Institution: The University of Edinburgh / Scotland's Rural College

Unit of Assessment: 6

Title of case study: E: Transforming genomic selection in commercial breeding programmes for pigs, dairy goats and poultry

Period when the underpinning research was undertaken: 2003 – 2020

Details of staff conducting the underpinning research from the submitting unit:

Name(s):	Role(s) (e.g. job title):	Period(s) employed by submitting HEI:
John Hickey	Chair of Animal Breeding	2013 – 2020
Mike Coffey	Chair of Livestock Informatics	1998 – present
Raphael Mrode	Chair of Animal Breeding	1998 – present
Joanne Conington	Reader in Applied Livestock Genetics	2007 – present
John Woolliams	Personal Chair of Mathematical Genetics	1977 – 2020
Alan Archibald	Personal Chair of Mammalian Molecular Genetics	1973 – present
Albert Tenesa	Personal Chair of Quantitative Genetics	2003 – present
Andreas Kranis	Senior Research Fellow / Group Leader	2016 – present
Peter Visscher	Reader	1995 – 2007

Period when the claimed impact occurred: August 2013 – December 2020

Is this case study continued from a case study submitted in 2014? N, but it builds on research and impact reported in REF2014/6/1f

1. Summary of the impact

Underpinning Research: We have developed an end-to-end package of theory, tools, technologies and implementation strategies that has enabled breeding companies locally and globally to deploy genomic selection in their routine breeding programmes.

Significance and Reach of Impact: Adoption of our genomic selection toolkit has led to the following benefits in these exemplar sectors:

- For **Genus PLC**, which provides 25% of the world's pig genetically improved breeding stock, genomic selection has since October 2013 doubled the accuracy of selection for female reproductive performance traits, resulting in an average annual increase in genetic potential for the number of piglets produced per sow per year from 0.65 in 2013 to 1.4 in 2020. Overall, genomic selection has enabled Genus customers to produce 2,000,000t more pig meat per year, resulting in GBP300,000,000 potential extra profit to producers.
- For **Yorkshire Dairy Goats**, which supplies 40% of the UK's goat milk and products, genomic selection (since 2014) has increased use of elite male goats, doubling the rate of genetic improvement and leading to 73% higher yields of milk, reduced costs of production and improved fertility and welfare.
- For **Aviagen Ltd**, the market leader for the world's chicken and turkey genetics with more than 50% market share in both species, genomic selection (since 2016) has resulted in increases in the accuracy of selection of approximately 20% for fertility traits and more than 50% for feed intake. Such improvements are associated with significant economic and environmental benefits, including an estimated saving of 673,651t of feed per year across that sector of the global market supplied by Aviagen.

2. Underpinning research

The Challenge: How to sustainably increase food production

The Food and Agriculture Organisation (FAO) estimate that to meet the challenge of producing enough food to feed the world's population sustainably for the next 50 years, the rates of livestock productivity need to double. Historically, selective breeding has accounted for 50% of the improvement in livestock productivity. In practice, therefore, this need for rapid improvement translates to a need for a step change in the current rates of genetic gain, i.e. the improvement in performance per generation achieved through breeding, in livestock breeding programmes.

From 2002 onwards, we have made substantial contributions to this goal by introducing the concept of genomic selection and demonstrating how it can be harnessed by the farming industry (reported in REF2014/6/1f). Since REF2014, we have facilitated and driven the practical uptake of genomic selection in commercial breeding programmes for multiple species through developing an end-to-end package of underpinning theory, tools, technologies and implementation strategies.

An end-to-end package of tools to enable genomic selection in multiple species and traits

Breaking the cost barrier
Genomic selection requires a large volume of high-density genomic data, which is expensive to analyse, and in the past represented a barrier to commercial implementation of genomic selection. Since REF 2014, we have overcome this barrier by recognising that it was possible to track desired genome segments passed from key males to their descendants using only a small number of markers; a process called imputation [3.1]. To enable imputation to be implemented in practice, we have contributed to high-quality reference genomes for key farmed animals via a leading role in the international Functional Annotation of Animal Genomes consortium and development of a software package containing the imputation algorithm [3.1].

Enabling and optimising genomic prediction
A key driver of the success of genomic selection is the accuracy of genomic prediction. This is based on establishing a set of genotyped and phenotyped individuals known as the “training set”, and using this to produce an equation that allows the value of the animals in the breeding programme for the trait(s) of interest to be predicted accurately from their marker genotypes. We were the first to set out the theoretical basis of training set design [3.2] and provide practical rules of thumb for the design process.

Through using these training sets, as well as genotyping and imputation strategies, breeding and recording organisations routinely generate extensive datasets. To maximise the accuracy of genomic selection based on these datasets, we have now developed a suite of scalable statistical methods [e.g. 3.3] and made them available to the academic community and industry.

Working collaboratively with Aviagen and Genus in landmark projects funded via the Innovate UK Agri-Tech Catalyst scheme, we have generated whole-genome sequence datasets for many thousands of elite chickens and pigs to further refine the accuracy of selection decisions.

Breeding programme designs to optimally exploit genomic technology
In addition to devising imputation strategies [3.1], we have made other pivotal contributions to breeding programme designs, including theory for the management of inbreeding under genomic selection [reported in REF2014] and methods for estimating linkage disequilibrium in mixed breed populations [3.4]. To facilitate uptake of these and other methodological developments we have since REF 2014 developed tools that simulate a wide range of mating designs, biotechnologies and selection strategies allowing both academic and commercial users to perform breeding simulations in any species using a wide range of strategies [3.5]. The newest open source version of this, AlphaSimR, has been downloaded 19,672 times since 2018.

Empirical analysis of prototype/emerging datasets
To achieve gains from this end-to-end package for genomic selection, we have worked with industry to apply it to routine commercial breeding programmes. For example, in collaboration with Yorkshire Dairy Goats, we were the first team to collate milk yield, pedigree and genotype data from UK commercial dairy goats. We then analysed these data to show, using methods described earlier [3.4], that crossbred populations were amenable to genomic selection. We demonstrated the additional accuracy that genomic data can provide compared to the

conventional pedigree-based approach to breeding, producing genomic evaluations for the first time for commercial crossbred dairy goats for milk production [3.6].

3. References to the research

[3.1] Anatolín R, Nettelblad C, Gorjanc G, Money D & Hickey JM, 2017. A hybrid method for the imputation of genomic data in livestock populations. *Genetics Selection Evolution* 49:30. doi: 10.1186/s12711-017-0300-y

[3.2] Daetwyler HD, Villanueva B, & Woolliams JA, 2008. Accuracy of predicting the genetic risk of disease using a genome-wide approach. *PLoS One* 3:e3395. doi:10.1371/journal.pone.0003395

[3.3] Canela-Xandri O, Law A, Gray A, Woolliams JA, & Tenesa A. 2015. A new tool called DISSECT for analysing large genomic data sets using a Big Data approach. *Nature Communications* 6:10162. doi: 10.1038/ncomms10162

[3.4] Hayes BJ, Visscher PM, McPartlan HC & Goddard ME, 2003. Novel multilocus measure of linkage disequilibrium to estimate past effective population size. *Genome Research* 13:635-43. doi:10.1101/gr.387103

[3.5] Faux A, Gorjanc G, Gaynor RC, Battagin M, Edwards SM, Wilson DL, Hearne SJ, Gonen S, & Hickey JM. 2016. AlphaSim: Software for breeding program simulation. *Plant Genome* 9. doi: 10.3835/plantgenome2016.02.0013

[3.6] Mucha S, Mrode R, MacLaren-Lee I, Coffey M, & Conington J, 2015. Estimation of genomic breeding values for milk yield in UK dairy goats. *Journal of Dairy Science* 98:8201-8. doi: 10.3168/jds.2015-9682

Key grants:
15AGRITECHCAT3 ‘Innovative NextGen pig breeding using DNA sequence data’, BBSRC BB/N004736/1 £1,170,166, Nov 15 - Oct 18 (PI Hickey; c. GBP3,000,000 in total with Genus contributions).

15AGRITECHCAT3 ‘Precision breeding: Broilers from sequence to consequence’, Innovate UK 102273, £524,854, Nov 15 - Oct 18 (PI Hickey; c. GBP3,000,000 in total with Aviagen contributions).

Innovate UK 101072 ‘Efficient goat breeding for sustainable milk production’. GBP682,042, Feb 12 - Mar 15 (PI Conington).

4. Details of the impact

The body of research described above has enabled major breeding organisations and individual farm businesses to deploy genomic selection in their breeding programmes. This has driven measurable improvements in productivity and efficiency of the global farming industry. We illustrate this using 3 example species: pigs, dairy goats and poultry.

Impact on pig breeding: Genus
The end-to-end package of tools developed through our research has had a “*transformative effect*” on the breeding programme at the world’s largest pig genetics company, Genus. With 25% share of the global market, Genus is the international leader in providing genetically superior breeding stock and technical support services in animal nutrition, health and management to pig producers across the world.

Genus confirm that they adopted genomic selection on a routine basis in October 2013, using the tools developed by our researchers amongst others [5.1]. Routine deployment of genomic selection has resulted in a doubling of accuracy of selection for female reproductive performance traits, such as the number of piglets born and time taken to return to reproduction following weaning, which were previously difficult and expensive to measure and thus to improve. As a result of this doubled accuracy of selection, the average annual increase in genetic potential for number of piglets produced per sow per year has more than doubled from 0.65 in 2013 to 1.4 in 2020 [5.1].

Overall, owing to the improvements in female reproductive performance and pig growth, robustness and efficiency, the annual rate of genetic gain for pig productivity and increased profit potential for customers of Genus has increased by 40% between 2013 and 2020 [5.1]. Genus estimate that "*At the global production level, this may translate to an annual increase of 2,000,000 tonnes of pig meat, which in turn may equate in up to GBP300,000,000 in extra profit potential per year for Genus customers worldwide (GBP3,500,000 for UK producers).*" *The genetic gain is cumulative, and as such will drive recurrent benefits to the farming sector as well as the pork-consuming market, through increased availability of high quality, nutritious and affordable protein. The continued advancement in genetic selection and impact from these advanced tools have also allowed improved rate of gain in traits such as feed efficiency, that drive positive contribution to improving the sustainability of global pork production, and animal welfare and well-being, via targeted improvements in leg structure and piglet mortality*." [5.1].

Impact on goat breeding: Yorkshire Dairy Goats (YDG)

Our collaboration with YDG, supported by Innovate UK funding, resulted in YDG implementing genomic selection in their breeding programmes in 2014; the first dairy goat company in the world to do so. By the end of 2018, 16,500 animals had been genotyped [5.2].

Genomic selection has enabled YDG to identify the male goats with the best milk-producing daughters at an earlier age. This has: 1) saved resources by allowing YDG to keep fewer of the males with less productive offspring, and 2) allowed the best males to be bred from an earlier age, resulting in greater numbers of offspring from these males. These advances have driven increased rates of genetic improvement and led to 73% higher average yields of milk and thus improved profitability for YDG and its customers [5.2; 5.3]. In addition, genomic selection has allowed YDG to apply selection to other key traits, including mastitis resistance, feed efficiency and out-of-season breeding [5.3].

Overall, YDG states that our collaboration with them: "*has enabled selection to be applied to a wider range of traits ensuring that future generations of YDG goats can produce high volumes of milk but remain healthy and fertile. These benefits will take years to manifest in the herd but are of vital importance for future sales*." [5.2].

In addition, our collaboration has created opportunities for YDG to export high genetic merit animals, embryos, and frozen semen, based on the genomic predictions we developed. YDG have already purchased a farm in New Zealand and are exporting superior embryos in order to establish a satellite goat herd there. High-value exports of improved embryos and breeding stock to China are already underway [5.3].

Impact on poultry breeding: Aviagen

Aviagen is the market leader for meat-type poultry, supplying broiler and turkey breeding stock to over 100 countries around the world. Collaboration with our team helped Aviagen to become the world's first poultry breeding company to implement genomic selection in its chicken and turkey breeding programmes; an innovation that was in place by 2016 [5.4].

Aviagen's use of genomics to inform selection decisions has resulted in a consistent improvement in many key traits in broilers, with a relative improvement in accuracy ranging from 20% for fertility to 45% for egg production, while for highly heritable traits, such as feed intake, this improvement can be greater than 50% [5.5]. Due to the structure and scale of the global poultry supply chain, such improvements have a profound impact in improving its efficiency and sustainability. Notably, improving the accuracy of predicting genetic merit for Feed Conversion Ratio (FCR), a measure of biological efficiency and a key driver of profitable and sustainable production, can significantly reduce the environmental footprint of the global poultry system. The 2019 global production of chicken meat was 118,017,161t, equivalent to 168,412,688t of body weight [5.6]. Our conservative estimate of the commercial field improvement in FCR is –0.020 kg/kg each year, [5.7a-c]. For the 50% share of the global broiler industry supplied by Aviagen, this equates to a cumulative annual saving of 0.02 × 168,412,688 x 0.5 = 1,684,127t of feed. Based on the evidence that 40% of this gain is due to implementation of genomic selection as described here [5.7], a conservative estimate of the saving in feed requirement is 673,650t – enough to feed at least 150,000,000 additional birds from the same quantity of feed grown.

This means that, despite the increase in demand requiring more birds to be reared globally, improvements in FCR driven by genomic selection enhance efficiency and reduce the economic cost and environmental footprint of the production of chicken meat [5.4].

5. Sources to corroborate the impact

[5.1] Testimonial from Genus PLC

[5.2] Testimonial from Yorkshire Dairy Goats

[5.3] Presentation by Yorkshire Dairy Goats, September 2018

[5.4] Testimonial from Aviagen Ltd

[5.5] Wolc A, Kranis A, Arango J, Settar P, Fulton JE, O'Sullivan NP, Avendano A, Watson KA, Hickey JM, De los Campos G & Fernando RL. 2016. Implementation of genomic selection in the poultry industry. *Animal Frontiers* 6:23-31. doi: 10.2527/af.2016-0004

[5.6] FAO data to show global chicken production in 2019

[5.7] Published papers corroborating the level of improvement in feed conversion ratio attributable to selection:
a. Havenstein GB, Ferket PR & Qureshi MA. 2003a. Growth, livability and feed conversion of 1957 versus 2001 broilers when fed representative 1957 and 2001 broiler diets. *Poultry Science* 82:1500-1508. doi: 10.1093/ps/82.10.1500.
b. Havenstein GB, Ferket PR & Qureshi MA. 2003b. Carcass composition and yield of 1957 versus 2001 broilers when fed representative 1957 and 2001 broiler diets. *Poultry Science* 82:1509-1518. doi: 10.1093/ps/82.10.1509.
c. Siegel PB. 2014. Evolution of the modern broiler and feed efficiency. *Annual Review of Animal Biosciences* 2:375-385. doi: 10.1146/annurev-animal-022513-114132.