

COLLECTION OF DATA FOR THE GENETIC IMPROVEMENT OF HEALTH TRAITS IN AUSTRALIAN DAIRY CATTLE

M. Abdelsayed¹, P. Douglas¹, J.E. Pryce²

¹Holstein Australia, Hawthorn East, VIC, 3122

² Department of Economic Development, Jobs, Transport and Resources, Government of Victoria
Bundoora, VIC, 3083

SUMMARY

There is growing interest in the Australian dairy industry in the genetic improvement of the health of dairy cows. In Australia, there is minimal storage or export of health data from some on-farm software systems into industry databases to assist in the research or reporting of health traits. The Health Data for Healthy Cows (HDHC) project aims to get a better understanding of the extent of health data recording in the Australian industry by collecting health data from the 100 Ginfo (genomic reference) herds. Health data obtained from herd test centres totalled 275,729 records from just 46 out of the 100 herds. The four most recorded groups of health diseases identified were mastitis, reproductive problems, lameness and metabolic disorders. Mastitis had the highest incidence with 20% of cows affected, followed by reproductive problems (12%), lameness and metabolic disorders (5% and 3% respectively). This project has provided an insight into what health information is actually being collected on farm and that there is a source of health data available which can be accessed and potentially used for the genetic improvement of health traits in Australian herds.

INTRODUCTION

Great improvements have been made genetically in milk production in dairy cows over the last 60 years. However unfavourable genetic relationships between milk production and most disease traits, such as mastitis, lameness, reproductive problems and metabolic disorder health traits have become apparent as milk production has increased (Pryce *et al.* 1997; Rauw *et al.* 1998; Koeck *et al.* 2012).

A growing concern for dairy farmers is the improvement of dairy cow health through genetic selection. Healthy cows are more productive, easier to manage, require less intervention, have improved animal welfare and contribute to profitability by reducing production costs. However, in many countries, including Australia, industry collection of data on common health events has been sub-optimal or absent, which means there is no ability to provide breeding values and apply genetic selection for common health disorders. Also, such traits are low in heritability, meaning that although genetic progress is feasible, it will be slower. While many farmers may collect some of this information on farm, there is likely to be variation in the completeness of these data sets. In Australia, there is little storage or export of such information from some on-farm software packages into industry databases for research or reporting purposes.

Before any work can begin on providing Australian farmers with breeding values for common health disorders, it is important to quantify what data is already being collected on farm and in veterinary practices. As a result of this challenge, the health data for healthy cows (HDHC) project has commenced to help improve our understanding of the extent of health data recording in the Australian dairy industry. The HDHC project will use infrastructure through the Dairy CRC in the form of the 100 'Ginfo' (Genomic information) herds to collect all health data that is currently being amassed on farm. The Ginfo data is being used as a genomic reference population for genomic breeding values. One of the advantages of having a genotyped population is that it opens up new opportunities for new breeding values, such as dairy health traits. Therefore the objectives

of the HDHC project are to:

1. Investigate and identify health data sources available within the herds participating in the Ginfo project
2. Assimilate health data into a database in order to summarise health data status
3. Estimate the incidence of common diseases and health occurrences on dairy farms
4. Estimate antibiotic usage on farms
5. Calculate provisional genetic parameters for health traits where incidence is high enough
6. Estimate the accuracy of genomic selection achievable for data identified health traits

For this paper the first three objectives are covered.

MATERIALS AND METHODS

Health data sources. On farm health data were collected from the 100 Ginfo participating herds.

Survey. A survey was used to get an understanding of the health data collection and storage methods that occur on farm. Before participating in the survey, privacy consent and data release authority documents were also provided to the participants to comply with privacy laws.

Obtaining health data. Once the survey, data release authority and privacy consent forms were returned by the farmers, an email was sent to each of the herds respective herd test centres to request all of the data collected for that farm, including the health data interchange format file.

Data analysis. Each of the herds' health data files were merged together to create a master health data file which contained the national cow ID, herd ID, health event, health treatment, date of health treatment, calving date, breed and cow date of birth. Statistical and graphical summaries of the surveys and master health data file were produced using Microsoft office Excel 2013 and the statistical program R version 3.1.1.

Disease incidence calculation. For the calculation of disease incidence the following equations were used:

Number of disease cases (disease occurrence) =

No. of disease cases over a lactation / No. of cows-lactations with disease

Disease occurrence is calculated for cows with a health event

Number of cows with cases (%) =

No. of cows with cases / Total No. of cows with test records

Cases refers to specific diseases, for this paper cases refers to mastitis, reproductive disorders, lameness and metabolic diseases.

RESULTS AND DISCUSSION

To date 51 of the Ginfo participants have returned surveys. Out of these, 46 herds have health data recorded, while 5 had no health records. Therefore, the results currently presented include 46 of the herds out of the total 100 participating in the HDHC project. The total number of raw health records (before any quality control) obtained only from herd test centres is 275,729 records between 1998 to 2011, from 42, 056 cows, representing multiple treatments per cow.

Survey. The main form of recording of health data on farm is electronically. Health events are mostly recorded daily across the Ginfo herds.

Figure 1 illustrates the health diseases that dairy farmers regard as most important and what they stated that they recorded on farm.

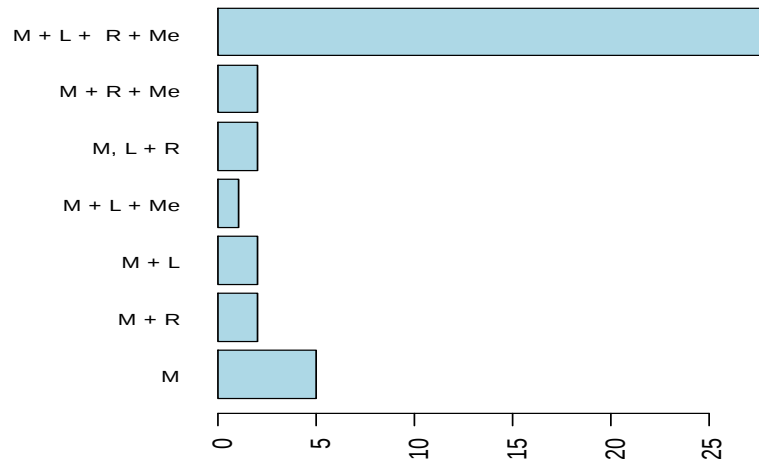


Figure 1. Health diseases farmers "say" they record and which they also regard as important. Mastitis (M), Reproductive (R), Lameness (L) and Metabolic (Me).

Data analysis. Analysis of the data indicated that the general health events most commonly recorded are mastitis, reproductive problems (retained foetal membranes, uterine infections, cystic ovarian disease), lameness (foot and leg disorders, injuries, footrot, abscess) and metabolic disorders (milk fever, ketosis, Grass tetany) (Figure 2). This is fairly consistent with the survey conclusions on what farmers indicated they record and what they think are most important (Figure 1).

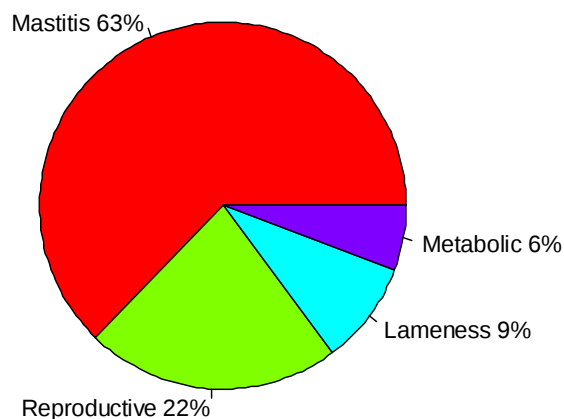


Figure 2. Health data that is actually being recorded on farm.

More mastitis health event data being identified and made available for analysis purposes will assist in improving the reliability of the mastitis resistance breeding value. With fertility being one of the most significant issues facing the dairy industry, knowing that reproduction disorder health data incidences are actually being recorded indicates that farmers are seeing the value and importance of such a trait to the health and production of their cows. Therefore, having a large health event data set would potentially increase the ability for farmers to improve their fertility, and in return profit, through the incorporation into a multi-trait genetic analysis model to improve

the reliability and confidence of the fertility breeding value.

Identifying what health event data is actually recorded on farm opens up new avenues of genetic analysis for potential new traits such as lameness and the development of new individual or integrated breeding values to become available to the industry.

Disease incidence. Disease incidence for the top four most recorded health events; mastitis, reproductive problems lameness and metabolic disorders were calculated (Table 1).

Table 1. Disease incidence of the most recorded health traits, total number of cow's with each disease and the total number of cases for each health trait

Disease	No. of cows	Total no. of cases	Disease occurrence	Cows with cases (%)
Mastitis	8495	21611	2.54	20%
Reproductive	4972	7730	1.55	12%
Lameness	2237	3124	1.40	5%
Metabolic	1425	1951	1.37	3%

For cows recorded with mastitis, on average there were 2.5 cases per lactation and 20% of cows affected. Cows reported with reproductive problems had 1.5 cases per lactation, affecting 12% of cows. At a lower level, lameness and metabolic problems in nominated health event cows have about 1 case per lactation with 5% and 3% of health event recorded cows being affected respectively. Incidences from this data set are less than those previously reported in other studies (Clarkson *et al.* 1996; Espejo *et al.* 2006; Clarkson *et al.* 1996; Parker-Gaddis *et al.* 2012). The number of cow cases for lameness, reproductive and metabolic problems were lower than previously reported while mastitis cow cases were fairly similar to findings reported in Norway (Osteras *et al.* 2007). No conclusions at this point can be drawn about whether the herds used in this study are generally healthier than other herds as only half of the herds were used in this analysis.

CONCLUSIONS

In Australian herds, mastitis, reproductive disorders, lameness and metabolic diseases are the most recorded health events. Mastitis is the most common occurring disease in dairy herds, followed by reproductive disorders, lameness and metabolic problems occur at lower incidence. As a result these findings provide information to make clearer decisions on future research priorities, and contribute a reference data set that may be applied for genomic correlation purposes.

REFERENCES

- Clarkson M.J., Downham D.Y., Faull W.B., Hughes J.W., Manson F.J. et al. (1996) *Vet. Rec.* **138**: 563.
- Espejo L.A., Endres M.I. and Salfer J.A. (2006) *J. Dairy Sci.* **89**: 3052.
- Osteras O., Solbu H., Refsdal A.O., Roalkvam T., Filseth O. and Minsaas A. (2007) *J. Dairy Sci.* **90**: 4483.
- Koeck, A., Miglior, F., Kelton, D. F., and Schenkel, F. S. (2012) *J. Dairy Sci.* **95**: 4099.
- Parker-Gaddis K.L., J. B. Cole J.B., Clay J.S., and Maltecca C.(2012) *J. Dairy Sci.* **95**:5422
- Pryce, J.E., Veerkamp, R.F. Thompson, R., Hill, W.G. and Simm, G. (1997) *Anim. Sci.* **65**: 353.
- Rauw, W. M., E. Kanis, E. N. Noordhuizen-Stassen, and F. J. Grommers. (1998) *Livest. Prod. Sci.* **56**:15.