



NSIP

National Sheep  
Improvement  
PROGRAM

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*PedigreeMaster*

*PedigreeMaster*

# Pedigree Master Software Manual

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v. 4.0

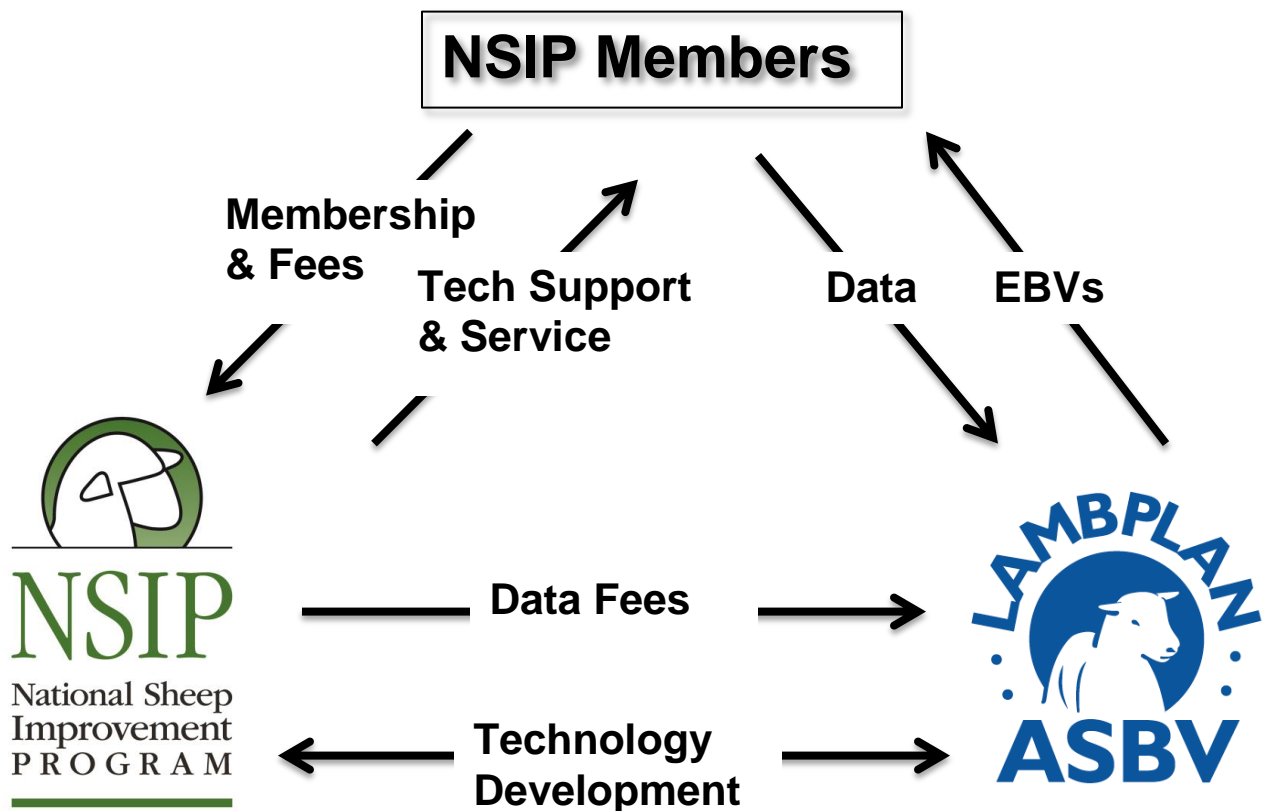
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## Chapter 1 -- Introduction

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.



NSIP 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 1258, Ames, IA 50014. Rusty Burgett is in charge of the office. His telephone number is 515-708-8850 and his email is [info@nsip.org](mailto:info@nsip.org). This information is also available online at <http://nsip.org/nsip-about/contact/>. 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 and worldwide. 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. Also, if you don't have data to submit but would like updated EBVs on animals in your flock, you can request this by emailing LambPlan at [database@sheepgenetics.org.au](mailto:database@sheepgenetics.org.au). In the subject line, write "EBV update requested" and write "EBV update only is requested" in the text area of the email along with your six-digit NSIP flock code.

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, grease fleece weight, clean fleece weight, fiber diameter, staple length, staple strength, coefficient of variation of fiber diameter, fiber curvature, yearling weight, hogget weight, adult 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. It has not been updated since August 2014. It is generally considered advisable to work with PedigreeMaster as it has more current software and is much more frequently updated. 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. There are other commercially available software programs that interface with LambPlan for a fee and can be found at <http://sheepgenetics.org.au/Getting-started/Software-for-managing-data>.

## Chapter 2 -- Downloading, Installing and Customizing

### Machine Usage

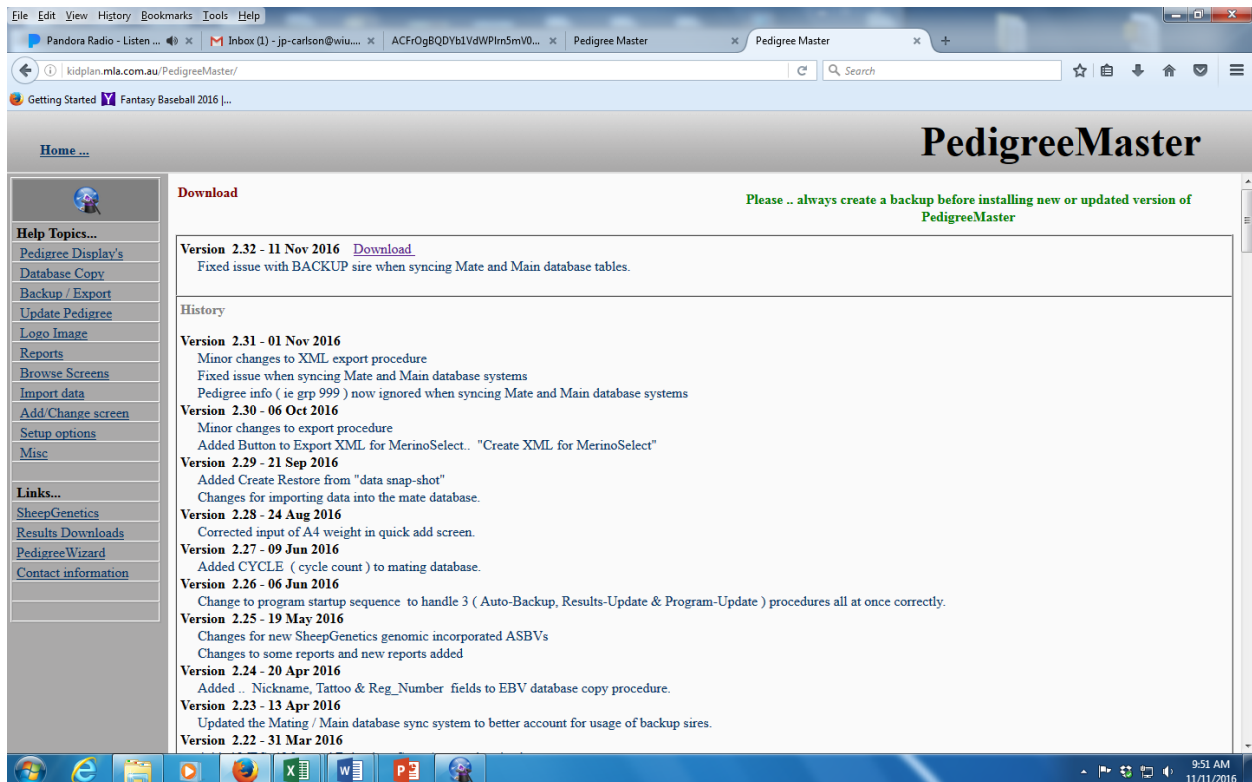
PedigreeMaster (PM) software may be used in either 32- or 64-bit PC machines. Ways are being researched to make PM easier to use on Apple computers. Currently, Apple users must have software such as BootCamp, VirtualMachine or another type of program that is capable of running PC programs. A program 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 several times each year for updated versions. There are typically 10 or more updates each year. Each new version has new features, is more efficient, and resolves problems encountered in previous versions. A good reminder is to check for updates and install them before adding any new data or installing EBVs that you have received from Australia. Before downloading any software update, it is a good idea to backup your existing data (see page 16). After downloading and installing the software update, it is a good idea to reboot the computer, just as it is with any new software update. Rebooting should help assure that the update will be seamless when working with new data.

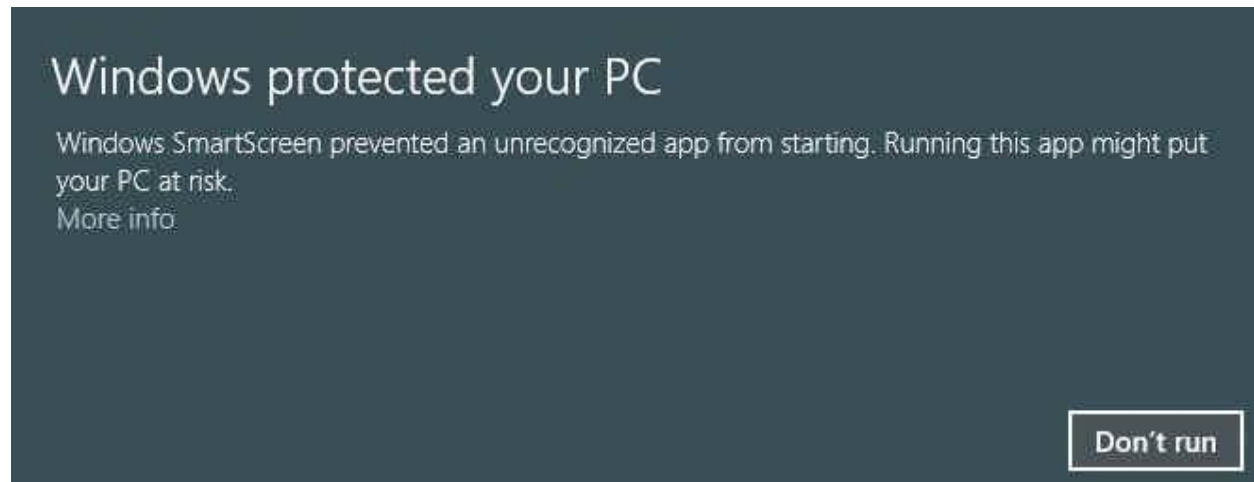


The screenshot shows a web browser window displaying the PedigreeMaster website. The page title is "PedigreeMaster" and the URL is "kidplan.mla.com.au/PedigreeMaster/". The main content area is titled "Download" and features a green banner that reads "Please .. always create a backup before installing new or updated version of PedigreeMaster". Below this, there is a list of software versions with their release dates and a "Download" link for each. The versions listed are:

- Version 2.32 - 11 Nov 2016: Fixed issue with BACKUP sire when syncing Mate and Main database tables.
- Version 2.31 - 01 Nov 2016: Minor changes to XML export procedure; Fixed issue when syncing Mate and Main database systems; Pedigree info ( ie grp 999 ) now ignored when syncing Mate and Main database systems.
- Version 2.30 - 06 Oct 2016: Minor changes to export procedure; Added Button to Export XML for MerinoSelect. "Create XML for MerinoSelect"
- Version 2.29 - 21 Sep 2016: Added Create Restore from "data snap-shot"; Changes for importing data into the mate database.
- Version 2.28 - 24 Aug 2016: Corrected input of A4 weight in quick add screen.
- Version 2.27 - 09 Jun 2016: Added CYCLE ( cycle count ) to mating database.
- Version 2.26 - 06 Jun 2016: Change to program startup sequence to handle 3 ( Auto-Backup, Results-Update & Program-Update ) procedures all at once correctly.
- Version 2.25 - 19 May 2016: Changes for new SheepGenetics genomic incorporated ASBVs; Changes to some reports and new reports added.
- Version 2.24 - 20 Apr 2016: Added . Nickname, Tattoo & Reg\_Number fields to EBV database copy procedure.
- Version 2.23 - 13 Apr 2016: Updated the Mating / Main database sync system to better account for usage of backup sires.
- Version 2.22 - 31 Mar 2016

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 next 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. Or, you may have Windows SmartScreen try to stop the process and the screen below will appear. If so, click on **More info** and then click on **Run anyway** when it appears.



The file name is typically PM-Y-XX.exe, 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**. If you have a previous version of PM installed on your computer, be sure that it is not actively running. When the download is completed, click on it and a dialog box will appear. At this point you want to be sure that – click on **Run**. The next box will welcome you to PM – click on **Next**. The next dialog box to appear asks you to set up a directory. The preferred choice by far is:

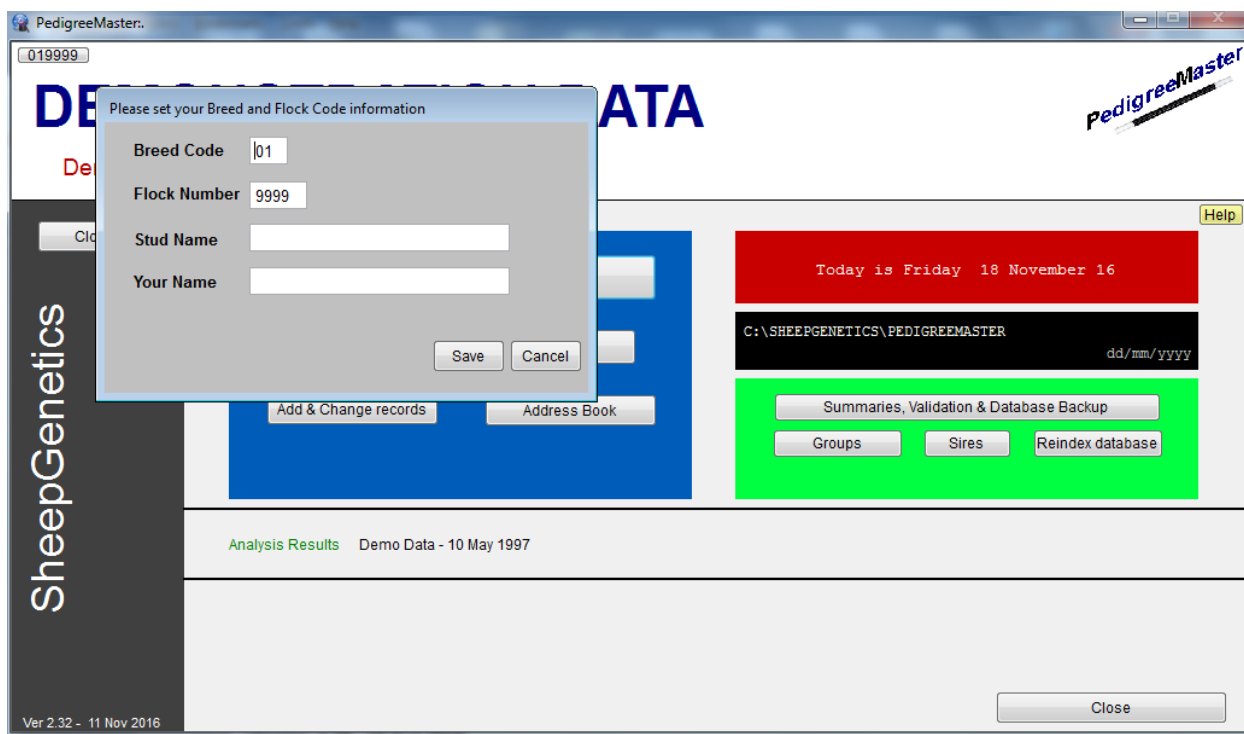
C:\SheepGenetics\PedigreeMaster

Click on **Next**. The dialog box that will appear next will allow you to put PM on the Start Menu, which is preferred. Click on **Next**. The next dialogue box then asks if you want to create a desktop icon and also if you want to create a Quick Launch icon. Those are choices that individual breeders may or may not want, although it is 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**.

If PM doesn't automatically launch, click on the Windows icon in the lower left corner of your screen and the Start Menu should appear with the Pedigree Master icon showing. Click on it to get started. First, the program will flash through some process to get initialized into your system.

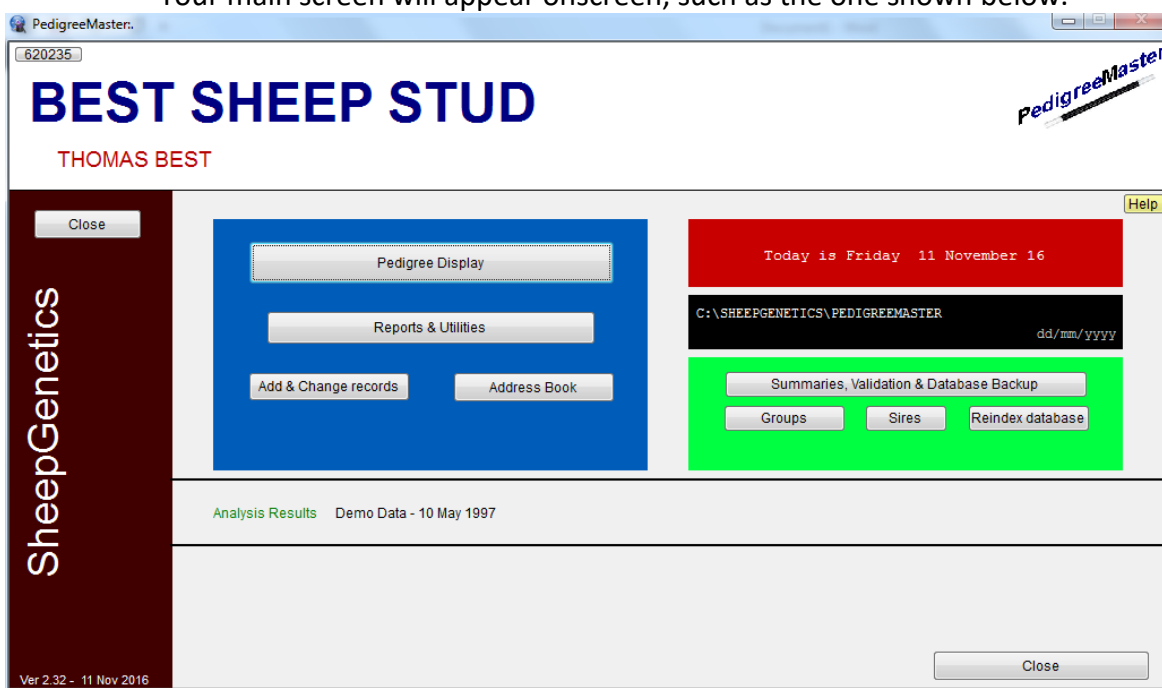
#### **Customization**

A screen will then appear asking you to input your breed code, flock number, name and stud name.

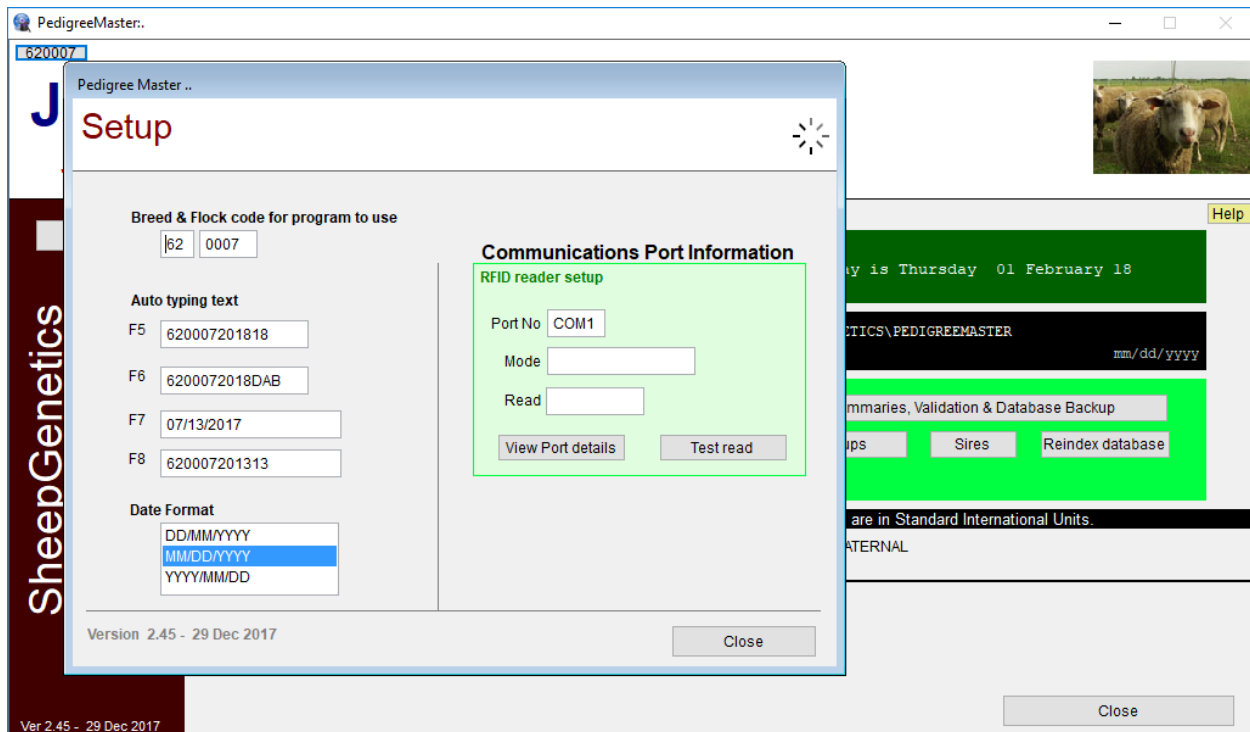


You should have earlier received a six-digit code from NSIP that is your LambPlan ID. The first two numbers of this code should be entered in the Breed Code section of the screen. The last four numbers should be entered in the Flock Code section. You should also enter information in the Stud Name (farm or ranch name) and Name sections as these will appear on the main screen. When finished, click on **Save**. A box will appear onscreen instructing you to restart the program. Click on OK and when the program screens disappear, restart the program as before if restart does not automatically occur.

Your main screen will appear onscreen, such as the one shown below.

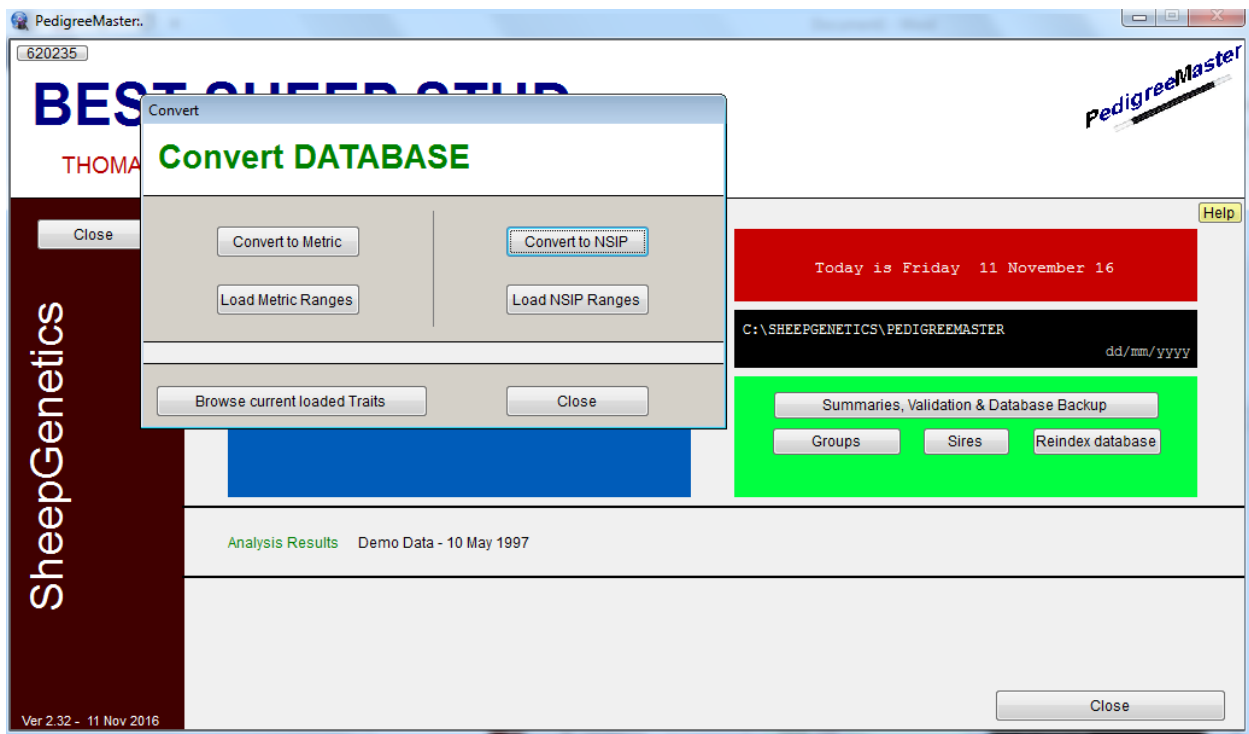


On the main screen, your flock's six-digit number in the upper left corner, just under PM. Click on this and a setup menu will appear.



The Breed Code and Flock Code sections of this screen should have the correct numbers for you and your flock. If not, you will need to input the correct values. 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. Instructions on how to use them are on page 26. 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. Highlight the format you like best. Typically in the United States the MM/DD/YYYY format is used, but you may choose whatever option you prefer. Remember that this is the format in which your data should be entered for the various weights and measurements. 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. Do not change any of the information in the Communications Port Information box unless you are using an RFID reader. When done, click on **Close**.

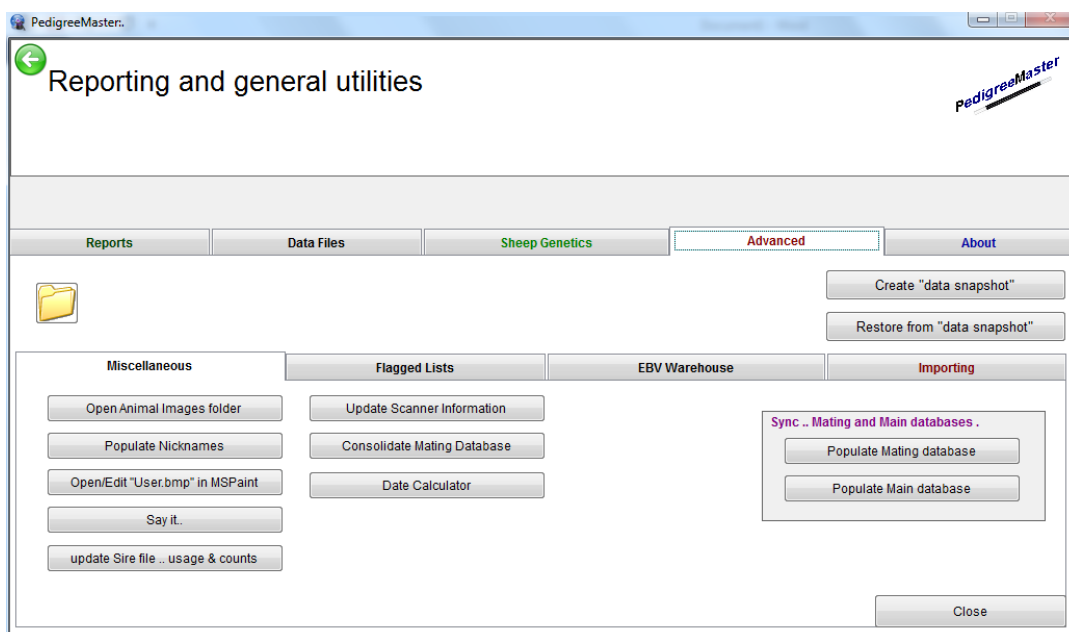
If you are downloading and installing PM and have data in PM but on a different computer or in Pedigree Wizard, you can import it as described on page 24. If you do NOT have any data previously in LambPlan, go to the main screen and push Ctrl-C. A screen will appear dealing with conversion setups.



Click on the **Convert to NSIP** button. If the screen does not disappear, click on the **Load NSIP Ranges** button. This tells PM that the program should run in NSIP mode with all weighs 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.

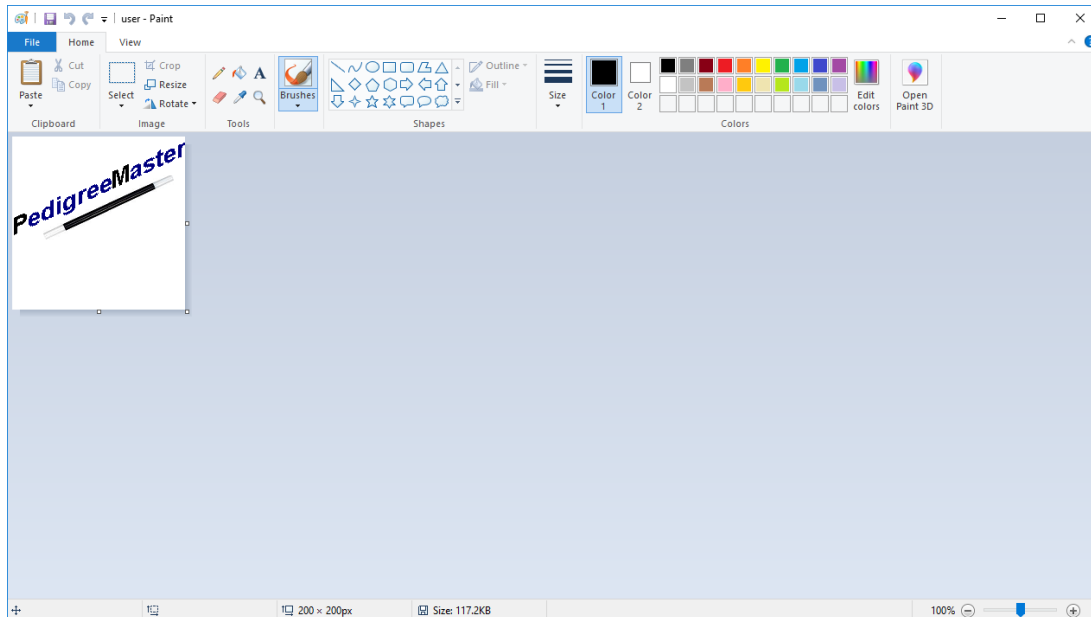
At the main screen, and on reports you will print later, the PM logo will appear. If you want to change this to a logo of your own, first have the image stored on the computer. For example, it could be a digital photo, clipart or a scanned image. You will need to know the exact location of this icon for the next step in using it.

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



Then click on the **Open/Edit “User.bmp” in MSPaint** tab. Click OK on the alert screen. A screen will also appear notifying you that PM will need to be restarted for the changes to be applied. Do NOT click OK on his until all of the work is done or you will find yourself starting over.

On the screen that appears as shown below, the PM logo will appear. Click on **File** and then on **Save As**. Change the filename to user-2 and click on Save. Then save the PM image if you should happen to want it in the future. Next, again click on **File** and then on **Open**.



Locate the image you want and double click on it.

Click on **Save As** and change the file name to **user** and the **Save as type** should be changed to **24-bit Bitmap 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**. Then exit the paint screen.

For the screen that tells you that you must exit PM for the change to take place – click on **OK**. PM will disappear. Re-start PM if it does not do so itself and your logo should be in the upper right area of the main screen, instead of the PM logo. This will also appear on reports you later generate.

To input your data, refer to Chapter 5 on page 33. First, though, it is a good idea to familiarize yourself with the various PM screens you will see, as described in Chapter 3.

## 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. By doing this early, you will be familiar with what your data can be used for. Before viewing the various screens, however, go through the glossary of terms in Appendix A so that you are familiar with the 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 brief and not too explanatory, but may provide you with some quick 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. If your version is not the most current, click on the **Download** link and follow the onscreen instructions as described on page three.

### Pedigree Display

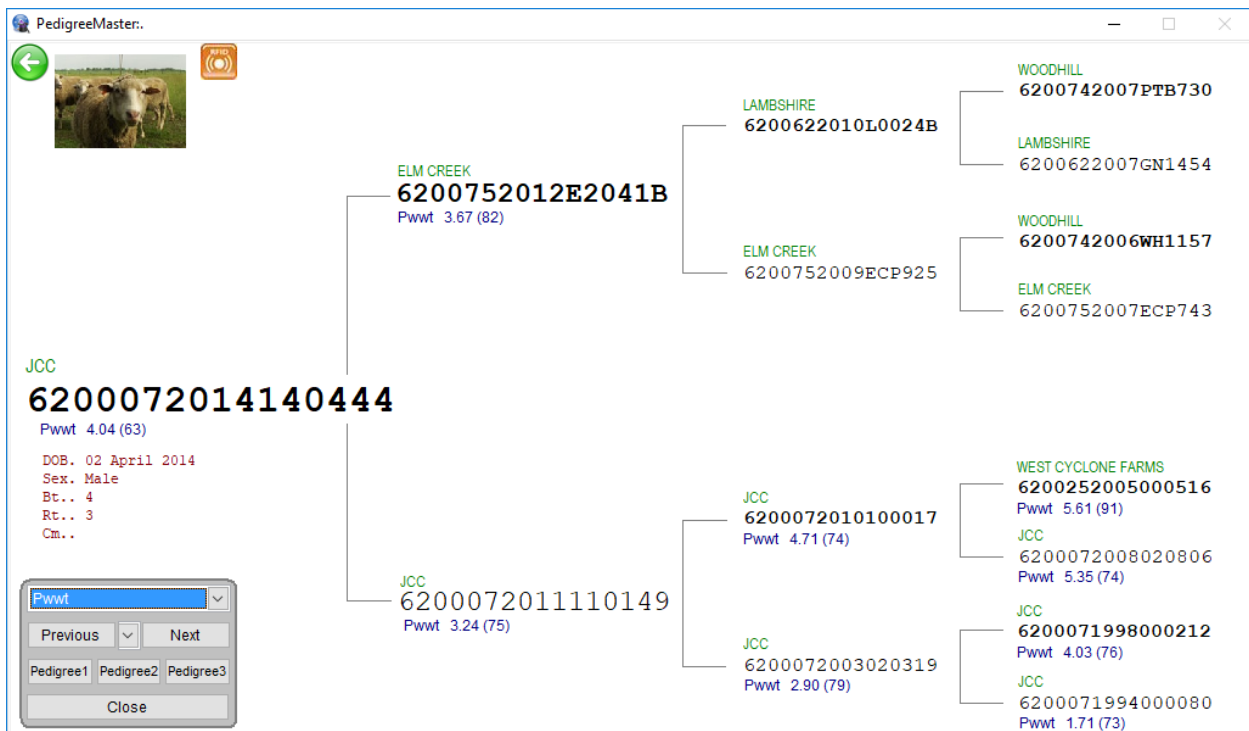
At the main screen, clicking on **Pedigree Display** reveals a screen with eight tabs.

The screenshot shows the PedigreeMaster software interface. At the top left, the animal ID **620007-2019-190920** is displayed in a blue box. Above it, the sire ID **620125-2018-P8092G** is in a red box, and the dam ID **620007-2016-160602** is in a green box. Below the animal ID, the sex is set to **1** (Male) and the date of birth is **01/17/2019**. The group is **1** with the name **early lambs**. A comment field contains the text **Ram to enter in the CNS sale**. The interface has several tabs: **Breeding** (selected), **Carcase**, **Fleece**, **Reproduction**, **Miscellaneous**, **(1) Breeding Values**, **(2) Breeding Values**, and **Visuals**. The **Breeding** tab contains fields for **Change Group** (set to 1), **Add new animal** (+), **Delete animal** (X), **Change / Edit Sire**, **Change / Edit Dam**, **Nickname** (1000), **FateCode**, **End of recorded life**, **Date** (//), **Pedigree method** (Sire and Dam), **Accuracy** (0.0), **Status** (Current), **Birth Type** (2), **Rear Type** (2), **Lambease**, **Conception** (Date //, Method), **Testicles**, **Jaw**, **Foster Ewe**, and **Recip ID**. On the right side, there is a list of animal IDs from **620007-2019-190905** to **620007-2019-190937**, with **620007-2019-190920** highlighted. A **Close** button is at the bottom right.

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 group name, if previously 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 that opens. 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. On the upper right part of the frame is a filter if you want to look at a particular individual or set of individuals. Input the ID of the animal and its ID will be highlighted in the list on the right with its information shown on the screen. Next to the ID input area is a filter switch. The default is for the filter to be off. If you click on that switch, the animal's ID and status will be displayed.

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 values are shown under all of the animals shown in the pedigree. The **Previous** and **Next** buttons will take you to other animals. To get a printable version of a performance pedigree, you can click on either **Pedigree 1**, **Pedigree 2** or **Pedigree 3**. All show the pedigree, along with the logo, sex, date of birth and other information, along with the EBVs. The difference between them 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 logo but includes the great-grandparent generation. **Pedigree 3** shows an additional generation beyond that shown in **Pedigree 2**. A **Print Preview** box will appear for all three that allows you to print the pedigree for sale display or other uses. Some printers also include an option to save the pedigree as a pdf image that is helpful to send via email to potential buyers interested in the animal. 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, click on **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 input or change 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 such as the same feed and in the same location. Otherwise, they will need to be listed in separate groups if, for example, they were fed different rations or were on different locations.

**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. For the most part, you only want to use **Delete** if you have started putting in a new record and there are numerous errors with it and you want to completely start over. Under no circumstances should you delete an animal simply because it is no longer in the flock! By doing that, you will eliminate its data which is extremely important in the subgroup comparisons as they are the basis of the analysis. If an animal is no longer in the flock, change its status on the right side of the page to one that is appropriate. The **Fate Code** and **Pedigree method** section have nothing to do with the EBV calculations but can be very useful for management information. A dropdown menu lists a variety of ways an animal could have left the flock. The bottom choice returns a blank record in case you make an error and need to get back to the base. You can also input the date. The **Pedigree method** section allows you to input the way the sire and dam of the animal were determined. You can also input the accuracy of those methods.

Having the status set correctly is important in some breeds so that animals which are no longer part of the genetic pool do not show up in summary reports. Sometimes there is confusion about which status to choose for an animal. Guidelines to be used are:

**Current** – an animal that is currently in your flock

**Sold** – an animal that was sold into another flock, not sold for slaughter

**Culled** – an animal that was deleted from the herd and will not be a part of the breeding herd

**Reference** – these animals are those who are not part of the breeding herd but are used to show a genetic relationship between animals. This status is usually assigned for flocks recently inputting new animals.

**Dead** – animals that have died

**Missing** – this status is for animals that were in the flock but currently are not yet are expected to return to the breeding flock

**Active** -- this status is mainly used for animals that have semen or embryos available. Thus they are active but not part of the current flock as such.

**Commercial** – for animals that are not purebred or are no longer considered part of the purebred flock

**Unknown** – Assign this status when an animal is not recognized or has disappeared from the flock.

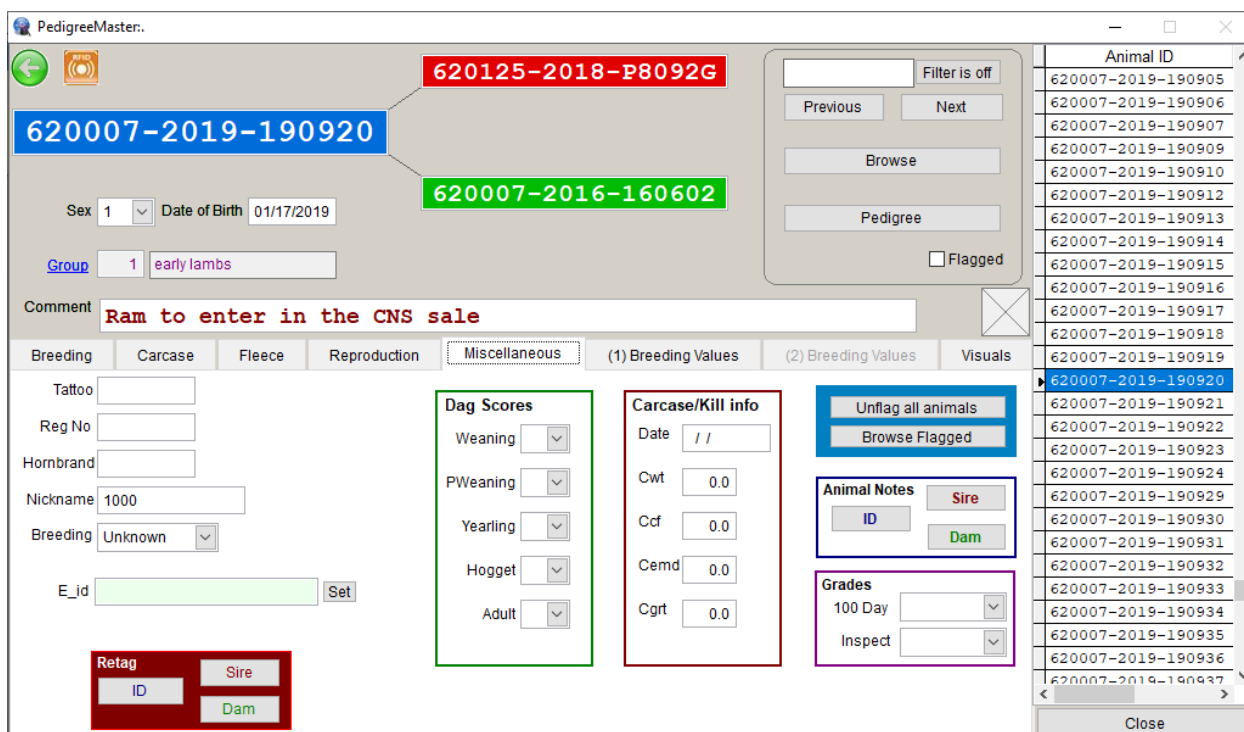
You can also make changes in such things as type of birth and type of rearing. You can input a lambing ease score but that is currently not used in any NSIP analysis. Other items that can be input on this page are conception date and method, as well as testicle measurement and jaw score (also from the drop down menu). If the animal had a foster mother, you need to input the ID of that mother into the space provided for it. Or, if a lamb was an embryo transfer lamb, its recipient mother needs to be identified in the appropriate space on this page. As you click on the other tabs such as **Carcase** (how the Aussies spell carcass), **wool**, **reproduction** and **Miscellaneous**, you can see how data may be input there. **Note:** EP weaning weight is for “early” postweaning weight, which is what most United States flocks will use, especially flocks in the Midwest and East. A hogget is a sheep that is 1-2 years old.

The screenshot shows the PedigreeMaster software interface. At the top, the animal ID **620007-2019-190920** is highlighted in blue. Above it, its parents are listed: **620125-2018-P8092G** (red) and **620007-2016-16060Z** (green). The interface includes fields for Sex (1), Date of Birth (01/17/2019), and Group (1 early lambs). A comment field contains the text "Ram to enter in the CNS sale". Below the comment are tabs for Breeding, Carcase, Fleece, Reproduction, Miscellaneous, (1) Breeding Values, (2) Breeding Values, and Visuals. The "Averages" table is shown below the tabs.

Averages							
	Date	Wt	cFat	Emd	Scrotal	Wec	Group
Birth	01/17/2019	13.0					
Weaning	03/24/2019	76.0	0.0	0.0			1
EP Weaning	05/13/2019	117.0	0.0	0.0	0.0		1
P Weaning	//	0.0	0.0	0.0	0.0		1
Yearling	//	0.0	0.0	0.0	0.0		1
Hogget	//	0.0	0.0	0.0	0.0		1
Adult 2y	//	0.0	0.0	0.0	0.0		1

On the right side of the interface, there is a list of Animal IDs from 620007-2019-190905 to 620007-2019-190937. The current animal ID, 620007-2019-190920, is highlighted in blue. Below the list is a "Close" button.

Under the miscellaneous tab, there are several useful functions. Most of these are for advanced and/or very specific use.



However, one very important function is the red **Retag** area at the lower left of the screen. This is the only place where you should attempt to retag animals other than newborns and it can also be used to retag newborns. This is because most other methods of retagging an animal do not account for making the necessary ID changes in offspring of the retagged animals. If these changes are not made, the important link of ancestry is broken. Here, when you make an ID change, you will be asked if you want to make the ID changes in relatives of the animal.

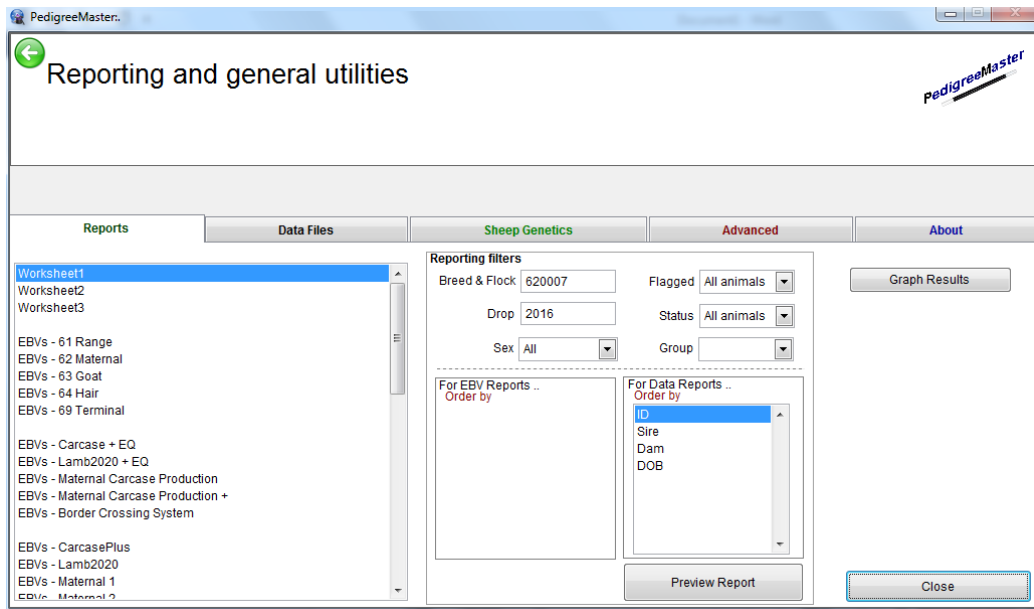
If you want to change an animal's ID, click on the **ID** button. A screen pops up with the animal's current ID and, under that, a space for the new ID. After you input the new ID and click on **Retag**, you will have a screen appear that asks if you want to make ID changes for animals that it is a sire of, and later a screen asking if you want to make ID changes for animals that it is a dam of, plus animals that are in the Visuals and Mating datasets. It is crucial that you input yes to these requests. Otherwise an animal will have two different IDs and, as mentioned before, there will be a break in connecting data among relatives. That is why this is the only acceptable way that IDs should be changed.

More about the use of this screen is explained in the **Data Input** section of this manual. The **(1) Breeding Values** tab reveals the EBVs sent to you from previous processing runs. The **(2) Breeding Values** is currently not active. The **Visuals** tab gives you the opportunity to add visual data and comments if you wish.

## Reports and Utilities

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, EBV, comments or notes on animals, as well as breed codes and trait codes.



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 how you would like the data ordered – individual **ID**, **sire**, **dam**, **date of birth** – and then click on **Preview Report**. For one of the EBV reports, click on either **ID**, **Sire**, **Dams** or one of the many traits listed. Also click on the box by **Descending sort** if you want to change the order of the sort. The default setting is for the lowest value to be listed at the top. Clicking on Descending sort will list the values from high to low. A **Print Preview** 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.

Print Preview .. Escape Key to close preview window

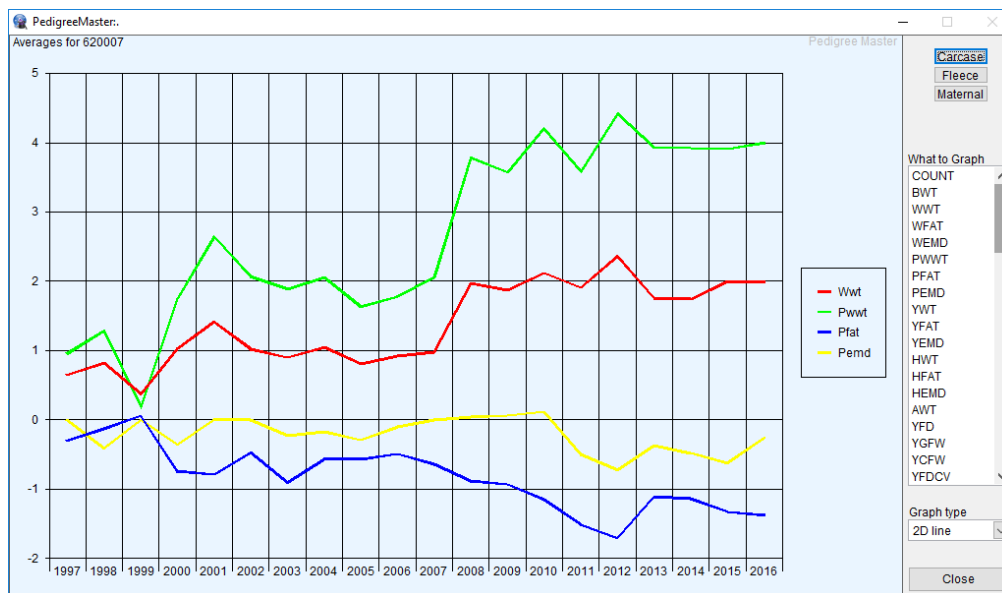
Print Preview

EBV Report..

Animal ID	Sex	Bwt	Mwvt	Wwt	PWwt	Pfat	Pemd	Ywt	Yfd	Ycfw	Ygl	NLB%	USA MATERNAL	Size	Dam
6200072016160601	M	0.4	2.4	1.9	3.8	-1.7		3.2					30.6	118.81	6200782014P14305
6200072016160602	F	0.5	2.4	1.9	3.9	-1.7		3.3					30.6	118.85	6200782014P14305
6200072016160603	F	0.5	2.4	2.1	4.3	-1.8		3.5					30.6	118.94	6200782014P14305
6200072016160604	M	0.5	1.4	1.6	2.4	-1.5		1.9					22.7	114.64	6200782014P14305
6200072016160605	F	0.5	1.4	1.7	2.7			2.1					22.7	114.72	6200782014P14305
6200072016160606	F	0.5	1.4	1.7	2.8			2.2					22.7	114.69	6200782014P14305
6200072016160607	M	0.4	1.7	2.3	4.6	-1.2	-0.2	3.5					35.3	114.16	6200742010PA0210
6200072016160609	F	0.3	1.8	1.3	3.0			2.9					29.6	116.75	6200782014P14305
6200072016160610	F	0.2	1.8	1.0	2.4			2.4					29.6	116.60	6200782014P14305
6200072016160611	F	0.6	1.5	2.3	4.0	-1.3		2.9					31.6	115.31	6200742010PA0210
6200072016160612	M	0.5	1.5	2.3	4.2	-1.2		3.0					31.6	115.31	6200742010PA0210
6200072016160613	M	0.5	1.5	2.5	4.9	-1.2		3.5					31.6	115.44	6200742010PA0210
6200072016160614	M	0.4	3.0	1.9	3.7	-1.2		2.4					21.5	115.47	6200742010PA0210
6200072016160615	F	0.5	3.0	2.3	4.2	-1.4		2.8					21.5	115.66	6200742010PA0210
6200072016160616	F	0.6	1.9	2.1	4.1	-1.7		3.3					37.9	119.04	6200072014140437
6200072016160617	M	0.6	1.9	2.6	5.6	-2.0		4.7					37.9	119.31	6200072014140437
6200072016160620	M	0.5	1.9	2.0	3.8	-1.2		2.6					29.3	114.86	6200742010PA0210
6200072016160621	M	0.4	1.9	1.9	3.5	-1.0		2.4					29.3	114.76	6200742010PA0210
6200072016160622	M	0.2	2.7	1.8	3.9	-0.9		2.7					33.0	117.90	6200742010PA0210
6200072016160623	F	0.4	2.7	2.4	5.0	-1.4		3.5					33.0	118.26	6200742010PA0210
6200072016160624	F	0.4	2.7	2.3	5.0	-1.4		3.7					32.9	118.22	6200742010PA0210
6200072016160625	M	0.5	2.7	2.7	5.9	-1.7		4.5					32.9	118.43	6200742010PA0210
6200072016160627	M	0.4	2.6	2.4	5.1	-1.4		3.7					24.8	114.57	6200742010PA0210
6200072016160628	F	0.5	2.1	1.8	3.2			2.6					26.6	116.91	6200782014P14305
6200072016160629	F	0.3	2.1	1.1	1.9			1.4					26.6	116.53	6200782014P14305
6200072016160631	M	0.4	2.2	2.4	5.3	-1.3		4.1					31.9	112.80	6200742010PA0210
6200072016160637	F	0.4	1.8	2.1	5.0			4.2					22.1	114.59	6200072014140437
6200072016160639	M	0.4	2.7	2.2	4.4	-1.2		2.9					22.7	115.47	6200742010PA0210
6200072016160640	M	0.3	2.7	2.2	5.0	-1.2		3.7					22.7	115.49	6200742010PA0210
6200072016160641	M	0.3	2.7	1.7	3.6	-1.0		2.5					22.7	115.19	6200742010PA0210
6200072016160642	M	0.3	1.8	1.0	1.9			1.8					24.8	113.35	6200782014P14305
6200072016160643	F	0.4	1.8	1.5	2.8			2.5					24.8	113.59	6200782014P14305
6200072016160645	F	0.3	2.1	1.8	4.1	-1.4		3.5					25.0	115.20	6200072014140437
6200072016160647	M	0.2	2.2	1.6	4.2			3.5					29.2	116.34	6200072014140437
6200072016160648	F	0.3	2.2	1.9	4.6			4.0					29.2	116.46	6200072014140437
6200072016160650	F	0.6	2.6	2.2	4.0			3.1					30.9	117.65	6200782014P14305
6200072016160652	F	0.6	2.5	2.8	5.7			4.4					31.3	117.52	6200072014140437

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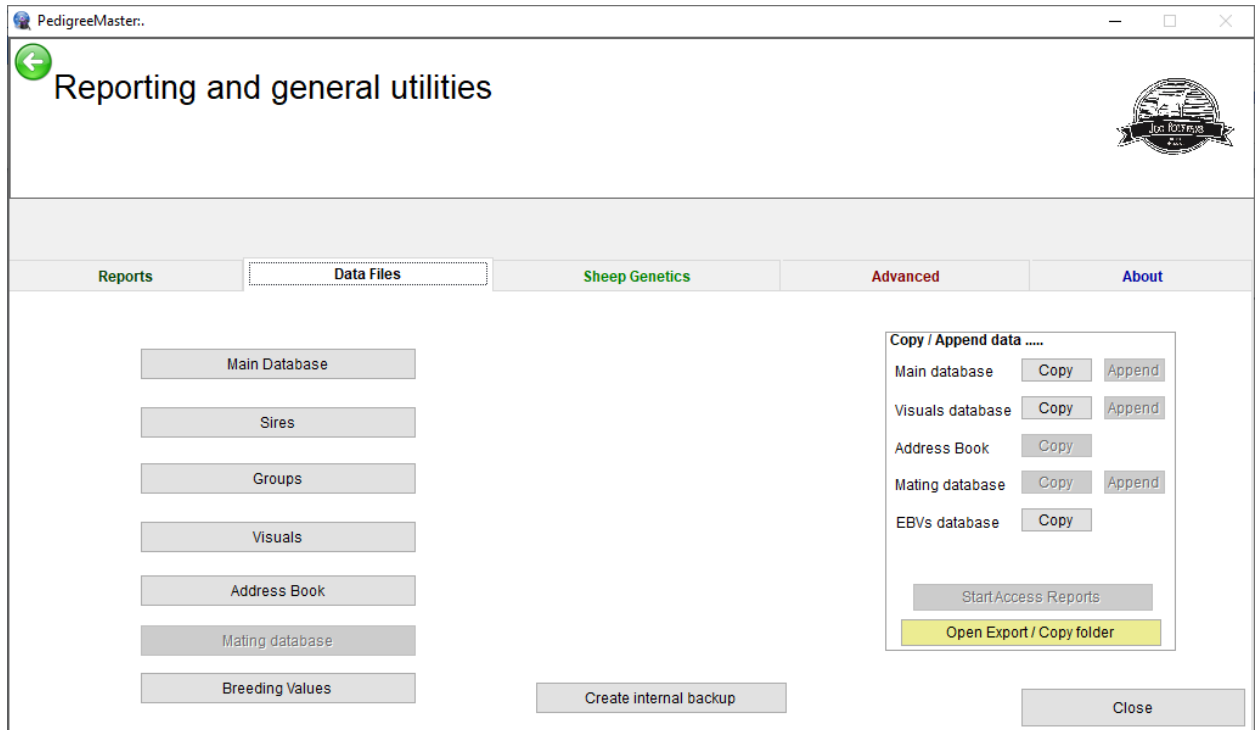
An interesting tab to hit is the **Graph Results** tab. Click on it and your progress over years will be shown in a graph.



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.



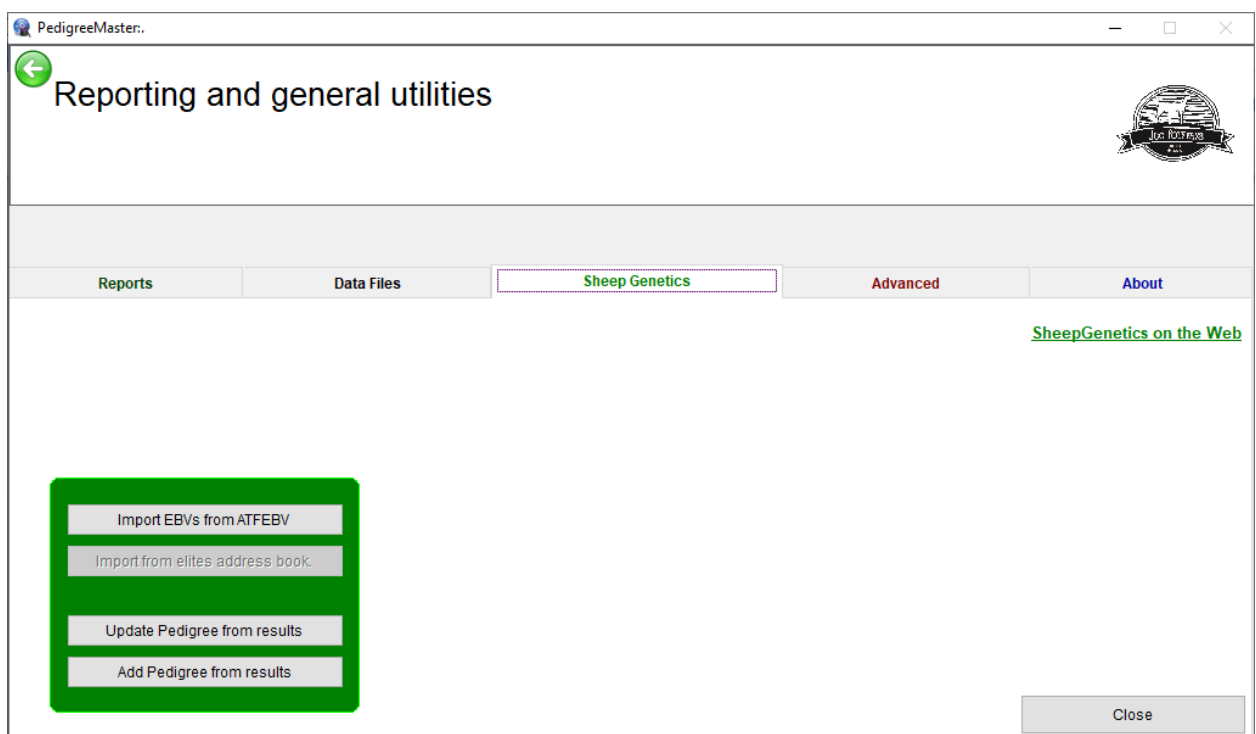
When you enter a new lamb, it will need to be assigned a group and the **Groups** tab will show you the names of the various groups from which you can choose. The groups come with pre-assigned names but you can customize these by selecting names that are more meaningful for you. Click on the **Groups** tab and then on **new record**. A line will be highlighted and you can type in the number for the group plus the group name, group sex and group drop. Click on **Close window** to exit. You can also edit a group's inputs or delete a group by putting the cursor on that row and clicking on **Delete record**. 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 initially submitted data, a listing of other NSIP flocks in your breed should appear, along with their flock codes. Later, you will need to manually update these. The **mating database** is currently not functional. 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, in tabular form.

Another function which can be performed from this screen is to create a backup file for your own use 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. When you click on the Create Internal Backup tab, a backup tab appears that show you where your backup file is located, normally C:\SheepGenetics\PedigreeMaster\backups. You can then go to that directory and copy the file to external storage if you want to have a backup located outside your computer, which is a good idea. You can also use this file when you submit data.

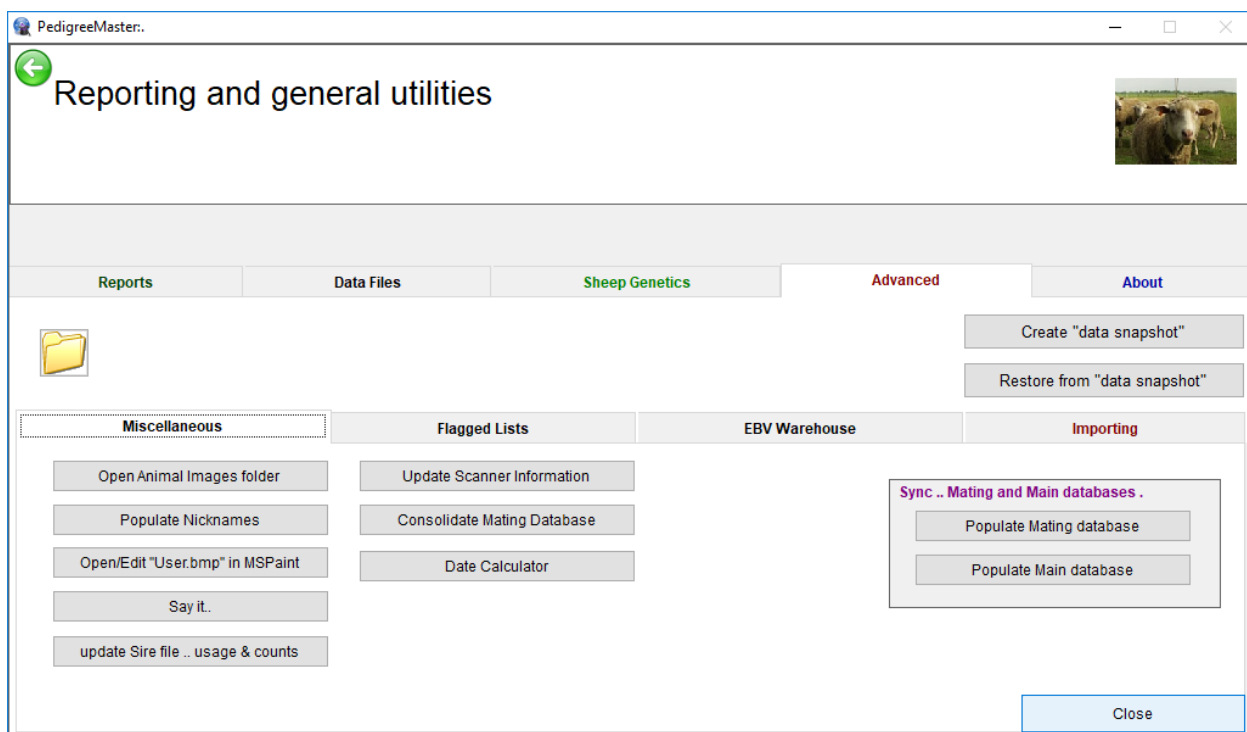
If you want to copy data, clicking on one of the copy tabs in the box with the **Copy/Append data** heading. The copy option is available for your **Main dataset, visuals database, and EBVs database**. The copy function is currently not available for **Address book or mating database**. When you click on the copy tab you are given a variety of options for what data should be copied. After making your selection and clicking on the copy tab, a pop-up screen appears showing where your data copy resides. This will normally be c:\SheepGenetics\PedigreeMaster\Export\. You can then access this copy and move it to external storage. An easy way to do this is to click on the **Open Export/Copy** folder at the bottom of the screen. By clicking on it, you are taken to the directory where data is stored and from there you can move it as you like.

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 currently not functional. It is very important to note the **Update Pedigree from results** and the **Add Pedigree from results** 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.

Clicking on the **Advanced** tab will produce four new tabs to appear: **Miscellaneous, Flagged Lists, EBV Warehouse and Importing**. Under **Miscellaneous** are five tabs.



The first is **Open Animal Images Folder**. Clicking on this will take you to where some images of sheep and the PedigreeMaster logo are located. Clicking on this **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 **Say it** 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.

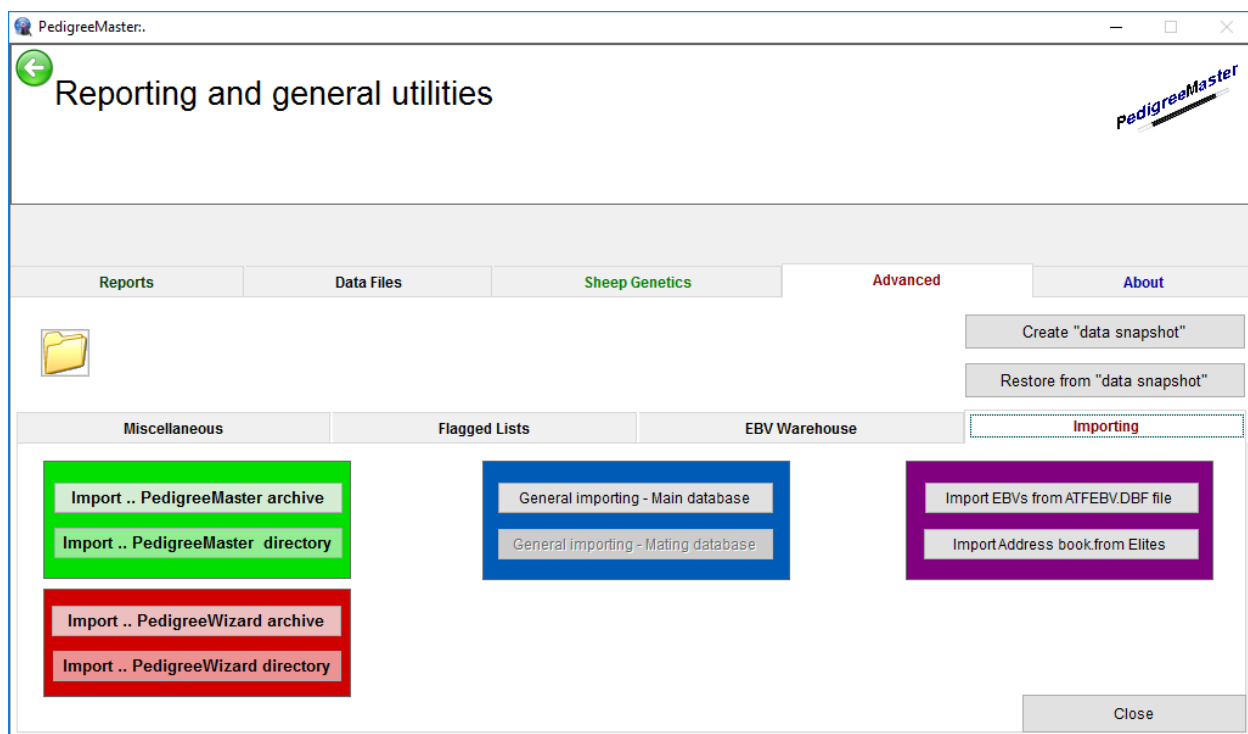
Clicking on the **update Sire file...usage and counts** will update the figures for number of progeny of various sires for various traits after a new set of data has returned from LambPlan processing. When you click on this tab, a screen appears asking if you want to limit the list to sires used in the 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 **Update Scanner Information** button is self-explanatory. The **Consolidate Mating Database, Populate Mating Data base** and **Populate Main Database** are currently not functional. **Date Calculator** is handy for tasks such as predicting when ewes will lamb. First input a date into the **Date One** area. For example, you might input a breeding date. Next input a value in the **Days** area, such as the expected gestation length. Then press Enter on your computer and a date will appear in the **Date 1 + Days** area of when the ewe should give birth. You can also input a value in the Date 1 – Date 2 area and the number of days difference between the two dates will appear.

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, a table appears with animal IDs, EBVs, and accuracies of those EBVs. This report is for viewing only. There is a sort option with this so that you can sort the values in

order of any of the table variables. 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 **Import ...PedigreeWizard archive** and **Import...PedigreeWizard directory** were described earlier in the manual. The **Import...PedigreeMaster archive** and **Import...PedigreeMaster directory** are to be used when bringing in archived data, such as when a data is to be transferred from an old computer to a new one. The remaining tabs on this screen deal with various ways to import external data. Clicking on the About tab gives you the address of Sheep Genetics as well as a link to the software update page.

## Other Opening Screens

The **Add & Change records** button is used for data entry, see page 26. **Address Book** is used to keep information on other breeders. It is initially stocked from your first data run but will need to be manually maintained and updated by you after that. The **Summaries, Validation and Database Backup** button is used mainly with data submission and is discussed on page 33. Click on the **Groups** button and a listing of contemporary group numbers and descriptions appears. These will be necessary to input data as described later in this manual. This screen gives you the opportunity to review the groups and make changes if needed prior to data entry. The **Sires** button, when clicked, reveals a list of sires of lambs. Keeping this list current will be very useful when later entering data. The button labeled **Reindex database** is to be used each time is received from processing.

## Chapter 4 – Data input

There are several situations in which you may find yourself involved 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](mailto: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 Burgett. To input data that was previously in PM, as would be the case of getting a new computer or wanting the data on an additional computer, please refer to Chapter 7.

### **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 same six digits of the NSIP code you use for animals you raised. Next input the year of birth in spaces 7-10, 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. In these situations it is often handy to input something into the nickname area of the animal so that you can more readily identify it because the NSIP number you just entered may not seem familiar to you later.

**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 of 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 in places 11 and 12, you

can input either CU or CO for animals that are culls, such as wethers or animals that may have a bad mouth, unsound feet or some other problem. 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. There is a limit to the number of CO and CU animals you can have, with no more than 25% of your flock labeled as CU or CO. Another possibility for identification is that if a lamb is born dead, the last six spaces can be DABxxx, where xxx is a number starting with 001, then 002 for the next dead lamb, etc.

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. Appendix C lists the combinations of letters that cannot be used in certain places in animal IDs as of November 2016. 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 except with through the process described on page 13. Otherwise, the changed ID may very well not be changed in the pedigrees of all other animals in which it appears.

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

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.

It is important to note that all "historic" data needs to be submitted on the first data submission in order to not be billable. If you later submit additional historical data, you will be charged for it. So it's good to think about things a bit and get all the data you want in the first submittal. On the first submission of data, only the 2 most recent lamb crops are considered billable and anything older than 2 years old will not generate a billing. In general, the more data you submit, the better things will be as the accuracy value will be higher due to having more records per individual and having more animals involved that are related to those you currently have in the flock. At a minimum, you should certainly at least submit data for all lambing season that include the first lambing for any ewes you have in the flock.

It is important that ALL lambing records be included for those years. In other words, don't just include the lambing records of ewes that you currently have in the flock. The lambing records of their contemporaries must be included as well. This is because the basis of this type of genetic analysis is in comparing how an animal performs relative to the others in its group. Thus as you input historical data, if you only include lambing records on ewes you currently

have and not on other ewes that lambed at that time, you will have a much poorer and somewhat biased comparison between the ewes.

If you have data on a spreadsheet, it can easily be input into Pedigree Master as explained below. If you are inputting the data from written records, remember that the first records you put on will take the longest as you will have limited use of the drop-down menus for sire and dam inputs. As the sires and dams are input, they should appear on the drop-down menus and speed the process up. This can be sped up even more by inputting the sires directly into the sire drop-down menu as described on page 28. Plus, in many cases, the first 10-13 digits of most IDs can be preset on one of the function keys as described on page 26, which speeds things up even more.

As with many things in life, the input process gets faster with each animal as the process becomes more routine. People who don't enjoy working with computers may tend to put in very little historic data as the work becomes tedious. However, it is much better to put the work aside if it becomes tedious, and input more data at a later date, than to give up because you're tired and submit what data you have. As you get data back from Lambplan, the benefits of putting in more historical data will become obvious. So, in summary, a) the more the better, b) be sure to input all historical data in the first run, and c) don't forget to use all of the available aids such as function keys and drop down menus, or spreadsheets, to make the process a lot faster.

**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. Before beginning, it is important to backup your current dataset as described on [page 16](#).

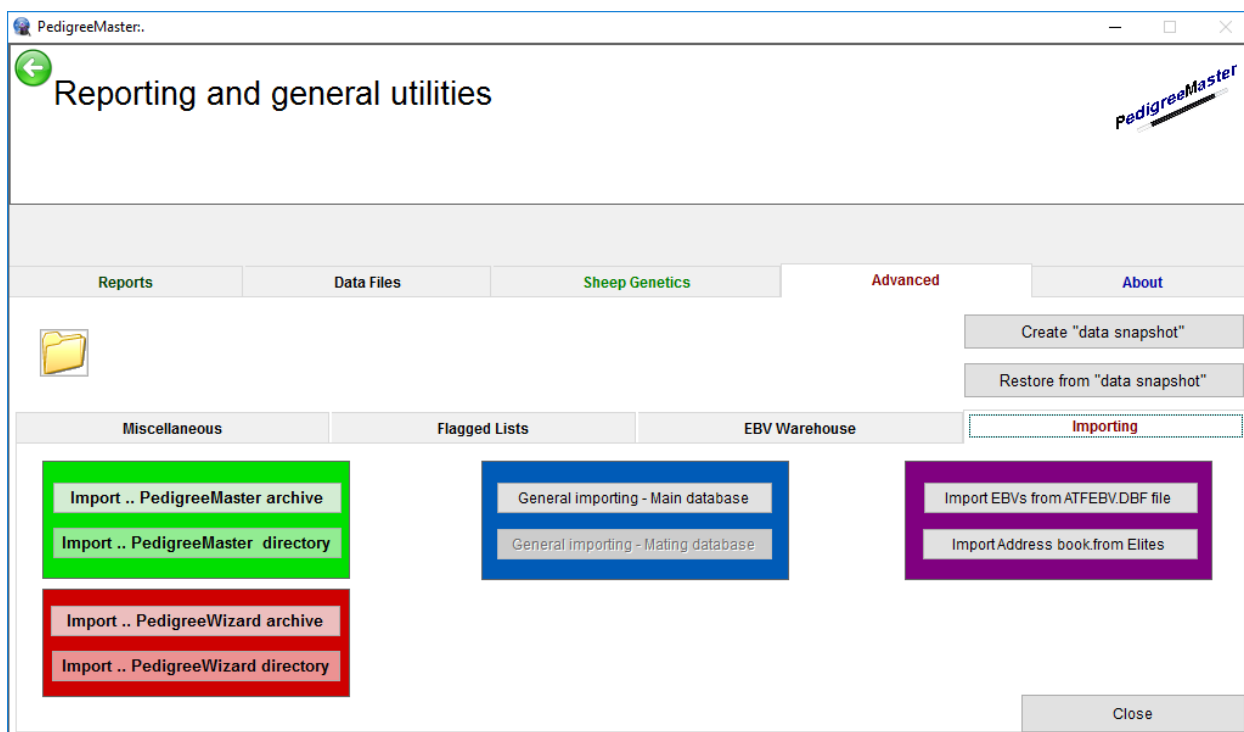
To successfully transfer the data from a spreadsheet to PM, the spreadsheet must have the required columns headings with appropriate data under the column headings. The columns do not need to be in any particular order right-to-left as PM will find each one during the import.

<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	Rear type- how many lambs were raised on the ewe 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
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 headings can be obtained at: <http://kidplan.mla.com.au/PedigreeWizard/> . At that site, click on **General Importing** on the left side menu. 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. If the sire of an animal is unknown, you can input UNKSRE. Some people find it helpful to use a fixed –width font such as Miriam Fixed to help spot errors in fields with a set length to them, such as the ID fields.

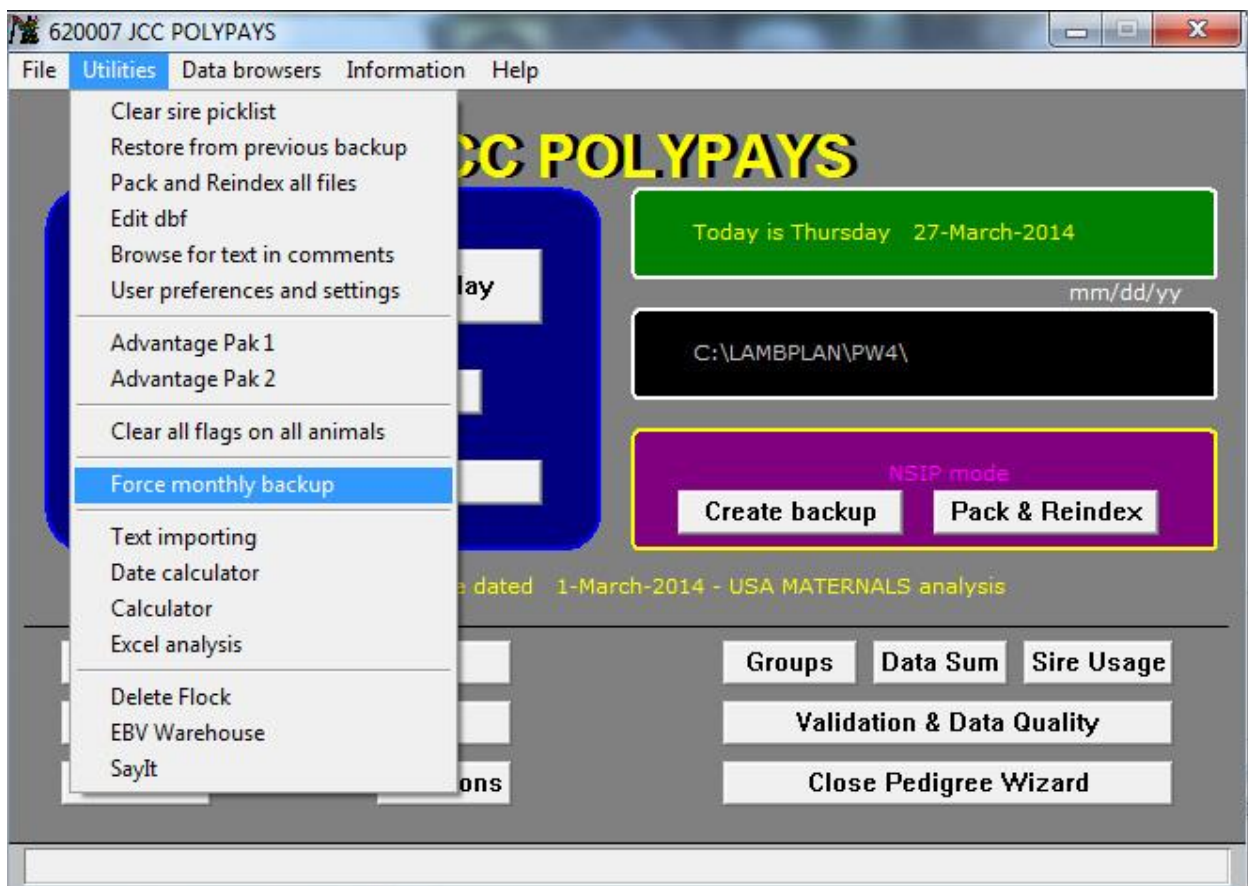
After all of the data is entered, save the file as you normally would so that you have a base set of data. Then do a **Save as** and save the file as a Text (tab-delimited) file. An alternative is to open Notepad as a blank file. Highlight all of the Excel Sheet’s data and column headings and copy and 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**. Be sure the import defaults are correct. You will be asked if you have a backup. If you do, then click on **yes**. If not, click on **no** and backup the file as described earlier in this manual. Again click on **Select file** and proceed. 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 an error appears, do not proceed to import. Go back to the spreadsheet and correct the error. If everything looks OK, click on **Import file** and then **OK**. Then click on **Check Main Data Table**. Check through the data carefully, especially ID inputs. If no errors appear, click on **Check Visual Table** if your data has any visual traits. After checking that data, click **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.

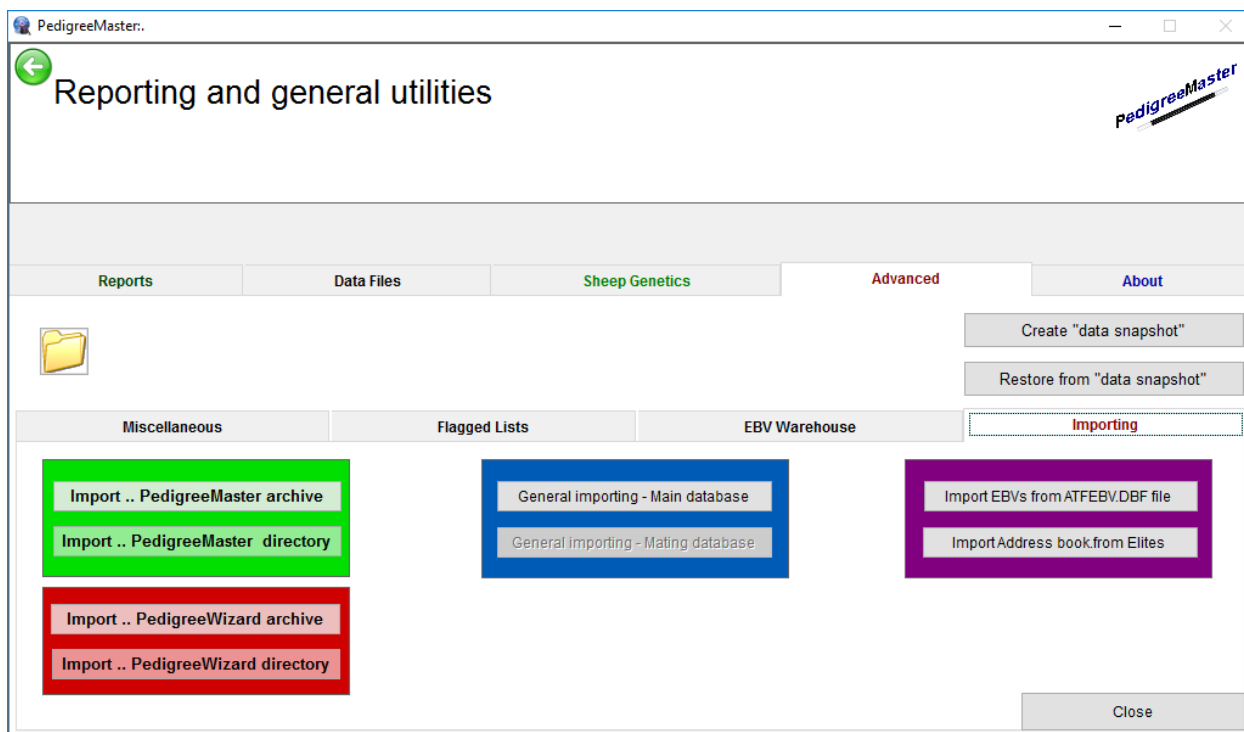
**Data transfer from Pedigree Wizard:** The first thing you need to do, of course, is to back up your PW data so that your data is secured should some computer malfunction occur. It is a good idea to frequently backup your data and back it up on different media in case your computer someday decides to 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

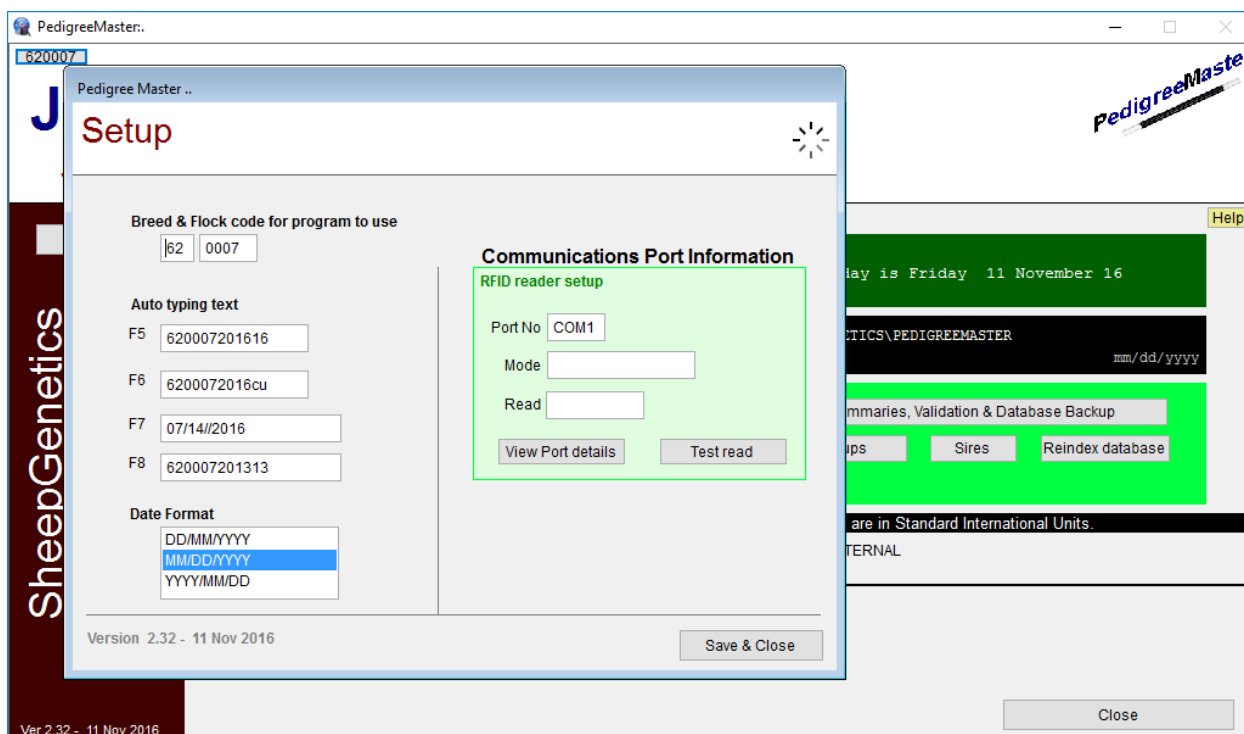
YYYYMMDD where YYYY is the current year, MM is the current month and DD is the day. If you will be using PM on a computer different from the one that has PW, you will need to get the backup file on cloud storage or other type of transferrable storage such as a thumb drive so that the other computer can 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](mailto: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 function keys can be used for years covering the data to be input, such as with F5 above, and CU or CO can be used in places 11-12 of the NSIP ID for animals that are to be culled as shown in F6. The use of CU and CO was previously 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 that are sires and dams 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**, or press tab or enter, and PM 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, enter its 16-character ID into the sire input area. After you do so and 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 sped 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 screen.

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	
	6200072011110126	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. The sex, birth type and rearing type menus are 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 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 the group that the animal

is in. See page 11 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 11 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 to click the Pedigree Display button on the main screen.

The screenshot shows the PedigreeMaster software interface. At the top, the animal ID **620007-2019-190920** is highlighted in blue. Above it, its parents' IDs are shown: **620125-2018-P8092G** (red) and **620007-2016-160602** (green). The interface includes a 'Sex' dropdown set to '1', a 'Date of Birth' field with '01/17/2019', and a 'Group' dropdown set to '1' with the label 'early lambs'. A 'Comment' field contains the text 'Ram to enter in the CNS sale'. Below this are tabs for 'Breeding', 'Carcase', 'Fleece', 'Reproduction', 'Miscellaneous', '(1) Breeding Values', '(2) Breeding Values', and 'Visuals'. The 'Breeding' tab is active, showing options to 'Change Group', 'Add new animal', and 'Delete animal', along with fields for 'Sire', 'Dam', 'FateCode', 'End of recorded life', 'Date', 'Pedigree method', 'Accuracy', and 'Status'. The 'Status' dropdown is set to 'Current'. On the right, a list of animal IDs is shown, with '620007-2019-190920' selected. The interface also includes fields for 'Birth Type', 'Rear Type', 'Lambease', 'Conception', 'Testicles', 'Jaw', 'Foster Ewe', and 'Recip ID'.

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 as explained in the Reports section of this manual. 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. Contact Rusty if you think that it absolutely must be done.

This is the screen to use if you have cross-fostered a lamb. In the Foster Ewe input area, type in the ID of the ewe to whom you gave an extra lamb. By doing so, the foster ewe will get credit for all of the lambs that she raised and their weights. Also, if a lamb is the result of an embryo transfer, input the ID of the recipient ewe that raised the lamb. Otherwise, the computer will assume that the ewe identified in the dam column is the ewe that raised it. This will not only give inaccurate values for some EBVs but may result in conflicts in lambing dates from other embryo transfer lambs from the same dam. If you click on the **Add new animal button**, you will see a different way to add animals. Autoprefix is there and, while the function keys do not appear on the screen, they 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 done.

Clicking on the **Carcass** button will bring up a screen allowing you to enter weights, carcass, scrotal and egg count data. If many animals had this data measured on the same day, a lot of time can be saved by programming the function keys to this date and inputting the date via the function keys for each animal. The **Fleece** and **Reproduction** tabs will bring up screens to allow you to enter data in those areas. The **Miscellaneous** 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. If you feel strongly about retagging an animal, contact Rusty Burgett at [info@nsip.org](mailto:info@nsip.org) to get explicit directions on how to proceed. 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 11<sup>th</sup> and 12<sup>th</sup> characters to CO or CU if you want to do so and for some reason did not enter them initially. In case of a tag change, you can use the nickname function to keep things more clear for you on who is who.

The **Breeding Values** 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. It is always a good idea to validate your data after entering it. 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, it is 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 **Main Database** and go to the first animal for which you have data to input.

The screenshot shows the PedigreeMaster software window. The title bar reads "PedigreeMaster." and the status bar indicates "2 of 793 - PMDATA". The window contains a table with the following columns: Id, Sire, Dob, Sex, Dam, Bwt, Wddmm, Wwt, Wcf, and Wemd. The table lists various animals with their respective IDs, sires, birth dates, sexes, dams, and weaning weight data.

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 **Close window** in the upper left corner. While 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 takes its data out of the group comparison which is the basis

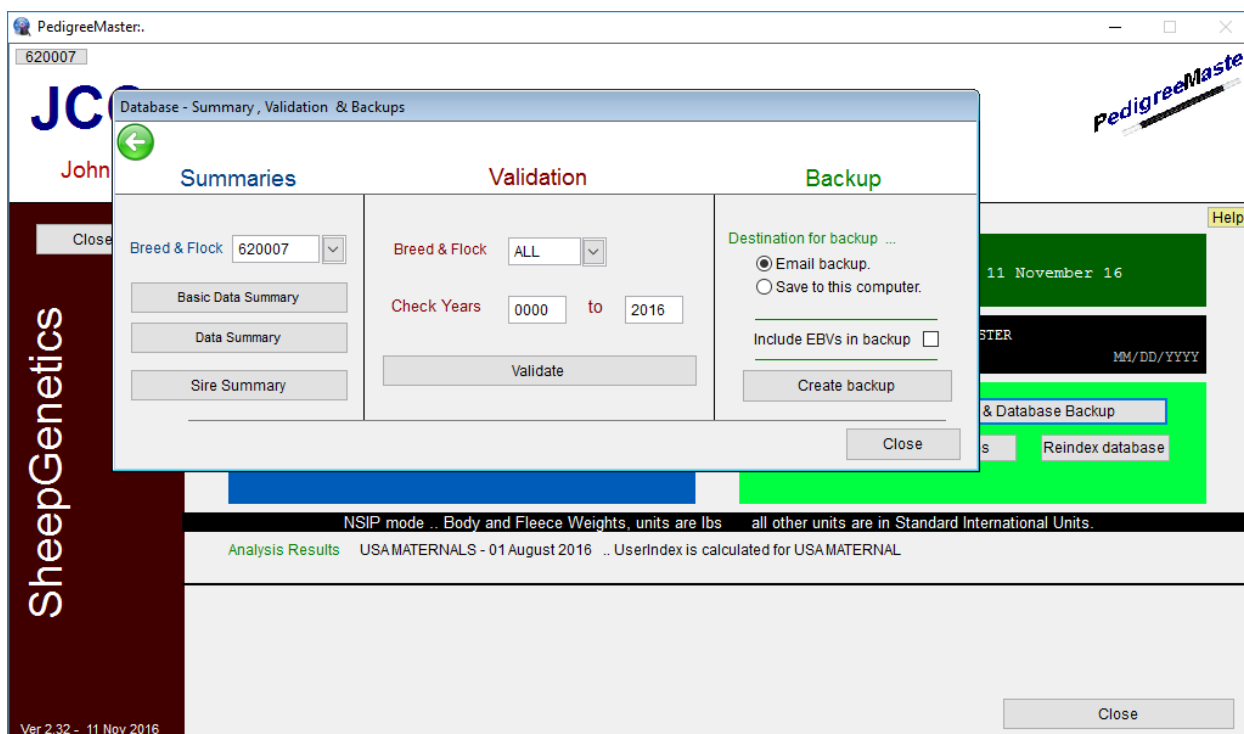
for the genetic analysis! If you have data that needs to be changed, you can easily do it in the **Main Database**. This is preferred to deleting a record and starting completely over.

## Chapter 5 -- Submitting data

Data can generally be submitted to LambPlan twice each month, if needed. Runs are generally around the 1<sup>st</sup> and 15<sup>th</sup> of each month. A calendar listing the submittal dates is online at: <http://nsip.org/nsip-member-services/data-run-calendar/>. If you do not have data but wish to have your EBVs updated, you can send an email to [database@sheepgenetics.org.au](mailto:database@sheepgenetics.org.au) and put EBV update in the subject line and in the text portion of the email, write that you do not have data but would like an EBV update and be sure to include your six-digit flock ID.

You will need to submit your data via email to LambPlan in Australia. The email to use is: [database@sheepgenetics.org.au](mailto: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 & Database Backup**. The first step is to validate your data. If there is an error, it needs to be detected and corrected now. If data with significant errors is submitted for analysis, it may be returned unanalyzed and will need to be corrected and resubmitted for a later analysis.



Under **Validation**, a popup screen will appear asking you to input what flocks you want checked, as well as the years over which data should be checked. Generally, you want to include all flocks and all years in which there are data. 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 message typically says 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. Submitting data that does not pass PM's validation can result in erroneous results or in LambPlan not being able to process your data.

Next, under the **Backup** heading, you need to fill in a circle either by **Email backup** or **Save to this computer**. Also, you should NOT check the box by **Include EBVs in backup** if you are submitting the data to Lambplan. If you fill in the circle by **Email backup**, a zip file will be created that is best used as a backup for the data that you want to be submitted. Warning: If you fill in the circle by **Email backup**, you **MUST** have your software configured to work with this. The method for doing this varies greatly from email software to email software. Because of this variation, this manual cannot tell you how to do the configuration. Use the Email backup option **ONLY** if you are sure you have the software configured to work with Pedigree Master. When the circle by **Email backup** is filled in, click on **Create backup** and a message will come up asking you if you have run the validation procedure and if you want to continue with the backup procedure. If you have just finished running this procedure, click on **Yes**. If you have not just finished running this procedure, you should run it, so click on **No** and run the validation procedure as previously described. If your email software is configured correctly, it should take care of things from here on.

If you are unsure about your email software configuration, a safer approach is to fill in the circle by **Save to this computer**. Click on **Create backup**. A message will come up asking if you have run the backup procedure and if you want to continue with the backup procedure. If you have just finished running this procedure, click on **Yes**. If you have not just finished running the backup procedure, click on **No** and run the validation procedure as previously described. After clicking on **Yes**, a screen will appear 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, click on OK.

Or, another location that many prefer is the desktop 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 and click on OK. If you have previously created a backup file, a box will appear asking if you wish to overwrite the existing/older backup file. Click on **Yes**. Then a message will appear informing you that the archive was successfully created. With some versions of Windows, a screen will pop up showing you where the file was created. If this occurs, be sure to check that the file is where you wanted it to be. Close out of the onscreen boxes. 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. The zipfile will be named with your six number NSIP code followed with a zip extension. Attach the file using your normal email attachment procedure. 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 3-7 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/>. Click on it and the update webpage will appear.

When you get to that website, scroll down until you come to a file in the far right column 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	<a href="#">00 Elites LPN 15Mar14.exe</a>
Thursday, March 20, 2014 10:35 AM	171427	<a href="#">00 Percentiles and TraitLeaders 15Mar14.zip</a>
Tuesday, March 18, 2014 9:52 AM	2138788	<a href="#">020041.EXE</a>
Tuesday, March 18, 2014 9:52 AM	734409	<a href="#">020163#.EXE</a>
Tuesday, March 18, 2014 9:53 AM	1126046	<a href="#">020645.EXE</a>
Tuesday, March 18, 2014 9:53 AM	975085	<a href="#">020863.EXE</a>
Tuesday, March 18, 2014 9:55 AM	3466037	<a href="#">021614.EXE</a>
Tuesday, March 18, 2014 9:56 AM	2424042	<a href="#">021929.EXE</a>
Tuesday, March 18, 2014 9:56 AM	653794	<a href="#">022272.EXE</a>
Tuesday, March 18, 2014 9:57 AM	1408324	<a href="#">022656.EXE</a>
Tuesday, March 18, 2014 9:57 AM	1018602	<a href="#">023151.EXE</a>
Tuesday, March 18, 2014 9:58 AM	873876	<a href="#">023270#.EXE</a>
Tuesday, March 18, 2014 9:58 AM	258830	<a href="#">023369.EXE</a>
Tuesday, March 18, 2014 9:59 AM	3741768	<a href="#">023626#.EXE</a>
Tuesday, March 18, 2014 10:01 AM	2942776	<a href="#">023666.EXE</a>
Tuesday, March 18, 2014 10:01 AM	817338	<a href="#">023691.EXE</a>
Tuesday, March 18, 2014 10:01 AM	1087413	<a href="#">023780.EXE</a>
Tuesday, March 18, 2014 10:02 AM	1021142	<a href="#">023881.EXE</a>
Tuesday, March 18, 2014 10:03 AM	2324664	<a href="#">024075.EXE</a>
Tuesday, March 18, 2014 10:03 AM	1242527	<a href="#">024166.EXE</a>

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. Or, you may have Windows SmartScreen try to stop the process and the screen below will appear. If so, click on **More info** and then click on **Run anyway** when it appears.

## Windows protected your PC

Windows SmartScreen prevented an unrecognized app from starting. Running this app might put your PC at risk.

[More info](#)

Don't run

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 **OK** to return to the main screen. If you click on the Pedigree Display button and then on the **Breeding Values** 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 check the box by **Include EBVs in backup**. Then click on **Create backup**. Click **Yes** to the questions about having validated the data, assuming you have. 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 explained in more detail on page 3. After installed, 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. 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, you need to click on OK to the box about restarting the program. 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.

If you have any questions, contact Rusty Burgett in the NSIP office via email at [info@nsip.org](mailto:info@nsip.org) or by phone at 515-708-8850 or your breed or group representative. Breed and group representatives are posted online at: <http://nsip.org/nsip-about/board-of-directors/>.

## 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 in terms of number of lambs born per 100 ewes lambing. For example, if an animal has an EBV of .20, its genetics have the ability to give birth to .20 more lambs per lambing. In the case of rams, this value is halved for his daughters' production.														
Number of Lambs Weaned	NLW	Weaning	Number of lambs a ewe gives birth to. Input as Bt with a 1 for single, 2 for twin, etc. EBV figures are in terms of number of lambs weaned per 100 ewes lambing. For example, if an animal has an EBV of .20, its genetics have the ability to wean .20 more lambs per lambing. In the case of rams, this value is halved for his daughters' production.														
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 their ability to grow to 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 to produce heavier weaning weights.
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 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 :** 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	Same as for Fiber Diameter (above)	Yield is the clean fleece weight as a percentage of the grease fleece weight. EBVs estimate																		

	for postweaning, yearling, hogget and adult yields, respectively.		the genetic differences between animals for 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	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

	hogget and Ass for adult values.		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																						
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																						
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 or low-cost 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. While this does entail some added costs, the benefit from improved genetics will more than cover the investment.

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. Programs that can satisfactorily run Windows programs on a Mac include Parallels Desktop, VMware Fusion, Boot Camp and 2-3 free ware programs. The choice of software is up to you, however several producers have reported good results using Parallels. As Mac operating systems upgrade, an upgrade in the previously mentioned software will likely be necessary as well. Pedigree Master does not require the latest versions of Windows and thus upgrades of the previously mentioned software may not be needed if it is to simply get a new version of Windows. 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. 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. A discussion on software to run Windows programs on a Mac, and the implications, is available at: <https://www.macworld.co.uk/feature/mac-software/best-virtual-machine-software-3671133/> .

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 versions. The newest versions of Window are not necessary to run Pedigree Master. 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. Or, some producers hire others to put the data onto a PC directly. Contact NSIP if you would like a list of data input contractors.

## Appendix C – Character sequences that should not be used in PM IDs

The table below lists various character sequences that should not be used when forming the 16-character identifications in Pedigree Master, along with the columns in which the character sequences should not be used.

<u>Code</u>	<u>Sire/Dan or Both</u>	<u>Starting Position in ID</u>	<u>Ending Position in ID</u>
00	both	1	2
0000	both	13	16
000000	both	1	6
000000	both	11	16
000077	both	7	13
2ND	both	11	16
9999	both	13	16
AG	both	15	16
ALD	both	14	16
AM	both	15	16
AMMR	both	11	16
BACKUP	both	7	16
BB	both	15	16
BK	both	15	16
CEDI	sire	11	16
CHA	both	12	16
CO	both	11	16
COB	both	14	16
CORR	both	11	16
CU	both	11	16
DAB	both	11	16
DRY	both	11	16
EWE	both	11	16
FINN	both	11	16
FK	both	15	16
FLK	both	7	16
FLK	both	11	16
FLOCK	both	7	16
GOOD	both	11	16
GORD	both	11	16
GP	both	15	16
GRP	both	11	16
HILC	both	11	16
JOHN	both	7	16
KEL	both	14	16
KIRK	both	11	16
LAMB	both	7	16
LATE	both	11	16
LLET	both	11	16
LM	both	15	16
LS	both	15	16
LS	both	15	16
LT	both	15	16
MAID	both	7	16
MDN	dam	11	16

MIC	both	13	16
MIL	both	14	16
MM	both	15	16
MS	both	15	16
MS	both	15	16
MSG	both	14	16
MSG	sire	11	16
MULTI	both	1	16
NAM	sire	11	16
NCY	both	11	16
NT	both	15	16
OWN	both	13	16
PGK	both	11	16
RAM	both	11	16
RAM	both	7	16
RET	both	13	16
RGP	both	11	16
RL	both	15	16
RLS	both	14	16
RLS	both	11	16
RLS	both	11	16
RR	both	15	16
RR	both	15	16
RS	both	14	16
RT	both	15	16
SIB	sire	11	16
SIRE	both	7	16
SN	both	15	16
SN	both	15	16
SRS	both	11	16
STD	both	11	16
STOCK	sire	1	16
STUD	both	11	16
SY	both	11	16
SYD	both	11	16
SYN	both	11	16
SYN	both	1	16
SYN	sire	11	16
TOP	both	12	16
UKN	both	7	16
UNSURE	both	11	16
UPS	both	11	16
XX	both	1	2
XXXX	both	7	16

## Appendix D – Top Ten FAQs and their answers

**1. I found out that I made a typo in the data on one of my lambs. How do I correct it?** The quickest and easiest way to correct most data input errors is to click on Pedigree Display at the opening menu and then on **Carcase** if the error is not regarding fleece data. If it is an error regarding fleece data, click on **Fleece**. The data you input will be shown and you can easily make the correction. When finished with the correction, click on **Close** and the situation is corrected.

**2. I made an error in one of my IDs. How do I correct that?** To easily correct an ID error, click on **Reports and Utilities** at the opening screen and then on **Data Files** and finally on **Main Database**. Make the needed change and click on **Close window**. Close the screens to go back to the opening screen and the change is completed.

**3. If I am just beginning to put in data, how far back should I go?** First it is important to note that all “historic” data needs to be submitted on the first data submission in order to not be billable. If you later submit additional historical data, you will be charged for it. So it’s good to think about things a bit and get all the data you want in the first submittal. In general, the more data you submit, the better things will be as the accuracy value will be higher due to having more records per individual and having more animals involved that are related to those you currently have in the flock. At a minimum, you should certainly at least submit data for all lambing season that include the first lambing for any ewes you have in the flock.

It is important that ALL lambing records be included for those years. In other words, don’t just include the lambing records of ewes that you currently have in the flock. The lambing records of their contemporaries must be included as well. This is because the basis of this type of genetic analysis is in comparing how an animal performs relative to the others in its group. Thus as you input historical data, if you only include lambing records on ewes you currently have and not on other ewes that lambed at that time, you will have a much poorer and somewhat biased comparison between the ewes.

If you have data on a spreadsheet, it can easily be input into Pedigree Master as explained on page 22, thus speeding up the process. If you are inputting the data from written records, remember that the first records you put on will take the longest as you will have limited use of the drop-down menus for sire and dam inputs. As the sires and dams are input, they should appear on the drop-down menus and speed the process up. This can be sped up even more by inputting the sires directly into the sire drop-down menu as described on page 28. Plus, in many cases, the first 10-13 digits of most IDs can be preset on one of the function keys as described on page 26, which speeds things up even more.

As with many things in life, the input process gets faster with each animal as the process becomes more routine. People who don’t enjoy working with computers may tend to put in very little historic data as the work becomes tedious. However, it is much better to put the work aside if it becomes tedious, and input more data at a later date, than to give up because you’re tired and submit what data you have. As you get data back from LambPlan, the benefits of putting in more historical data will become obvious. So, in summary, a) the more the better, b) be sure to input all historical data in the first run, and c) don’t forget to use all of the

available aids such as function keys and drop down menus, or spreadsheets, to make the process a lot faster.

**4. How often do I need to update this software?** Not working with the latest version of PedigreeMaster is one of the main reasons that people encounter an unexpected problem. Software updates come up somewhat irregularly, depending on the number of problems that are encountered and how long it takes to fix them or to make general improvements. So the best rule-of-thumb on updating the software is that each time you add data or download EBVs, first see if an update is available and install it. Download and install the software **before** making any other changes. It is quick and easy to check for updates. Just click on the Help button on the opening screen and then on PedigreeMaster on the screen that follows. Then you will see a page that lists the recent updates, including the one that is available. Updates are cumulative, so don't worry about the past ones – just get the one that is available. Before downloading any update, make sure you have a current backup of your data. Also, when downloading, make sure your current version of Pedigree Master is closed and only open it once the download is completed. It is also a good idea to reboot the computer after you have loaded an update, just as it is with a software update for any program.

**5. I ran the validation procedure and some errors showed up. The deadline to submit data is close, however, and I really want to get new EBVs. How important is it to clear up the validation errors?** If you have severe errors in your data, LambPlan may not be able to process your data and you will have missed the processing deadline anyway. Plus, even if the error is smaller and will allow processing, the EBVs you get back may not be too meaningful. The error will not go away on its own – it will show up each time you validate. So while it will take some extra time to track down, the best thing to do, without a doubt, is to take the necessary time to correct the errors before you submit the data. Otherwise, it will be a constant problem for you.

**6. I'm going to a sale next week and want to print out some performance pedigrees to help promote my sale sheep. How do I do that?** This process is described in a little more detail on page 10 but the general procedure is to click on Pedigree Display, then on Breeding Values and then on Pedigree. Select your favorite pedigree format from the three types and then click on the printer icon that shows up in the Print Preview window. With some printers there is a pdf option. By using that option and saving the pdf file, you can later send the pdf file via email to a prospective buyer.

**7. I would like to have my EBVs in Excel so that I can sort and work with them. Is it possible to do that?** There are several ways to do this, however the handiest way is to click on **Reports and Utilities** and then on **Data Files**. Next click **Copy** that is by **EBVs database**. From the popup screen that next appears, input the flock number for the animals you would like to see. This is the first six digits of the NSIP ID of your animals. If you want animals from every flock that is in your data base, leave the value set to **ALL**. Then select the year of birth for the animals you want included, the sex if you want only males or females, the status (normally this is **current**) and then on **Copy**. If you do not set the status to **current**, animals that are no longer in your flock will appear. This assumes that you have previously set the status of all animals in your flock to **current**. By doing this, you won't have to deal with animals no longer in your

flock, if that is what you want. A message will then appear telling you that the process is completed, and click on OK. If you next click on **Open Export/Copy folder**, you will see the file that has been saved for you: Exp\_ebv. If you do not see it, be sure that you have “All files” listed as the file type, not just Excel files. Double click on it and it should open in Excel. This file is saved as a .dbf file, a database file, and not as an Excel file., although it can be opened by Excel. If it does not open in Excel right away when you double click it, open Excel, and click “open”. Then find the “SheepGenetics” folder on your C: drive, then click “PedigreeMaster” then “Export”. Then, to the right of the “File name” dialog box, click the dropdown menu that says “All Excel Files” and select “dBase Files”. Then your exports should appear in the selection box.

**8. I don't have any data to submit but would like to see if my EBVs have changed due to data submissions from people who have animals with genetics similar to mine. Do I have to submit data to get updated EBVs?** No, you can send an email to LambPlan at [database@sheepgenetics.org.au](mailto:database@sheepgenetics.org.au) requesting updated EBVs without having to submit data. In the subject line of the email, and in the body, print “EBV update only requested” and include your six-digit flock ID. You will get a link to new EBVs after the next data run and follow the normal procedure for downloading them to your computer.

**9. I have a new computer. How do I copy everything from my old computer to the new one.** The procedure for this is given in Chapter 7 on page 37. The most important part of the procedure is to back up your file, as explained there, and store the backup somewhere other than on your old computer. For example, attach it to an email to yourself or copy it onto a flash drive. That way, if the old computer would crash and burn in the process of transfer you still have a copy of your data.

**10. From reading through this manual, it looks like PedigreeMaster is designed for a PC. I have a Mac. Does that mean I can't use PedigreeMaster?** You can use PedigreeMaster on a Mac but will need to incorporate some software such as Bootcamp or Parallel to allow it to run in a PC environment. Producers are doing this. See Appendix B for more details on this.