THE FUTURE OF GENOTYPING

J.C. McEwan¹, K.G. Dodds¹, T.P. Bilton¹, R. Brauning¹, S.J. Rowe¹, M.K. Hess¹, K.M. McRae¹, A.F. McCulloch¹, R.A. Anderson¹and S.M. Clarke¹

¹AgResearch, Invermay Agriculture Centre, Mosgiel, New Zealand

SUMMARY

The future of genotyping is sequencing. A wide variety of technologies are available, but costeffective low coverage methods need further development. The downstream bioinformatics and statistics also have to be able handle the incomplete and noisy data produced. DNA sequencingbased technologies separate into 3 classes: whole genome or skim sequencing, random sampling of the genome typically 0.05X coverage or less, and amplicon or equivalent technology for defined segments and variants. There will be a place for all three, possibly combined into a single sequencing assay. However, the most cost effective for genomic selection currently are random sampling methods: best known as genotyping by sequencing (GBS). Currently, most flavors of GBS are based on restriction enzyme reduced representational sequencing or RE-RRS. In the longer-term methods based on random selective primers and PCR may prevail. Increasingly, opportunities will be taken to contemporaneously explore DNA methylation, structural variation and the host microbiome. Nanopore and long read technologies will also be used, in part, to reduce infrastructure costs and reduce turn-a-round time. There is still a niche for array-based technologies, at least for the next decade, but if they are to persist beyond that date the ability to manufacture small runs of chips, cost effectively, coupled with further cost reductions will be required. As sequencing costs decline, research emphasis will shift to better DNA sampling and DNA extraction techniques.