# Research Stimulus Fund

# <u>Final Report</u>

*'Multi-breed genomic selection in dairy and beef cattle- MultiGS'*

**DAFM Project Reference No:** 11/S/112

**Start date:** 01/11/2012

**End Date**: 31/07/2018

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**Collaborating Research Institutions and Researchers:** Irish Cattle Breeding Federation

**Please place _one_ "x" below in the appropriate area on the research continuum where you feel this project fits**

| Basic/Fundamental $\longrightarrow$ Applied $\longrightarrow$ Pre Commercial | | | | | | |
|---|---|---|---|---|---|---|
| 1 | 2 | 3 | 4 | 5 | 6X | 7 |

**Please specify priority area(s) of research this project relates to from the National Prioritisation Research Exercise\* (NRPE) report;**

| Priority Area (s) | I |
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**Key words:** Genetics, genomics, breeding, cattle

## 1.	Rationale for Undertaking the Research

Within-breed genomic selection has the potential to increase genetic gain by at least 50% in dairying. Little was known on the expected benefits in beef but the expectations were similar, if not greater in Ireland. Genomic selection uses information on the DNA of an animal to supplement the traditional genetic evaluations; this results in increased accuracy of selection. The increase in accuracy of selection is a function of, amongst others, the size of the population used to estimate the SNP (i.e., pieces of DNA) effects.

Many countries have now implemented genomic selection in national breeding programs for dairy cattle; to our knowledge no national across-breed genomic selection program was operational in beef cattle at the time that the project began, although within-breed genomic selection using customised panels were operational in some beef breeds in the US/Canada. Within-breed genomic selection for Holstein-Friesian dairy cattle using a two-step approach is already implemented internationally including in Ireland. Across-breed genomic selection in beef cattle had not been undertaken at the time of the project beginning although multi-breed genomic evaluation in Holstein-Friesian and Jersey cattle, again using a two-step approach, was undertaken in New Zealand. Based on preliminary research in Ireland, the size and structure of the beef population in Ireland does not lend itself to accurate within-breed genomic selection as currently implemented in dairy cattle in Ireland; therefore across-breed genomic selection must be pursued. The same will be true of sheep in Ireland (and probably most other countries). Furthermore, other dairy cattle breeds in Ireland (e.g., Jersey and Scandinavian breeds) also are not sufficiently represented in Ireland to exploit the full benefits of within breed genomic selection. Across breed genomic selection could facilitate greater accuracy of selection in these breeds thereby also increasing genetic gain and providing more accurate genetic evaluations of alternative breed bulls for use in on-farm crossbreeding schemes which is increasing in Irish dairy herds. This project is a "close to implementation" project developing on the knowledge already generated in Ireland on genomic selection in dairy cattle.

## 2.	Research Approach

The MultiGS project used quantitative research approaches focusing on three main tasks; Imputation, genomic prediction and genome-wide association studies; optimal breeding programs (both nationally and on-farm) were also considered using stochastic and deterministic simulations.

**Imputation**: Several different imputation software suites (Beagle, FImpute and Findhap) were tested for both accuracy and efficiency. Accuracy of imputation as a function of the quantity of genotyped back-pedigree available was also compared across algorithms. A novel approach to impute the back pedigree of genotyped animals was developed and showed that once >6 genotyped progeny per animal exist, the genotype of the parent can be accurately imputed. A simulation study on the long term consequences of imputation was completed which emphasized the necessity to routinely generate high density genotypes on influential animals to maintain genotype imputation accuracy.

**Genomic prediction:** Several genomic prediction methods were testing for their efficiency including two-step, one-step, APY, ssRBLUP and BOLT. Many of these software approaches were redeveloped to take into account the vast quantity of genotype data within the Irish population. The one-step prediction approach was not feasible to be implemented in the national genomic evaluations due to the computational difficulty and efficiency of inverting large scale matrixes; currently there are >1million genotyped cattle. To reduce the delay in delivering genomics to beef farmers, a two-step genomic approach (similar to that in dairy) was implemented in 2016. Considerable research was also undertaken on using different algorithms for the development of the genomic relationship matrix; the final decision was to use the Euclidian distance. The correct approach to validating the accuracy of genomic predictions was also widely tested throughout the duration of Multi-GS. A standardised protocol to correctly choosing the validation population was widely discussed with the International Scientific Advisory Committee and is now implemented when testing all genomic prediction approaches.

**Genome-wide association studies:** Both Bayesian and linear mixed model GWAS approaches were used throughout this task, as well as a variety of different software (Gcta64, AsReml, Wombat, Gensel, BayesRC). Genotypes were either imputed to high density (770.000 SNPs) or to whole genome sequence (40 million SNPs). Efficient linux scripts were created to facilitate the handling of large datasets. The benefits of using a weighted GWAS approach over a standard un-weighted GWAS were also demonstrated.

## 3.    Research Achievements/Results

*Task 1: International pedigree file of genotyped non-Holstein animals.*
An international list of 8265 AI bulls from different breeds with provided information on the genotypes available from different countries was collated. Ireland has used this list to exchange several hundred genotypes with participating countries- a cost saving of approximately €250,000.

*Task 2: Efficient and accurate genotype/sequence imputation pipelines.*
Several imputation software suites were tested for their accuracy and efficiency. Based on the results, FImpute software was chosen for imputation in beef cattle to medium density genotypes for use in the national genetic evaluations. Manuscripts outlining the results were published in the Journal of Animal Breeding and Genetics and Animal. The imputation pipeline has since been incorporated into the ICBF genomic selection software suite thus reducing the cost of genomic selection to Irish stakeholders. In addition, pipelines created for the imputation of microsatellites to undertake parentage testing have also been incorporated; saving the breed societies >€200.000 on re-genotyping older samples. Imputation from chip genotypes to whole genome sequence data was also evaluated. Genotypes were firstly imputed to HD using a two-step approach in FImpute2 which involved imputing the IDB genotypes to the Bovine SNP50 density and consequently imputing all resulting genotypes to HD using a population of 5,504 influential sires from multiple breeds genotyped on the HD. Imputation to whole genome sequence was then

undertaken using a reference population of 2,333 *Bos Taurus* animals of multiple breeds from Run6.0 of the 1000 Bulls Genomes Project. To assess the accuracy of imputation to whole genome, a validation set of 175 animals that were genotyped on either the Bovine SNP50 or HD genotype panels, as well as being sequenced, were used. This involved using the animal's original genotype panel calls, and imputing these genotypes to whole genome using both Eagle and minimac3, whilst removing the validation animals from the reference population. The average genotype concordance, defined as the proportion of correctly called SNPs versus all SNPs, was estimated to be 0.98.

### Task 3: Across breed genomic predictions

Two-step national genomic evaluations, developed in this project, are now available in beef cattle since 2016. This genomic evaluation incorporates >1 million genotyped cattle, making this by far the largest multi-breed genomic evaluation being undertaken in any livestock species globally. The research underpinning these evaluations was developed in Multi-GS and the benefit observed by Irish farmers is strongest when the reliability of the breeding value without genomics is least. Validation of the genomic evaluations was undertaken and an increase in prediction accuracy for nearly all traits (excluding age at first calving) was detected. This increase is expected to improve over time as new prediction approaches are developed. A one-step prediction approach was tested during Multi-GS; however at the present time it is not scalable to the large number of animals genotyped. Research on improving this approach is on-going and pipelines created during Multi-GS will facilitate an easy transition. Furthermore, improvements have been continuing on dairy genomic predictions; all evaluations have now transitioned to a more efficient and flexible software that allows the evaluation to scale up with the addition of new genotypes.

### Task 4: Genome-wide association study for performance traits in dairy and beef cattle.

Association studies have been completed for a suite of performance traits including calving difficulty, fertility, tuberculosis, carcass performance, milk production, parasites, Johnes and linear type traits. Results have been presented at many (inter)national conferences and multiple manuscripts have been published. Significant SNP associations have also been incorporated into the Irish custom genotyping panel for further validation. While a few regions were detected to be associated (small effect) with performance traits, of note was that these regions were few, implying that most of the genetic variation in performance traits complies with the infinitesimal model in that there are a very large number of genes affecting the trait, each with a very small effect. This therefore implies that to be successful at detecting genomic regions associated with performance with some level of confidence, hundreds of thousands of animals are required.

### Task 5: Genomic selection breeding schemes

The breeding program research task (industry and on-farm) focused on three main areas: 1) number of animals to genotype to maximise genetic gain, 2) whether investing in a

breeding program for another breed would be useful (in particular Jersey, 3) evaluation of bull movement as they accumulate more progeny and thus the impact on the breeding program. From an Irish national perspective, there was little marginal benefit of genotyping >3000-4000 bull calves annually. If evaluating sires from another breed in the national breeding program, then obviously the greater the number of young bulls evaluated the better, but also a larger number of semen straws per young bull should be used to aid in achieving high reliability genetic evaluations thereby minimising the regression of breeding values to the mean. Equations were developed (and deployed) to set the limits of bull movements between genetic evaluation runs based on the increase in reliability observed from one evaluation to the next.

## 4. Impact of the Research

### 4(a) Summary of Research Outcomes

(i) Collaborative links developed during this research

*Irish Cattle Breeding Federation*; This project strengthened the existing collaboration between Teagasc and ICBF. All pipelines that were developed in Multi-GS were constructed and tested to be compatible with existing ICBF infrastructure to ensure ease of implementation and roll out of the results.

*International Scientific Advisory Committee:* It is the role of the international scientific advisory committee to advise and ensure the correct development of beef multi-breed genomic predictions within the Irish national evaluation system. As such, there was strong collaboration between members of the committee (Roel Veerkamp, Dorian Garick, Esa Mantysaari, Ismo Stranden, Theo Meuwissen, Peter Amer, Fiona Hely, Jeremie Vandenplas, Jan ten Napel) and participants in Multi-GS when both testing and implementing genomic prediction approaches. Members of the committee are recognised as international leaders in the development of genomic prediction approaches and computing approaches.

*AgriBio, Centre for AgriBioscience, Department of Economic Development, Jobs, Transport and Resources, Bundoora, Victoria, Australia.* Research completed during Multi-GS was used as a part of a meta-analysis genome-wide association approach to elucidate the genomic variation behind cattle stature. This study was an international project involving 58 researchers across 30 research institutes and was published in 2018 in Nature Genetics. Deirdre Purfield, the post-doctoral researcher hired under Multi-GS spent five months in Agribio, Australia completing this research work under the supervision of the paper lead Dr Ben Hayes in 2015. This collaboration and time spent abroad helped establish strong collaborative links between both Agribio and Teagasc.

*Jerry Taylor Animal Genetics Research group, University of Missouri, USA.* Deirdre Purfield, the post-doctoral researcher hired under Multi-GS spent 3 months from February till May 2017 as part of Jerry Taylor's lab group in the University of Missouri. Research during this time focused on creating the pipelines for efficient and precise large scale imputation to whole genome sequence and comparison of genome-wide

association approaches. The pipelines created during this placement where used to impute 635,000 animals to whole genome sequence (40 million genotypes). This data is now available for genome-wide analysis for multiple traits of economic importance.

(ii)     Outcomes where new products, technologies and processes were developed and/or adopted

**Development of multi-breed beef genomic evaluations:** Two-step national beef genomic evaluations were officially launched in 2016 as a result of work completed during the Multi-GS project. These evaluations are currently the largest official national genomic evaluation globally in cattle.

**Custom genotyping panel- Irish Dairy and Beef:** The custom genotyping panel has been redeveloped twice during the lifetime of Multi-GS and version 4 is currently in development. Research completed during Multi-GS has contributed to both developments; SNP markers identified from association studies on fertility, calving difficulty and stature have been included in both builds. This allows these associations to be validated in separate populations and to test their ability to improve genomic prediction accuracy. In addition SNP markers identified in the present study to increase imputation accuracy to high density have also been incorporated into these genotyping panels.

**Development of imputation pipelines:** Imputation pipelines for the efficient and accurate imputation of SNP panels to medium (50k), high density (770k) and whole genome sequence (40 million) have been created. The pipelines for imputation to medium density are implemented within the national genomic evaluations.

**Breeding programs:** the mathematical methodology to set limits to animal movement in genetic merit between consecutive genetic evaluation runs has been incorporated into the ICBF quality assurance system; the impact of relationships among bulls and unequal bull usage within a bull team for a herd's breeding program have been incorporated in the national sire advise system run by the ICBF.

(iii)    Outcomes with economic potential

**Development of multi-breed beef genomic evaluations:** The Beef Genomics and Data Program is based on genomic evaluations of females; the pipelines and approaches (i.e., imputation, data editing, revised genetic evaluations, genomic predictions, blending) developed in MultiGS, now run routinely by the ICBF, are used to generate these genomic evaluations. A reversal in the trend in genetic merit for the beef replacement index is being observed implying increased profitability at farm level for beef farmers.

**Developments in dairy cow genomic evaluations;** the dairy cow genomic evaluations are now more efficient than prior to MultiGS and are less prone to human error. The equations used to calculate the reliability of a team of bulls if related and not used equally has been integrated into the back-end of the national dairy sire advise system as well as recommendations by Teagasc advisors. The outcome is greater genetic gain for profit.

(iv)    Outcomes with national/ policy/social/environmental potential

The ability to undertaken large-sale genomic evaluations was of fundamental importance in the national policy underpinning the beef genomic scheme. Through an improvement in genetic gain, the economic benefit is greater profitability for farmers while the social

benefit (over and above that due to increase spendable income by farmers in the respective communities) is that higher replacement index females are environmentally more efficient.

## 4 (b) Summary of Research Outputs

### (i) Peer-reviewed publications, International Journal/Book chapters.

- McClure, M.c, et al., (2013) Imputation of Microsatellite Alleles from Dense SNP Genotypes for Parentage Verification Across Multiple Bos taurus and Bos indicus breeds. Frontiers in animal genetics. 4: 176
- Berry, D.P., McClure, MC and Mullen MP (2014). Within and across-breed imputation of high density genotypes in dairy and beef cattle from medium and low density genotypes. Journal of Animal Breeding and Genetics:131(3):1665-72
- Berry, D.P., McParland, S., Kearney, J.F., Sargolzaei M, and Mullem M.P. (2014) Imputation of un-genotyped parental genotypes in dairy and beef cattle from progeny genotypes. Animal 8(6):895-903
- Purfield, D.C, Bradley, D.G, Kearney, J,.F, and Berry, D.P. (2014) Genome-wide association study for calving traits in Holstein-Friesian cattle. Animal 8(2):224-235
- Meredith, B.K, Berry, D.P, Kearney, J.F, Finlay, E.K, Fahey, A.G, Bradley, D.G, Lynn, D.J (2013).A genome-wide association study for susceptibility to bovine mastitis identifies a novel QTL that encodes a previously uncharacterized small non-coding RNA. Frontiers in Genetics 4 (229) : 1-10
- Purfield, D.C, Bradley, D.G, Evans R.D, Kearney, F.J., and Berry. D.P. (2015)Genome wide association study for calving performance using high-density genotypes in dairy and beef cattle. Genetics Selection Evolution;47:47
- Zhao, F., McParland, S, Kearney, J. F, Du, L., and Berry, D.P. (2015). Detection of selection signatures in dairy and beef cattle using high density genomic information. Genetics Selection Evolution 47:49
- Richardson, I.W., Berry, D.P., Wiencko, H.L, Higgins, I.M, More, S.J., McClure, J., Lynn D.J and Bradley, D.G., (2016). A genome-wide association study for genetic susceptibility to Mycobacterium bovis infection in dairy cattle identifies a susceptibility QTL on chromosome 23. Genetics Selection Evolution 48:19
- Purfield,D.C., McClure, M.C and Berry, D.P. (2016) Justification for setting individual animal genotype call rate threshold at 85%. Journal of Animal Science 94(11):4558-4569
- Kelleher, M.M., Berry, D.P., Kearney, J.F., McParland, S., Buckley, F, Purfield, D.C., (2017). Inference of population structure of purebred dairy and beef cattle using high density genotype data. Animal 11(1):15-23
- Purfield, D.C., McParland, S., Wall, E., and Berry, D.P. (2017) Runs of Homozygosity and Selection Signatures in Six Commercial Meat Sheep Breeds. Plos One 12(5)
- Berry, D.P., Wolfe, A., O'Donovan, J., Byrne, N., Sayers,R., O'Connor, R.E., McClure, M., and Purfield, D.C. (2017) Characterisation of a X-chromosomal non-mosaic monosomy (59, X0) dairy heifer detected using routinely available genotype data.Journal of Animal Science 95(3):1042-1049
- Judge, M.M, Purfield, D.C., Sleator, R.D., and Berry, D.P.(2017) Impact of multi-generational genotype imputation strategies on imputation accuracy and genomic predictions. Journal of Animal Science 95(4):1489-1501
- Berry D. P., O'Brien A, O'Donovan J, McHugh N, Wall E, Randles S, McDermott K, O'Connor R.E., Patil MA, Ho J, Kennedy A, Byrne N, Purfield D.C. (2018).Aneuploidy in dizygotic twin sheep detected using genome-wide single nucleotide polymorphism data from two commonly used commercial vendors. Animal 15:1-8.
- Bouwman et al. Meta-analysis of genome wide association studies for cattle stature identifies common genes that regulates body size in mammals (2018). Nature Genetics 50(3):362-367
- Gobikrushanth, M, Purfield, D.C., Colazo, M. G., Butler, S. T., Wang, Z., and Ambrose, D.J. (2018). The relationship between serum anti-Müllerian hormone concentrations and fertility, and genome-wide associations for anti-Müllerian hormone in Holstein cows. Journal of Dairy Science 101(8):7563-7574
- Gobikrushanth, M, Purfield, D.C., Colazo, M. G., Butler, S. T., Wang, Z., and Ambrose, D.J (2018). The relationship between serum insulin-like growth factor-1 (IGF-1) concentration and reproductive performance, and genome-wide associations for serum IGF-1 in Holstein cows. Journal of Dairy Science(preprint)/

- Rafter, P., Purfield, D. C., Berry, D. P., Parnell, A. C., Gormley, I.C., Kearney, J.F., Coffey, M.P., and Carthy, T. R. Characterization of copy number variants in a large multi-breed population of beef and dairy cattle using high-density single nucleotide. Journal of Animal Science. Accepted.


## (ii)    Popular non-scientific publications and abstracts including those presented at conferences

- Mullen M.C, McClure, M.C. Kearney, J.F, Waters, S.M, Weld, R., Flynn, P. Creevey, C.J, Cromie, A.R and Berry. D.P. (2013) Development of a custom SNP chip for dairy and beef cattle breeding, parentage and research. Interbull Meeting No. 47
- Berry et al., (2013). Development of a custom genotyping panel for dairy and beef cattle breeding and research.  Proceedings, British Society of Animal Science
- Purfield  D.C., Bradley, D.G., Kearney, J.F and Berry, D.P. Genome wide association study for calving performance in Irish cattle (2013). European Association for Animal Production p. 606
- Mullen, M.C, Waters, S. M., McClure, M.C., Kearney, J.F., Cromie, A.R., Weld, R., Flynn, P. and Berry D. P. (2013) Animal breeding using DNA technologies. Tresearch Winter.
- Berry et al., (2013). Across breed, beef dairy cattle genotype imputation to high-density genotypes. Agricultural Research Forum, Tullamore Court Hotel, 12-Mar-2013, 70
- Berry  et al., (2013). Across and within-breed imputation across several genotyping densities in dairy and beef cattle. Proceedings of the Association for the advancement of Animal Breeding and Genetics (AAABG), Napier, New Zealand, 20-Oct-2013, 20
- Mullen M.C, McClure, M.C. Kearney, J.F, Waters, S.M, Weld, R., Flynn, P. Creevey, C.J, Cromie, A.R and Berry. D.P  (2013) The development of a custom genotyping chip for beef and dairy cattle in Ireland. Agricultural Research Forum, Tullamore Court Hotel, 11-Mar-2013, 56
- Mullen, M.C et al (2013) Imputation of parental genotypes in dairy and beef cattle from progeny genotyped at different genotyping densities. Agricultural Research Forum, Tullamore Court Hotel, 11-Mar-2013, 57
- Purfield, D. C, Bradley, D.G, Kearney, J.F and Berry, D.P (2013). Genome wide association study for calving performance in Irish cattle. Agricultural Research Forum, Tullamore Court Hotel, 11-Mar-2013, 55
- McHugh, N and Berry, D.P (2013). Genomic selection, past, present, future - Irish Dairying-Harvesting the Potential. Moorepark Open Day Booklet 3/7/13
- McParland S., et al., (2014). Retrospective analysis of the accuracy of genomic selection in Irish dairy cattle. Agricultural Research Forum, Tullamore Court Hotel, 11-Mar-2014
- Richardson I, et al., (2014). Genome wide association study for genetic susceptibility to Mycobacterium bovis infection in dairy cattle. Agricultural Research Forum, Tullamore Court Hotel, 11-Mar-2014
- Purfield, D.C.,  et al (2014) Genome wide association study for calving performance in Irish dairy and beef cattle using high-density genotypes. Agricultural Research Forum, Tullamore Court Hotel, 11-Mar-2014
- Berry, D.P (2014). Low density genotyping panels for genomic selection in Irish dairy cattle. Agricultural Research Forum, Tullamore Court Hotel, 11-Mar-2014
- Mullen, M.C., et al. (2014)Performance of the International Dairy and Beef (IDB) custom genotyping chip for beef and dairy cattle in Ireland, Agricultural Research Forum, Tullamore Court Hotel, 11-Mar-2014
- Purfield, D.C et al., (2014). Characterisation of copy number variation in Holstein-Friesian cattle. Agricultural Research Forum, Tullamore Court Hotel, 11-Mar-2014
- Pryce, J. E and Berry, D.P. (2014). Implementation of genomic breeding values for novel traits such as feed efficiency through female nucleus reference populations. ICAR Berlin
- Berry, D.P (2014). Selection for Novel Traits: An international genomics perspective. Beef Improvement Federation, Annual Conference, Nebraska
- Cromie et al (2014). Genomics for Pedigree and Cross-bred Beef Cattle Populations; Some experiences from Ireland. World Congress on Genetics Applied to Livestock Production, Vancouver B.C
- Purfield et al (2014). Genome-wide Association using High Density Genotypes for Calving Difficulty in Dairy and Beef Cattle. World Congress on Genetics Applied to Livestock Production, Vancouver B.C 2014
- Judge et al., (2014). Development of Low Density Genotype Panels for Dairy and Beef Cattle. World Congress on Genetics Applied to Livestock Production, Vancouver B.C

- Tsairidou et al., (2014). A meta-analysis for bovine tuberculosis resistance in dairy cattle. *World Congress on Genetics Applied to Livestock Production*, Vancouver B.C
- Richardson et al., (2014). Variance Components and Genome Wide Association Analysis of Mycobacterium bovis Infection in Dairy and Beef Cattle. *World Congress on Genetics Applied to Livestock Production*, Vancouver B.C
- McClure et al., (2014). Accelerating the shift to SNP-based parentage verification through microsatellite imputation in Ireland. *World Congress on Genetics Applied to Livestock Production*, Vancouver B.C
- Purfield, D.C, Kearney. J.F, and D.P. Berry. (2015).   Strong genomic associations for reproductive performance identified on chromosome 18 in Holstein-Friesian cattle. *Agricultural Research Forum*, Tullamore p99
- Carthy, T.R. Kemper, K.E., Berry, D.P.  Evans, R.D. and Pryce, J.E. (2015). Regional heritability mapping to identify genomic regions associated with reproductive traits in Holstein-Friesian bulls. . *Agricultural Research Forum*, Tullamore p920
- Berry, D.P, Purfield, D.C., Evans, R.D., Pabiou, T. and Kearney, J. F. (2015). Whole genome-enabled predictions of carcass merit in a multi-breed cattle population. *Agricultural Research Forum*, Tullamore p144
- Purfield, D.C., Evans, R.D., Kearney, J.F.,  and Berry, D.P. (2015). Refinement of the genomic regions on chromosome 18 associated with direct calving difficulty using sequence data. *Agricultural Research Forum*, Tullamore p145
- Kelleher, M.M., Kearney, J.F and Purfield, D.C. (2015). Genomic breed prediction in Irish dairy and beef cattle. *Agricultural Research Forum*, Tullamore p152
- Purfield, D.C (2015). Imputation accuracy from high density genotypes to whole genome sequence in cattle. *Agricultural Research Forum*, Tullamore p153
- Berry, D.P., Judge, M.,  and M. McClure (2015). High accuracy of imputation from the Irish custom bovine genotype panel to higher density genotypes. *Agricultural Research Forum*, Tullamore p154
- Berry, D.P, Buckley, F and Butler. S. (2015) Reducing replacement cost on Irish dairy farms. *Moorepark Open Day Booklet* 01/07/15
- Judge, M., McHugh, N., McParland, S., Kearney, J.F., and Berry, D.P. Genomic selection is delivering genetic gain in profit. *Moorepark Open Day Booklet* 01/07/15
- Purfield, D.C (2015) Exploiting Whole Genome Sequence. *TResearch Winter*
- Berry, D.P., (2015) Integration of genomic information into national cattle and sheep evaluations – past, present and future. *AAABG conference*
- Purfield, D.C, McClure, M and Berry, D.P. (2016). The impact of call rate on genotype accuracy. *ADSA-ASAS Joint Annual Meeting*.
- Purfield, D.C, MacLeod, I., Hayes, B. J., Butler, S.T, Moore, S.G..Moran, B., Kearney, J.F. and Berry, D.P. (2016). The use of Bayesian methods, biological priors and sequence variants to identify genomic regions associated with dairy cow fertility. *International society for animal genetics conference*
- Purfield, D.C, McClure, M and Berry, D.P. (2016). Justification for setting individual animal genotype call rate threshold at 85%. *European Association for Animal Production* p342
- Purfield, D.C, Wall, E and Berry, D.P. (2016). Runs of homozygosity profiles in five sheep breeds. *European Association for Animal Production* p167
- Carthy, T.R, Purfield, D.C, McClure, M and Berry, D.P. (2016). Characteristics of haplotypes in a multi-breed dairy and beef cattle population. *European Association for Animal Production* p343
- Carthy, T.R, Evans, R.D, and Berry, D.P. (2016) Refining cattle breed proportion using genomic data. *European Association for Animal Production*
- McHugh, N., Purfield, D.C, Kearney, J.F, Cromie, A.R, and Berry, D.P.(2017) Genomic evaluations-Maximising genetic gain. *Moorepark Open Day booklet* 04/07/2017
- Purfield, D.C, Evans,R.D., and Berry, D.P. (2018) GWAS using imputed sequence data for fertility related traits in dairy and beed cattle. *World Congress on Genetics Applied to Livestock Production 2018*
- Purfield, D.C and Berry, D.P.(2018). Genomics of Animal Stature. *Tresearch Summer*

(iii)    National Report

(iv)    Workshops/seminars at which results were presented
- Project Team. Genomics-a new era for cattle breeding: Portlaoise 14 Nov 2012
- Berry D.P Canadian Simmental Conference. 01/07/2013
- Berry, D.P., et al., Canadian Simmental conference      01/07/13
- Berry, D.P., et al., Grassland Alliance meeting   25/07/13
- Berry, D.P., et al., Blonde d'Acquitine breed society meeting      10/05/13
- Berry, D.P., et al., Joint IRL-UK Angus society meeting  18/03/13
- Berry, D.P., et al., Munster AI group   24/01/13
- Berry, D.P., et al., Irish Angus meeting 24/01/13
- Berry, D.P., et al., Irish pedigree council meeting 09/01/13
- Berry, D.P. INIAC, Urguary, Genomic research in Ireland .01/04/14
- Berry, D.P.  Dawn Dally visitor Genomics and breeding research in Ireland. 14/04/14
- Berry, D.P. IDB user group meeting. Update on IDB developments 04/06/14
- Berry, D.P. SRUC meeting. Beef genomic research update 09/06/14
- Berry, D.P. ABP. Beef genetics & genomics research update 10/06/14
- Berry, D.P.  Scottish NFU. Update on beef genetics and genomics research and plans 07/08/14
- Berry,D.P Beef genomics scientific advisory group. Update on beef genomics research 19/08/14
- Berry,D.P. Bord Bia, Results of using genomics in breeding. 28/08/14
- Berry,D.P. FBD advisors. Genomics in breeding. 04/09/14
- Berry,D.P. Teagasc discussion group, killmallock mart. Breeding (including genomics) of profitable cattle
- Berry,D.P. IDB user group meeting. Update on the developments of the IDB chip. 21/10/14
- Berry, D.P.  NCBC conference. Genomic selection in Ireland 14/10/15
- Berry, D.P.  Farmer group, Moorepark. Past present and future of genomic selection in Ireland 16/09/15
- Berry, D. P. Farmer group, Moorepark. Past present and future of genomic selection in Ireland 07/09/15
- Berry, D.P  Australasian dairy science symposium. Breeding the cow for the future - what do we need 19/11/14
- Berry, D.P Beef inservice training update on beef genomics 25/02/15
- Berry, D.P Inservice training.  Past present and future of genomic selection in Ireland 23/06/15
- Berry, D.P International group Moorepark.Past present and future of genomic selection in Ireland. 16/06/15
- Berry, D.P.  Trade mission to Russia. Past present and future of genomic selection in Ireland. 19/05/15
- Berry, D.P. Beef herdbooks meeting. Update on beef genomics. 08/04/15
- Berry, D.P Professional dairy farm managers lectures. Past present and future of genomic selection in Ireland. 02/04/15
- Berry, D.P International group Moorepark. Past present and future of genomic selection in Ireland. 18/03/15
- Berry, D.P. Farmer discussion group.Past present and future of genomic selection in Ireland. 05/03/15
- Berry, D.P. UCD lecture. Past present and future of genomic selection in Ireland. 19/01/15
- Berry, D.P. Angus society. Update on major gene research. 25/05/15
- Berry, D.P & MacHugh D. Agricultural science association meeting. Update on genomics research. 01/05/15
- Berry, D.P Hermintage genetics. Update on the state of genomics research in Irish cattle 30/06/15
- Berry DP & Cromie AR. National beef genomics scheme review group. Update on research on beef genomics. 17/10/15
- Purfield, D.C.  CIT lecture Introduction to genomics. 21/11/16
- Purfield, D.C.  & M. M. McClure DNA in the Agri-Food Industry. Overview of genetics and genomics 15/12/15
- Berry, D.P.  Scientific advisory group meeting. Update on beef genomics. 05/11/15
- Berry, D.P.  Sheep breeders round table.  Research update on cattle genomics to sheep breeders 20/11/15
- Berry, D.P.  National dairy conference. Retrospective analysis of dairy genomics 08/12/15
- Berry, D.P. ICBF industry meeting. Update on genomics research 09/12/15

- Berry, D.P.  DNA workshop. Genomics research update to industry include DAFM.15/12/15
- Berry, D.P. Teagasc inservice training. Update on genomics research. 12/01/16
- Berry, D.P.  EU Simmental conference. Update on genomics research in Ireland. 17/01/16
- Berry, D.P.  Positive farmers conference. Retrospective analysis of dairy genomics and potential foR the future 13/01/16
- Berry, D.P. British cattle breeders conference. Potential of genomics in cattle breeding. 19/01/16
- Berry, D.P. Virginia show. Potential of genomics in cattle breeding. 26/02/16
- Berry, D.P. ICBF industry meeting. Update on genomics research. 29/01/16
- Berry, D.P.  Scientific advisory group meeting. Presented update on beef genomics. 10/02/16
- Berry, D.P.  SRUC meeting. Update on multi-breed genomics research in Ireland. 15/02/16
- Berry, D.P. Teagasc dairy inservice training. Performance of dairy genomics. 24/02/16
- Berry, D.P.  Teagasc beef inservice training for beef genomics scheme. Genomics in breeding 24/02/16
- Berry, D.P. Affymetrix seminar. Genomics research in Teagasc. 02/03/16
- Berry, D.P.  Nuffield scholars. Usefulness of genomics in cattle breeding. 08/03/16
- Berry, D.P.  ICBF industry meeting. Update on genomics research. 30/03/16
- Berry, D.P.  Discussion group. Dairy genomics. 01/04/16
- Berry, D.P.  ICBF industry meeting. Update on genomics research. 06/04/16
- Berry, D.P.  Discussion group. Dairy genomics. 08/04/16
- Berry, D.P.  Discussion group. Dairy genomics. 15/04/16
- Berry, D.P.  World Hereford conference. Usefulness of genomics in cattle breeding. 19/04/16
- Berry, D.P.  ICBF industry meeting. Update on genomics research. 17/05/16
- Berry, D.P. Eurogenomics. Update on genomics research. 09/06/16
- Berry, D.P.  Teagasc beef open day. Beef  genomics. 05/07/16
- Berry, D.P.  Joint animal science meetings. Update on genomics research. 19/07/16
- Berry, D.P.  World Limousin conference. Usefulness of genomics in cattle breeding. 21/08/16
- Berry, D.P. Scientific advisory group meeting. presented update on beef genomics. 25/08/16
- Cromie + berry. EAAP. irish beef genomics scheme. 29/08/16
- Berry, D.P. UCC lectures. genomics in agriculture. 28/09/16
- Berry, D.P. Teagasc national beef conference. Usefulness of genomics in cattle breeding. 04/10/16
- Purfield. D.C., Genetics Group, University of Missouri. Overview of Irish Agriculture and imputation to whole genome sequence. 28/03/2017
- Purfield. D.C., Beef Genomics Scientific advisory committee. Update on imputation to full sequence. 24/08/2017
- Purfield, D.C., Discussion Group. Benefits of Genotyping Female Cattle. 10/08/2017
- Purfield, D.C., Origin Green Ambassadors. Overview of animal breeding and genetics. 20/10/2017
- Purfield, D.C., Sheep Industry Meeting. Major Genes and GWAS. 18/04/2018
- Purfield, D.C., UCD Dairy Business. Introduction to Genomics. 01/04/2018
- Purfield, D.C., Russian Genomic Technology in Agriculture. Application of Genomic Technology to Irish Livestock. 31/05/2018

       (v)     Intellectual Property applications/licences/patents N/A
       (vi)   Other

Berry, D.P.  Ear to the ground TV. Presented details on potential of genomics. 26/11/15
Purfield, D.C., and Berry, D.P. Irish Times. Interview about Nature Genetics paper on stature. 01/03/2018
Purfield, D.C., That's Farming media website. Interview on career path. 21/06/2018

## 5.   Scientists trained by Project

Total Number of PhD theses:                                    0

Total Number of Masters theses:                                0

## 6.    Permanent Researchers

| Institution Name | Number of Permanent staff contributing to project | Total Time contribution (person years) |
|---|---|---|
| Teagasc | 1 | 1.4 |
| ICBF | 4 | 1.8 |
| **Total** | **5** | **3.2** |

## 7.    Researchers Funded by DAFM

| Type of Researcher | Number | Total Time contribution (person years) |
|---|---|---|
| Post Doctorates/Contract Researchers | 1 | 3.4 |
| PhD students | 0 | |
| Masters students | 0 | |
| Temporary researchers | 0 | |
| Other | 0 | |
| **Total** | **1** | **3.4** |

## 8.    Involvement in Agri Food Graduate Development Programme

| Name of Postgraduate / contract researcher | Names and Dates of modules attended |
|---|---|
| Deirdre Purfield | How to write successful grant applications, 2015 |
| Deirdre Purfield | Statistics for Agri-Food Researchers-UCC, 2016 |
| Deirdre Purfield | Preparing for recruitment, May 2016 |

## 9.    Project Expenditure

Total expenditure of the project:                               € 345,605.30

Total Award by DAFM:                                            € 376,735.00

Other sources of funding including benefit in kind and/or
cash contribution(specify):                                     € 0

Breakdown of Total Expenditure

| Category | Teagasc | ICBF | Name Institution 3 | Name Institution 4 | Total |
|---|---|---|---|---|---|
| Contract staff | | | | | |
| Temporary staff | | | | | |
| Post doctorates | 158,501.25 | | | | 158,501.25 |
| Post graduates | | | | | |
| Consumables | 2,341.68 | | | | 2,341.68 |
| Travel and subsistence | 22,236.99 | 7,524.83 | | | 29,761.82 |
| Sub total | 183,079.92 | 7,524.83 | | | 190,604.75 |
| Durable equipment | 6,039.36 | | | | 6,039.36 |
| Other | | 101,310.00 | | | 101,310.00 |
| Overheads | 45,769.98 | 1,881.21 | | | 47,651.19 |
| **Total** | **234,889.26** | **110,716.04** | | | **345,605.30** |

## 10. Leveraging
Funding has been received for new projects on the back of the data and skills developed in this project including:
GenTORE – H2020 – Berry is WP leader
SMARTER – H2020 – Berry is WP co-lead
VistaMilK Centre – SFI – Berry is director

## 11.    Future Strategies
Genetic evaluations using BLUP have been actively researched for the past 70 years with improvements continually being observed. The same will be true for genomic evaluations. It was originally thought that one-step genomic evaluation would be relatively easy to

implement but the exponential increase in numbers of animals genotyped have questioned the scalability of such evaluations. Approaches to circumvent the necessity to invert the genomic relationship matrix are well underway and will continue.  Also, the complex models used in especially the Irish beef genetic evaluations do not lend themselves easily to one-step genomic evaluations. Research is currently underway to reduce the complexity of the models without sacrificing much in accuracy. The algorithms developed in selecting SNPs for use in genotyping platforms is now being developed for sheep populations.

## 12.    Consent to Publish Final Report on the DAFM Website and/or Through Other Dissemination channels

I consent to this report being made available to the public, through the Department's website and other dissemination channels.

Yes    X                    No       ☐

## 13.    Declaration

I declare that the information contained in this final report is complete and true to the best of my knowledge and belief.

Signed:                                 Project Coordinator

Date:          08/09/2018