herds are low heritability reproductive traits including age at first calving, reproductive success and replacement rate (Roughsedge *et al.* 2005). Research results suggest that large numbers of records will be required to obtain accurate DNA tests for low heritability traits (Goddard 2009). Further, such tests are the most difficult to validate as there is a paucity of cattle populations with sufficient phenotypic data to estimate the accuracy of new genetic tests for those traits. The value of using DNA information in making replacement heifer selection decisions will depend upon the information available at the time of selection, the accuracy (r) explained by the test, and the selection intensity (i.e. proportion of available heifers that are selected). The latter will be dependent upon the calving and replacement rates. In the absence of accuracy estimates it is not possible to model the value such tests might have for heifer selection. In practice, selection for replacement heifers is frequently driven by age and size as heifers that are born later in the calving season are too immature to be cycling in time for the first potential breeding season. This criterion tends to put indirect selection on fertility (i.e. selects for heifers that were conceived in the first estrus cycle). Additionally phenotypic considerations (feet, legs, udders, reproductive tract score, and pelvic area measurements) are likely to enter heifer selection decisions, further reducing selection intensity. In this study calves born during the first 21 days of the calving season were not randomly distributed among sires in multi-sire breeding pastures: highly prolific sires produced more early calves and hence their descendants were overrepresented in replacement heifers.

TECHNICAL DIFFICULTIES

During the course of this trial we encountered numerous technical difficulties of maintaining data integrity. Although in the field or at weaning we married the electronic ID and DNA barcode electronically, errors sometimes occurred emphasizing the need for a single “foolproof” DNA collection and animal identification system. Additionally in five consecutive Ranch A calf cohorts, the carcass misidentification rate in the processing plant ranged from 3.5 to 19.3%, with an average misidentification rate of 10.8% (Weber *et al.* 2012b). In this study paternity assignment of sampled calves using a 99 SNP panel was very high, but despite concerted efforts in working with the commercial producers DNA samples were not collected on 9.4% of the progeny with birth records. These considerations may influence whole herd results in commercial settings.

ACKNOWLEDGEMENTS

The author acknowledges the USDA National Institute of Food and Agriculture National Research Initiative competitive grant no. 2009-55205-05057 for funding support.

REFERENCES

Burns B.M., Gazzola C., Holroyd R.G., Crisp J. and McGowan M.R. (2011) *Reprod. Domest. Anim.* **46**: 534.

Goddard M (2009) *Genetica* **136**: 245.

Holroyd R.G., Doogan V.J., De Faveri J., Fordyce G., McGowan M.R., Bertram J.D., Vankan D.M., Fitzpatrick L.A., Jayawardhana G.A. and Miller R.G. (2002) *Anim. Reprod. Sci.* **71**:67.

Roughsedge T., Amer P.R., Thompson R. and Simm G. (2005) *Anim. Sci.* **81**: 221.

Van Eenennaam A.L, van der Werf J.H. and Goddard M.E. (2011) *J. Anim. Sci.* **89**: 307.

Van Eenennaam A.L., Weaber R.L., Drake D.J., Penedo M.C., Quaas R.L., Garrick D.J. and Pollak E.J. (2007) *J. Anim. Sci.* **85**: 3159.

Weaber R. L. (2005) PhD Thesis, Cornell University, Ithaca, NY.

Weber K.L., Thallman R.M., Keele J.W., Snelling W.M., Bennett G.L., Smith T.P., McDaneld T.G., Allan M.F., Van Eenennaam A.L. and Kuehn L.A. (2012a) *J. Anim. Sci.* **90**: 4177.

Weber K.L., Drake D.J., Taylor J.F., Garrick D.J., Kuehn L.A., Thallman R.M., Schnabel R.D., Snelling W.M., Pollak E.J. and Van Eenennaam A.L. (2012b) *J. Anim. Sci.* **90**: 4191.