

“StockTake” – GENETIC AUDIT SOFTWARE FOR AUSTRALIAN SEEDSTOCK BEEF PRODUCERS

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SUMMARY

New software called StockTake has been developed as a tool to assist beef cattle breeders assess and improve the rate of genetic progress in their breed and herds. StockTake uses existing data, recorded by each breed on their NBRIS databases, to compute descriptive statistics for the breed that are used to describe and monitor changes in the basic “genetic” structure of the breed. Secondly, stepwise regression is used to determine key variables that explain differences in the rate of genetic progress, for a given period, across herds within a breed. Herds are rated for their performance in these variables to provide a benchmark of their breeding program against the average of other herds recorded in the breed.

Key words: beef cattle, selection, genetic progress, key performance indicators

INTRODUCTION

Selection of beef cattle has allowed beef producers to breed more profitable cattle. Genetic trends in individual estimated breeding values (EBV) or selection indexes can be used to assess genetic change in a breed, or individual herd. However it is often difficult to determine the reason for different rates of genetic progress across herds. Therefore the aim of developing StockTake was to use existing files to compute variables associated with the theoretical prediction of genetic progress (e.g. selection differentials and generation interval) and determine which variables explain differences in genetic progress across herds, within a breed.

STOCKTAKE SOFTWARE

StockTake is written in Fortran 90 and is compatible with the BREEDPLAN system (Reverter 2002). It is used to generate results for a breed and also for individual herds. The program uses data recorded by each breed on their national pedigree/performance databases and their EBV files from BREEDPLAN evaluations, including breed standard BreedObject \$Indexes. StockTake uses breed specific controller files to remove herds with insufficient structure (e.g. too few animals, too few years of recording). Breed results are described using a set of variables to characterize the genetic structure of a breed, and the changes that occur over time. Results at the herd level are computed using a reduced set of variables and stepwise regression is used to determine which variables (if any) significantly explain differences between herds in rate of genetic gain in a given \$Index. These significant variables ($P < 0.01$) are termed key performance indicators (KPI). Genetic progress is computed as the regression of each \$Index on a 5 year period e.g. 1999 to 2004. The software has the capacity to define 2 periods to compute results. However it is only the second period that is used in the stepwise regression analysis.

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Variables. StockTake computes numerous variables using the input data file. Many of the variables are highly related and some variables are more meaningful at the whole breed level. Table 1 presents the descriptive variables used for the 2 functions of StockTake. All variables are computed for a breed and herd and a sub-set of these are considered for the KPI analysis.

Table 1. Variables computed and used in StockTake as the average of all animals born in the nominated 2 periods, as well as breed average.

Variables computed for breed and herds	Variables computed for breed and herds and considered for KPI analysis
Genetic progress in period 1 (prior period)	1. Correlation between sire and dam EBVs
Correlation between sire EBV and number of progeny	2. Herd size
Ratio of number of dams per sire	3. Average herd EBV in prior period
Average EBV of all males, females, steers	4. Sex ratio of recorded calves
Average EBV of sires (weighed number of progeny)	5. % calves by artificial insemination (AI)
Average EBV of dams (weighed number of progeny)	6. % calves born by embryo transfer (ET)
% of inbred animals	7. % males castrated
Average % inbreeding of inbred animals	8. Selection differential of sires
Replacement rates sires and dams	9. Selection differential of dams
Mean age of sires to breed sires	10. Selection differential of ET donor cows
Mean age of sires to breed dams	11. Selection differential of sires mated to 2 year old cows
Mean age of dams to breed sires	12. Inbreeding of all animals
Mean age of dams to breed dams	13. Age of dams at first calf
Number of herds with progeny of common sires	14. Mean age of sires
Maximum selection differential of sires	15. Mean age of dams
Maximum selection differential of dams	16. % sire connectedness of herd (i.e. number of progeny of common sires as a ratio total animals)
	17. Standard deviation of EBV of all animals
	18. Mean square error of birth date for day of the month (i.e. 1-31)
	19. Mean square error of birth day for day of the week (i.e. Mon-Sun)

Output. The output is a comprehensive summary of the input data and for the variables in Table 1, summary statistics are computed for each year in the nominated periods. For the individual herds, the output contains their average genetic progress and average performance of all KPI (average of all animals born in the nominated 2 periods) as well as the breed average. Also provided for each KPI is their herd's percentile ranking against all herds considered (e.g. top 10% of herds for KPI 1). For all other variables (i.e. non-KPI) the mean performance of the herd and breed is listed. All results files are outputted as a printable report and can be uploaded into a web page.

EXAMPLES OF KPI

StockTake analyses were performed on all breeds with breed standard BreedObject \$Indexes. This included 8 breeds and 23 \$Indexes. KPIs were identified for each breed and \$Index using stepwise regression in SAS (SAS, 1989).

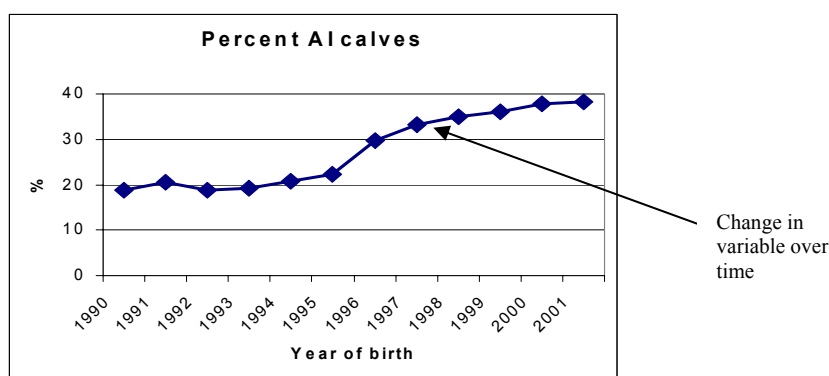


Figure 1. Example StockTake output describing changes in the variable %AI calves in this breed over years

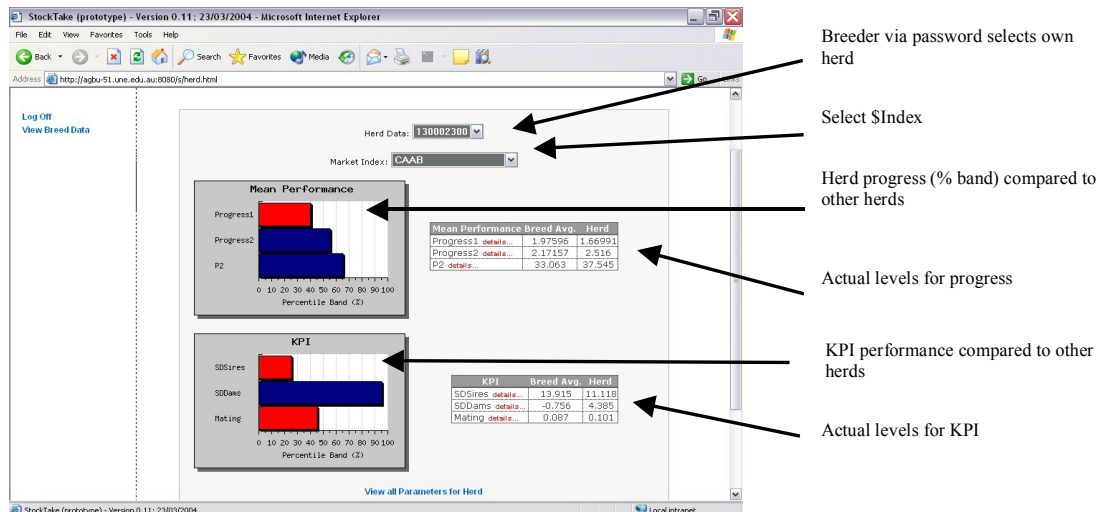


Figure 2. Example StockTake output for an individual herd showing its performance for genetic progress and KPIs for a given \$Index compared to the average of other herds in the breed

Results. StockTake results show clear differences in the “genetic” structure across the 8 breeds for many of the computed variables e.g. %AI, age at first calving. This information can be used as

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general information about each breed and also provides a mechanism by which changes at the breed level over time can be documented and monitored. Different sets of KPIs were identified for the different breeds and for their different \$Indexes. Table 2 presents results for each breed for their \$Index with the highest R² from the stepwise regression models. Commonly only 2-5 variables were significant for each breed, with selection differential of sires (KPI 8) always being present and almost always the most significant (with a positive regression coefficient). This means that herds that were using sires of superior \$Index (compared to the average EBV of males in the herd from previous 3 years) were making significantly more genetic progress over time in that \$Index. Also common across most of the breeds and \$Indexes were the variables: selection differential of dams (KPI 9) and the correlation between the sire and dam EBV (KPI 1), with positive assortative mating resulting in increased gain.

Table 2. StockTake results including KPI and their partial R² for each breed and \$Index

Breed	Example \$Index	Total R ²	Significant variables* and their partial R ²									
			8	9	1	17	3	11	15	5	19	7
Angus	Japan B3	58	21	3	10					1		
Shorthorn	Supermarket	50	18	10	5						13	
Brahman	JapOx	62	14		13					5		12 7
Hereford	EU	44	14	5	11		1					
Charolais	Export	52	47	10								
Murray Grey	Long Fed Export	59	19	6	4	3	2					
Limousin	Self Replacing	42	16	8	5					13		
Simmental	Supermarket	59	43	4					6			

* see Table 1 for a description of each variable.

CONCLUSIONS

StockTake provides a retrospective examination of the variables that significantly explain differences between herds for genetic progress in a given \$Index. The KPI vary according to breed and \$Index, and are likely to change over time e.g. as a breed develops its genetic evaluation or as the level of AI increases. The StockTake report will provide a useful guide to breeders on the types of variables that are likely to have the greatest impact on rate of genetic gain and therefore should be considered in their breeding program.

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