

GENOMICS AND THE HAYS CONVERTER BREED

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INTRODUCTION

The Hays Converter (HC) was the first Canadian breed to be recognized in terms of the Canadian Livestock Pedigree Act and combines the genetics of the Hereford, Holstein and Brown Swiss breeds.

HC is a total performance breed that has been rigorously tested in field production and under harsh Canadian climate conditions.

THE HERD

The breed is maintained by Red Bow Ranching Ltd and it is used in commercial beef production by three producers in Manitoba and Quebec. There is interest for use in Australia as part of a new synthetic with Brahman cattle to improve crossbred production. The size of the nucleus herd has been reduced to only 100-120 cows, and inbreeding is a significant concern.

OBJECTIVES

To develop a new improvement strategy based on genomic information to help control inbreeding and increase the rate of improvement of feed efficiency, carcass traits, and meat quality.

To provide the Canadian beef industry with improved performance cattle.

METHODOLOGY

- Genotype the DNA samples already collected.
- Calculate breeding values (EPDs) for the HC population using existing data, including >10,000 full pedigree, >600 mid- and low-density genotypes, >600 ultrasound, and >250 with complete carcass data.
- Develop new selection index.
- Estimate genomic relationship matrix, calculate inbreeding and correct pedigree.
- Analyze the genomic architecture (breed origin) of the HC and use to design a prediction for HC based on the UofA database.
- Develop genomic predictions for feed efficiency and carcass traits and rank HC finishing animals for validation of predictions.



RESULTS TO DATE

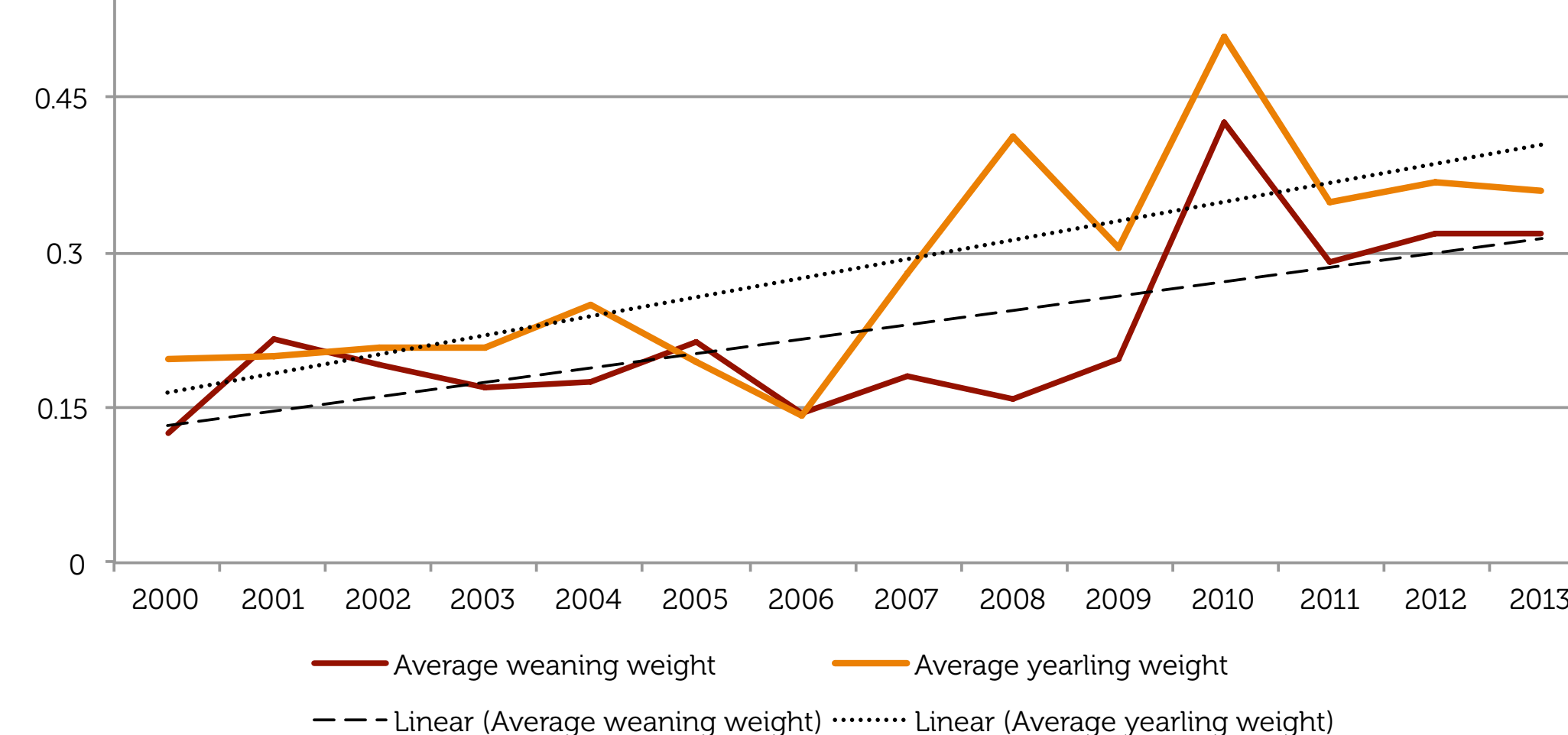


Figure 1. Average EPDs by year of birth for weaning and birth weight.

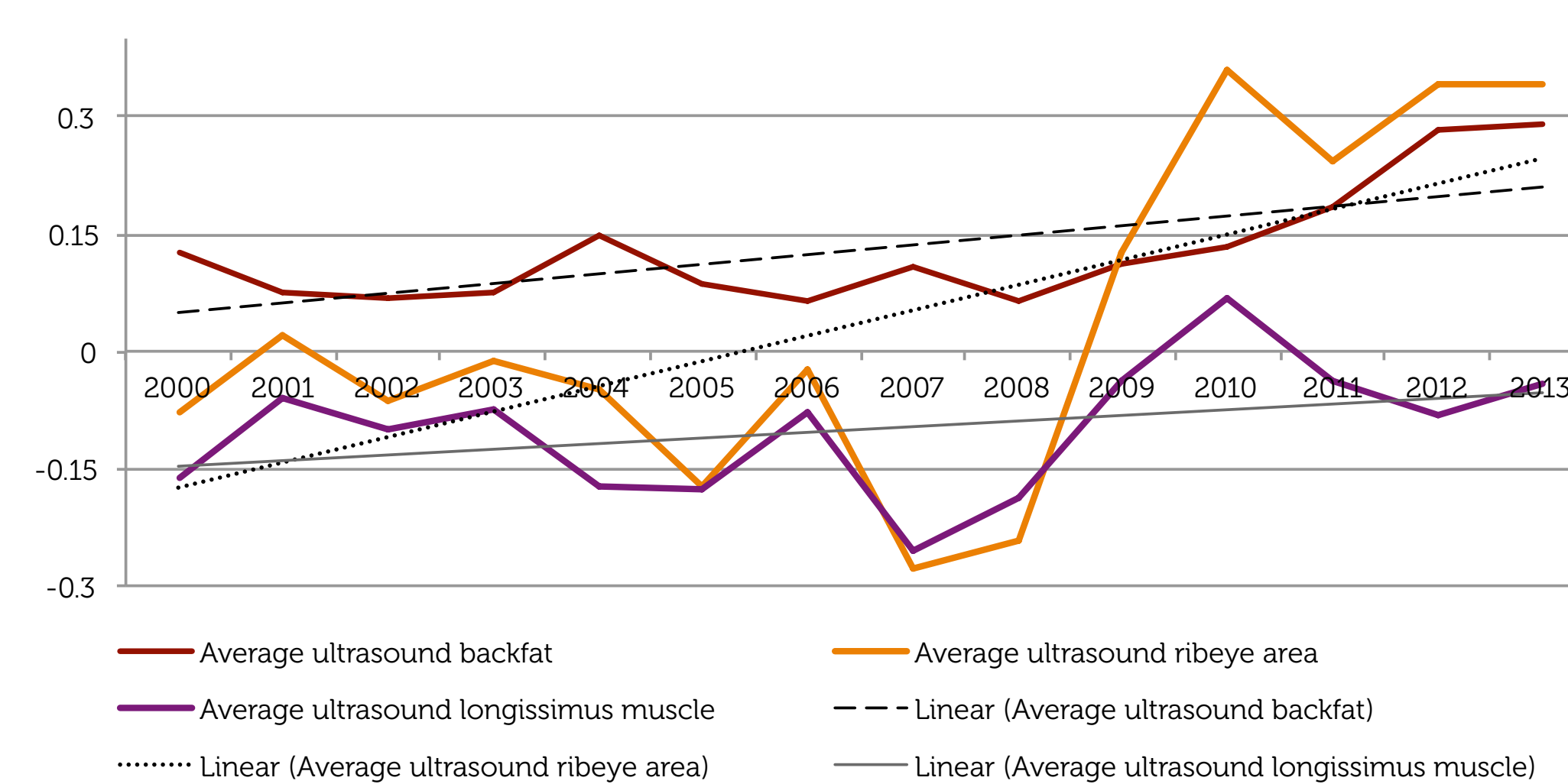


Figure 2. Average EPDs by year of birth for ultrasound measured traits - backfat, ribeye area, longissimus muscle.

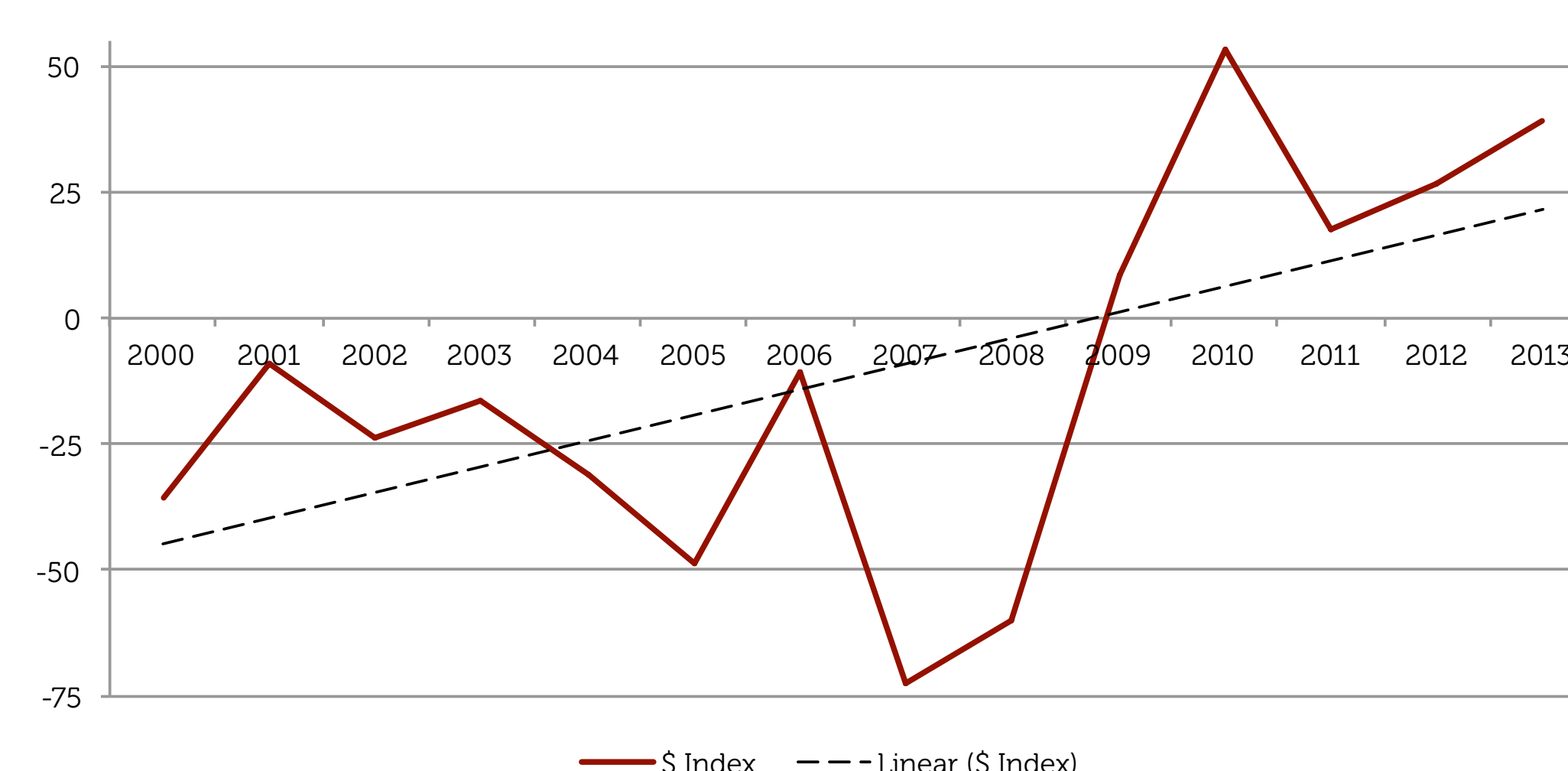


Figure 3. Calculated \$ Index by year of birth.

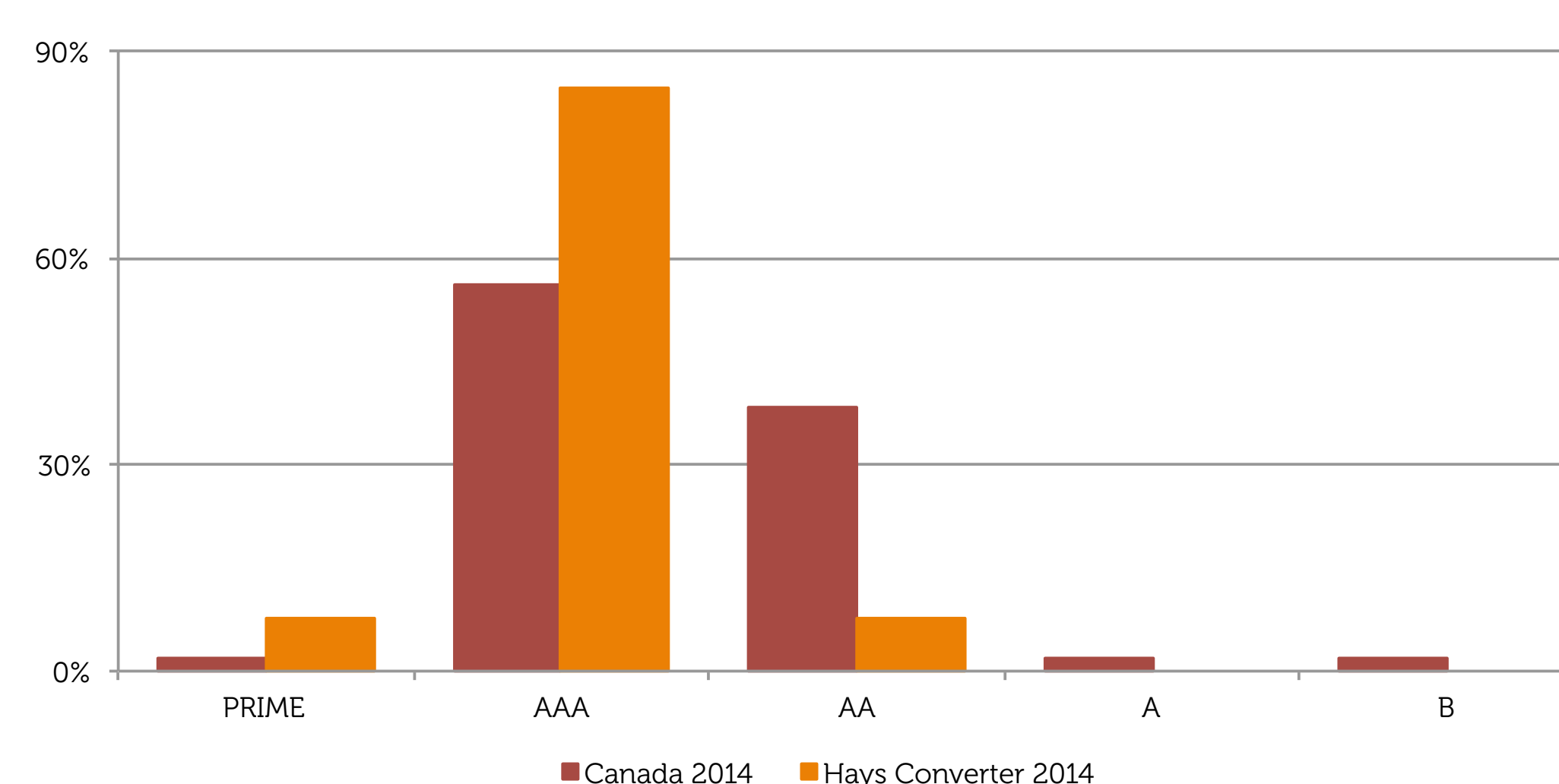


Figure 4. Quality grade proportions for 2014 Canadian youthful maturity^a and HC (Canada N = 2.3M; HC N = 52)



CONCLUSIONS

The work to date has generated genomic information on historical samples. There has been significant progress over the past 15 years in the HC breed. Average weaning and yearling weights are trending up, as are lean muscle yields (ribeye and longissimus muscle area). However, backfat is also trending up, meaning there is still progress to be made in selecting for animals to efficiently convert feed to lean muscle.

\$ Index is calculated by combining the economically relevant traits and predicting the total value. The selection program has seen great benefit over the past 5 years, but there is still improvement to be made in refining the index and continuing to optimize progress.

The project will provide immediate benefit to Canada's first breed of beef cattle to help determine its sustainability (including managing inbreeding). The tools developed will potentially be of benefit to other small beef breeds as well as creating knowhow and HQP to help maintain Canada's position as a leader in livestock genomics and beef improvement. Improving feed efficiency of beef populations will contribute to reducing the environmental footprint of Canadian beef production.

FUTURE RESEARCH

Research to provide more accurate inbreeding estimation by analyzing the genomic relationship of all animals in the herd and enable future matings to take into account genomic relatedness will begin late 2015. This project will enable genotyping of the latest progeny within the herd and provide the basis for establishing a genomically enhanced breeding program for HC, which will be useful for selecting bulls and cows for the production of embryos for export to Australia and the development of a new market for HC cattle.

REFERENCES

^aCANFAX 2014 Annual Report.

ACKNOWLEDGEMENTS

