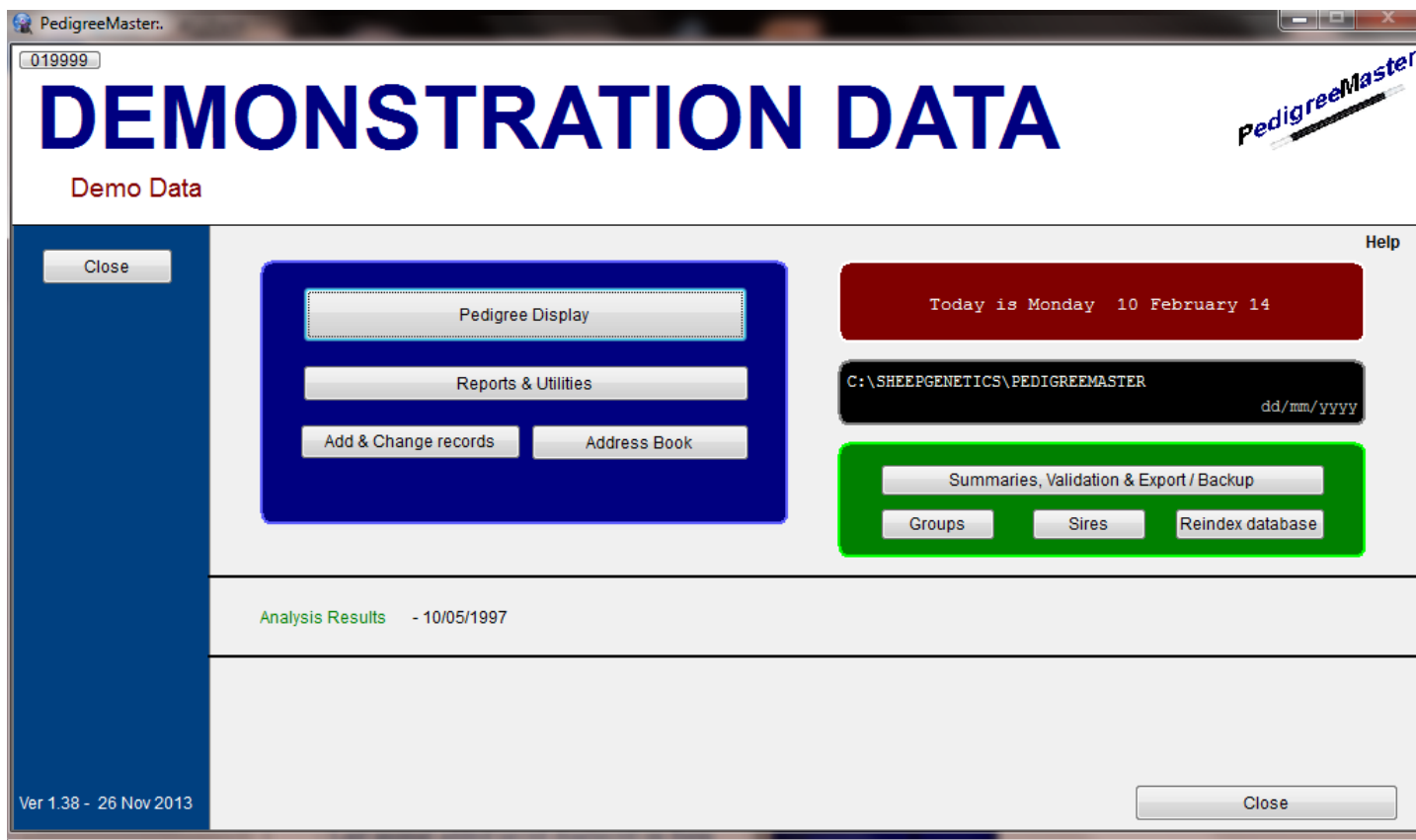
At the dialog box, click on **Save file**. When the download is completed, click on it and a dialog box will appear – click on **Run**. The next box will welcome you to PM – click on next. The next dialog box to appear will want you to set up a directory. The preferred choice by far is:

C:\SheepGenetics\PedigreeMaster

Click on **next**. The dialog box that will appear next will allow you to put PM on the Start Menu, which is preferred. It is also suggested that you create a desktop icon. This can be deleted later if you so desire but many find it useful to have. Click on Next and then click on Install. When it is installed, click on Finish. You may be asked if you wish to include demo data to be installed, or the demo data may automatically be installed, depending upon the PM version and your configuration. This will show you what some of the screens will look like after you have added animals with data. If demo data is on your machine, do not delete it as at least one record of the demo data must be there until you put on your own data. Then the demo data is deleted.

If PM doesn't automatically launch, you will be asked if you want to launch PM and if you plan to immediately input some data or work with the program in general--click on **Yes**.

Customization



One of the first things you will want to do is to have your name appear on the main screen. To accomplish this, at the main screen, click on the **Address Book** button. On the new

The screenshot shows the 'PedigreeMaster' software window with the title 'DEMONSTRATION DATA'. The interface includes the following elements:

- Navigation:** A green back arrow in the top left corner.
- Header:** 'DEMONSTRATION DATA' in large red letters, with 'Demo Data' below it.
- Form Fields:**
 - Breed Code: 01
 - Flock Code: 9999
 - Stud Name: DEMONSTRATION DATA
 - Stud Master: Fred the computer
 - Name: Demo Data
 - Address: (empty)
 - City / Town: (empty)
 - State: (empty)
 - Postcode: (empty)
 - Profile: Pedigree Wizard
 - Phone: (empty)
 - Fax: (empty)
 - Mobile: (empty)
 - Group: Demo Data
 - Web: (empty)
 - Email: (empty)
- Order records by:** A dropdown menu with options: Breed & Flock, Stud, Name.
- Find:** A search box with a green search icon and a 'Browse' button.
- Comment:** A text area containing: 'Demonstration data set', 'Breed : 01', 'Flock : 9999'.
- Buttons:** Previous, Next, Browse all records, New record, Delete record, Close.

screen, note the green **back** arrow in the upper left corner to be used to get back to the main screen. This will be seen on most screens in PM. The new screen may be blank or it may have demo data on it, depending on what option you chose earlier. The first thing to do in filling this screen out is to put your flock ID and other information into the system. You should have earlier received a six-digit code from either NSIP or LambPlan that is your LambPlan ID. The first two numbers of this code should be entered in the Breed Code section of the screen. The last four numbers should be entered in the Flock Code section. You should also enter information in the Stud Name and Name sections as these will appear on the main screen. The other sections are self-explanatory and optional. When finished, click on **Close**. This will take you back to the main screen.

On the main screen there is a six-digit number in the upper left corner, just under PM. Click on this and a setup menu will appear.

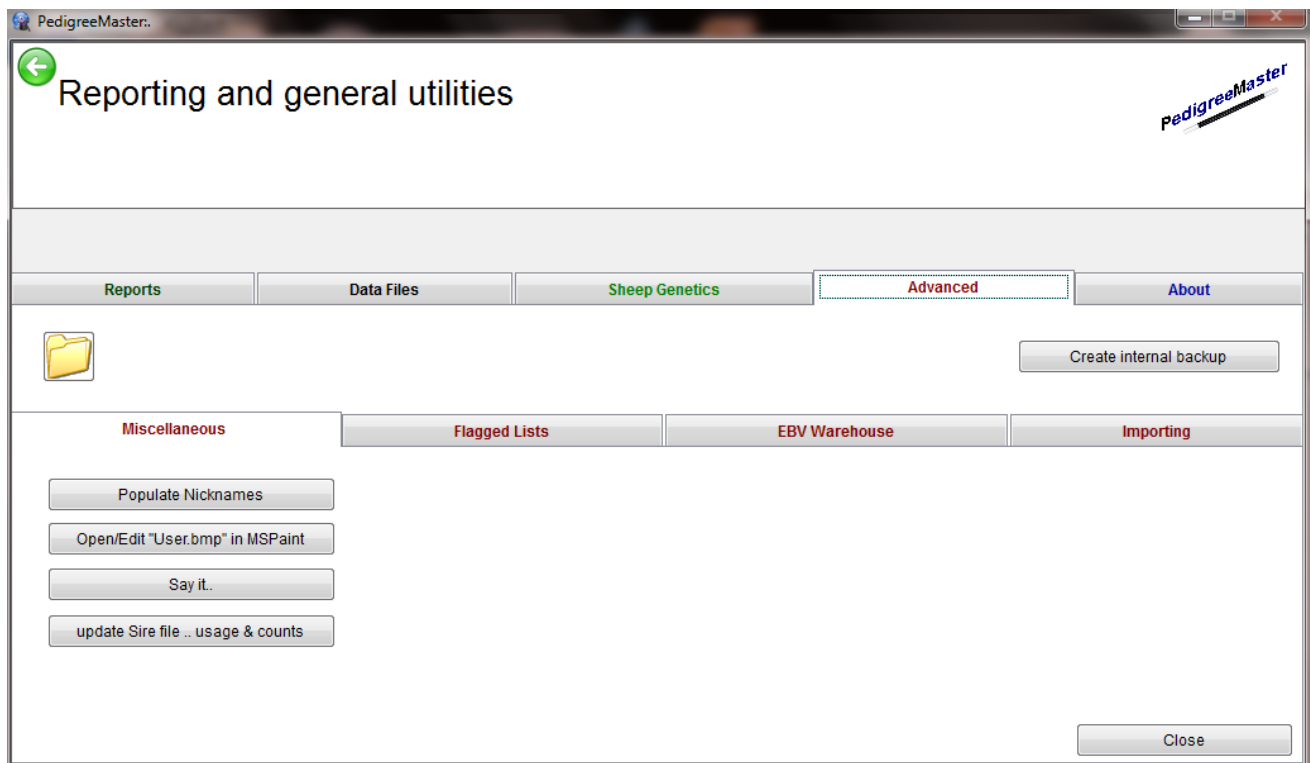
In the Breed Code and Flock Code sections of this screen, put in the same numbers you entered on the last screen for those fields. Under that are four auto typing text inputs. These are texts that you can use as shortcuts when entering data. The advantages of using these will become apparent when you later enter data. For now, simply remember where these are as you will later want to use them. Under those boxes is a box for you to select the format in which you would like dates displayed. Choose the format you like best and then click on Save and Close. Your flock name and your name should now appear on the main screen. Note that the data in the lower left corner of the main screen is in DD/MM/YYYY format and will not change as it is in the format commonly used in Australia and denotes the creation date of the software you are using.

If you are downloading and installing PM and do NOT have any data previously in Lambplan, go to the main screen and push Ctrl-C. A screen will appear dealing with conversion setups.

Click on the **Load NSIP Ranges** button. This tells PM that the program should run in NSIP mode with all weights in pounds. A black band should now appear on the main screen, about 2/3 of the way down from the top, and in the band it should say that the program is in NSIP Mode.

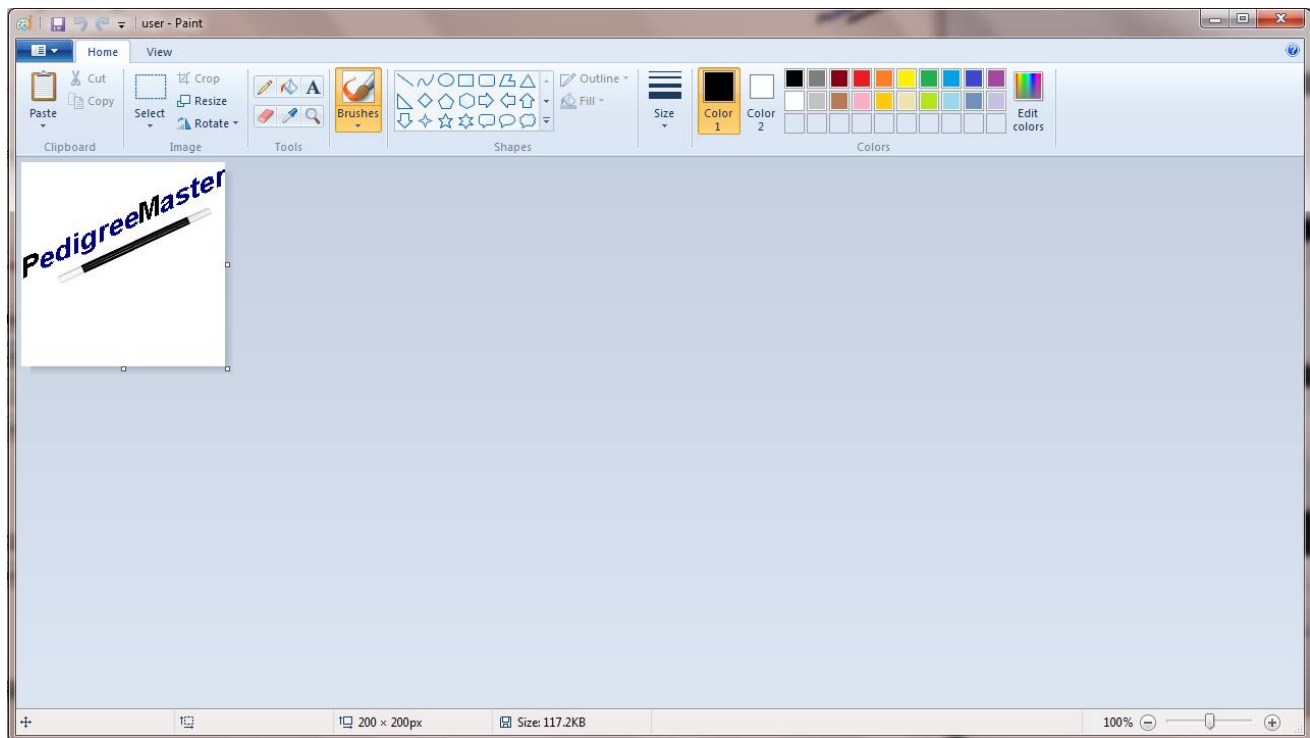
At the main screen, and on reports you will print later, the PM logo will appear. If you want to change this to a logo of your own, first have the image stored on the computer. For example, it could be a digital photo, clipart or a scanned image.

At the main screen, click on the **Reports and Utilities** button and then on the **Advanced** tab.



Then click on the **Open/Edit "User.bmp in MSPaint"** tab. Click OK on the alert screen.

On the screen that appears, the PM logo will appear. Toward the upper left you will see a blue area with what appears to be a page and a "down" arrow.



Click on it and then click on **Save As**. Change the filename to user-2 and click on Save. Next, click on **Open**. Locate the image you want and double click on it.

Click on the resize button. In the **Resize and Skew** screen, be sure the circle by **Pixels** is filled in. The numbers by Horizontal and Vertical do not have to necessarily be the same, however neither should exceed 200. If one or both are larger than 200, first be sure that the **Maintain aspect ratio** box is checked. Then change the largest number to 200. The other number will change as well. Click on **OK**.

Again click on the **down** button in the blue area and then on **Save As**. Change the file name to **user** and the **Save as type** should be changed to **24-bit image**. Next change the directory to c:\SheepGenetics\PedigreeMaster and click on **Save**.

A screen will appear asking if you want to replace "user.bmp" and you should click on **Yes**. A screen will then appear telling you that you must exit PM for the change to take place and so you will want to exit the MSPaint screen. PM will disappear. Re-start PM and your logo should be in the upper right area of the main screen. This will also appear on reports you later generate.

If you already have data in Lambplan but are now changing to PM, see the data input section at page 20 to get your data into the program.

Chapter 3 -- PedigreeMaster screens

Before entering data and looking for specific items in the software, it is advisable to go through all of the various screens to familiarize yourself with all of the capabilities of the software. Before viewing the various screens, however, it is advisable to look through the glossary of terms in Appendix A so that you are familiar with many of the various terms and trait abbreviations used in PM. At the opening screen, the first thing to note is the **Help** button near the upper right corner. If you click on it, a web browser will open with a PM link. Clicking on that link will bring up a screen with a variety of help items in a frame on the left side. The help here is a bit brief and not too explanatory, but may provide you with some answers. Also, it is important to verify that you are using the most recent version of PM that is listed at the top of the page.

Pedigree Display

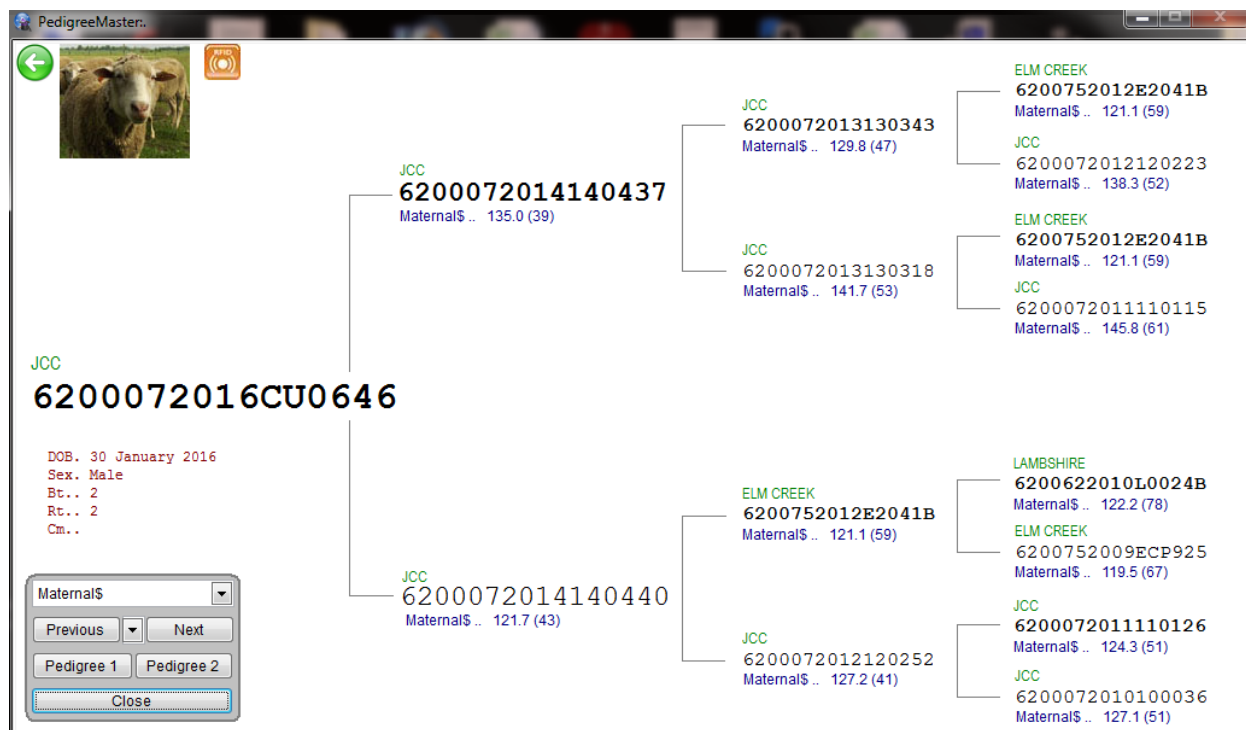
Clicking on **Pedigree Display** reveals a screen with seven tabs.

The screenshot shows the PedigreeMaster software interface. The main window displays a pedigree for animal ID 0199991995950006. The sire is 0199991992920099 and the dam is 0199991992920001. The animal's sex is 2 (Female) and its date of birth is 23/04/1995. The group is 1 (Stud). The interface includes a filter section with 'Filter is off', 'Previous', 'Next', 'Browse', and 'Pedigree' buttons, and a 'Flagged' checkbox. Below the pedigree, there are tabs for Breeding, Carcase, Wool, Reproduction, Mics, EBVs, and Visuals. The Breeding tab is active, showing options to change group, add new animal, delete animal, and edit sire/dam. A status dropdown menu is open, showing options: Current, Sold, Culled, Reference, Dead, Missing, Active, and Unknown. The animal's nickname is 950006. At the bottom, there are fields for Birth Type (2), Rear Type (2), Lambease (0), Conception Date (//), Method (3), Foster Ewe, Testicles, Jaw, and Recip ID. On the right side, there is a list of animal IDs in the system, with 0199991995950006 highlighted. The window title is 'PedigreeMaster:' and the window has standard OS controls.

From the upper left, the animal ID is shown, along with the IDs of its sire and dam. Under that is the animal's gender, date of birth and group number and name, if input. There is also a comments section available if you want to include management notes, such as scrapie genotype or other management information. The "Breeding" tab is the default tab to be open. On the right side is a frame with the ID of animals in the system. You can move up and down with the computer's arrow keys, or use the slide on the right side to see another animal displayed. To the left of the frame is a filter if you want to look at a particular individual or set of individuals. The **previous** and **next** buttons under that can also be used to display different

animals. By clicking on the **Browse** button, a screen will appear with a listing of basic pedigree and other data. To return to the previous screen, click on the X in the upper right corner of the screen, or press the ESC key.

Clicking on the **Pedigree** button will reveal a pedigree with grandparents and great-grandparents, along with basic information of interest such as date of birth, gender, etc., under the ID.



At the top of the box located to the lower left, you can select a trait or index from the drop-down menu whose value is then shown under the animal's ID. The **Previous** and **Next** buttons will take you to other animals. The **Pedigree Preview** button is the first step in viewing and printing performance pedigree forms. To get a printable version of a performance pedigree, you can click on either **Pedigree 1** or **Pedigree 2**. Both will show the pedigree, along with the logo, sex, date of birth and other information, along with the EBVs. The difference between the two is that **Pedigree 1** produces a performance pedigree with a large logo and the parents and grandparents, plus the animal, while **Pedigree 2** shows a smaller graphic but includes the great-grandparent generation. Also, a **Print Preview** box will appear which allows you to print the pedigree for sale display or other uses. To go back, hit the ESC key or click on the folder in the Print Preview Box. To return to the main **Pedigree Display** screen, press **Close** or hit the ESC key.

Breeding

By clicking on the **Breeding** tab you can change the group number, add or delete an animal, change the sire or dam and even give it a nickname, plus other items such as birth type, or lambing ease. The importance of group designation cannot be overemphasized. A management group is a group of sheep that were born under similar management conditions at one site and over a period no longer than 42 days. Ram lambs and ewe lambs can be considered in one group if they were managed together under the same conditions.

CAUTION: Deleting an animal is usually NOT a good idea because deleting it means that all of its production values are deleted from the database. Thus even if an animal has died and has no relatives in the flock, its data is still of value in determining the group average in which it performed and removing it will artificially change the EBVs of animals in the flock. Deleting an animal is rarely a good idea so be absolutely sure you do not want this animal, or its data, included if you hit **Delete**. For the most part, you only want to use **Delete** if you have put in a new record and there are numerous errors with it. Under no circumstances should you delete an animal simply because it is no longer in the flock! If an animal is no longer in the flock, change its status on the right side of the page to one that is appropriate. You can also make changes in such things as type of birth and type of rearing. As you click on the other tabs such as **Carcase** (how the Aussies spell carcass), **wool, reproduction and Mics**, you can see how data may be input there.

The screenshot shows the PedigreeMaster software interface. At the top, a pedigree chart displays three animals: a central blue box (6200072003020319), a red box (6200071998000212), and a green box (6200071994000080). Below the chart, there are input fields for Sex (2), Date of Birth (01/22/2003), Group (1 early lambs), and a Comment field. A navigation panel on the right includes buttons for Previous, Next, Browse, and Pedigree, along with a Filter is off indicator and a Flagged checkbox. The main data table is divided into tabs: Breeding, Carcase, Wool, Reproduction, Mics, EBVs, and Visuals. The Carcase tab is active, showing a table with columns for Date, Wt, cFat, Emd, Scrotal, Wec, Group, and Date Wt. The table contains rows for Birth, Weaning, EP Weaning, P Weaning, Yearling, Hogget, and Adult 2y. To the right of the table is a list of animal IDs, with 6200072003020319 highlighted. A Close button is at the bottom right.

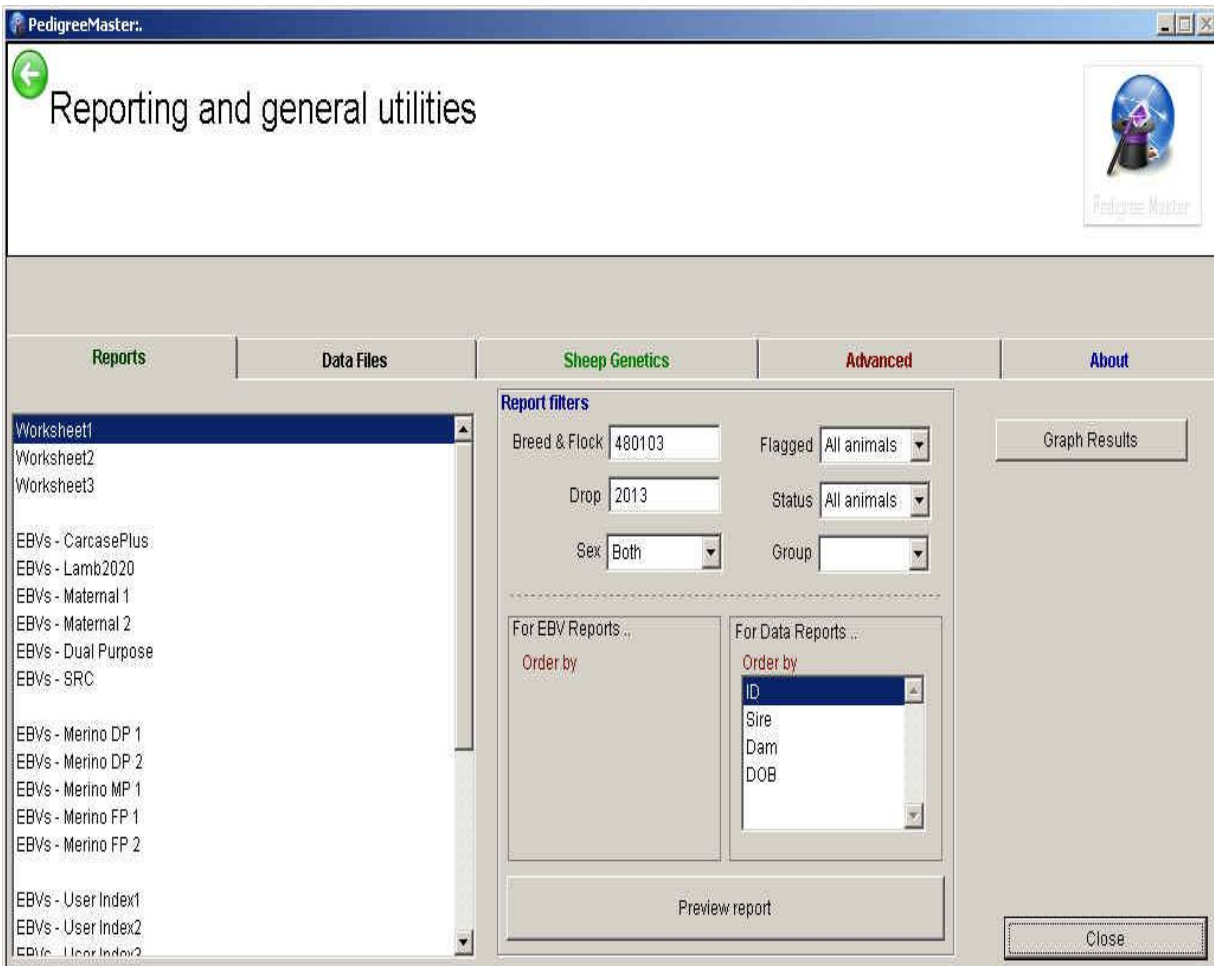
	Date	Wt	cFat	Emd	Scrotal	Wec	Group		Date	Wt
Birth	01/22/2003	10.0							Adult 3y	//
Weaning	03/19/2003	47.2	0.0	0.0			1	+	Adult 4y	//
EP Weaning	05/07/2003	89.3	0.0	0.0			1	+	Adult 5y	//
P Weaning	//		0.0	0.0			1	+		
Yearling	//		0.0	0.0			1	+		
Hogget	//		0.0	0.0			1	+		
Adult 2y	//		0.0	0.0			1	+		

Note: EP weaning weight is for “early” postweaning weight, which is what many United States flocks will use, especially those in the Midwest and East. Also, a hogget is a sheep that is 1-2 years old, usually around a year and a half old.

More about the use of this screen is explained in the **Data Input** section of this manual. The **EBVs** tab reveals the EBVs sent to you from previous processing runs. The **Visual** tab gives you the opportunity to add visual data and comments if you wish.

Reports and Utilities

Activities under this tab are numerous and greatly varied in their results.



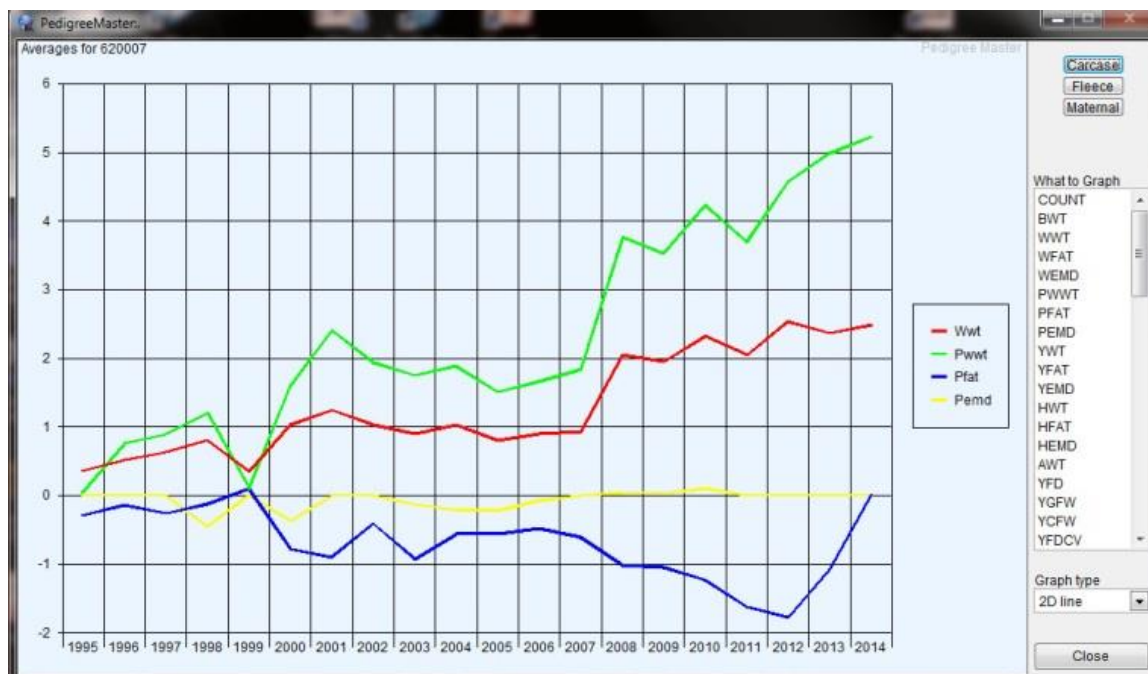
Under the **Reports** tab, you will find a wide variety of reports to view or print. Some may not have much information for you as they do for those with other breeds, while some reports will provide your flock with a wealth of information. In the box at the left, select the type of report such as a general worksheet, or EBV type or comments. The report filters section allows you to have only certain groups be included in the report. Then select how you would like the data in the report to be ordered. For a worksheet report, click on **Preview Report**. For one of the EBV reports, click on either **Sire**, **Dams** or **Progeny**. A **Print Preview**

EBV Report ..

Animal ID	Sex	Bwt	Wwt	PWwt	Ywt	Pfat	Pemd	Pwec	NLW%	Lamb2020	Carcase+	Sire	Dam
6200072004020409	F	0.2	1.3	2.8	2.3	-0.6	-0.1	0.4	5.1	101.81	113.92	6200252002000259	6200072000000194
6200072006020616	F	0.2	1.1	2.1	1.6	-0.5	-0.0		9.5	101.57	111.51	6200252002000259	6200072001000219
6200072007020712	F	0.3	1.2	2.6	2.2	-0.8			2.6	101.45	111.38	6200072000000238	6200072004020409
6200072008020806	F	0.5	2.6	5.2	4.1	-1.2	-0.0		22.2	104.12	128.68	6200252005000516	6200072004020408
6200072008020837	F	0.3	1.7	3.5	2.8	-0.7	0.1		5.5	103.07	120.76	6200252005000516	6200072007020712
6200072009020912	F	0.3	1.9	3.9	3.3	-0.9	0.0		10.2	103.37	122.72	6200252005000516	6200072006020620
6200072009020914	F	0.4	1.9	3.8	3.2	-1.0	-0.0		1.4	103.27	122.12	6200252005000516	6200072006020620
6200072010100027	F	0.3	1.6	3.0	2.4	-0.7	0.1		1.9	102.91	119.36	6200252005000516	6200072006020620
6200072010100028	F	0.5	2.2	4.1	3.4	-1.2	-0.1		9.1	103.42	123.38	6200252005000516	6200072006020620
6200072010100029	F	0.8	2.7	3.9	2.9	-1.4	-0.1		33.6	103.49	124.65	6200252005000516	6200072003020319
6200072010100030	F	0.6	2.2	3.3	2.5	-1.0	0.0		18.6	103.16	121.93	6200252005000516	6200072003020319
6200072010100031	F	0.6	2.8	4.9	3.7	-1.4	-0.0	-12.3	12.2	104.25	128.89	6200252005000516	6200072008020821
6200072010100035	F	0.4	2.0	3.5	2.6	-0.6	0.4	-12.4	15.2	103.78	124.96	6200252005000516	6200072008020804
6200072010100036	F	0.8	3.0	5.7	4.5	-2.1			18.3		126.15	6200782009009379	6200072009020904
6200072010100037	F	0.7	2.6	4.5	3.4	-1.9			11.7		121.43	6200782009009379	6200072009020904
6200072011110103	F	0.6	2.4	4.8	3.8	-1.8			5.7	102.55	119.98	6200782009009379	6200072004020409
6200072011110115	F	0.8	3.0	5.4	4.1	-2.0			35.0	103.48	125.81	6200782009009379	6200072008020804
6200072011110130	F	0.7	2.5	4.5	3.5	-1.9			10.1	102.83	120.87	6200782009009379	6200072008020837
6200072011110133	F	0.5	2.4	4.9	4.0	-1.6			8.2		123.06	6200782009009379	6200072008020813
6200072011110138	F	0.5	2.3	4.1	3.1	-1.0			11.0	103.80	125.84	6200072010100017	6200072010100030
6200072011110141	F	0.7	2.6	4.8	3.8	-2.0			8.7	103.04	122.32	6200782009009379	6200072010100028
6200072011110149	F	0.7	2.6	4.1	3.0	-1.3			25.0	103.34	123.98	6200072010100017	6200072003020319
6200072012120206	F	0.7	2.3	4.1	3.2	-1.8			10.1	102.63	119.34	6200782009009379	6200072008020837
6200072012120208	F	0.4	2.1	4.2	3.4	-1.3			11.1	102.79	120.17	6200782009009379	6200072008020837

bar will appear with printer commands if you wish to print out the report. Press either the ESC key to exit or click on the folder in the Print Preview box.

An interesting tab to hit is the **Graph Results** tab. Click on it and your progress over years will be shown in a graph.



You can choose from the list of traits on the right side of the graph. This is a great way to see long-term progress. A variety of interesting graph types are available to choose from in the lower right corner. To go back, press the ESC key or click on the **Close** tab.

DATA FILES

The **Data Files** tab will show you a variety of datasets. The **Main Database** tab will display your actual dataset and you can make changes if necessary. By clicking on the **Sires** tab, you can see how many progeny are in the dataset from each individual sire. You can add a sire by clicking on **New Record** and adding the appropriate information. Similarly, you can delete a sire if you don't need him in the sire list any longer. The sire list will show up later when you add new animals into your dataset.

Each lamb will need to be assigned a group when its data is entered and the **Groups** tab will show you the names of the various groups from which you can choose. The groups come with pre-assigned names but you can customize these by selecting names that are more meaningful for you. By clicking on the **Visuals** tab you can view, add and delete data regarding visual aspects of animals in your flock. This is not data that will be analyzed but is a good reference set for visual and other non-analyzable data such as genotype for scrapie. If you click on the **Address Book** after you have submitted data, a listing of other NSIP flocks in your breed should appear, along with their flock codes. Clicking on the **Breeding Value** tab will reveal all of the EBVs for animals in your flock, as well as the accuracies of those EBVs.

Another function which can be performed here is to create a backup file. You can do this by clicking on the **Create Internal Backup** tab. It is very important to keep backup datasets! Keep one not only on your computer but also on cloud storage and/or a jump drive so that if your computer should someday fail, you don't have to put all of the data back into the system! No one wants to think about that happening, but it can. Thus it is advisable to keep backup datasets somewhere other than on your computer, such as on a cloud drive or a thumb/jump drive. The location of the backup will be shown in a pop-up screen.

Or, you can save the data by clicking on **Main Database...DBF Format**. Again, the location is shown in a pop-up screen. While neither of these two options allow you to name an auxiliary directory, you can do that as explained in Data Submission. These two options do, however, give you a backup on your computer, which is a valuable option. If you click on **Open export folder**, the datasets are available for you to interact with them. You can view them or save them to a different location if you wish. For example, one good use is to double click on Exp_ebv file. This will produce a file of all animals with their EBVs and other basic information in Excel. This is the easiest way to get the data into Excel for you to sort or rank animals by different variables.

Information and processes under the **Sheep Genetics** tab include the **Import EBVs from ATFEBV** button which can be used to import EBVs from another location. This is a button that is rarely used but nice to have if needed. The **Import from elites address book** is discussed in the first section of this manual. It is also important to note the Update Pedigree from results and the Add Pedigree from Result buttons. Each time that data comes back from processing, these two buttons should be clicked. This will update results that are shown on the pedigree printouts.

When you click on the **Advanced** tab, several new tabs appear.



Clicking on the **Create internal backup** tab will make a backup file and the directory location will appear. There are four other tabs that appear: **Miscellaneous, Flagged Lists, EBV Warehouse and Importing**. Under **Miscellaneous** are four tabs. The first is **Populate Nicknames** which, when clicked, puts the last six digits of an animal's 16-digit ID in the nickname spot if the nickname area is blank. The **Open/Edit "User.bmp in MSPaint"** tab is discussed in the **Getting Started** section of this manual. The **Sayit** tab appears to have no significant function, although it is interesting to work with. Click on the tab and type some words into the **Dribble Creator** space that appears. When you click on **Sayit**, a voice will verbalize what you typed in.

Clicking on the **update Sire file...usage and counts** will update the figures for number of progeny of various sires for various traits after a new set of data has returned from Lambplan processing. When you click on this tab, a screen appears asking if you want to limit the list to sires used in the last three years and you can respond Yes or No. This option is available because often people do not care about the usage of sires in the distant past, yet sometimes are. This will update the figures that show up under **Data Files – Sires**.

The **Flagged Lists** tab is for advanced users where specific groups are desired for reports. This has its greatest advantage in very large flocks and is of limited use in small flocks. **EBV Warehouse**, when clicked on, reveals a tab titled **View Current Breeding Values**. When that tab is clicked on, a report appears with animal IDs, EBVs, and accuracies of those EBVs. This report is for viewing only. The **New Record** and **Delete Record** tabs are currently not working. **WARNING** – you rarely, if ever, want to delete animals. Deleting them is not the route to take if you have animals no longer in the flock or ones that you just don't want to see. If you delete them, their data is deleted also and this data is important in determining the subgroup values, which is the basis for the entire analysis. The large and small **A's** determine font size, while the **Lock** tab functions as it does in Excel to allow you to look at data to the far right of the spreadsheet while still viewing the first column, which is the animal ID.

The **Importing** tab is used to import data from Pedigree Wizard or from PM archives.



The use of this tab is explained in the **Initial Data** section of the manual.

Add/Change records

Use of this tab is described in the **Data Input** section of the manual.

Address Book

Use of this tab is described in the **Downloading, installing and customizing** section of the manual. It is basically an address book of contact information on other breeders. You must have your information entered for it to be displayed on the main screen

Chapter 4 – Data input

There are several situations that you may find yourself involved in when it comes to entering data. The different situations are separated here by letter with instructions following for that particular situation.

A. Need to input previous NSIP data

If you have data from NSIP prior to the processing of data by LambPlan and would like to include that data, contact the NSIP coordinator, Rusty Burgett, at info@nsip.org or phone him at 515-708-8850. If you filled out the enrollment form (a link to the enrollment form is: <http://nsip.org/nsip-become-a-member/>) this situation should have been taken care of when you enrolled in NSIP. If, however, it was not and you find yourself with data that was previously submitted to NSIP prior to LambPlan processing and you would like to get that data into Lambplan, please contact Rusty.

B. Need to create or input an animal ID

Before proceeding, you need to know how to form animal ID numbers. Without proper IDs, flocks may not be connected, animals may be mistaken for others and data may not be meaningful. Be aware that animals who were enrolled in NSIP before LambPlan will have their IDs changed when converted to LambPlan. Do NOT try to change these or it may cause serious problems in regard to tying animals together throughout your flock and into other flocks. If you prefer to think of these animals by their previous ID, you can put that ID in the nickname blank to help you identify them by their old ID.

Animals in NSIP but not from your flock: Before you enter any animals into the dataset, you first need to take care of animals that came from outside your flock but were born into an NSIP flock and thus already in the system. You need to get their NSIP number from the NSIP breeder and the IDs of their sire and dam to be sure that you can use that animal to connect to existing NSIP flocks. The methodology of inputting the data is explained below.

Animals from a non-NSIP flock: These animals do not have an NSIP ID and you will need to provide one for them when you enter them as a sire or dam. You do not need to enter them as an individual. When creating an ID for them, the 16-digit NSIP number for one of these animals starts with the six digits of the NSIP code for animals you raised, followed by their four-digit year of birth, followed by the last two digits of the animal's year of birth, followed by a four-digit number that identifies the animal, usually some numbers from its eartag. Be absolutely sure that this number does NOT duplicate another tag already in your system.

Animals from your flock: NSIP animals have a 16-digit identification. The standard Lambplan ID for a lamb is to start with the first six digits same as your NSIP ID. Of those six numbers, the first two are for the type of flock, such as terminal sire, maternal/wool, etc. The next four numbers are for your flock within that group. The six-digit code is unique for your flock. Following that, the next four numbers are the year of birth of the animal. Next, generally, are the last two digits of the animal's birth year. For example, an animal born in 2014 would have characters 7-12 as 201414. However, instead of those two numbers, you can input either CU or CO in some cases. The animals for which you use CU or CO are cull animals, such as wethers or animals that may have a bad mouth, unsound feet or some other problem. By putting CU or CO in their identification, EBVs will not be printed for those animals. Their

production data will be used in helping predict the EBVs of close relatives but animals with CU or CO will not appear in printouts, thus not creating confusion by printing an EBV on a non-breeding animal. Also, you are not charged for data submittal on CU and CO animals if the CU or CO is in the ID prior to input of post 90-day inputs. There is a limit, however, in that no more than 25% of your flock can be CU or CO animals.

In general, Lambplan does not like to have letters in animal identifications. If you routinely use letters in an animal's identification, it would be advisable to either switch to an identification system that does not use letters or have a system whereby a number represents a code for a letter. For example, perhaps you use the number 1 for the letter A and the number 2 for the letter B and so on. Then an animal whose tag is A331 would be coded in Lambplan as 1331. An animal with a tag of B879 would be coded in Lambplan as 2879. This system works well for those who use tags of various colors and want to somehow have that color included in the ID. Being unable to use letters in an animal's ID may seem like a problem at first to some producers, but it can be easily worked out with a little imagination and producers report that after a generation or two it is no longer a problem. If for some reason you absolutely must include a letter in the identification, contact Rusty Burgett at the NSIP office. He can contact LambPlan and see if it is possible to use that letter. As of May 2014, combinations of letters that are not allowable are DA,RT,NT,LT, AG, RL, AM, SN, MS,LS, RR, BK, MM, FK, LM, OO and WR. Never assume that a letter you put in an ID without permission from LambPlan will be acceptable!

IMPORTANT: NEVER change the ID of an animal who might appear in the pedigree of another animal. If you change this ID, the ID would have to be similarly changed in the pedigrees of other animals in which it appears. There is too much of a chance that one or more will be missed. If it is absolutely important to make a change like this, contact the NSIP office who can contact LambPlan to see if it is possible.

C. Need to input past data to get started on NSIP

Number of years: The first thing you need to do is decide how many years of past data you would like to input. The more data you include, the more accurate the estimates will be on the animals currently in the flock. However, the increase in accuracy is less for each additional generation that is included. There is no set guideline for how many generations should be included, however most producers will at least include all data for animals currently in the flock. It is **IMPORTANT** that when you include data from a lambing group that ALL data be included from that group. For example, when you include lambing data for your oldest ewe, you must include the data for all of the ewes that lambed in that group, even if they are no longer in the flock. This is because the NSIP analysis relies on comparing how animals perform with the performance of their contemporaries. Thus if you only put in the data from the ewe that is still in your flock, and not her contemporaries as well, there would be no comparison and the data would have little value. Most producers include enough data from past years to either include all of the data on ewes in the current flock, and their contemporaries, or they may go further back to include an additional generation on animals currently in the flock. The decision as to how far back to go is up to you.

Spreadsheet Entry: There are three main ways to enter data into PM. One way to get data into PedigreeMaster is from a spreadsheet. In general, you want to use this option **ONLY** if you already have the data in a spreadsheet for some other program. Otherwise, it is much

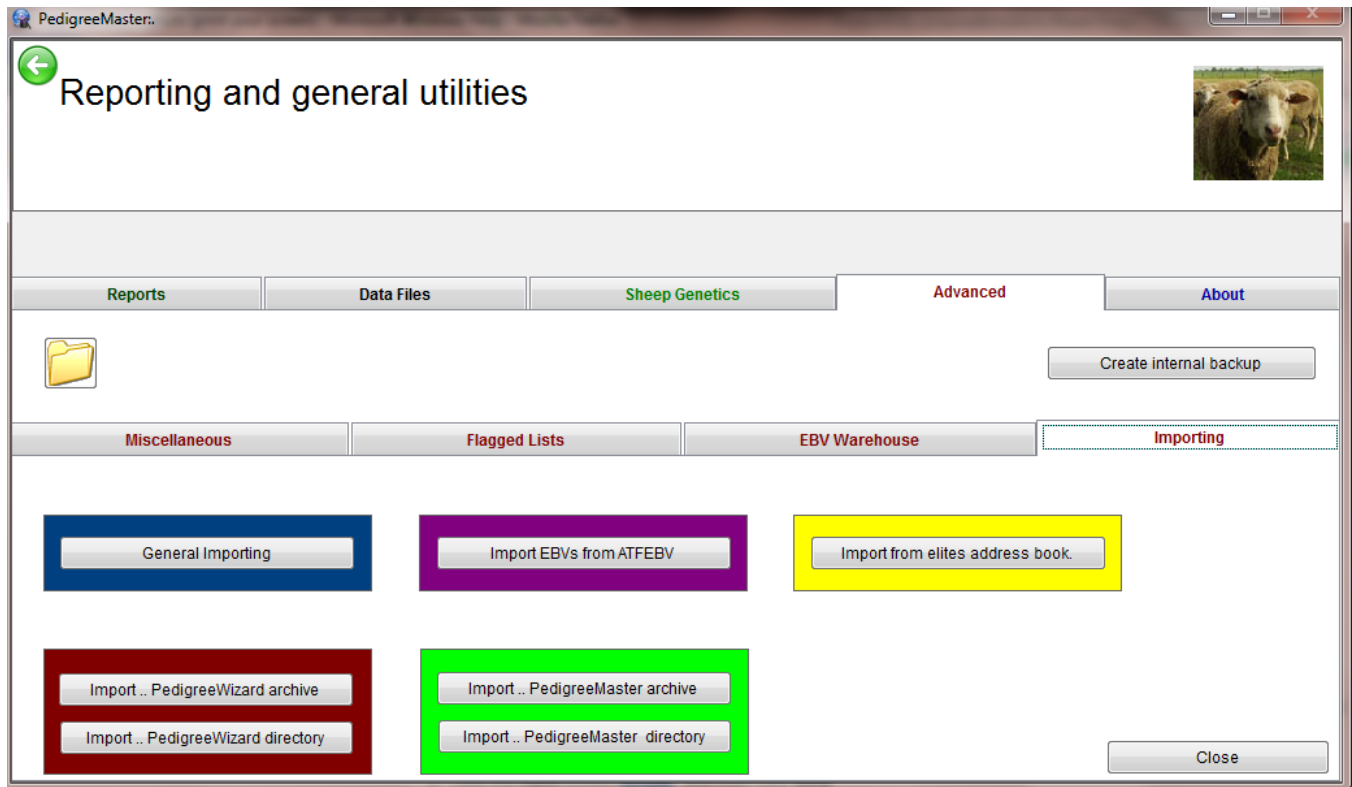
easier to input data directly into the program than to enter it into a spreadsheet and then transfer it.

To successfully transfer the data from a spreadsheet to PM, the spreadsheet must have the required columns headings with appropriate data under the column headings. The columns do not need to be in any particular order right-to-left as PM will find each one during the import.

<u>Column Heading</u>	<u>Description of Data</u>
ID	This is the 16-digit NSIP ID for the sheep you are adding.
Sex	1 for male, 2 for female
BT	Birth type, 1 for single, 2 for twin, 3 for triplet, and so on, up to 9.
RT lamb?	Rear type- how many lambs did the ewe raise in this batch with this lamb?
CM	Conception method – 1= Natural, 2= ET, 3= AI, 4= JivET
LAMBEASE	Lambing ease for this birth. 0 – Unobserved, 1 - No Assistance, 2 - Some Assistance, 3 - Hard Assistance, 4 - Abnormal presentation, 5 - other
Status	Current, Culled, Dead, Missing, Reference, Sold , Unknown
BWT	Birth weight value
DOB	Date of birth – PM uses standard American formatting: MM/DD/YYYY
Sire	This is the 16 digit NSIP ID of lamb’s sire.
Dam	This is the 16 digit NSIP ID of lamb’s dam.
GRP	Group number of birth group
WDDMM	Date of weaning weight (in MM/DD/YYYY format)
WWT	Weaning weight
EPDDMM	Date of early post-weaning weight (in MM/DD/YYYY format)
EPWT	Early post-weaning weight (120 d)
PWDDMM	Date of post-weaning weight (in MM/DD/YYYY format)
PWWT	Post-weaning weight [this may be PWT; WFEC puts it in WWT time]
FEC	Fecal egg count

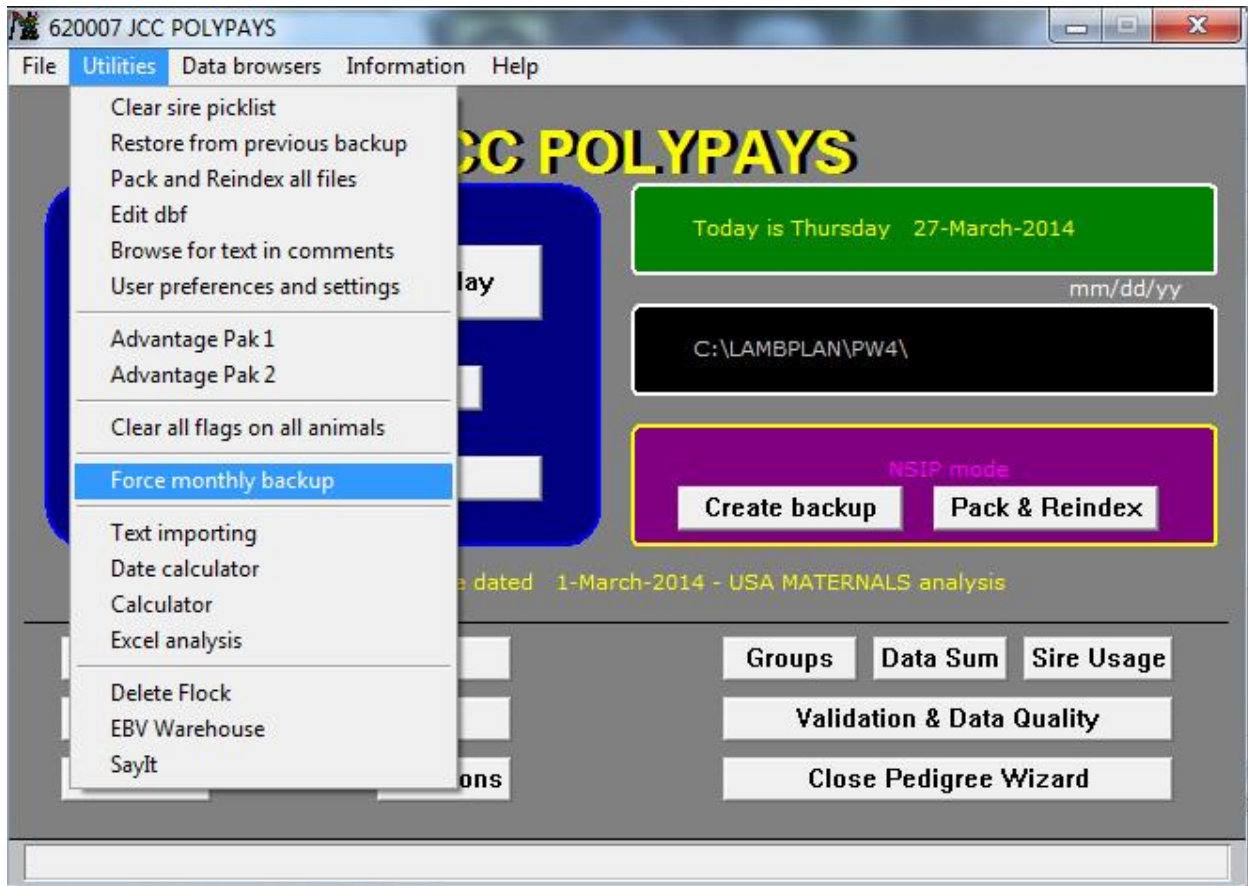
Other column headings can be obtained at: <http://kidplan.mla.com.au/PedigreeWizard/>. You do not need all of the above columns if you do not have data for that trait on any animal. After all of the column headings are in place you can then enter data. Be sure there are no blank cells or the fields may become offset when imported. If there is no data available for a particular trait for an animal, put a * in the cell.

After all of the data is entered, save the file as you normally would in Excel format but do not close it. Open Notepad as a blank file. Highlight all of the Excel Sheet’s data and column headings and copy and paste the file into Notepad. Save the file and remember where you saved it and what you named it. Next go to PM’s main screen and click on the **Reports and Utilities** button. Then click on the **Advanced** tab and then on the **Importing** tab. Next click on **General Importing** and then on **Select file**. Choose the file you want to work with and click OK.



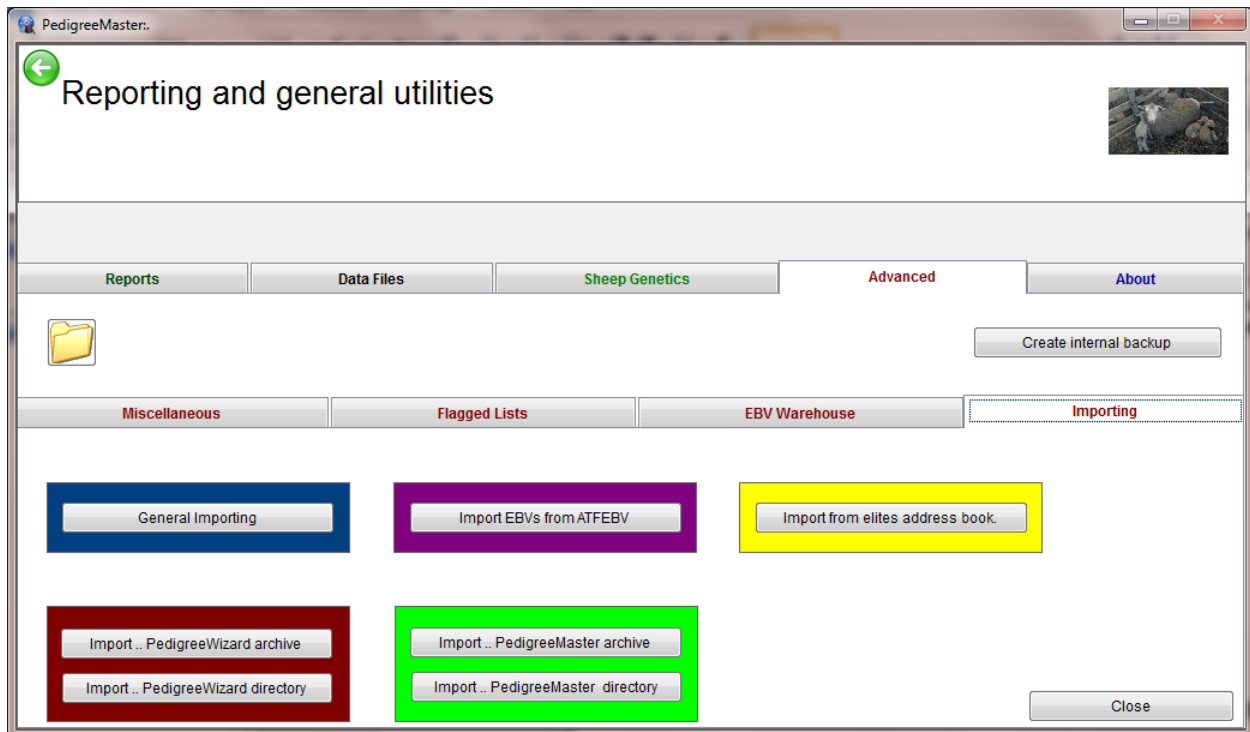
Then click on **View file to Import** and look at the file to see if you detect any errors. If everything looks OK, click on **Import file** and then on **Check Main Data Table**. If no errors appear, you can click on **Update to main database**. Your data should be successfully onboard. You can use this same procedure to update data after the initial data is in place to combine new data with your original data. Also, if you notice an error after importing a file, you can go through this process again only making a change the next time when you view the file prior to importing. It will overwrite the incorrect file. If you see some serious mistakes and want to start all over, you can click on the Undo import button to get you back to where you were before you started the import.

Data transfer from Pedigree Wizard: The first thing you need to do, of course, is to back up your PW data so that your data is secured should some computer malfunction occur. It is a good idea to frequently backup your data and back it up on different media in case your computer someday decides to die. There are several ways you can back up your data but the easiest way to do this is to open PW and click on the **Utilities** button on the bar at the top of the screen.



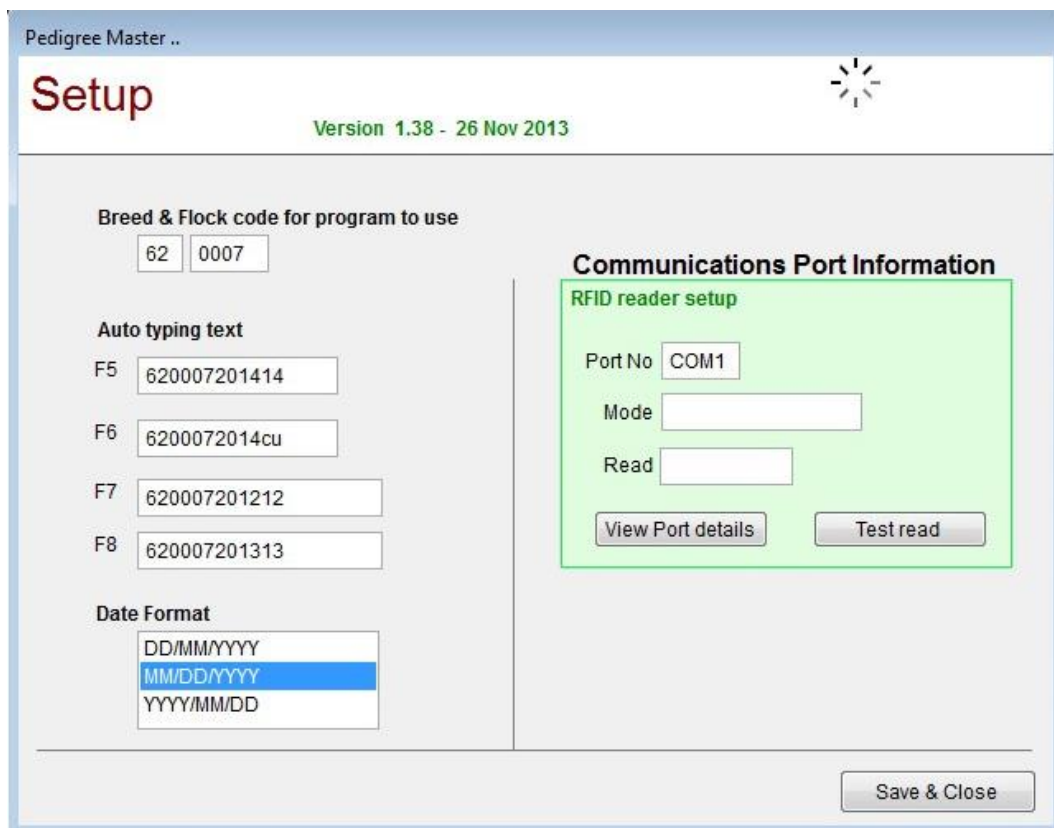
Click on **Force monthly backup** and the program will do its job. A popup screen will appear telling you that the process is completed and you should click on OK. Another popup screen will then appear telling you where your backup file is located. Write this down as you will need it later. Normally the file is located in the PW4 folder and the dataset is named YYYYMMDD where YYYY is the current year, MM is the current month and DD is the day. If you will be using PM on a different computer than the one that has PW, you will need to get the backup file on cloud storage or other type of transferrable storage such as a thumb drive so that the other computer can access it.

If you have not already downloaded and setup PM, you need to do that before proceeding. See the section at the beginning of this manual that has instructions on how to install and setup PM. If all is OK, then click on **Reports & Utilities**. Next click on **Advanced** and then on **Importing**.



If you backed up your data as described above, you need to click on the **Import.. Pedigree Wizard directory** tab. If you used some other method of backing up your data, you will likely need to click on the **Import..Pedigree Wizard archive** tab. After clicking on **Import..Pedigree Wizard** directory, you will be asked if you backed up the data and you should click on yes, assuming you backed up the data. A screen will then come up asking you to find the backup file which you made earlier. A warning will appear that you are going to overwrite the file in PM but it is OK to do so, so click on yes. When it is done moving the data, close PM and then reopen it. Everything should be complete – check to see that your flock ID and name are on the main screen. Click on Pedigree Display and see if your animals are there. Also, the black bar in the middle of the main screen should say that you are in NSIP mode. If not, try re-transferring your data. If you are still experiencing a problem, contact Rusty Burgett at info@nsip.org.

Direct input into PM: Most producers will input their initial data directly into PM and certainly most will input additional data by this method. A recommended way to begin with this process is to click on the Lambplan ID number located at the upper left of the opening screen. That will open a screen displaying the option of changing the values associated with various function keys. Changing those values will make data entry much easier.



The best use of the function keys that PM uses (F5, F6, F7 and F8) is to reduce the amount of work needed to input the first ten digits of an animal's ID. As shown in the graphic, different years can be used for years covering the data to be input, and CU or CO can be used in places 11-12 for animals that are to be culled, as discussed in the section on animal identification numbers. Setting and re-setting these when data from various years is to be entered can save a lot of time and greatly reduce errors.

Remember, the data entry will go much easier if you start with the oldest animals first. This is because as you enter new animals, previously entered animals can be entered with a few keystrokes, rather than needing to type in the entire ID. After the function keys are set to what you want them to be, click on **Save & Close** to return to the main screen.

There are different ways data can be directly entered into the PM software, but the easiest way to enter at least the pedigree portion of a new animal is through the **Add & Change records** button. First review the buttons at the top of the page. The **Edit Auto Build text** button will greatly speed up data entry. It is similar to the function keys but a bit faster. If you have the first ten digits of an animal's ID set in the **Edit Auto Build text** area, then all you need to do when you input the animal's ID is to put in the last four characters and either click on the **Edit Auto Build text** button or press the tab key or the enter key and the first twelve characters are automatically set in place for you. If, however, you want either CO or CU in places 11 and 12, you can enter the last six characters of the ID and when you click on **Edit Auto Build text**, the first 10 digits will be automatically entered. **Edit date 1** and **Edit date 2** are valuable items when entering data on a set of animals in the data input section. For example, if you are want to enter the weaning weights on a group of animals, you should set the **Edit date 1** to the

weaning date for the group of animals. Then as each animal's weaning date needs to be entered, you can simply drag the **Edit date 1** value into the appropriate date blank. **Edit date 2** functions the same way. Or, if you have set the date in one of the available function keys (F5, F6, F7 and F8), you can use them to enter the date by holding down the fn key while pressing the appropriate function key. The next button limits what age areas can be used for data entry. The areas that are then allowable appear in white and the non-allowable are in grey. Thus if you are only going to be entering weaning weight, you might want to specify that in the limits. This would keep you from entering data in one of the other areas by mistake. If you check the box for wool and fleece data, then you can input data for wool and fleece traits that are in the age range you previously checked in the button to the left. The last area on the top bar is a drop-down menu that tells you to what the various function keys are currently set.

You are now ready to start entering an animal ID, the 16-digit ID. You can either enter all sixteen digits, or, if you have the first ten digits of the animal's ID set in the **Edit Auto Build text** area, then input the last four characters of the animal's ID and either click on the **Edit Auto Build text** button or press the tab key or the enter key and the first twelve characters are automatically set in place for you. If, however, you want either CO or CU in places 11 and 12, then you should input the last six characters and click on **Edit Auto Build text** and it will put the first ten characters in place for you.

There are several ways that you can input the sire identification. The quickest way is that if the animal you are entering has the same pedigree as the previous animal (for example, you are entering an animal that is a twin or triplet to the animal just entered) then click on the **Repeat last animal's pedigree** button and the sire and dam identifications will automatically fill

in. You **MUST** have the animal ID entered before you click the **Repeat last animal's pedigree** button or you will have to click that button again after entering the animal ID. Note: A sire must be at least 297 days of age when offspring are born for him to be accepted as the sire.

If, however, the sire and dam are not the same as the previous animal, then you will need to use another method. The first button at the end of the Sire blank will give you a drop down list of all males who have "current status" and you may be able to find the sire there. This button is particularly helpful to find sires that are animals you raised yourself but have not yet been entered as sires. The next button with a drop down menu provides you a list of animals already identified as sires. So if the sire of the lamb you are entering has already been identified as a sire, it should appear in this drop down list.

If the sire is an animal that has not yet been entered or not identified as a sire, the quickest way to get it into the system is to directly enter its 16-character ID into the sire input area. When you press the ENTER key, a question will pop up asking you if you want to add it to the Sire picklist/database. You should click on Yes unless you are absolutely sure you will never enter another animal with that sire. By having sires in the database, data entry is greatly speeded up. The dam portion works the same way as the sire input.

Another way to enter sires, but which takes more time, is to click on the **Sires** tab at the beginning menu.

The screenshot shows the PedigreeMaster software window. At the top, there are menu options: 'Close window', 'New record', 'Delete record', 'A A', and 'Lock'. The main area is a table with the following columns: 'Picklist', 'Sire', 'Sire_ref', 'Progeny', and 'Sire_note'. The table contains several rows of data, with the first row highlighted in blue.

Picklist	Sire	Sire_ref	Progeny	Sire_note
	6200782009009379	09009379	72	
	62000720111110126	110126	19	
	6200752012E2041B	12E2041B	75	
	6200252011W1030C	11W1030C	5	
	6200622010L0024B		1	
	6200072013130315	130315	2	
	6200622010L0024B		1	
	6200072013130343	130343		

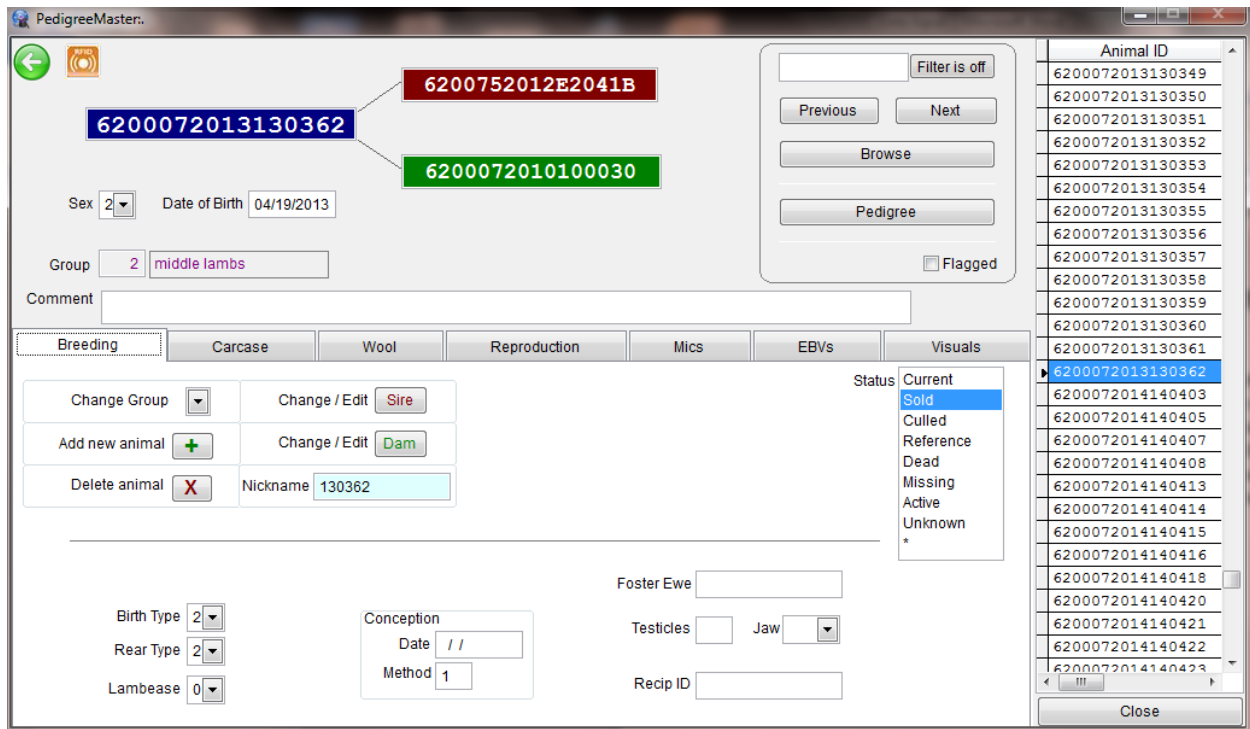
Click on the **New record** tab and enter the new sire's ID and nickname, if it has one, under the Sire_ref column. When finished, click on **Close window**.

You can tab to most of the other fields on the **Add & Change records** input screen except for the input areas in the upper right of the screen. The sex, birth type and rearing type menus as self-explanatory, as are the conception area inputs. It is important to know that

lambs reared artificially should have their type of rearing be input as a single. Lambs that die before weaning should, of course, be input as 0 for type of rearing. Choosing a pedigree method is optional. For pedigree method, choose normal management unless some DNA type of analysis was used. Lambing ease is self-explanatory and also optional.

The nickname is automatically set to the last six digits of the animal's ID but you can change that on this screen to something that is more meaningful to you if you wish to do so. For example, maybe the animal has been retagged with a new tag number or color and you wish to have the nickname area with the other ID. To the left, choose a group that the animal is in. See page 13 for instructions on how to change group names so that they are meaningful to you. It is EXTREMELY important that you select an appropriate group as all comparisons in the analysis are made within a group. See page 13 for information about the importance of selecting a group. The comments section can be used if you have something significant to input on an animal and status of the animal has a self-explanatory drop down menu. At that point you can save the record if you have no other data to enter. For most animals, however, you will want to enter the birth date, birth weight and other data. The other data entries and the Save Record button are fairly obvious. The E_ID input area is if you have an electronic ID that you wish to input. The **Discard changes** button is to be used if you came into this screen to make changes but then decided the changes weren't appropriate. See Appendix A for information on the other data input areas as to what the abbreviations stand for and the limits of the various values.

Another way to enter data is by clicking on the Pedigree Display button on the main screen.



Click on the **Breeding** button and the screen that appears allows you to do editing and enter new data as well. Across the top of the screen is the animal's pedigree along with its sex, date of birth and group. You can change the sex and date of birth at this point if you so desire. To the right of the pedigree is a filter if you only want to look at a certain group. The **Previous** and **Next** buttons move you to different animals. Or, you can click on the **Browse** button which will open up a spreadsheet of animals. Move the cursor on the far left side to the animal you want to see and then press the ESC button. The selected animal will now appear in the pedigree. Or, you can go up and down on the column of animal IDs on the far right side to select the animal you want. Clicking on the pedigree button will display an extended pedigree of the animal. By clicking on the **Breeding** button, you can see how to change groups, edit the sire and dam, add a new animal, delete an animal or change the nickname. CAUTION: When you delete an animal you are also deleting all of its data and thus changing the group comparisons. There are very, very few instances where you will want to delete an animal. Changing their status from current will keep them from appearing in the sire and dam lists but their data almost always needs to be in the database. Think more than twice before deleting an animal – they should rarely be deleted for the reasons just stated. If you click on the **Add new animal button**, you will see a different way to add animals. Autoprefix is there and, while they do not appear on the screen, the function keys work on this screen as well. The remaining input areas are similar to what is discussed above. It usually takes longer to input animals through this screen as the sires will appear in a drop-down screen only after you type in the first few characters and you must type in the entire dam ID. Click on **Save** when you are through.

Clicking on the **Carcase** button will bring up a screen allowing you to enter weights, carcass, scrotal and egg count data. The **Wool** and **Reproduction** tabs will bring up screens to allow you to enter data in those areas. The **Mics** tab brings up a screen to allow you to change identification data. While there is a button on this screen to retag animals, it is advisable to **NOT** retag animals because of the possibility of losing missing an animal and thus losing connections in pedigrees. There is a major difference between retagging an animal and simply changing its ID because it was input incorrectly. Retagging means that all animals with the original ID will have their ID changed to a new value. If you are using the Retag option to change a number on a lamb because it was input incorrectly, you could be making a catastrophic error because there might be an animal already in the system with that ID. If you simply have an incorrect ID for the animal, its sire or its dam, it is best to click on the Add & Change records, pull up the animal to which you need to make changes, make the changes and then save the results. Then delete the animal that has the incorrect ID. By making the change this way, you do not have to be concerned about disturbing the pedigrees that might occur in a retag. However, the retag option is a viable way to change the 11th and 12th characters to CO or CU if you want to do so and for some reason did not enter them initially.

The **EBV** and **Visuals** tabs do not allow you to enter data but are very valuable as they display the EBV information on the animal and visual factors that have been entered. The EBV values will change each time data is returned from Australia if you follow the protocol outlined in the Receiving Data section. Be sure to click on the Summaries, Validation & Export/Backup button and validate all of the data that you have just entered. Then backup the data – always backup your data after entering or changing it.

D. Need to input new data into an existing database

The procedures described above in section C can be used to input additional data to update your system. Whenever inputting new data, is it highly advisable to back up your past data so that your data is secured should some computer malfunction occur. If you are not entering data via a spreadsheet, it is a good idea to backup your data before beginning to add more. In addition, before beginning to add new data, it is a good idea to run through the animals via the Pedigree Display tab and make sure that animals which will no longer be sires or dams are not listed as Current. That will give you fewer animals to have to wade through when you are selecting sires and dams for the new lambs that you are going to enter. When you have done that, you can add data as described above in the **Spreadsheet Entry** and **Direct input into PM** sections.

Another way to input additional data is via the **Master Database**. This is a very slow option for entering new animals as it lacks some of the quick inserts available with the options described above. However, it can be a good way to input update data on animals whose pedigree and base data has already been input. For example, weaning weight data and ultrasonic scan data can be easily and quickly entered here. To input data into the **Master Database**, click on **Records & Utilities** at the opening screen. Then click on **Data Files** and then on **Master Database** and go to the first animal for which you have data to input.

Id	Sire	Dob	Sex	Dam	Bwt	Wddmm	Wwt	Wcf	Wemd
6200071987000003	6200241983000223	09/11/1987	2	6200241985000103	/	/	0.0	0.0	
6200071987000004	6200241983000223	09/13/1987	2	6200241985000119		05/10/2014	0.0	0.0	
6200071988000001	6200241985000059	02/20/1988	2	6200070000QD0001	/	/	0.0	0.0	
6200071988000002	6200241985000059	02/20/1988	2	6200070000QD0001	/	/	0.0	0.0	
6200071988000005	6200070000QS0078	03/07/1988	1	6200070000QD0078	/	/	0.0	0.0	
6200071988000078	6200070000QS0078	02/25/1988	1	6200070000QD0078	/	/	0.0	0.0	
6200071989000006	6200071988000005	02/05/1989	1	6200071987000003	9.9	/	0.0	0.0	
6200071989000007	6200071988000005	03/20/1989	1	6200071987000004	11.0	/	0.0	0.0	
6200071989000008	6200071988000005	03/20/1989	1	6200071987000004	9.0	/	0.0	0.0	
6200071989000009	6200071988000005	03/20/1989	2	6200071987000004	9.0	/	0.0	0.0	
6200071989000010	6200071988000005	02/18/1989	1	6200071988000001	7.9	/	0.0	0.0	
6200071989000011	6200071988000005	02/18/1989	2	6200071988000001	7.1	/	0.0	0.0	
6200071989000012	6200071988000005	03/14/1989	1	6200071988000002	7.9	/	0.0	0.0	
6200071989000013	6200071988000005	03/14/1989	1	6200071988000002	9.9	/	0.0	0.0	
6200071989000028	6200070000QS0030	10/05/1989	1	6200070000QD0028	/	/	0.0	0.0	
6200071989000030	6200070000QS0030	10/03/1989	2	6200070000QD0030	/	/	0.0	0.0	
6200071990000014	6200071988000005	01/15/1990	1	6200071987000004	13.0	/	0.0	0.0	
6200071990000016	6200071988000005	01/29/1990	1	6200071987000003	11.0	/	0.0	0.0	
6200071990000017	6200071988000005	02/02/1990	1	6200071988000001	11.0	/	0.0	0.0	
6200071990000018	6200071988000005	02/02/1990	2	6200071988000001	11.0	/	0.0	0.0	
6200071990000019	6200071988000005	02/03/1990	1	6200071988000002	13.0	/	0.0	0.0	
6200071990000020	6200071989000013	03/10/1990	2	6200071989000011	9.0	/	0.0	0.0	
6200071990000021	6200071989000013	03/10/1990	1	6200071989000011	11.0	/	0.0	0.0	
6200071990000022	6200071989000013	03/27/1990	2	6200071989000009	11.0	/	0.0	0.0	
6200071990000023	6200071988000005	10/01/1990	1	6200071987000004	11.0	/	0.0	0.0	
6200071990000031	6200071988000005	01/29/1990	2	6200071987000003	12.1	/	0.0	0.0	

You can use the function keys to input dates, as described earlier, which will speed up the process. Then input the data, such as weaning weight, and repeat the process for all lambs in the group. When finished, click on the **Close window** tab in the upper left corner. While it is possible to add records by clicking on the **New record** tab, it is a much slower process to input new records this way because the aids in repeating pedigrees and choosing sires and dams is not available with this screen. There is also a tab for deleting records but rarely will you want

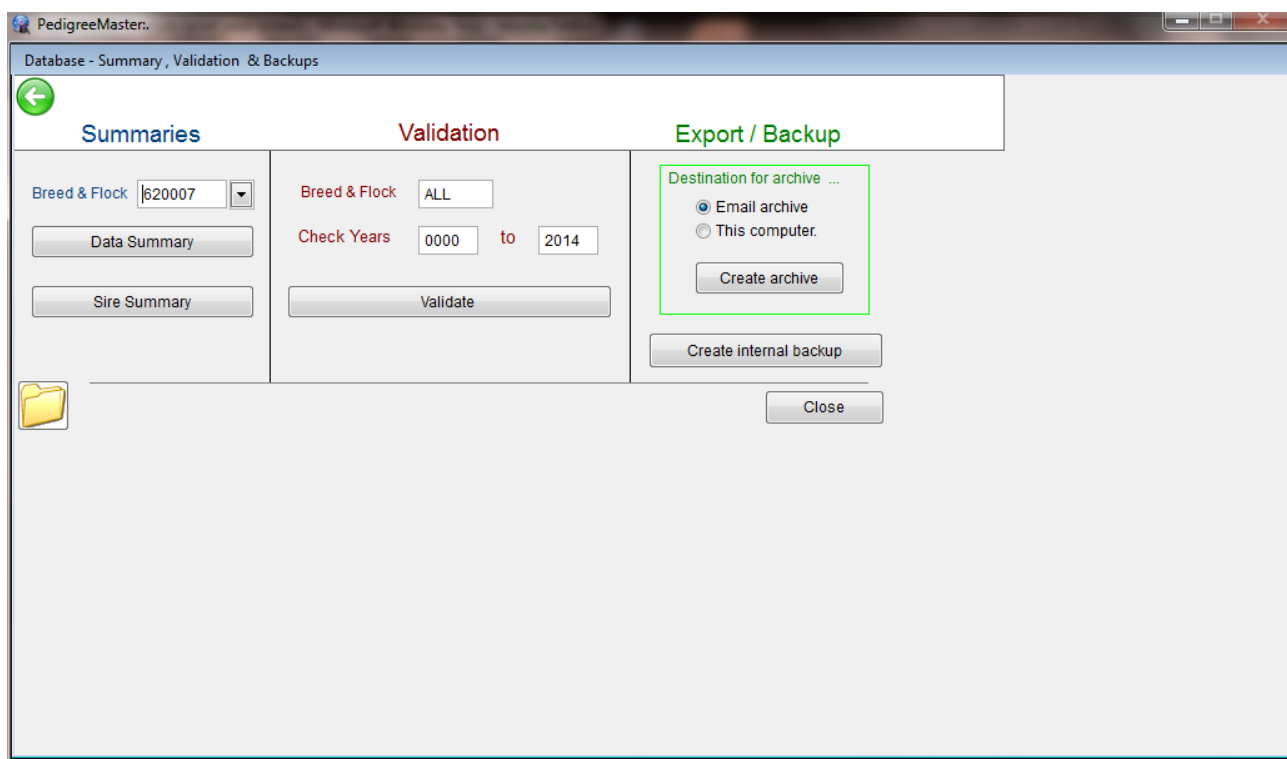
to use this. Remember that deleting an animal also takes its data out of the group comparison which is the basis for the genetic analysis! If you have data that needs to be changed, you can easily do it in the **Master Database**. This is preferred to deleting a record and starting over with new input.

Chapter 5 -- Submitting data

Data can generally be submitted to Lambplan twice each month, if needed. A calendar listing the submittal dates is online at: <http://nsip.org/nsip-member-services/data-run-calendar/>

You will need to submit your data via email to Lambplan in Australia. The email to use is: database@sheepgenetics.org.au. It is usually best to open your email and address a message to go to Lambplan and then proceed with PM while the email file is still open.

At the opening screen, click on the button labeled **Summaries, Validation & Export/Backup**.



Under **Validation**, a popup screen will appear asking you to input the years over which data should be checked. You should include whatever years in which you think there might be possibilities of errors. Generally, if you have validated your data in the past, you will need to only input the current year in both of the input areas. Click on **Validate**. If an error comes up, you should correct the error or there may be validity problems in the results that you get back, possibly some of the data will not be included. The error messages seldom use individual animal IDs to point out where the error is. More commonly, you will get a message saying that something is wrong with an animal of a certain sex and in a certain group in a certain birth year, along with what is wrong, such as too short of a weaning age, a ewe is reported to have lambed twice in a month or whatever the problem is. You then need to go through the various animals in that group, find the error and correct it. When the errors are corrected, validate again until

you get a message that says “Nothing to report.....” and ends with the year(s) within which you had data checked.

Next, under the **Export/Backup** heading, you need to fill in a circle either by **Email archive** or **This computer**. If you fill in the circle by Email archive, a zip file will be created that is best used as a backup for the data that you want to be submitted. When the circle by Email archive is filled in, click on **Create archive** and a message will come up “Include Breeding Vales in backup?” and except for very unusual circumstances, you should click on No. A message then appears telling you that an archive file was created and it lists the location. If you don’t feel the need for an email archive or you have already created one, the handiest way to get your data to the email is to fill in the circle by **This computer** and click on **Create archive**. A message will come up “Include Breeding Vales in backup?” and if you are sending the file to Lambplan, you should click on No. The only reason to save the breeding values in a backup would be to backup your data for your own use when you won’t be submitting any data in the near future. Then a box will appear onscreen asking you to browse for a folder in which to put the zip file. You can choose whatever location you like but the easiest is to use the default location that appears in the box. This will be the C:\SheepGenetics folder. The file will be named with your NSIP ID and have a zip extension. To use the default location, all you need to do is click on OK.

Or, another choice is to use the desktop as an option because it is easy to locate the file and once you are done with it, it will be easy to remember to erase the file. Choose your location, click on OK and a message will come up informing you that the archive was successfully created. If you have not already addressed your email, do so and you will then need to attach the zip file that is to go to Lambplan. You can do that through your normal email attachment procedure or click on the folder icon in the lower left part of the screen. The folder works as an explorer folder and the default opening is to the default location when you created the zip file. Some email software systems will allow you to drag the zip folder, named with your NSIP ID, into the email and attach it. When the file is attached to the email, press send. Be sure to check your sent file to make sure it was sent without problems. Within one or two business days of the data run, you will receive an email from Lambplan acknowledging that they received your data. It is then a good idea to move the sent message to a local folder or delete it to keep room free in your email system. Usually within 5-7 days of the data submission deadline you will receive your results.

Chapter 6 -- Receiving Data

After LambPlan has processed your data you will receive an email from LambPlan telling you that new EBVs are available. There are two important parts to the email. One is that there will be several reports attached to the email. These are printouts of your new EBVs as well as printouts of a sire summary, an error report dealing with any pedigree problems that were detected, a general database summary and a report on genetic trends of your flock. Pedigree error problems should be addressed as completely as possible.

The other important part is that in the body of the email there is a link to a website that you will need to go to in order to update the EBVs in PM. Be sure you know your LambPlan ID and the password that comes to you in the subject line of the email in brackets. In the email will be a link: <http://legacy.sheepgenetics.org.au/updates/>

When you get to that website, scroll down until you come to a file in the far right column (shown here in blue) that is named with your LambPlan ID followed by an EXE extension.

[legacy.sheepgenetics.org.au - /updates/](http://legacy.sheepgenetics.org.au/updates/)

[\[To Parent Directory\]](#)

Thursday, March 20, 2014 10:30 AM	2028072	00 Elites LPN 15Mar14.exe
Thursday, March 20, 2014 10:35 AM	171427	00 Percentiles and TraitLeaders 15Mar14.zip
Tuesday, March 18, 2014 9:52 AM	2138788	020041.EXE
Tuesday, March 18, 2014 9:52 AM	734409	020163#.EXE
Tuesday, March 18, 2014 9:53 AM	1126046	020645.EXE
Tuesday, March 18, 2014 9:53 AM	975085	020863.EXE
Tuesday, March 18, 2014 9:55 AM	3466037	021614.EXE
Tuesday, March 18, 2014 9:56 AM	2424042	021929.EXE
Tuesday, March 18, 2014 9:56 AM	653794	022272.EXE
Tuesday, March 18, 2014 9:57 AM	1408324	022656.EXE
Tuesday, March 18, 2014 9:57 AM	1018602	023151.EXE
Tuesday, March 18, 2014 9:58 AM	873876	023270#.EXE
Tuesday, March 18, 2014 9:58 AM	258830	023369.EXE
Tuesday, March 18, 2014 9:59 AM	3741768	023626#.EXE
Tuesday, March 18, 2014 10:01 AM	2942776	023666.EXE
Tuesday, March 18, 2014 10:01 AM	817338	023691.EXE
Tuesday, March 18, 2014 10:01 AM	1087413	023780.EXE
Tuesday, March 18, 2014 10:02 AM	1021142	023881.EXE
Tuesday, March 18, 2014 10:03 AM	2324664	024075.EXE
Tuesday, March 18, 2014 10:03 AM	1242527	024166.EXE

Click on that link and you will be asked if you want to save the file. Save it somewhere where it will be easy to find. After the download is complete, click on the file. **WARNING:** Some anti-virus software such as Norton may think that the file is a virus. If it is the file you got from the above website, it is not a virus. Click whatever you need to in order to get your antiviral software to accept it. Then you will see a message pop up that says the program will install a Sheep Genetics Breeding Values update. You will be asked if you wish continue and you should click on **Yes**. A screen will pop up welcoming you to the update program. Click on **Next**. Once it clears this step, you will need to input your password. Remember that the password, in the subject line of your email, is case sensitive. Input the password and click on **Next**. Click **Next** on the following screen and then you will then be asked where you want the

data stored which will be c:\SheepGenetics\PedigreeMaster if you followed the default values when installing PM. If you did not use the default directory, you will need to change the directory to the one you designated at installation. When the correct folder is highlighted, click on **Next** and then click on **Install**. The next screen will appear if an index is being calculated for you, telling you that an index is being calculated and you should click on **Next**. The next screen will tell you to click on **Finish** to exit Setup.

Sometimes you may get a screen that asks if you want new screen icons. If you have the icons that you want, uncheck the boxes or another set will appear on your computer screen.

The program will have now put new values into PM, based on your latest data submittal. Bring up PM and a message will appear saying that new EBV files have been found and are being updated/imported into PedigreeMaster. Click on **OK**. Also, on the opening screen there will be a date next to Analysis Results. That date should be the date of the most recent analysis. You next want to click on the **Reports & Utilities** button on the main screen and then on **Sheep Genetics**. Click on both the **Update Pedigree from results** and **Add pedigree from results** buttons. By clicking on these two buttons, your performance pedigrees will be updated with new values. You should also click on the **Reindex database** button on the opening screen. Click on **Close** to return to the main screen. If you click on the Pedigree Display button and then on the EBVs tab, you will see new EBV values for your animals. It is important to go through this step so that you can view the up-to-date EBVs on your computer and also so that if you wish to print out performance pedigrees, they will have the latest EBVs on them.

Chapter 7 – Adding a computer/New computer

Some producers like to have Pedigree Master on two or more computers for flexibility in working with records. Also, as producers add a new computer to replace their old one, they will need to seamlessly move Pedigree Master and their data to the new machine. The first step in the process of putting data onto a new machine is to use a backup file to transfer the data. At the opening screen, click on **Summaries, Validation & Database Backup**. You should first validate the data so that if there is any invalid data, it will be corrected. There is no sense in transferring invalid data to the new computer. Click on **Validate** and the validation process will begin. You can print out the invalid data if you so desire using the pop up box that appears. If there is nothing invalid, or after printing, you can leave this screen by pressing the Esc key.

Next fill in the circle by **Save to this computer** and click on **Create backup**. Click **Yes** to the two questions about having validated the data and about excluding EBV. The process runs smoother if EBVs are later added from the download site that is normally accessed after a data processing run. Browse for a folder or spot to place the backup file. The desktop is highly recommended for this as it is easily accessed and very visible. After highlighting the desired spot, hit OK. Click on OK when the statement occurs that says a backup file was created. The file should be named with your NSIP Id with the zip extension, such as 620007.zip. Transfer this file to the other computer via email, jump drive or cloud storage.

If the other computer does not have Pedigree Master, you will need to download it <http://kidplan.mla.com.au/pedigreemaster/>. After it is downloaded, run the file, normally by double clicking it, to install it. The steps to do this are straightforward. After it is installed, run the program. You will be asked to input your two-digit breed code and your four-digit flock code. The program will then close. Run the program again and at the main screen, click on **Reports & Utilities**, then on **Advanced** and then on **Importing**. Then click on **Import Pedigree Master Archive**. Click on Yes for the question regarding having a current backup. The select the backup file from wherever you transferred it and click on Import. Click on Yes to the question about overwriting current databases, if it appears. After transferring the data, the program will shut down. Re-start the program and check if all transferred. Remember that the EBVs will not be there. The EBVs can be included by either going to a past EBV update page and following past procedures, but to this computer, or by updating it after future data processing.

Appendix A – Traits/EBVs -- Terminology and abbreviations

Recommended age ranges – the ages in the table below are the recommended age ranges within which data should be submitted for various age brackets. However, ages outside these ranges are accepted by the program and are listed further in the chapter by each trait.

General Age Ranges

Age Bracket	Recommended Range	Age Bracket	Recommended Range	Age Bracket	Recommended Range
Weaning	40-120 days	Early Postweaning	80-240 days	Postweaning	160-340 days
Yearling	290-430 days	Hogget	410-550 days	2 yr	530-1000 days
3 yr	890-1300 days	4 yr	1260-1660 days	5 yr	1600-2030 days

Fertility Traits

Trait	Abbreviation	When to record data	Explanation														
Number of Lambs Born	NLB	Birth	Number of lambs a ewe gives birth to. Input as Bt with a 1 for single, 2 for twin, etc. EBV figures are a percentage above or below a breed average for superiority of the animal. For example, if an animal has an EBV of 20, it's genetic value for number of lamb born is 20% above average.														
Number of Lambs Weaned	NLW	Weaning	Number of lambs a ewe weans. Input a Rt with a 1 for single, 2 for twin, etc. EBV figures are a percentage above or below a breed average for superiority of the animal. For example, if an animal has an EBV of 20, it's genetic value for number of lambs weaned is 20% above average.														
Scrotal Circumference	Scrotal for input, Pwsc, Ysc, Hsc and Asc for postweaning, yearling, hogget and adult EBVs	<table border="0"> <tr> <td><u>Age</u></td> <td><u>Input range</u></td> </tr> <tr> <td>Early postweaning</td> <td>64-264 days</td> </tr> <tr> <td>Postweaning</td> <td>128-374 days</td> </tr> <tr> <td>Yearling</td> <td>232-473 days</td> </tr> <tr> <td>Hogget</td> <td>320-660 days</td> </tr> <tr> <td>2 yr.</td> <td>421-1107</td> </tr> <tr> <td>days</td> <td></td> </tr> </table>	<u>Age</u>	<u>Input range</u>	Early postweaning	64-264 days	Postweaning	128-374 days	Yearling	232-473 days	Hogget	320-660 days	2 yr.	421-1107	days		Circumference of the scrotum, measured in centimeters. Rams with great circumference tend to have greater servicing ability and their daughters tend to be more fertile. Input values must be between 9 and 40 cm for early postweaning, and between 11 and 49 cm for all other ages.
<u>Age</u>	<u>Input range</u>																
Early postweaning	64-264 days																
Postweaning	128-374 days																
Yearling	232-473 days																
Hogget	320-660 days																
2 yr.	421-1107																
days																	

Worm Load

Trait	Abbreviation	When to record data	Explanation
Weaning Fecal Egg Count	WEC for input, Wfec for EBV	At weaning, between 32 and 132 days of age	Estimates the genetic difference in worm load/burden at weaning time.
Post-weaning Fecal Egg Count	WEC for input, EPfec of Pfec for EBV	For early postweaning, between 64 and 264 days of age. For later postweaning, from 128 and 374 days of age.	Estimates the genetic difference in worm load/burden at time of postweaning.
Yearling Fecal Egg Count	WEC for input, Yfec for EBV	Between 232 and 473 days of age.	Estimates the genetic difference in worm load/burden at around one year of age.
Hogget Fecal Egg Count	WEC for input, Hfec for EBV	Between 320 and 660 days of age	Estimates the genetic difference in worm load/burden at around one and a half years of age.
Adult Fecal Egg Count	WEC for input, Afec for EBV	Between 421 and 1107 days of age	Estimates the genetic difference in worm load/burden as an adult animal.

Weight Traits

Trait	Abbreviation	When to record data	Explanation
Birth weight	BW	Within 24 hrs of birth	The genetic differences between animals for birth weight. Must be at least 1.8 pounds and less than 21.0 pounds.
Weaning Weight	WWT	At weaning, between 32 and 132 days of age	The genetic differences between animals for weight at weaning. Weight must be between 17.6 pounds and 143.0 pounds.
Maternal Weaning Weight	MWWT	There is no data to record for this trait. It is calculated from the other data.	MWWT estimates the genetic differences between females for milk production and the ability to provide a better maternal environment
Early Postweaning Weight	EP Weaning for input, PWWT for EBV	At weaning, between 64 and 264 days of age	Both this and the later possible weaning weight input (below) result in EBVs labeled as PWWT. However, they have different acceptable data input ranges. This trait must be between 35.2 and 220.0 pounds. This is most applicable to farm flocks.
Postweaning Weight	P Weaning for input, PWWT for EBV	At weaning, between 128 and 374 days of age.	As noted above, both this and Early Postweaning Weight result in EBVs labeled as PWWT. This trait, however,

			must be between 52.8 and 242.0 pounds. This is more applicable to some range flocks.
Yearling Weight	YWT	Between 232 and 473 days of age.	EBV for yearling weight. The input value must be between 44 and 286 pounds.
Hogget Weight	HWT	Age must be input between 320 – 660 days of age.	EBV for weight at around a year and a half of age. Weight input must be between 44 and 308 pounds.
Adult Weight	Adult 2y, Adult 3y, Adult 4y or Adult 5y for input, AWT for EBV	<u>Age</u> <u>Input range</u> 2 yrs. 421-1107 d 3 yrs. 655-1549 d 4 yrs. 918-1990 d 5 yrs. 1181-2553d	Shows estimated genetic differences for adult weight. Weight input must be between 52.8 pounds and 330 pounds.

Wool Traits

Note: EBVs for wool traits will not be generated unless the data is taken at an age of 300 days or greater.

Trait	Abbreviation	When to record data	Explanation																		
Fiber Diameter	FD for data input, Pwfd for postweaning, Yfd for yearling, Hfd for hogget, Afd for adult	<table border="0"> <tr> <td><u>Age</u></td> <td><u>Input</u></td> </tr> <tr> <td><u>range</u></td> <td></td> </tr> <tr> <td>Postweaning</td> <td>64-374 d</td> </tr> <tr> <td>Yearling</td> <td>232-473 d</td> </tr> <tr> <td>Hogget</td> <td>320-660 d</td> </tr> <tr> <td>2-yr</td> <td>421-1107 d</td> </tr> <tr> <td>3 yr</td> <td>655-1549 d</td> </tr> <tr> <td>4-yr</td> <td>918-1990 d</td> </tr> <tr> <td>5-yr</td> <td>1181-2553 d</td> </tr> </table>	<u>Age</u>	<u>Input</u>	<u>range</u>		Postweaning	64-374 d	Yearling	232-473 d	Hogget	320-660 d	2-yr	421-1107 d	3 yr	655-1549 d	4-yr	918-1990 d	5-yr	1181-2553 d	This estimates the genetic differences between animals for fiber diameter, in microns. Animals with negative EBVs should produce finer wool. Input values must be between 11.0 and 49.0 microns.
<u>Age</u>	<u>Input</u>																				
<u>range</u>																					
Postweaning	64-374 d																				
Yearling	232-473 d																				
Hogget	320-660 d																				
2-yr	421-1107 d																				
3 yr	655-1549 d																				
4-yr	918-1990 d																				
5-yr	1181-2553 d																				
Fleece Weight	For data input, Gfw for grease fleece weight and Cfw for clean fleece weight. EBVs are Pwgf, Ygfw, Hgfw and Agfw for grease weights, and Pwcfw, Ycfw, Hcfw and Acfw for clean weights.	Same as for Fiber Diameter (above)	This estimates the genetic differences between animals for fleece weight – either clean or grease basis may be used. For data input, postweaning grease values must be between 1.1 and 17.6 pounds, while values for other weights must be between 2.2 pounds and 30.8 pounds. For clean weight input, values must be between 2.2 and 13.2 pounds for postweaning, and between 2.2 and 26.4 for all other ages.																		

Yield	Yld for data input. EBVs are Pwyld, Yyld, Hyld and Ayld for postweaning, yearling, hogget and adult yields, respectively.	Same as for Fiber Diameter (above)	Yield is the clean fleece weight as a percentage of the grease fleece weight. EBVs estimate the genetic differences between animals for the this percentage. Input values must range between 40.0 and 99.0.
Fleece Comfort Factor	Fcf for data input, Pwfcf, Yfcf, Hfcf and Afcf for EBVs.	Same as for Fiber Diameter (above)	This is the percentage of fibers less than 30 microns. Values should be input between 0 and 100. Estimates the differences between animals for this percentage. A higher value indicates more comfortable fibers.
Fiber Diameter Coefficient of Variation	FDcv for data input. EBVs are Pwfdcv for postweaning, Yfdcv, for yearling, Hfdcv for hogget and Afdcv for adult.	Same as for Fiber Diameter (above)	Coefficient of variation for fiber diameter. Input values should be between 10.0 to 35.0. EBV estimates the genetic differences between animals for this trait.
Fiber Diameter Standard Deviation	FDsd for data input. EBVs are Pwfdsd, Yfdsd, Hfdsd and Afdsd for postweaning, yearling, hogget and adult, respectively.	Same as for Fiber Diameter (above)	Estimates the genetic differences between animals for the variability of fiber diameter. Input values should be a positive number. A lower number indicates less variability.
Curve	Data input is Curve. EBV for postweaning is Pwcurv, for yearling is Ycurv, for hogget is Hcurv and Acurv for adult.	Same as for Fiber Diameter (above)	Estimates the genetic differences between animals for curvature in the fiber.
Staple Length	Sl is the term for data input. EBVs are Pwsl for postweaning, Ysl for yearling, Hsl for hogget and Asl for adult values.	Same as for Fiber Diameter (above)	Estimates the genetic differences between animals for staple length, in mm. Greater EBVs indicate longer staple length. Input values must be between 10.0 and 120.0

Staple Strength	Ss is the term for data input. EBVs are Pwss for postweaning, Yss for yearling, Hss for hogget and Ass for adult values.	Same as for Fiber Diameter (above)	Estimates the genetic differences between animals for strength of a fiber. Greater EBVs indicate stronger fibers. Input values must be between 0.1 and 150.0
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Carcass Values

Note: Lambs must be weigh at least 66 pounds for scan data to be accepted.

Trait	Abbreviation	When to record data	Explanation																				
Fat Depth	cFat for input, EBVs are Wfat for weaning, Pfat for postweaning, Yfat for yearling, Hfat for hogget and Afat for adult values.	<table border="1"> <thead> <tr> <th>Age</th> <th>Input range</th> </tr> </thead> <tbody> <tr> <td>Weaning</td> <td>32–132 days</td> </tr> <tr> <td>Early postweaning</td> <td>64–264 days</td> </tr> <tr> <td>Postweaning</td> <td>128–374 days</td> </tr> <tr> <td>Yearling</td> <td>232–473 days</td> </tr> <tr> <td>Hogget</td> <td>320-660 days</td> </tr> <tr> <td>2 yrs.</td> <td>421-1107 days</td> </tr> <tr> <td>3 yrs.</td> <td>655-1549 days</td> </tr> <tr> <td>4 yrs.</td> <td>918-1990 days</td> </tr> <tr> <td>5 yrs.</td> <td>1181-2553 days</td> </tr> </tbody> </table>	Age	Input range	Weaning	32–132 days	Early postweaning	64–264 days	Postweaning	128–374 days	Yearling	232–473 days	Hogget	320-660 days	2 yrs.	421-1107 days	3 yrs.	655-1549 days	4 yrs.	918-1990 days	5 yrs.	1181-2553 days	Depth of fat from ultrasonic scan measurements, in mm. EBVs estimate the genetic differences between animals for depth of fat with smaller values indicate leaner animals. Input values at weaning must be between 0.5 and 9.0 mm, at postweaning must be between 0.5 and 15.0, and for all others, between 0.5 and 20.0.
Age	Input range																						
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Eye Muscle Depth	Emd for input, EBVs are Wemd for weaning, Pemd for postweaning, Yemd for yearling, Hemd for hogget and Aemd for adult ages.	Same as for fat depth (above)	Estimates the genetic differences between animals for eye muscle depth. A greater value indicates more depth of muscle. The input weaning value must be between 6 and 40 and inputs for the other ages must be between 11 and 59 mm.																				

Appendix B -- Use of PM if the primary computer is a Mac

James Morgan and John Carlson

The originators of PedigreeMaster designed it to work with computers using Windows. However, this does not preclude Mac users from working with Pedigree Master. For Mac users, there are several options:

1. Running Windows Programs on Macs via Partition Programs or Virtualization Software
2. Obtaining a used PC that can run Pedigree Master
3. Contracting with a NSIP Data Processor

Each of the above options has advantages. The best option for your flock depends on your needs, knowledge, patience and current computer hardware and software. Also, as operating systems and PM software change, some of the information on compatibility and features may change.

Option 1 – Running Windows Programs on Mac can be affected by how much extra room you have on your hard drive and how you use your computer. Viruses should not be an issue if you use a Mac email program and web browser to send to Australia and to receive data. Use a Mac browser to download your flock *.exe file after each data run for updating Pedigree Master. A problem that some users have encountered with the Yosemite version of a Mac is that the default program to open the zip file that is downloaded. If a problem is encountered, change the program that is used to download this file.

You also need to check the compatibility of the partition/virtualization program with the version of Windows you will run. Compatibility varies between the different programs, different versions of the program and the version of Windows. For example, recent versions of the Bootcamp utility requires Windows 7 or later. Parallel can run with Windows XP, 7.0 or 8.0. Make sure you factor in the cost of purchasing Windows. To run Pedigree Master, you will not need the most recent Windows and can probably find used legal copies on the internet.

A recommended way to enter data into a Mac is to use a spreadsheet program. This is particularly helpful if you are using a sheep management program that typically allows you to import your data into a spreadsheet. Information on using a spreadsheet to enter data into PM is included in Chapter 4 of this manual.

In regard to running partition programs, the main one used is Bootcamp. It is a utility program that currently comes as part of the more recent MAC OS. Partition programs do require that you boot up with either the Mac OS or Windows – you can't run both at the same time. First, be sure to backup your hard drive. The install Bootcamp, then install Windows. When that is done, install Pedigree Master.

Virtualization programs allow simultaneous running of Mac OS & Windows OS. Some also allow drag and drop. As for types of virtualization programs, Virtual Box is freeware while Parallel 9 is less than \$100 and Parallel 8 is even cheaper. Some NSIP Mac users prefer Parallel as they don't have to shut their Mac down to run it and they like the drag and drop. Another type is VM Ware – VM Fusion is the software and there are freeware copies.

Option 2 -- Buying or obtaining an older, used PC is another option. These should be available for a minimal price or perhaps or sometimes obtainable from family or friends might

even. The PC needs to be of sufficient capacity to run Windows XP or later. Typically, the only function for this machine is to run PM, thus they can be streamlined for this function and thus provide adequate speed and capacity. PM works with either 32 bit or 64 bit machines. Since you don't need to hook the PC up to the internet, you don't need to purchase virus software. Download the PM installation program with your Mac and use a jump drive to ferry installation material from your Mac to the PC. After creating a file for submission to LambPlan, as described in Chapter 5 of this manual, ferry the file from the PC to your MAC to email it to LambPlan. Also download PM updates to the Mac and then ferry them to the PC.

Option 3 -- Using a data processor consists of hiring a person familiar with PM to handle the aspects of working with PM on a PC. The process starts with the Mac user entering the data on an Excel spreadsheet or exporting it to Excel from a sheep management program to Excel. The spreadsheet would then be emailed to a data processor. A list of current data processors is online at: <http://nsip.org/data-processors> and their fees vary. The data processor would import the spreadsheet into Pedigree Master, validate the data and return any error messages or validation needs to the flock. The data processor then emails the file for submission back to the MAC user who then would email the file to Lamb Plan. After the data is processed, the data processor can update the participant's PM files and export EBVs to an Excel File to be mailed to the Mac user, although there is generally little need of this because LambPlan sends reports to each participant with EBVs of the main traits of interest.