

# DEERSELECT STANDARD OPERATING PROCEDURES

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## RECORD OF AMENDMENTS/REVISIONS

No	Date	Revision Description	By
1	22/11/13	First draft	JW
2	11/12/13	Amendments by Sharon	SM
3	17/12/13	Formatting by Helen	HMD
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5			
6			

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## **2 Purpose**

### **DEVELOP AND DOCUMENT STANDARD OPERATING PROCEDURES FOR**

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**DEERSELECT**

### **3 DEERSelect Red Deer Across-herd Evaluation and Sire Summary Reporting**

#### **3.1. Timing**

DEERSelect red deer Across-herd Sire Summary reporting is to be carried out in the following months:

March  
May  
July  
October  
November  
December

Cut-off date for data inclusion = 1st of the Month

Publication by 10th Month (allows time for error checking, rerunning and weekends.

Sire Summary reports published; - October, November, December, March, May and July

Note in 2013 October run was completed by the 1st October under the previous schedule

The expectation is that the GE run will be done on or as soon as possible after the 1<sup>st</sup> of the month in order to report the results by the 10<sup>th</sup> of the month (barring a major technical or data issue that would prevent reporting).

#### **3.2. Criteria for inclusion in across-herd summaries**

These runs are currently for red deer only, at present there is no across-herd reporting for wapiti and wapiti crossbreds (including progeny of recorded red deer mated to wapiti or wapiti crossbreds). Wapiti herd connectedness should be checked periodically. If acceptable connectedness is established and there is agreement from the DEERSelect Manager then a wapiti Sire Summary report could be published.

#### **3.3. Bureaux**

It is courteous to remind the three bureaux at least a week before the run is to be executed that you will be initiating the run and that they should have all deer data loaded before that date and then refrain for loading any more deer data until you have issued the reports to them, as new data will cause variation between runs, should more than one run be required.

The three bureaux are: Focus Genetics (Marius Van Niekerk), Genetic Gains (Julia Aspinall) and NZPRS (Ken Moore).

#### **3.4. Reporting**

This Sire Summaries reported are of all (red deer) sires on DEERSelect with progeny born in the last three years, that come from herds linked for growth, have a W12eBV accuracy of >74% and >4 progeny recorded.

There are currently two lists: English, and a European and Composite. For animals to be reported on the English list their owner must nominate them as being English (i.e. they consider them to be of "pure" English type according to pedigree, English herds include:

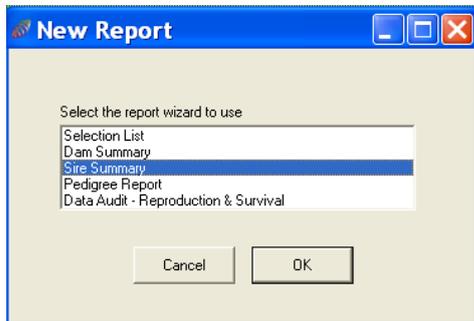
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Warnham Park, Woburn Abbey, Furzeland, Normanby Hall, Whittlebury Park, Scottish types/herds and others including many original New Zealand wild captured stock.)

The published Sire Summary lists/reports are the primary way herds that do not record on DEERSelect especially commercial producers who purchase stags are able to view breeding values and indexes. It is unlikely that this list will ever represent the maximum breeding values within the recorded herds. This is because there is a time lag for animals to enter the list as sires and progeny within the breeders herds should be bettering their parents breeding and economic index values.

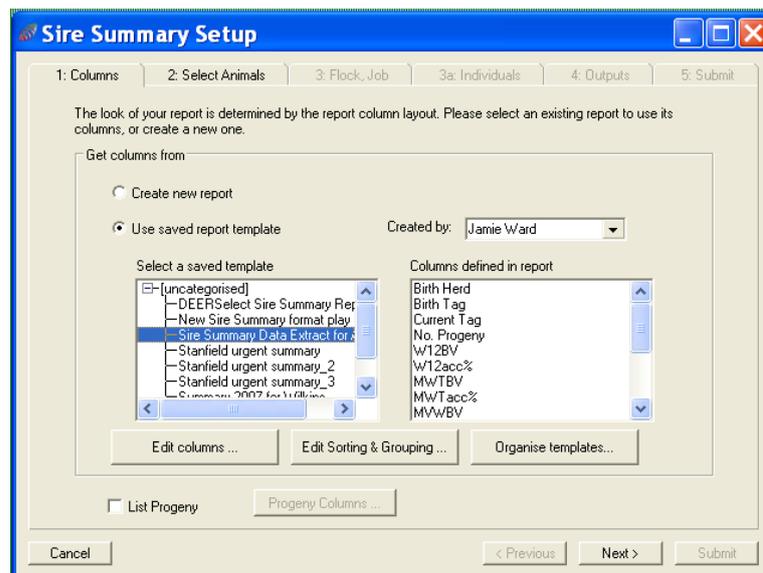
## 4 Running DEERSelect Sire Summary Reports in SIL

Open **Reports** menu, select **Report Writer** from drop down  
**New Report** window opens, select **Sire Summary** from list hit **OK** button.



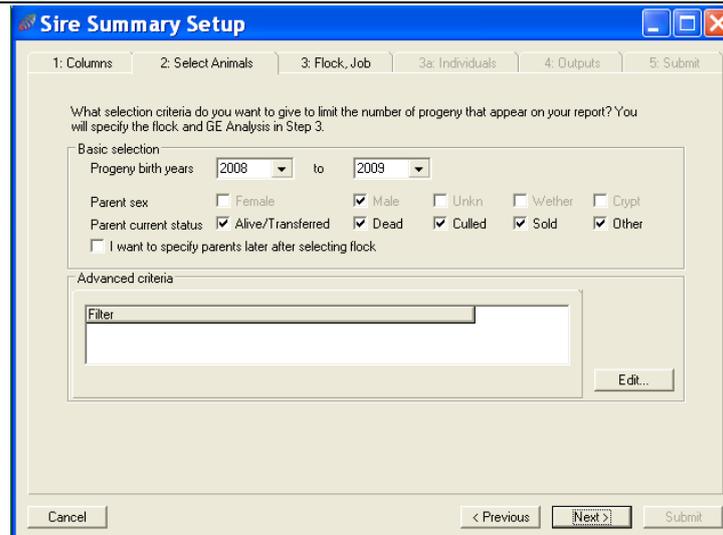
### 7.1. Columns tab

Select **Used saved report template**, select a **saved template** from the box, expand the selection options using the plus sign choose **DEERSelect Sire Summary Data Extract for Access**, wait for the columns list to populate. Hit **Next >** button. Note you will require created by Jamie Ward to access this version.



## 5 4.2 Select Animals

**Progeny Birth Years** fields choose last 3 birth years. Hit **Next >**



1: Columns 2: Select Animals 3: Flock, Job 3a: Individuals 4: Outputs 5: Submit

What selection criteria do you want to give to limit the number of progeny that appear on your report? You will specify the flock and GE Analysis in Step 3.

Basic selection

Progeny birth years: 2008 to 2009

Parent sex:  Female  Male  Unkn  Wether  Crypt

Parent current status:  Alive/Transferred  Dead  Culled  Sold  Other

I want to specify parents later after selecting flock.

Advanced criteria

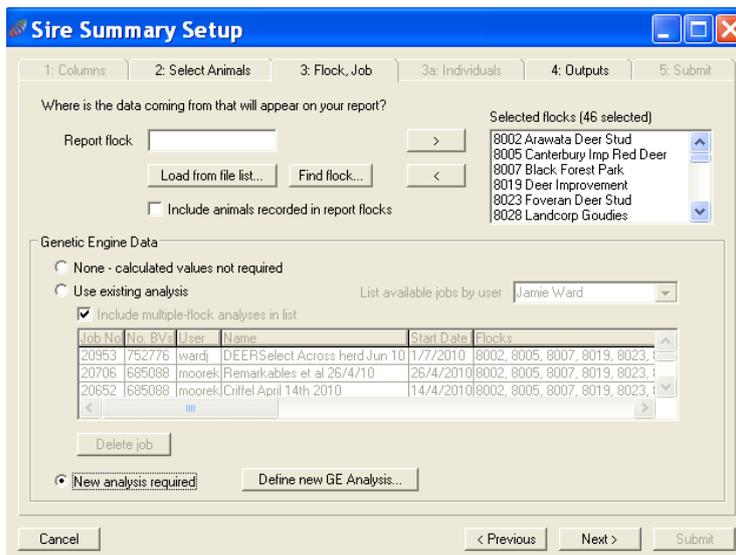
Filter:

Edit...

Cancel < Previous Next > Submit

## 6 4.3 Flock, Job

In **Report Flock** field type **Deer** hit **>** button to populate: **Selected Flocks**. Check with **Sharon** what (if any) new herds should be included in (or excluded from) the run. If herds are to be excluded select them then push the **<** button to remove. In **Genetic Engine Data** window, check **New analysis required**, the hit **Define new GE analysis** button.



1: Columns 2: Select Animals 3: Flock, Job 3a: Individuals 4: Outputs 5: Submit

Where is the data coming from that will appear on your report?

Report flock:  > <

Load from file list... Find flock...

Include animals recorded in report flocks

Selected flocks (46 selected)

- 8002 Arawata Deer Stud
- 8005 Canterbury Imp Red Deer
- 8007 Black Forest Park
- 8019 Deer Improvement
- 8023 Foveran Deer Stud
- 8028 Landcorp Goudies

Genetic Engine Data

None - calculated values not required

Use existing analysis

List available jobs by user: Jamie Ward

Include multiple-flock analyses in list

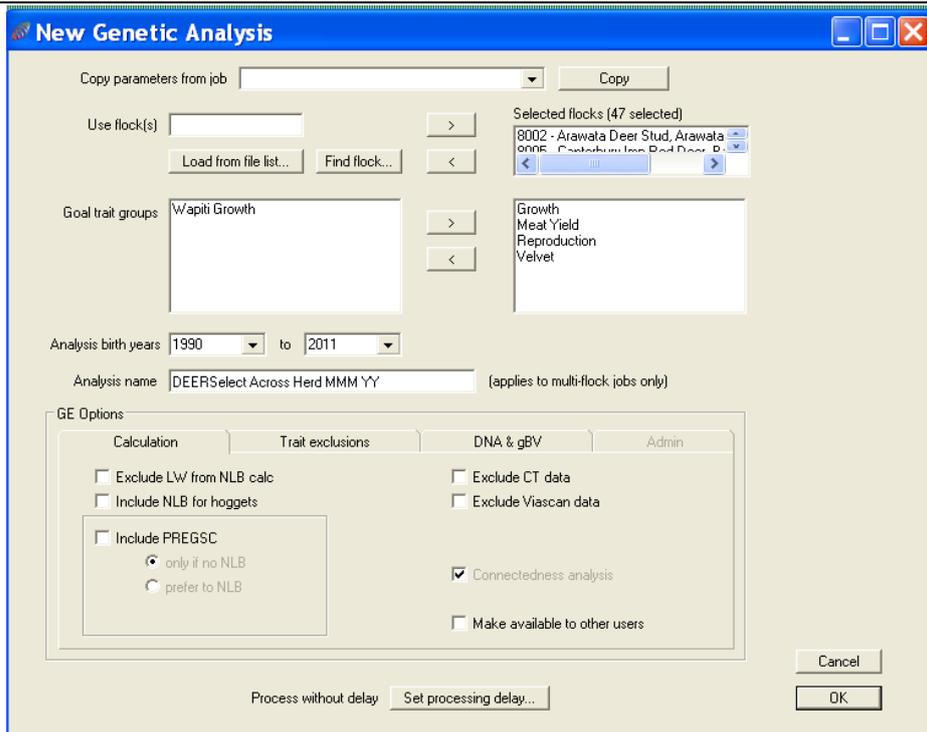
Job No.	No. BVs	User	Name	Start Date	Flocks
20953	752776	wardj	DEERSelect Across herd Jun 10	1/7/2010	8002, 8005, 8007, 8019, 8023, 1
20706	685088	moorek	Remarkables et al 26/4/10	26/4/2010	8002, 8005, 8007, 8019, 8023, 1
20652	685088	moorek	Criffel April 14th 2010	14/4/2010	8002, 8005, 8007, 8019, 8023, 1

Delete job

New analysis required Define new GE Analysis...

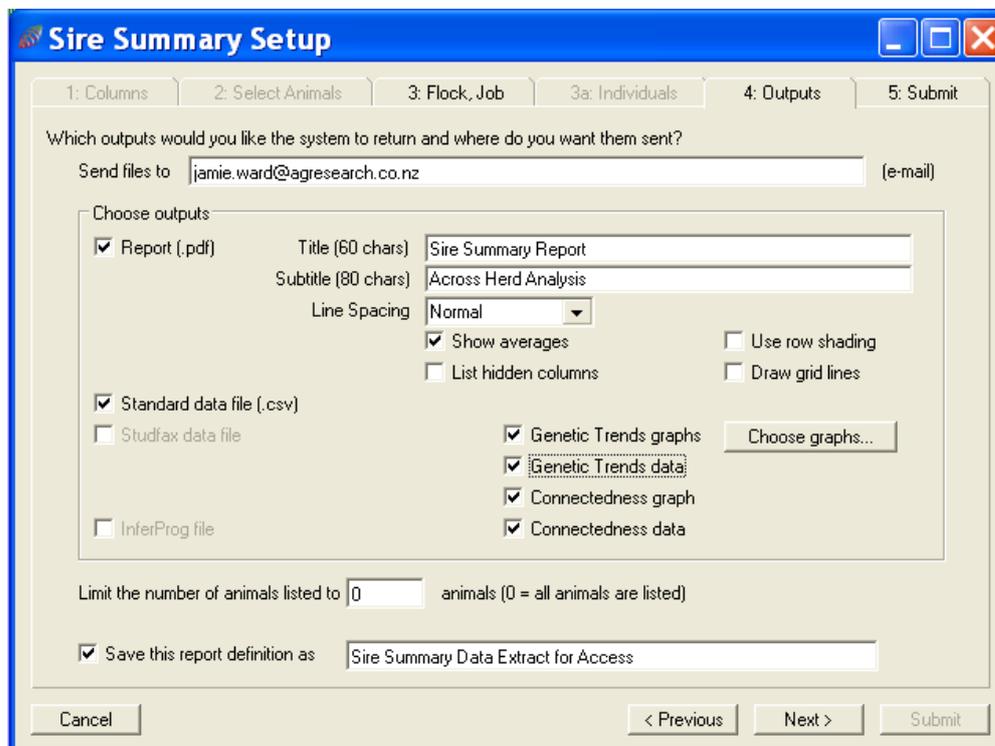
Cancel < Previous Next > Submit

In **New Genetic Analysis** window select **Goal Traits**; click on **Growth, Meat Yield, Velvet** and **Reproduction** then hit **>** button to transfer them across. In the **Analysis birth years** fields choose 1990-Present and in GE options, **Analysis name** field name file (e.g. DEERSelect Across herd date) check **Make available to other users** tick box. You can set a processing delay here if desired. You will be asked which job you want to delete also, as you can only store 2 GE runs jobs at one time. Hit **OK** button you return to **3: Flock, Job** window; hit **Next>** button.



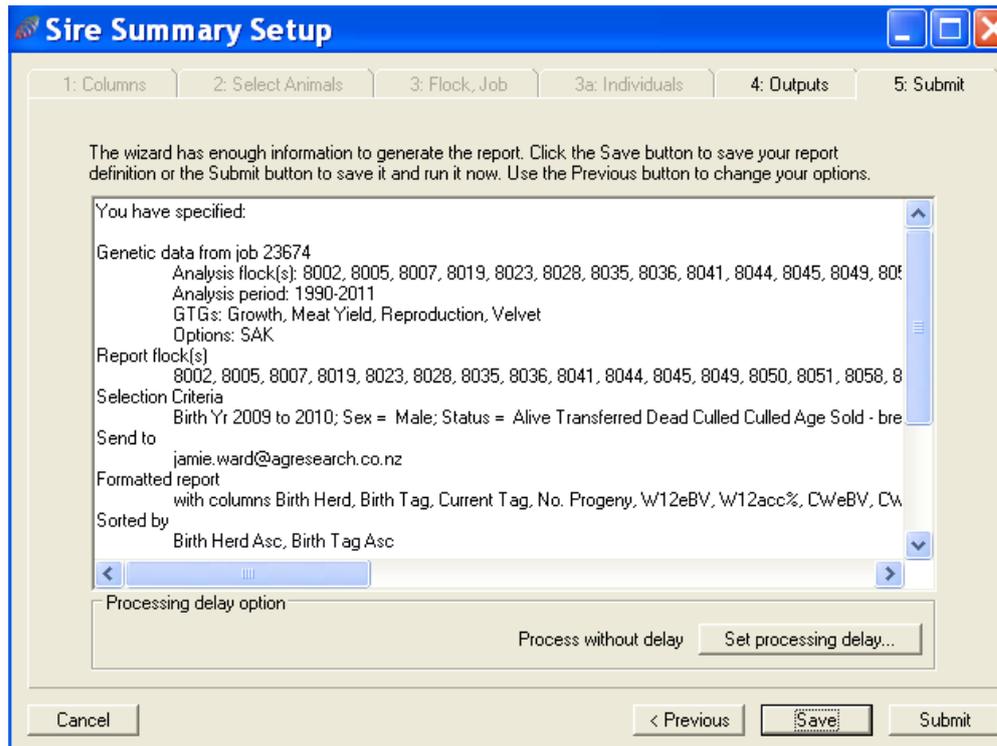
## 7 4.4 Outputs

Check **Report Title** and **Save this report definition as** (ensure tick box checked) fields. They should not require any changes, currently we report all genetic trends graphs for all herds combine, four graphs per page (use **Choose graphs**) button to change this. Hit **Next >** button. You will be told the report name has been used before. Choose **Yes** to overwrite it. Note you can e-mail to any e-mail address in 'Send files to'

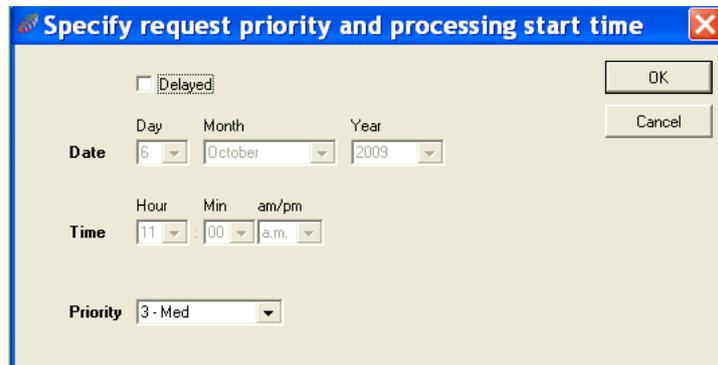


## 8 4.5 Submit

Check specifications. Hit in **Process without delay** hit **Set processing delay** button.



Uncheck the **Delayed** tick box (unless you want to delay run), ensure **Priority** is **3-Med** hit **OK** button to return to **5:Submit** window



Hit **Submit** button, wait until you get a message (**Run Report**) telling you it has been submitted, hit the **OK** button and wait for your email of the analysis (this may take some time ( could be >1 hour depending on usage). Close/cancel the **Sire Summary Setup** window. You can check your report in **Reports** menu, **Report History** drop down.

## 9 Outputs from SIL

When you receive the e-mail from SIL open the **zipped file** file and save it to **ivydeer\$, into a QA folder for the run i.e. QA/QA Nov 2013**. Copy all of the individual files within the zipped file to the new QA folder.

Open the traffic light connectedness pdf and the TL\_connectedness graph for **growth**. Check that all herds being reported on are connected for growth. You can check the individual sires which connect herds by opening the following .csv file:

ConnectSires\_XXXXXX\_DGROWTH (remember as this is a .csv file if you open it with excel sire tag formatting can be lost, best to open in wordpad). If not re-open SIL and run the Sire Summary report again: To do this repeat steps 1, 2 4 and 5, but **modify step 3** as follows:

At the **Select Flocks** step select the unlinked flocks from the list and use the < button to remove the unlinked flocks so they will not be reported on. Once the Select Flocks list contains only the herds linked for growth rerun the GE analysis.

In **Genetic Engine Data** select **Use existing analysis** and make sure **Include Multiple Flock analysis in list** is ticked. Then select use the **same GE run** you have previously just created (you are only reporting at this stage not running a whole new run through the GE).

Proceed through the remainder of step 3, then steps 4 and 5 as usual. As you are only running a report this time you will very quickly be sent an e-mail of the results.

Once this run is complete repeat the steps above, but create another file on Ivydeer\$ for the connected herds only run (and ensure you use only this file for all reporting from this point, do not delete the earlier files though as they show what herds were unconnected). Send the zip file to Sharon McIntyre, so she can do her QA. Notify Sharon which herds (if any have are unlinked in the report).

## 10 Reporting and formatting in MS Access

Open **Access**. Open **DEERSelect Sire Summary V4 – R-LK** Database (on ivydeer\$ share (N: in my case). Click security warning to enable content/macros etc.

**Import** the **reportxxxxxx.txt** file. Just import as report name and **don't** add a **Primary key**, ensure all tag fields and the N progeny field are set as text.

Open the **SIL Output** table. **Delete** all of the rows. Run a **Query** to **append** all of the data from you imported **reportxxxxxx** table to **SILOutput** table.

Open the **SIL Output** table and asterisk (\*) the current tag of the DPT sires. There is a file in ivydeer\$/DEERSelect documentation called DPT sires to asterisk in Sire Summaries.xlsx, this file tells you which sires to asterisk in which reporting years (as DPT sires will only be asterisked for the years they have progeny reported in the summaries).

Check **CD≥40** table is empty, if not delete all lines. Run the **All CD** query. This query drops the CDeBV for any sires with an accuracy for CDeBV of <40%.

Run the 2 percentile queries; **European and composite percentile** and **English percentile**, note down the percentile results as you need these to modify the conditional formatting in the reports below. This is to bold the top 10% of BV's and indexes.

Open the **Reports** in Design view (European and Composite Sire Summary and English Sire Summary). Change the **Analysis Date** to the date the GE analysis was run. Change the **conditional formatting** (right click) on **W12eBV**, **CDeBV**, **CWeBV**, **R-Early Kill**, and **Terminal** headers in the **Detail** section of the report, to the appropriate percentiles you noted down earlier (this bolds the BV's and indexes which are in the top 10%). Close the design view, then **open** the report(s) and **print** it/them off as a .pdf file. Save them to ivydeer\$ \BVReports\DEERSelect Sire Summaries\Sire Summaries Mmm YYYY (create new folder for this, and save all other files to this folder also.)

Run the other 4 queries: **English**, **English sorted W12**, **European and Composite** and **European and composite sorted W12** and export these, save versions as .xlsx and .xls for users of older Office versions. Save the whole extract file from DEERSelect in the quarter run folder with everything else.

The queries which produce the reports in the database operate on 4 different sets of criteria which determine which sires and what data is reported:

- Sires are not reported if their W12eBV accuracy is <75%, or if they have <5 progeny.
- Their CDeBV is not reported if the accuracy is <40%.

- They are assigned to the English list by having **English** entered into the **DBRD field** in DEERSelect, all other sires go to the European and Composite list regardless of what is entered in DBRD.

If you should have to add a sire to the English list at late notice you can just enter English in the DBRD field in the SIL Output table.

## 11 Quality Assurance (QA) process

In access or excel align the latest European and Composite list with that from the previous month or months and do the same for the English list (use excel the list is so small).

Create columns to examine the deviations in the breeding values and indexes from the new run to the previous run(s), do this by subtracting the old BV from the new BV. Sort the list by these BV change columns, I primarily used W12 and R-EK index as these are the two most looked at when the lists are released.

I generally carefully examine any changes > 1 kg in the W12 BV also look at any movement in DPT sires (asterisked) or well used sires. For sires with > 1 kg movement look to see if they are young sires with their first crop of progeny and if there are unders and overs within the same herd (likely same sire birth year if young sires.)

The movements may be due to progeny records being uploaded and providing a progeny proven BV. If there are very large movements of isolated individuals with large changes discuss with Sharon and between you contact the breeders concerned to see if you can discern how the changes occurred if they are genuine, or if a recording error has been made.

Decide how to progress for reporting following these discussions; it may be that an offending herd might have to be dropped from the reporting if there is a recording error. If possible see if the herd's bureau can amend the data if you/they believe they can identify the problem.

Under a good run with no concerning deviations from previous BV use the aligned files to plot correlation graphs for selected BV's and indexes, as second a QA check. This way you can easily identify outliers and check the general trend (plot  $r^2$  on graph).

Sharon QA:

Track and record: Mean, Min, Max and Standard Deviation of Breeding values, Accuracies, Indexes, Herd and Sire numbers for All, European and English lists. Produce percentile bands from standard deviation and check against previous percentile band.

Keep separate the reporting and QA files, so QA files are not sent to everybody.

Consult with Sharon as to her QA and when both of you are happy you can release the results. You do not have to wait until the 10<sup>th</sup> to release. Sharon will organise publishing the tables on the Deer Industry Information Hub.

It is of value to add a commentary to the e-mail when you release the results, this should include such things as : asking bureaux to forward to their clients, notifying the next data entry cut off and reporting dates, indicating traits bureaux could expect to load in the near future, indicating any changes in the reporting for that report, indicating any movements in the breeding values, notifying if any herds have been dropped from the report due to lack of linkage, highlighting any interesting observations you have made while reporting e.g. new high value, number of new sires.

Delete the data in **CD≥40** table, to prevent using old information in new (future) runs.

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Zip your DEERSelect Sire Summaries Mmm YYYY folder (which should contain: the .xlsx files of the English and European and composite and sorted files, .pdf files of GTGraphs, Connect\_TL, ConnectGraph\_T\_ for meat, growth repro and velvet, and the English and European and Composite Sire Summaries). Make sure that this folder only contains reporting files, not any QA or raw files.

Send the zipped file to Sharon McIntyre and BCC (blind carbon copy) everybody else: Julia Aspinall, Ken Moore, Julie Everett-Hincks, Helen Mathias-Davis, Sheryl-Anne Newman, Catharine Sayer, Geoff Nicoll, Marius Van Niekerk and Tony Pearse. July and December reports should also be sent to Phil Stewart Deer Industry News. I now also send it to a group of Alliance staff as stakeholders in the DPT and the DPT farms Invermay farm, Whiterock Station and Haldon Station and Adam Whaanga (Stock agent who requests it).

All files that you have created are backed up on the AgResearch servers and being saved to ivydeer\$ many users can access them. Other users who access files please create your own copy of any files you work on and save them elsewhere. If your new files are of value to the QA process please clearly name and save to the appropriate QA folder.

The GE runs are at present all backed up by Sheryl-Anne Newman; even though they are deleted from SIL once > 2 have accumulated to your user account. Do however also check periodically with Sheryl-Anne to ensure this process is still continuing.

Updated 11 Dec 2013

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## 12 Policies for Across-herd Genetic Evaluation of Deer

*Updated: 11 December 2011*

### 12.1 Participation – herd eligibility

- The intention of the scheme is to provide genetic evaluation for red deer and wapiti/wapiti crossbreds to allow valid within breed to comparison across different herds.
- Membership is open to any deer breeder within New Zealand (other cases by consideration), provided that they collect and submit pedigree and performance records which meet the technical requirements for across-herd breeding value analysis.
- A major requirement for membership is the need to have sufficient genetic linkage with other herds to support valid comparisons across different herds.
- Membership of the scheme is taken as agreement to support principles of transparent, across-herd evaluation of deer and a willingness to evaluate deer on the same base as all other participants of the scheme.
- All members agree to abide by the attached code of practice for deer genetic evaluation.
- Red deer is defined as including English, Eastern and NZ Red genotypes, but excluding deer with known significant Wapiti & Elk content.
- Wapiti is defined as including progeny from recently imported elk from North America (registered with the EWSNZ) and upgraded animals (i.e. from Fiordland captured origins).

### 12.2 Publication of results

- A full breeding value report will be produced for each participating herd, as part of their BV analysis. The report will contain information on all animals born in that herd and all sires and dams used in the herd (irrespective of whether used by natural service, AI or ET). Thus a report can potentially contain information on animals not actually owned by the herd (e.g. sire used by AI, or an embryo-donor dam).
- The herd BV report will also give the genetic trends calculated for that particular herd. The genetic trends in the herd are confidential to that herd, but may be released by the herd owner

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if desired. Overall “all herds” genetic trends will be reported publically with Sire Summary Reports.

- In principle, the BVs of all animals evaluated in across-herd analysis will be publically available, and may be released by either the herd owner (based on their herd report) or by the BV service provider.
- Lists of BVs will be released (to scheme participants or to the public) by the service provider for various purposes. For example, a major output of across-herd evaluation would be expected to be a list of sire BVs, based on certain criteria (e.g. a list of trait leaders, or a list of all sires with >5 recorded progeny in the last 3 years).

### **12.3 Data ownership & access**

- Performance data submitted to the scheme remains the property of the herd owner submitting the data. Once data is submitted to the group genetic evaluation scheme, it cannot be withdrawn. This does not preclude the herd owner from using the data for other purposes, and providing the data to other people or organisations. The intention is simply to avoid large variations in calculated BVs due to data previously available being withdrawn. At any point a participant can withdraw from the group evaluation and no longer supply annual updates to performance records.
- Breeders should be aware that BVs of animals in across-herd analysis are calculated using information from several herds, and that data from their herd will likely contribute to BVs of animals in other herds and vice versa. By submitting data to the scheme a breeder is giving permission for the data to be used by all contributing herds in current and future across-herd BV analyses.
- When an animal is sold, right to use any data on the animal transfers to the new owner.
- Performance data supplied to the scheme is confidential, and will not be supplied in any form (other than BVs) to anyone other than the owner of the herd supplying the data or to the owner of the animal(s) concerned.
- Pedigree information will be treated as public information, and may be released.

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- Data and samples generated from the scheme may be used for research purposes, by agreement in writing between the research provider and the breeder(s) involved.
  - The service provider will conduct BV analysis in good faith and will make every effort to ensure that BV analyses are of the highest standard possible. However, no responsibility is taken for losses (real or opportunity losses) arising from use of the analysis results in any way.

### **13 Code of practice for across-herd genetic evaluation of deer**

#### **13.1 Performance recording**

- The onus is on the breeder to be responsible and record information accurately and with integrity.
- All performance data will be measured (not estimated) using appropriate equipment according to guidelines provided. Scales and other equipment used to measure performance will be regularly checked for correct function. Data will be submitted as measured, without any adjustments applied.
- Animals will be recorded in contemporary groups (mobs) and managed to ensure that all animals within each contemporary group have equal opportunity to perform. Animals given preferential treatment, and sick or disadvantaged animals will be identified and then allocated to separate contemporary groups when data is submitted.
- Breeders submitting pedigree and/or performance records will ensure they have adequate information to correctly record parentage, performance and contemporary groups of all animals. This will include ensuring an adequate DNA sample is held on file by the breeder or designee.
- Breeders will not exclude any animal from a contemporary group based on its performance alone. The breeding value analysis system may impose some checks and balances to exclude animals where performance is extreme (high or low) relative to contemporaries.

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### 13.2 Publication of BVs

- It is the responsibility of those publishing information, whether for advertising, sale catalogues or any other purpose, to ensure that information provided on the BVs of any animal is accurate.
- Any BVs presented will be the most recent BVs available from an Official Across Industry Run whenever possible.
- Any raw performance data provided on an animal will be clearly identified, and will not be used instead of available BVs.
- BVs will be shown with a clear positive (+) or negative (-) sign.
- A herd is free to publish its own BVs and genetic trends, and the average BVs and genetic trends across the group evaluation. However, a herd must not publish another herd's BVs and genetic trends without written permission of the herd owner except a reproduction of the most recently available DEERSelect Sire Summary list.
- Any advertisement using the DEERSelect name or reference to DEERSelect information (except sales catalogues) must be reviewed by Deer Industry New Zealand. This is to ensure use of data and its format is consistent and clear to readers and the advertising is consistent with the intentions of DEERSelect which is fair comparison between animals.

### 14 Publication of individual herd results

Default position is Herds have approved availability for publication when first sign onto DEERSelect unless they opt out on the form at the time or at a later date.

- Herds must be connected for Growth to be published.
- If connected for Growth then publish Index.
- Must be connected for Meat and Conception Date to publish information on these traits.
- Minimum 75% accuracy for W12 to be reported on Sire list
- Lists sires with progeny born in last three years- potential sires of sale stags.
- European red and English published separately – although BVs are completely comparable.
- Publish Elk/Wapiti data for connected herds.

## 15 Frequency of publication

Cut-off date for data inclusion = 1<sup>st</sup> of the Month

Publication by 10<sup>th</sup> Month (allows time for error checking and rerunning and weekends)

Published; - October, November, December , March, May and July.

On website – addition of abbreviation explanation and disclaimer.

## 16 Appendices

### 16.1 DEERSelect Goal Trait groups

<b>Recorded Traits</b>			
<b>GROWTH</b>	<b>MEAT YIELD</b>	<b>REPRODUCTION</b>	<b>VELVET</b>
W02 - W12	CTEMA	CD	LVW
W15	CTFAT	MATEDATE	RVW
W18	CT LEAN	MWT	TVW
W21	CTLGLEAN	NLB	W09
W24	CTLNLEAN	PREGSC	W10
MWT	CTSHLEAN	SNLB	W11
	EMA (ultrasound)	W01-W12W15	W12
	W02 - W12	W18	
		W21	
WWT		W24	
		MWT	
<b>Analysis traits</b>			
<b>GROWTH</b>	<b>MEAT YIELD</b>	<b>REPRODUCTION</b>	<b>VELVET</b>
WWT	WWT	W12	W12
AWT	AWT	MWT	VW2
W12	W12	CDOY	MVW
W15	CWT		
MWT	CTFAT		
	CTLEAN		
	CTEMA		
	CTHQ		
	CTLN		
	CTSH		
	USEMA		
<b>Breeding Values</b>			
<b>GROWTH</b>	<b>MEAT YIELD</b>	<b>REPRODUCTION</b>	<b>VELVET</b>
WWT	CW	CD	VW2
WWTM	New BV carcass wt adjusted	(conception date)	MVW
AWT	EMAc		

W12 MWT	FATY LEANY HQLY LNLY SHLY  old BVs - age adjusted FAT LEAN HQLEAN LNLEAN SHLEAN			
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AOD	3 AGES	2,3 MA
Weights	WWT	Month W02, 03,04
	AWT	Months W05,06,07
	SWT	Months W08, 9,10
WEIGHTS	W12	Month W11 & 12
	W15	Month W15 & 18
Mature Wt	MWT	W21-24 Repeat

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**16.2 Trait Abbreviations**

On the SIL website under help 0 PDFs

**16.3 Trait Bounds**

On the SIL website under help 0 PDFs

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**16.4 Uploading data for conception date eBV**



## Uploading trait data for conception date eBV.

There is now a module to produce estimating breeding values for conception in DEERSelect. This module allows the calculation of these BV's so long as the hinds have had an opportunity to naturally express early breeding, that is; the hind was joined with a stag (or stags) for natural mating on or before the 10<sup>th</sup> of March.

These traits are not to be used for any hinds that have been artificially mated or manipulated (i.e. synchronised) in that breeding season. This is not to be used as a repository for all mating information; it is for trait recording of naturally mated hinds.

For the module to estimate conception date BV's four different traits are required to be entered. While there may appear to be duplication within these traits, they are all necessary. These 4 traits can be subdivided by mating traits and pregnancy traits.

### Mating traits are:

- **MDATE**, the first date which any stag was joined with the hinds (dd/mm/yyyy)
- **MATEGP**, the mob/sire(s) which the hinds were mated in/to (text)

The important information to include with these traits :

- **Mob**, numerical mob hind was in, when stag was joined
- **Trait Date**, the first date which any stag was joined (same as MDATE)
- **Trait Value**,
  - MDATE; date first stag(s) was joined (this defines if the CD trait can be estimated i.e. needs to be on or before 10 March),
  - MATEGP; stag(s) joined with tags/names or mating group number (note no commas for multiple stag mating groups).

### Pregnancy traits are:

- **PREGSC**, result of the pregnancy scan 1 = pregnant : single foetus visible, 0 = no visible pregnancy, 2 = pregnant: twins visible
- **CD**, date of conception estimated from pregnancy scan (dd/mm/yyyy)

Important information to include with these traits:

- **Mob**, numerical mob the hind was pregnancy scanned in
- **Trait Date**, date the ultrasound pregnancy scanning occurred
- **Trait Value**,
  - PREGSC = 1 pregnant, 0, not pregnant, 2 twins,
  - CD = estimated date of conception (dd/mm/yyyy) i.e. date of PREGSC – estimated foetal age (determined by ultrasound estimated foetal age scanning)
- Sanity check for Sex, so you may have to update the odd animal incorrectly sexed in earlier life!

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**16.5. Loading carcass traits for meat yield module**



## Loading carcass traits for meat yield module

### Background

A new module has been added to DEERSelect in October 2011. This module is based on recent ultrasound scanning of eye muscle (longissimus dorsi) research by AgResearch, and whole animal CT (computed tomography) scanning from InnerVision and hence uses live animal data. In the future we anticipate that actual carcass data will be able to be incorporated into this module also. There are separate modules available for red deer and wapiti.

Aligned to the meat yield module are a large number of new traits, the majority of which are generated from the CT scanning data. All of the CT scan traits are provided by InnerVision and hence should already be correctly formatted.

The ultrasound eye muscle data has three traits and is currently undertaken by Stockscan, on animals around 12 months of age between the 12<sup>th</sup> and 13<sup>th</sup> rib. Animals are targeted for scanning around 12 months of age, in order to align the trait with slaughter live weights and times. Ultrasound eye muscle area traits are non-repeat traits, as they should only be recorded once for the animal at an appropriate age to reflecting slaughter live weight targets.

In the near future a full standard operating procedure (SOP) for ultrasound scanning will be available to the industry and other scanning operators will have the opportunity to up skill and provide deer ultrasound eye muscle scanning if they chose to do so.

Both the ultrasound and CT traits require a live weight to be recorded within a week (ideally on the same day) of the scan, so appropriate weight adjustments can be made.

These new traits contribute to a number of new eBV's and to updated versions of the three economic indexes (more information on this is available in the Meat Yield Module Report by John Rendel October 2011).

### Ultrasound Eye Muscle Traits

Trait name	Trait code	Trait unit	Trait use in DEERSelect
Ultrasound eye muscle traced area	<b>EMAUS</b>	cm <sup>2</sup>	Contributes to meat yield module, hence breeding values and indexes
Ultrasound eye muscle depth	<b>EMD</b>	cm	Reference data, does not presently contribute to reported eBV's or indexes.
Ultrasound eye muscle width	<b>EMW</b>	cm	Potential to be used in future to estimate EMA

Please ensure all ultrasound eye muscle traits are loaded in cm or cm<sup>2</sup>, as for sheep, not mm. All 3 traits are numeric. The associated live weight should be entered as the appropriate monthly weight trait.

## 16.6 Equations for economic indexes

### Explanation of Indexes

**Deer Replacement - Early Kill** (\* DeerR-EK)  $\phi = 5 \times \text{WWT}e\text{BV} + 6 \times \text{W12}e\text{BV} - 45 \times \text{MWT}e\text{BV} - 25 \times \text{AWT}e\text{BV} + 615 \times \text{LNLY}e\text{BV} + 89 \times \text{HQLY}e\text{BV} - 24 \times \text{SHLY}e\text{BV} - 39 \times \text{CDeBV}$

**Deer Replacement - Late Kill** (\* DeerR-LK)  $\phi = -28 \times \text{WWT}e\text{BV} + 31 \times \text{W12}e\text{BV} - 37 \times \text{MWT}e\text{BV} - 6 \times \text{AWT}e\text{BV} + 640 \times \text{LNLY}e\text{BV} + 93 \times \text{HQLY}e\text{BV} - 25 \times \text{SHLY}e\text{BV} - 16 \times \text{CDeBV}$

**Deer Terminal** (\* DeerTerm.)  $\phi = 5 \times \text{WWT}e\text{BV} + 6 \times \text{W12}e\text{BV} - 25 \times \text{AWT}e\text{BV} + 353 \times \text{CWeBV} + 926 \times \text{LNLY}e\text{BV} + \text{HQLY}e\text{BV} - 37 \times \text{SHLY}e\text{BV}$

### Explanation of Breeding Values

AWTeBV = Autumn Weight eBV

CDeBV = Conception Date eBV

CWeBV = Carcass weight eBV

HQLYeBV = Hind quarter lean yield eBV

LNLYeBV = Loin lean yield eBV

MVWeBV = Mature velvet weight eBV

MWTeBV = Mature weight eBV

SHLYeBV = Shoulder lean yield eBV

W12eBV = Yearling weight eBV

WWTeBV = Weaning weight eBV