THE GLOBAL STANDARD FOR LIVESTOCK DATA

DNA Working Group Webinar Meeting
Monday, 20 February 2017
(15h00 Paris time)

AGENDA

1. Call to Order - Brian Van Doormaal
2. Roll Call of Participants
3. Appointment of Meeting Recorder (seeking volunteer(s) from among WG members)
4. Review of Agenda
5. Summary of Previous Meeting held January 9, 2017
6. ICAR Accreditation for DNA Data Interpretation Centres (Attachments)
   - 6.1 CDN Chile Paper - Parentage Analysis Services for Dairy Cattle in Canada
   - 6.2 Test Files Distributed to Experts for Parentage Analysis Accreditation
   - 6.3 ISAG Guidelines for Cattle Parentage Verification Based on SNP Markers
   - 6.4 Recommendation for Guidelines for Cattle Parentage Discovery Based on SNP Markers
   - 6.5 Draft ICAR Accreditation Application Form (Labeled as Annex V)
7. Status of GenoEx-PSE Service
   - 7.1 Database and Software Development at Interbull Centre
   - 7.2 Revisions to Service Agreement
8. Proposed Interbull Service for Exchange "Genetic Trait" Codes Based on Genetic Tests
9. Emerging DNA Technologies
   - 9.1 Gene Editing (attachments)
10. Future Meetings
    - 10.1 Webinar meetings on 21 April and 19 May at 15h00 Paris time
    - 10.2 Live meeting during ICAR meetings in Edinburgh, Scotland (attachment)
11. Summary of Actions
12. Adjournment

Parentage Analysis Services for Dairy Cattle in Canada

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Abstract

Since the implementation of genomic evaluations in 2009, Canadian Dairy Network (CDN) has used SNP genotypes to verify the reported parents if genotyped and, when missing or incorrect, to discover the animal's sire and/or dam based on all existing SNP genotypes. To date, for breeds with official genomic evaluations in Canada, CDN has over 1.4M genotypes including 1.2M Holstein, 163,000 Jersey, 29,000 Brown Swiss, 6,000 Ayrshire and 3,000 Guernsey. These genotypes involve 23 different genotype panels, including low (3K-30K), medium (44K-140K) and high (over 600K) density. For parentage analysis, a list of 2,683 SNP in common from the 3K and 50K genotype panels are used as the basis for parentage verification, parentage discovery and for identifying families of genetically identical animals. Using the list of SNP proposed for inclusion in GenoEx-PSE for parentage verification (200) and parentage discovery (additional 675 or 354), it was concluded that the 200 SNP recommended by ISAG for parentage verification performed very well compared to the SNP routinely used by CDN for dairy cattle breeds in Canada. It was also concluded that parentage discovery using either set of additional 675 or 354 SNP also provided accurate results. To avoid a possible misuse of the additional SNP for parentage discovery, the reduced set of 354 SNP, selected from only 10 chromosome, are recommended for GenoEx-PSE due to the higher level of imputation error and lower accuracy of GEBV estimation compared to results based on the additional 675 SNP.

Key words: SNP parentage analysis, parentage verification, parentage discovery, GenoEx-PSE

Introduction

The International Committee of Animal Recording (ICAR) plans to introduce a new service effective early 2017, referred to as GenoEx-PSE (**P**arentage **S**NP **E**xchange). This service will be offered through the Interbull Centre and aims to facilitate the international exchange of SNP genotypes for the purpose of parentage analysis in dairy and beef cattle populations.

Within the context of GenoEx-PSE, parentage analysis consists of three principle processes:

- Parentage Verification - The process by which the SNP genotypes of the recorded parents (sire and/or dam) of an animal are examined relative to the SNP genotype of the animal to determine if one or other does not qualify as a parent.
- Parentage Discovery - The process by which a set of SNPs from an animal's genotype are compared to a database of SNP genotypes for older animals in order to identify the most likely sire and/or dam, if not already confirmed by Parentage Verification.
- Microsatellite Imputation - The process by which the microsatellite (STR) profiles of an animal may be imputed from SNP genotypes and the resulting SNP genotype is used for the purpose of parentage verification.

A fundamental component of the service is the establishment of a standard set of SNP to be included in the exchange process. The GenoEx-PSE service agreement offers flexibility for the service user to define its level of participation, which then defines the list of SNP to be routinely uploaded to the GenoEx-PSE database at the Interbull Centre and therefore also the list of SNP that are accessible for downloading. The basic level of participation includes the exchange of the 200 SNP (Group A) recommended by the International Society for Animal Genetics (ISAG) for parentage verification in cattle. A second level of service includes the exchange of additional SNP (Group B) to provide more accurate results for parentage discovery. The third level of participation includes another group of SNP (Group C) required for the imputation of microsatellite profiles from the SNP genotypes.

Prior to the official implementation of GenoEx-PSE, ICAR and the Interbull Centre published the proposed list of SNP to be included in each of Groups A, B or C. Interested countries were encouraged to assess these SNP in terms of application for parentage analysis within their national breed populations. Therefore, the objectives of this research include: (a) quantify the minor allele frequency (MAF) of the SNP in Groups A and B within each of the five dairy breed populations with genomic evaluations in Canada, (b) compare official parentage analysis results at Canadian Dairy Network (CDN) with those that would have resulted based on the SNP in either Groups A or B, and (c) examine the accuracy of imputation from SNP profiles based on Groups A and B to 50K genotypes and the accuracy of genomic breeding value (GEBV) estimation based on these GenoEx-PSE SNP.

Data and Methods

Given the SNP recommended by the International Society for Animal Genetics (ISAG) for parentage verification have been widely accepted and used by various organizations, GenoEx-PSE defined the same 200 SNP within Group A. The distribution of these SNP across chromosome 1 to 29 is presented in Table 1 and shows a range from 4 to 11 on all these chromosome. For the Group B SNP, an initial proposal for GenoEx-PSE included a total of 675 SNP with 75 defined by work in Australia and 600 based on research in United States and Ireland (McClure, 2015).

Later, the list of SNP in Group B was reduced by limiting the initial set defined by McClure to include only those from the ten chromosome that had the most, specifically chromosome 1, 2, 3, 5, 7, 8, 11, 13, 19 and 21. These two SNP groups are labelled as B-675 and B-354, respectively (Table 1). For Group C, a list of 980 SNP were selected (McClure, 2015) that are densely located near the 12 short-tandem-repeat (STR) on chromosome 1, 2, 3, 5, 9, 15, 16, 18, 19, 20, 21 and 23 that have been used for microsatellite parentage verification globally for many years (Table 1).

Table 1. SNP count by chromosome (Chr) for each group in GenoEx-PSE.

Chr	Group*				Total (675)	Total (354)
	A	B-675	B-354	C		
1	11	40	40	70	121	121
2	9	42	42	80	131	131
3	8	32	32	110	150	150
4	9	22	4		31	13
5	9	33	33	90	132	132
6	8	17	2		25	10
7	11	26	26		37	37
8	6	31	31		37	37
9	6	19	3	110	135	119
10	9	24	2		33	11
11	10	27	27		37	37
12	5	21	3		26	8
13	6	30	30		36	36
14	5	20	1		25	6
15	7	14	3	40	61	50
16	5	21	1	80	106	86
17	9	24	2		33	11
18	7	23	2	40	70	49
19	8	27	27	80	115	115
20	5	16	5	120	141	130
21	8	25	25	80	113	113
22	7	20	1		27	8
23	4	16	2	80	100	86
24	4	24	2		28	6
25	4	18	2		22	6
26	4	17	2		21	6
27	6	14	1		20	7
28	6	16	1		22	7
29	4	16	2		20	6
Total	**200**	**675**	**354**	**980**	**1,855**	**1,534**

** - Group A = SNP for parentage verification, B = SNP added for parentage discovery and C = SNP added for microsatellite imputation.*

Minor Allele Frequency

The value of a SNP for parentage analysis is highly dependent upon its minor allele frequency (MAF) within the population of animals in question. SNP with low MAF will have more limited value for parentage analysis since only homozygous genotypes in both parent and progeny are informative. The SNP defined in Groups A and B for GenoEx-PSE

were selected based on MAF within several dairy and beef cattle breeds with genotypes at the Irish Cattle Breeding Federation (ICBF) in Ireland. Given that CDN offers genomic evaluation services in the Ayrshire, Brown Swiss, Guernsey, Holstein and Jersey breeds in Canada, all genotypes available for each of these breeds were used to estimate the MAF of each SNP proposed for Group A and Group B-675. Since Group B-354 is a subset of those included in B-675, the analysis was not repeated based solely on this reduced SNP. This analysis serves as a general indication of how well the SNP could perform for parentage analysis.

Comparison of Parentage Analysis Results

As part of the routine processing at CDN to produce Canadian genomic evaluations for each breed, CDN has implemented an internal process to carry out parentage verification as well as parentage discovery, when needed. The genotypes at CDN currently involve 23 different genotype panels, including low (3K-30K), medium (44K-140K) and high (over 600K) density. For parentage analysis, a list of 2,683 SNP in common from the 3K and Illumina 50K genotype panels are used as the basis for parentage verification, parentage discovery and for identifying families of genetically identical animals. In order to compare results for parentage verification based on the 2,683 SNP routinely used by CDN versus either (a) the 200 ISAG SNP in Group A or (b) the combination of Group A and Group B-675 SNP, the genotypes of 5,372 Ayrshire, 23,144 Brown Swiss, 1,771 Guernsey, 573,988 Holstein and 63,248 Jersey animals were included in each analysis.

To define a SNP parentage conflict within the routine process at CDN, a maximum limit of 2% conflicts among informative SNP is allowed prior to excluding the recorded parent. For the analysis using the Group A SNP, the published guidelines established by ISAG for parentage verification analysis in cattle (ISAG, 2012) were applied. For the Group B-675 SNP some rules based on number of conflicts, similar to the ISAG guidelines for the 200 SNP in Group A, were established and applied. To compare the results across the three sets of SNP, the process was applied only for conducting parentage verification of the recorded sire and the cases that led to differing results were assessed in more detail.

To compare results of parentage discovery between the routine CDN process and one that would be limited to include Group B-675 or Group B-354, in addition to Group A, known parentage information was removed for a group of 26,691 animals across the five breeds that were born in recent years. In this manner, the three sets of SNP applied for parentage discovery can be compared to each other.

Accuracy of Imputation and Estimation of Genomic Breeding Values

The exchange of SNP genotypes via GenoEx-PSE is restricted for the use of parentage analysis only. Nonetheless, it is valuable to verify the level of accuracy that could be achieved for genomic prediction if the exchanged SNP were used in such a manner by any service user of GenoEx-PSE. To assess this objective the 50K genotypes for a group of 27,324 Holsteins born in 2016 were reduced to include either (a) 200 ISAG SNP in Group A, (b) Group A and Group B-675 SNP, or (c) Group A and Group B-354 SNP. The FImpute software (Sargolzaei, 2014) used routinely at CDN for imputation of all genotypes to 50K genotypes was applied to the reduced genotypes of the Holsteins selected for analysis. After imputation, the routine genomic evaluation system at CDN, based on GBLUP methodology (VanRaden, 2008), was applied to all genotyped Holsteins to estimate Direct Genomic Values (DGV) for each of the selected animals born in 2016.

Imputation error was quantified by comparing each animal's imputed 50K genotype based on each of the three subsets of SNP available for imputation to the 50K genotype used for the routine evaluation at CDN. Similarly, simple correlations among resulting GEBV were used to assess the accuracy of genomic breeding value (GEBV) estimation based on each subset of SNP considered for GenoEx-PSE.

Results and Discussion

Minor Allele Frequency (MAF)

Table 2 shows the average MAF of the SNP included in Groups A (n=200) and B-675 (n=675) as proposed for exchange within GenoEx-PSE for parentage verification and discovery, respectively.

Table 2. Average minor allele frequency of GenoEx-PSE SNP groups.

Breed	Group A	Group B-675
Ayrshire	0.342	0.343
Brown Swiss	0.352	0.353
Guernsey	0.322	0.322
Holstein	0.391	0.381
Jersey	0.291	0.316

Table 3 provides the percentage of the SNP in each group that have a MAF of at least .30 within each of the five dairy cattle breeds with genomic evaluations in Canada.

Table 3. Percentage of GenoEx-PSE SNP with minor allele frequency ≥.30.

Breed	Group A	Group B-675
Ayrshire	66.0%	69.4%
Brown Swiss	70.0%	73.2%
Guernsey	60.5%	62.8%
Holstein	83.5%	81.0%
Jersey	51.0%	58.0%

Results from these tables indicate that the proposed SNP for GenoEx-PSE can be expected to perform well for parentage analysis, noting that the Jersey breed has the lowest average MAF and lowest percentage of SNP with a minimum MAF of .30. Even here, of those with MAF ≥.30, there are at least 100 of the 200 SNP in Group A for parentage verification and a total of almost 500 when combining Group A and Group B-675 for parentage discovery.

Comparison of Parentage Analysis Results

For sake of brevity, results for only the Holstein breed are presented. Of the 573,988 animals included in the analysis for assessing if the reported sire can be verified, a total of 558,828 (97.4%) did not have any SNP conflicts in any of the analyses conducted, leaving a total of 15,160 animals for the further assessment. Table 4 provides a summary of the parentage verification results based on the 200 SNP in Group A for GenoEx-PSE versus the list of 2,683 SNP used routinely by CDN.

Table 4. Comparison of parentage verification results when using Group A SNP versus the 2,683 SNP used in Canada.

Group A Conflicts*	CDN Result		
	Conflict	Verified	Total
0	1	9,067	9,068
1		3,306	3,306
2	3	126	129
3	3	11	14
4	2		2
5	4	2	6
6	8		8
7	9		9
8	22		22
9	27		27
10	52		52
>10	2,517		2,517
Total:	**2,648**	**12,512**	**15,160**

** - 0-3 conflicts = Parent accepted, 4-5 = Parent in doubt, >5 = Parent excluded.*

The CDN process identified a total of 2,648 animals with a sire parentage conflict of which seven were found to have three or fewer conflicts based on the Group A SNP alone. Among the remaining 12,512 animals for which the CDN process verified the reported sire, all but two received the same status based on Group A SNP, having 3 or less conflicts. These results show that using the Group A SNP for parentage verification yield results that are 99.9984% consistent with the official CDN results studied (558,819 out of 558,828), which translates to differences for 16/1,000,000.

Table 5. Comparison of parentage verification results when using Group A (ISAG 200) as well as Group B-675 SNP versus the 2,683 SNP used in Canada.

Group A and B-675 Conflicts	CDN Result		
	Conflict	Verified	Total
0	1	274	275
1		11,153	11,153
2		892	892
3		137	137
4		41	41
5		8	8
6	2	4	6
7			
8	2	1	3
9		2	2
10			
>10	2,643		2,643
Total:	**2,648**	**12,512**	**15,160**

The GenoEx-PSE service also allows the user to participate at a level that includes the exchange of SNP genotypes for the purpose of parentage discovery in addition to parentage verification. The analysis examined any differences found in terms of discovering a valid sire for each of the 26,691 animals included. The sire considered to be discovered was the male that had the fewest SNP conflicts among those with less than 1% conflicts based on the informative SNP each sire had with the animal in question. Technically, 99.865% of the discovered sires based on using SNP from Groups A and B-675 were the same as the results based on the full set of 2,683 SNP routinely used by CDN. That said, in all other cases but one the two SNP groups ended up with different males discovered as the sire but they were identical twins. Only one case resulted in the two processes identifying full brothers as the discovered sire, which translates to a concordance rate of 99.996% in terms of discovering the correct genotype as the animal's sire. In practise, any parentage discovery procedure would have to include pre- and/or post-processing for handling genetically identical parents in addition rules associated with birthdates to avoid discovering a progeny as a potential parent.

Based on the comparative results of parentage verification and parentage discovery carried out in this study, there is no reason to not accept the use of the 200 SNP recommended by ISAG for parentage verification and the additional B-675 SNP for parentage discovery as the basis of the SNP genotype exchange for GenoEx-PSE.

Accuracy of Imputation and Estimation of Genomic Breeding Values

A key step in the calculation of GEBV is the imputation of genotypes from lower density panels to the current international standard of using 50K genotypes. More importantly, however, is the accuracy of any GEBV estimated using such imputed genotypes. Initially, the intent was simply to quantify imputation accuracy (i.e.: error rates) and GEBV correlations that would be derived from genotypes that only included SNP from Groups A and B-675. During the course of the research, it was decided to repeat the analysis using SNP from Groups A and B-354 (reduced set from Group B-675) and from Group A alone. Table 6 presents the distribution of animals by the level of imputation error for the group of 27,324 Holsteins born in 2016 that had their 50K genotype reduced to include only the three subsets of SNP considered for use by GenoEx-PSE. As expected, the overall level of the imputation error increased as the number of SNP included decreased. In fact, all animals but one had an imputation error of at least 5% when only Group A (200 ISAG) SNP were used. Of particular interest is the important difference in imputation accuracy when the SNP from Group B-354 were added to Group A rather than those from Group B-675, which reduced the percentage of animals with less that 5% imputation error from roughly 66% to 13% (Table 6). This loss in imputation accuracy with B-354 is due to the fact that over 80% of those SNP are located on only 10 of the chromosome so relatively little information is available for imputation of SNP on the other chromosome.

Table 6. Percentage of animals by level of imputation error when SNP from three different groups defined for GenoEx-PSE were used to impute to a 50K genotype (n=27,324).

Imputation Error	Group A	Groups A and B-354	Groups A and B-675
0 - 4.99%	0.004%	12.919%	65.840%
5 - 9.99%	18.167%	54.231%	6.822%
10 - 14.99%	47.003%	3.594%	7.880%
15 - 19.99%	4.271%	4.853%	10.240%
20 - 24.99%	2.302%	9.852%	5.610%
25 - 29.99%	5.991%	7.678%	2.049%
30 - 34.99%	9.896%	4.531%	1.215%
35 - 39.99%	5.406%	1.998%	0.307%
40 - 44.99%	6.024%	0.326%	0.026%
45 - 49.99%	0.926%	0.018%	0.011%
50 - 54.99%	0.011%	0.000%	0.000%
Total	**100%**	**100%**	**100%**

In terms of assessing the accuracy of the second step, namely the estimation of GEBV, it is important to recognize there are two key components to a GEBV. In Canada, GEBV is calculated as a combination of the animal's traditional EBV (or Parent Average) and its Direct Genomic Value (DGV) derived by GBLUP, weighted by the relative estimated reliability of each value. Given that EBV/PA is constant for each animal, the analysis conducted here focused on the impact on the DGV resulting from the genotypes imputed from the three sets of SNP considered for GenoEx-PSE. Table 7 provides various correlations with the DGV of the official evaluation published by CDN for one of Canada's national selection indexes, the Lifetime Performance Index (LPI). Even with the use of only the 200 SNP recommended by ISAG for parentage verification (Group A) for imputation and GEBV estimation, a correlation of 0.87 was obtained with the DGV of the official evaluation published by CDN. While this may be considered reasonably high, this approach shows no improvement in accuracy compared to what would be obtainable simply by knowing the animal's pedigree for calculation of its Parent Average, which also yielded a correlation of 0.87 in this study (Table 7).

Table 7. Correlation between the official Direct Genomic Value (DGV) for Lifetime Performance Index (LPI) and DGV resulting from 50K genotypes imputed using three subsets of SNP considered for GenoEx-PSE.

SNP Used for Imputation to a 50K Genotype	Correlation with Official DGV
No genotype available, only pedigree*	0.87
Group A (n = 200)	0.87
Groups A and B-354 (n = 554)	0.92
Groups A and B-675 (n = 875)	0.96

** Correlation between the animal's Parent Average without any genotype and the official DGV.*

When SNP added for parentage discovery within the GenoEx-PSE service were included in the analysis, the correlation with the official DGV increased to 0.92 for Group B-354 and to 0.96 for Group B-675 (Table 7). This resulting correlation for Group B-675 is considered too high to use this set of SNP within the GenoEx-PSE service. The lower correlation of 0.92 for Group B-354 provides a better balance between accuracy of parentage discovery and obtaining only a moderate level of accuracy for GEBV estimation, which is a prohibited use of the genotypes exchanged according to the GenoEx-PSE service agreement. In addition, the level of GEBV accuracy that was obtained in this study from the imputation of SNP from Groups A and B-354 to derive 50K genotypes is highly dependent upon having a large population of ancestors that have a 50K genotype available for accurate imputation. For this reason, any such misuse of the SNP genotypes exchanged within GenoEx-PSE will not be beneficial even if not prohibited.

Conclusions

From the results of this analysis, based on genotypes available in Canada for five dairy cattle breeds, the following conclusions can be drawn:

1. An analysis of the within breed minor allele frequency of the SNP proposed for exchange within GenoEx-PSE did not reveal any

concerns with the potential use of such SNP for parentage analysis in the Ayrshire, Brown Swiss, Guernsey, Holstein and Jersey populations with genotypes at CDN in Canada.

2. The 200 SNP recommended by ISAG for parentage verification in cattle populations performed very well with results highly consistent with those based on roughly 2,600 SNP that have routinely been used by CDN. These SNP should be included in the GenoEx-PSE exchange of genotypes for parentage verification.

3. For parentage discovery, two possible sets of SNP were analyzed in addition to the ISAG 200 SNP for parentage verification, referred to as Groups B-675 and B-354. The latter set includes a subset from B-675 with 80% being from only 10 chromosome. This study found that both sets perform very well for parentage discovery compared to the larger set of roughly 2,600 SNP used by CDN.

4. The comparison of imputation error rates and accuracy of GEBV estimation showed that the use of SNP from Groups A and B-354 was most desired for accurate parentage discovery analysis without resulting in high levels of accuracy of imputation to 50K genotypes and estimation of GEBV.

References

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ISAG INTERNATIONAL SOCIETY FOR ANIMAL GENETICS

Guidelines for cattle parentage verification based on SNP markers

Approved at ISAG conference in Cairns, July 2012

SNP profile:

Minimum number of SNPs in reference core panel (published in ISAG WEB site): 100
Minimum number of SNPs available in profile: 95
(If less than 95 SNPs can be scored, retest the sample or request a new sample).

If mismatches occur in a supposed parentage, the general rule is to first retest the samples involved or request new samples to confirm the determined genotypes. If the genotypes are confirmed the following guidelines are suggested.

Case with offspring and one parent tested
Minimum number of common SNPs in verification offspring: 90
Number of mismatches*: 0-1 -> parentage accepted
Number of mismatches*: 2-3 -> parentage doubtful, backup panel required**
Number of mismatches*: >3 -> parentage excluded.
*: example: offspring = GG, sire = AA
**: When the parentage is doubtful, first genotype the samples with both panels (ISAG and backup). If results remain doubtful, ask customer for the other given parent and or another candidate parent. If there are no other possible parents, then qualify the parentage.

Case with offspring and both parents tested
Minimum number of common SNPs in verification offspring: 85
Number of mismatches*: 0-2 -> parentage accepted
Number of mismatches*: 3-4 -> parentage doubtful, backup panel required**
Number of mismatches*: >4 -> parentage excluded.
*: example: offspring = AG, sire = AA, dam = AA
**: When the parentage is doubtful, first genotype the samples with both panels (ISAG and backup). If results remain doubtful, ask customer for other possible parents. If there are no other possible parents, then qualify the parentage.

In any case, it is recommended that samples be retested if there is parentage exclusion with ISAG and/or back up panels.

ACTIVITY AREA REFERENCE DOCUMENT

CERTIFICATION SERVICES – GENETICS
ICAR Accreditation of DNA Data Interpretation Centres

Doc number	05_CER_GNTX_0003
Author	Martin Burke
Date First Draft	19th July 2016

Latest revision author	Martin Burke (for discussion with input from Brian Van Doormaal, Toine Roozen, Andie Dimitriadou, Brian Wickham)
Latest revision date	26th September 2016

PURPOSE

ICAR offers two separate areas in Accreditation for Organisations involved in DNA analysis and interpretation ;

1) ICAR Accreditation of laboratories (so called wet labs) who analyse biomaterial to produce DNA Genotypes (DNA Data) and is described in ICAR SOP 05_CER_GNTX_0002.

2) ICAR Accreditation of **DNA Data Interpretation Centres** who take the DNA Data from the 'wet labs' in 1) above and interpret the data for a number of purposes as is described in this ICAR SOP 05_CER_GNTX_0003.

DNA Data Interpretation covered by this accreditation procedure includes applications for;

1. Parentage verification
2. Parentage discovery
3. Microsatellite imputation from SNPs (will not be part of the initial offering in 2016)
4. Animal identification verification.

For definitions see the 'Terms & Definitions' table below and for further technical background see ICAR Guidelines Section 4 – Guideline B.

SCOPE

This SOP concerns the Organisations involved in DNA analysis and interpretation, the DNA Working Group, the Interbull Centre, the ICAR Secretariat and Service-ICAR. Given that it is a commercial activity, it is also related to area 02_ADM (Admin/Finance).

TERMS & DEFINITIONS

Term	Definition
Animal Identification verification	The process by which a DNA analysis of a tissue sample is used to determine if the sample can be excluded as originating from a particular animal.
DNA Data Handling and Interpretation Test	This is a prerequisite compliance test which each DNA Data Interpretation Centre Applicant has to pass before ICAR Accreditation can be granted. ICAR's reference institute sends a predetermined set of SNPs to the Applicant with a series of accompanying animal and/or parentage analysis tasks to complete. The Applicant is asked to complete the interpretation tasks and return the required answers/results which are then assessed by ICAR's reference institute. Applicants must pass this assessment to gain Accreditation status.
ICAR accreditation	Formal Recognition by ICAR that an organisation has provided sufficient evidence that it has the competency, authority and experience to conduct DNA data interpretation for the purposes outlined in this Standard Operation procedure.
MAF	Minor allele frequency.
Microsatellite	Refer to definition of STR in this table.
Microsatellite imputation from SNPs	The process by which the microsatellite (STR) profiles of an animal may be imputed from SNP genotypes for the purpose of parentage verification.
Parentage discovery	The process by which a set of SNPs from an animal's genotype are compared to a database of SNP genotypes for older animals in order to identify the most likely sire and/or dam, if not already confirmed by Parentage Verification.
Parentage verification	The process by which the genotypes of the recorded parents (sire and/or dam) of an animal are examined relative to the genotype of the animal to determine if one or other does not qualify as a parent.
SI	Service ICAR
SNP	Single nucleotide polymorphism
SOP	Standard Operating Procedure in ICAR
STR	Abbreviation for short-tandem-repeat and commonly referred to as a microsatellite.

RESPONSIBILITIES

Services Executive: Administration of the Accreditation Applications in Service-ICAR for applicant DNA Data Interpretation Centres.
Administration Executive: Contractual and financial transactions between the Accredited DNA Data Interpretation Centres, the Interbull Centre and Service-ICAR.
Information Executive: Maintenance of ICAR web listing of Accredited DNA Data Interpretation Centres.
DNA Working Group (WG): Maintenance of Guidelines, policies as well as review and approval / rejection of Accreditation Applications (including design of the 'DNA Data Handling and Interpretation Test'.
Interbull Centre: Provide SNP database exchange and validation service for 'DNA Data Handling and Interpretation Test'.

PROCEDURE

ICAR Accreditation of Centres Performing DNA Data Interpretation

The DNA Data Interpretation Centre Accreditation process comprises the following steps:

1. Application for accreditation.
2. Review of application.
3. Data handling and interpretation test
4. Granting of accreditation and on-going compliance monitoring.

1. Application

Organisations requesting DNA Data Interpretation Centre Accreditation from ICAR must apply by downloading, filling in and submitting the Application form and administration fee to ICAR. The Application form will be found in Annex V Guidelines Section 4 and must be filled out accurately and completely, providing necessary documentation as required, and submitted.

2. Review of Application

The form will be evaluated by the Chair and/or nominated members of ICAR's DNA Working Group (WG). The DNA WG will review the application in line with criteria specified in the ICAR Guidelines, specifically in Section 4 Guideline B.

Based on this review and the successful passing of the 'DNA Data Handling and Interpretation Test' therein, the DNA WG shall either approve, request further information or reject the application through a letter from ICAR. In the case of rejection, ICAR advises that no resubmission is allowed within ninety days of the failed application. After the ninety days have elapsed then the Applicant is entitled to submit again.

3. DNA Data Handling and Interpretation Test

The DNA WG will define the DNA Data Handling and Interpretation Test protocol, quantity of SNPs, file exchange rules, pass/fail criteria, etc. This test will be outsourced to and coordinated by the Interbull Centre on behalf of Service ICAR. This test will be detailed as an Annex in our Guidelines.

4. Granting of accreditation and on-going monitoring

Notice of successful DNA Data Interpretation Centre Accreditation will be sent to the Organisation by ICAR and the Organisation's name will be added to ICAR's Website listing of Accredited DNA Data Interpretation Centres. To ensure the ongoing compliance of Accredited DNA Data Interpretation Centres, ICAR's reference centre will send, every two years, a version of the DNA Data Handling and Interpretation Test to each Centre. The Centre will return test files and their results will be assessed and filed as a record of ongoing compliance.

To maintain its Accreditation status, the DNA Data Interpretation Centre must participate in and pass all DNA Data Handling and Interpretation Tests.

Service ICAR Fees for Accreditation of DNA Data Interpretation Centres *(Under Proposal)*

Application Fee: Service ICAR have yet to announce fees for the Application and the two yearly compliance test – expected Quarter 4 2016.

RELATED DOCUMENTS

ICAR Guidelines Section 4 – Guideline B.
GenoEx-PSE Service Agreement
05_CER_GNTX_0002 ICAR Accreditation of DNA Analysis Laboratories (Wet Labs)
DNA Working Group Terms of Reference
Application Form Annex V Guidelines Section 4
Data Handling and Interpretation test protocol – Annex X Guidelines Section 4

Annex V *(19th August 2016)*

ICAR DNA Working Group
Application Form for Centres seeking ICAR Accreditation status for DNA Data Interpretation

To be returned by e-mail to: DNA@icar.org

---

1. APPLICANT ADDRESS DETAILS (fill out)

Country: .....

Organisation Name: .....

Organisation Dept.: .....

Contact person: .....

Address: .....

Telephone: .....

E-mail: .....

EU VAT no.....

or Tax Registration no. (For non EU applicants).....

2. ICAR MEMBER WHO NOMINATES APPLICANT CONTACT/ ADDRESS DETAILS (fill out) (N/A if Applicant in 1. is already an ICAR Member)

Country: .....

ICAR Member Organisation: .....

Contact person: .....

Address: .....

Telephone: .....

E-mail: .....

3. APPLICANT EDUCATION, TRAINING, AND EXPERIENCE OF EMPLOYEE RESPONSIBLE FOR CONDUCTING DNA DATA INTERPRETATION

a. Level of education of the head of the DNA Data Interpretation activities (tick the box and describe)

- ☐ Ph.D. in .....
- ☐ Masters of Science in .....
- ☐ Bachelors of Science in .....
- ☐ Other .....
- ☐ None

b. Experience of senior employee in conducting DNA Data Interpretation (tick)

- ☐ More than 5 years
- ☐ More than 2 years but less than 5 years
- ☐ Less than 2 years

Annex V *(19th August 2016)*

4. EXPERIENCE USING SNPS FOR DNA DATA INTERPRETATION

a. Describe briefly:

Overview of your Organisations SNP Parentage Analysis Software/Process (Cite scientific reference publications when available)

.....
.....
.....
.....

List key Customers of your existing DNA Data Interpretation Services and estimated annual volume for each in the table below;

DNA Data Interpretation Service	Customer	Annual Volume
1. Parentage verification		
2. Parentage discovery		
3. Microsatellite imputation from SNPs		
4. Animal identification verification		

Comments: .....
.....
.....
.....

Procedure and key statistics for error and repeatability checking (for SNP genotypes incoming and Parentage Analysis results outgoing) Define, Unresolved figures, Mismatches,

.....
.....
.....
.....

b. Other pertinent information to add? (describe)

.....
.....
.....
.....
.....
.....
.....
.....

Annex V *(19th August 2016)*

5. NAME & CERTIFICATION STATUS OF THE LABORATORIES WHICH PROVIDES THE DNA DATA TO YOUR CENTRE.

Table 1. The Top 5 Laboratories (by volume) supplying genotypes to your Centre.

Name of Lab supplying genotypes?	What % of your supply	% Call Rate	ISAG Accredited?	ICAR Accredited?

Other Comments re your source(s) of genotypes?

.....

.....

6. LEVEL OF ICAR ACCREDITATION FOR WHICH YOUR ORGANISATION IS APPLYING?

a. Please indicate to what level of DNA Data Interpretation (tick) you wish your Organisation to be listed (will be indicated on ICARs Accreditation Listing on our website):

☐ (1) Parentage Verification
☐ (2) Parentage Discovery
☐ (3) Microsatellite Imputation from SNPs
☐ (4) Animal Identification Verification

Note: Please tick each that applies to your application.

Applicant Name (Print):_____

Applicant Signature:_____ Date:_____

This Box for ICAR Office Use Only;

Application No.:

Date Rec'd:

Date To DNA WG:

Date Interbull Centre send out:

Date back from Applicant to Interbull

Interbull Pass/Fail:

Date Notification to Applicant:

NATURE | **NEWS**

Gene-edited animals face US regulatory crackdown

Last-minute proposal from Obama administration addresses CRISPR and other cutting-edge technologies.

Amy Maxmen

19 January 2017 Clarified: 19 January 2017

Michael Conroy/AP

Some dairy cattle have their horns removed, a practice that has raised animal-welfare concerns.

Researchers transforming animals with the latest genome-engineering tools may be disappointed by draft rules released by the US Food and Drug Administration (FDA) on 18 January — two days before US President Barack Obama leaves office. It is not clear how the administration of incoming president Donald Trump will carry the proposals forward, however.

The most controversial of three proposed regulations declares that all animals whose genomes have been intentionally altered will be examined for safety and efficacy in a process similar to that for new drugs.

Many researchers had hoped that the FDA would be less stringent about evaluating organisms whose genomes have been edited with precise tools — such as CRISPR and a separate technique called TALENs — than it is for animals that have been given DNA from different species or created using less-sophisticated

means. Alison van Eenennaam, an animal geneticist at the University of California, Davis, calls the draft FDA proposals “insane”.

“The trigger for their regulation is whether the animal was intended to be made, and what does intention have to do with risk?” she says. “The risk has to do with the attributes of the product.”

Related stories

- Gene-edited CRISPR mushroom escapes US regulation
- CRISPR: gene editing is just the beginning
- CRISPR tweak may help gene-edited crops bypass biosafety regulation

More related stories

Swimming upstream?

Some scientists, including van Eenennaam, are afraid that the proposed rules would prompt businesses, universities and non-profit organizations to abandon development of genetically engineered animals. They see a cautionary tale in the genetically engineered salmon created by AquaBounty Technologies in the early 1990s.

The company — based in Maynard, Massachusetts — spent US$60 million on developing the fish, an Atlantic salmon (*Salmo salar*) with genes from Chinook salmon (*Oncorhynchus tshawytscha*) that allow it to grow rapidly. But the firm had to wait 20 years for the FDA to review more than 50 studies demonstrating that the salmon posed no unusual risks before the agency approved the fish in November 2015. Even then, the salmon cannot be sold until the FDA decides whether it must be labelled as genetically modified.

AquaBounty’s story terrifies Scott Fahrenkrug, chief scientific officer at gene-editing company Recombinetics in St Paul, Minnesota. The firm has produced hornless dairy cattle by inserting a gene from naturally hornless beef cattle into a breed of the same species that is used in milk production. The animals could help to reduce the practice of surgical ‘dehorning’, a controversial practice that has raised animal-welfare concerns.

On 21 December, Recombinetics told the FDA that it intended to market food from its cows without FDA approval, and with a label reading ‘generally recognized as safe’. The company’s decision was bolstered by the US Department of Agriculture’s announcement in April 2016 that it would forgo regulation of a mushroom that has been genetically modified to resist browning. The agency said that the fungus, which was created using the CRISPR–Cas9 method, did not require approval because it did not contain genes from other species. Recombinetics’ cattle were also created without foreign genes, using TALENs.

Enter Trump

Fahrenkrug was taken aback by the FDA’s new proposal, and says that the agency has “gone off the rails”. “They’re suggesting that an already existing allele we have been eating for thousands of years now needs to be evaluated for risk because we’ve intentionally put it into this cow’s genome,” he says.

The company plans to protest against the agency’s plan to the incoming administration of president-elect Donald Trump, which will oversee finalization of any new regulations. The draft regulations will be open for public comment until 19 April, and the FDA may modify its approach according to the feedback it receives.

Others welcomed the Obama administration's last-minute overture. "The public is leery of genetic engineering of animals, in particular," says Jennifer Kuzma, a social scientist at North Carolina State University in Raleigh. "With gene editing we do see off-target effects, so it is wise on the part of the FDA to include all of these organisms in the near term while they build up data."

But having had her own transgenic projects frozen in the past owing to arguably baseless fears from the public and regulators, van Eenennaam disagrees. "Because of measures like this, almost everything in genetic engineering will have to be done by huge multinational companies," she says. "If the scientific community doesn't stand up and say this is crazy, we've done a disservice to innovation."

Nature doi:10.1038/nature.2017.21331

Clarifications

Clarified: The story has been updated to reflect that Jennifer Kuzma is a social scientist.

Related stories and links

From nature.com

- **Gene-edited CRISPR mushroom escapes US regulation**
  14 April 2016
- **CRISPR: gene editing is just the beginning**
  07 March 2016
- **CRISPR tweak may help gene-edited crops bypass biosafety regulation**
  19 October 2015
- **CRISPR, the disruptor**
  03 June 2015
- **Seeds of change**
  08 April 2015
- **US regulation misses some GM crops**
  20 August 2013

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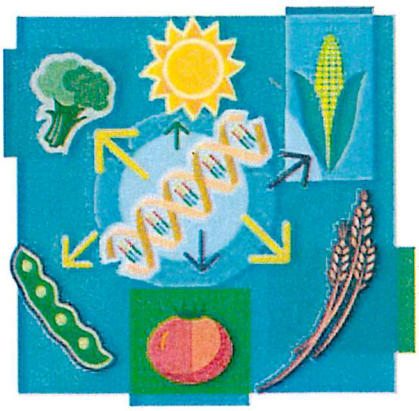
FDA proposal to regulate gene edited animals is 'nonsensical'

Alison Van Eenennaam | January 23, 2017 | Genetic Literacy Project

Editor's Note: This article discusses the US Food and Drug Administration guidance on "Regulation of Intentionally Altered Genomics DNA in Animals" which was released on Jan. 18, 2017. Alison Van Eenennaam, an animal geneticist at the University of California-Davis, analyzed the paper.

The recently released FDA guidance for producers and developers of genetically improved animals and their products defining all intentional DNA alterations in animals as drugs, irrespective of their end product consequence, is nonsensical.

FDA "Guidance for Industry #187" updates the never finalized 2009 document "Regulation of Genetically Engineered Animals Containing Heritable rDNA Constructs" to the much more expansive "Regulation of Intentionally Altered Genomic DNA in Animals" to expand the scope of the guidance to address animals intentionally altered through use of genome editing techniques. No longer is it the presence of an rDNA construct (which conceivably COULD have encoded a novel allergen or toxic protein) that triggers FDA regulatory oversight of genetically engineered animals, but rather it is the presence of ANY "intentionally altered genomic DNA" in an animal that triggers oversight. Intention does not equate to risk. This trigger seems to be aimed squarely at breeder intention and human intervention in the DNA alteration.



DNA is generally regarded as safe. We eat it in every meal, and along with each bite, we consume billions of DNA base pairs. Each individual differs from another by millions of base pair mutations – we are always consuming DNA alterations – the mutations that provided the variation that enabled plant and animal breeders to select corn from Teosinte and Angus cattle from Aurochs. DNA does alter the form and function of animals – and all living creatures – it is called the genetic code, the central dogma, and evolution. If DNA is a drug then all life on Earth is high.

The guidance states that "intentionally altered genomic DNA may result

from random or targeted DNA sequence changes including nucleotide insertions, substitutions, or deletions", however it clarifies that selective breeding, including random mutagenesis followed by phenotypic selection, are not included as triggers. So the random DNA alterations that result from *de novo* or chemical-induced mutagenesis with not be a trigger, but intentional precise and known alterations and any off-target random changes that might be associated with the intended edit will trigger regulation, irrespective of the attributes of the end product. This is beyond process-based regulation, it is regulation triggered by human intent. That is if a breeder was involved, then it is regulated. If random mutations happened in nature or due to uncontrolled mutagenesis – not regulated.

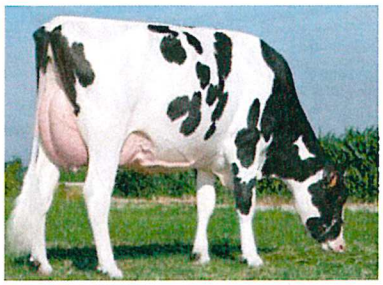
This sounds a lot like what Greenpeace is arguing for when they state that a GMO is when "the genetic modification is enacted by heritable material (or material causing a heritable change) that has, for at least part of the procedure, been handled outside the organism **by people**." The problem is that risk is associated with the attributes of the product, not the fact that it is handled by people or carries the taint of human intention.

This approach is the polar opposite of what the 2016 National Academies report concluded that the distinction between conventional breeding and genetic engineering is becoming less obvious. They reasoned that conventionally bred varieties are associated with the same benefits and risks as genetically engineered varieties. They further concluded that a process-based regulatory approach is becoming less and less technically defensible as the old approaches to genetic engineering become less novel and as emerging processes — such as gene editing — fail to fit current regulatory categories of genetic engineering. They recommended a tiered regulatory approach focused on intended and unintended **novel characteristics of the end product** resulting from the breeding methods that may present potential hazards, rather than focusing regulation on the process or breeding method by which that genetic change was achieved.

The new FDA Guidance, released two days before Trump's inauguration, then goes on to state "a specific DNA alteration is an article that meets the definition of a new animal drug at each site in the genome where the alteration (insertion, substitution or deletion) occurs. The specific alteration sequence and the site at which the alteration is located can affect both the health of the animals in the lineage and the level and control of expression of the altered sequence, which influences its effectiveness in that lineage. Therefore, in general, **each specific genomic alteration is considered to be a separate new animal drug subject to new animal drug approval requirements.**" So every SNP is potentially a new drug, if associated with an intended alteration.

To put this in perspective, in one recent analysis of whole-genome sequence data from 234 taurine cattle representing 3 breeds, >28 million variants were observed, comprising insertions, deletions and single nucleotide variants. A small fraction of these mutations have been selected owing to their beneficial effects on phenotypes of agronomic importance. None of them is known to produce ill effects on the consumers of milk and beef products, and few impact the well-being of the animals themselves.

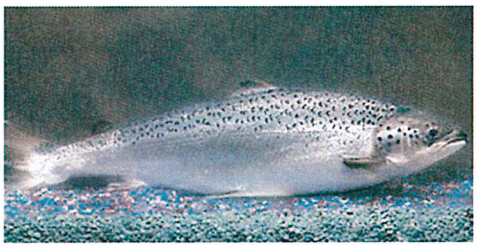
What is not clear is how developers are meant to determine which alterations are due to their "intentions", and which result from spontaneous *de novo* mutations that occur in every generation. Certainly, breeders can sequence to confirm the intended alteration especially if they are inserting a novel DNA sequence, but how can they determine which of the random nucleotide insertions, substitutions, or deletions are part of the regulatory evaluation, and which are exempt as random mutagenesis. And if there is risk involved with the latter, why are only the random mutations associated with intentional modifications subject to regulatory evaluation? And what is the if intended modification is a single base pair deletion – will the regulatory trigger be the absence of that base pair – something that is not there?


Holstein cow

Many proposed gene editing applications will result in animals carrying desirable alleles or sequences that originated in other breeds or individuals from within that species (e.g. hornless Holsteins were edited to carry the Celtic polled allele found in breeds like Angus). As such, there will be no novel combination of genetic material or phenotype (other than hornless). The genetic material will also not be altered in a way that could not be achieved by mating or techniques used in traditional breeding and selection. It will just be done with improved precision and minus the linkage drag of conventional introgression.

Does it make sense to regulate hornless dairy calves differently to hornless beef calves carrying the exact same allele at the polled locus? Does it make sense to base regulations on human intent rather than product risk? Regulatory processes should be proportional to risk and consistent across products that have equivalent levels of risk.

There is a need to ensure that the extent of regulatory oversight is proportional to the unique risks, if any, associated with the novel phenotypes, and weighed against the resultant benefits. This question is, of course, important from the point of view of technology development, innovation and international trade. And quite frankly the ability of the animal breeding community to use genome editing.



Given there is currently not a single "genetically engineered animals containing heritable rDNA construct" being sold for food anywhere in the world (see my BLOG on AquAdvantage salmon), animal breeders are perhaps the group most aware of the chilling impact that regulatory gridlock can have on the deployment of potentially valuable breeding techniques. While regulation to ensure the safety of new technologies is necessary, in a world facing burgeoning animal protein demands, overregulation is an indulgence that global food security can ill afford.

I urge the scientific community – including those not directly impacted by this proposed guidance because animal breeders are a small community – to submit comments to the FDA on this draft revised guidance #187 during the 90-day comment period which closes April 19, 2017. There are several questions posted there asking for scientific evidence demonstrating that there are categories of intentional alterations of genomic DNA in animals that pose low to no significant risk. Centuries of animal breeding and evolution itself would suggest there are many.

There is also a request for nomenclature for the regulatory trigger as outlined in the draft revised guidance. The FDA used the phrase "animals whose genomes have been altered intentionally" to expand their regulatory reach beyond genetically engineered animals containing heritable rDNA constructs (aka drugs), but suggested that other terms that could be used include "genome edited animals," "intentionally altered animals," or expanding the term "genetically engineered" to include the deliberate modification of the characteristics of an organism by manipulating its genetic material. They encourage the suggestion of other phrases that are accurate and inclusive. I can think of a couple!

A version of this article originally appeared on the UC Davis

BioBeef Blog as "FDA seeks public comments on regulation of genetically altered animals" and has been republished here with permission from the author.

Alison Van Eenennaam, Ph.D. is an animal geneticist and Cooperative Extension specialist in the Department of Animal Science at the University of California, Davis. Follow her on Twitter @BioBeef

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October 3, 2012

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October 28, 2014

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EVENT PROGRAMME

The ICAR Conference is an important forum to exchange experiences and to help to improve the systems needed for animal recording.

DOWNLOAD FULL PROGRAMME

SUNDAY 11 JUNE 2017

EVENING
Dinner for Board and working groups

MONDAY 12 JUNE 2017

MORNING
ICAR Board and working group meetings
Lunch for ICAR Board, WG SC members

AFTERNOON
ICAR Board and working group meetings

EVENING
ICAR Board + ICAR Secretariat + SC and WG Chairpersons Dinner

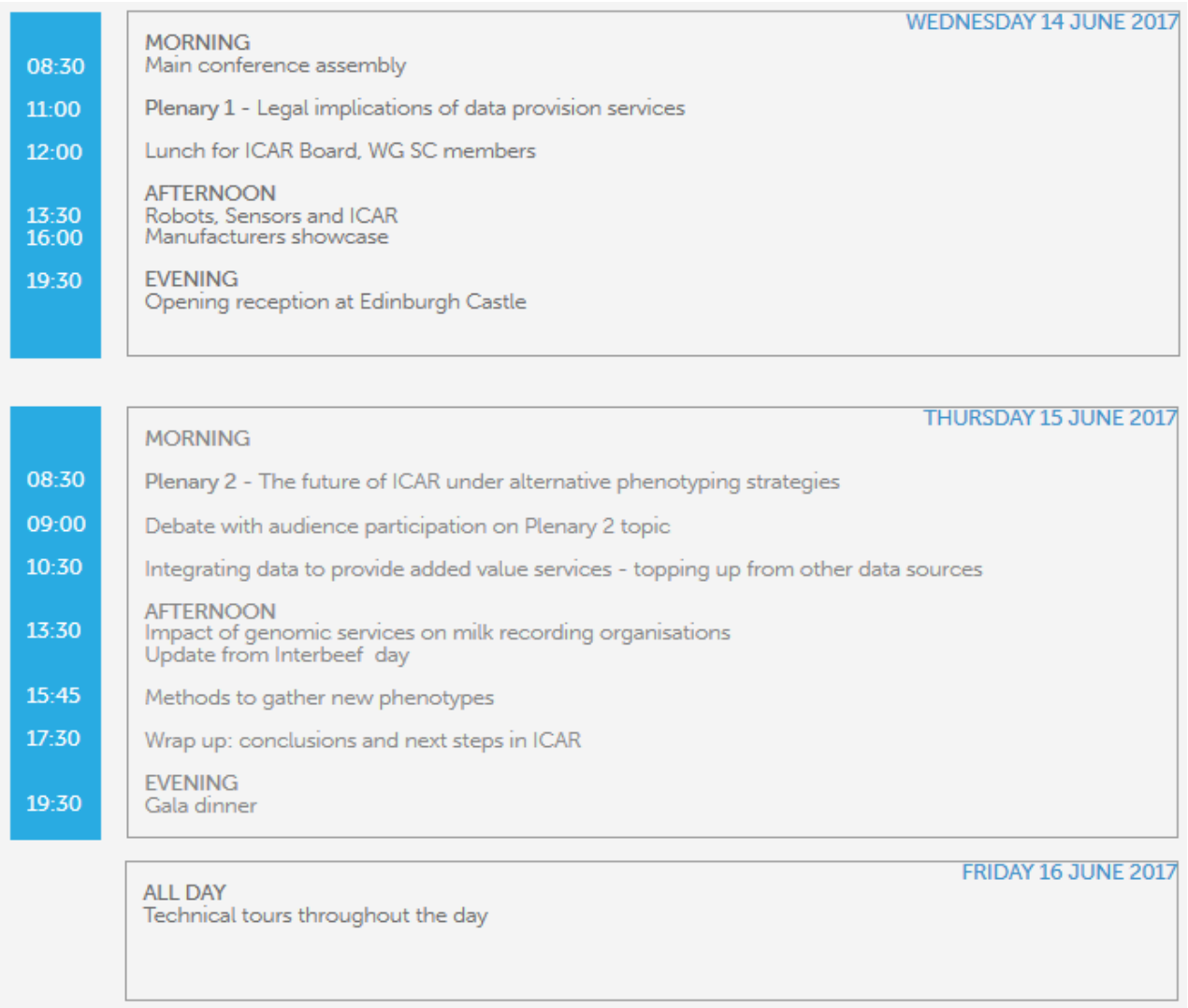
TUESDAY 13 JUNE 2017

MORNING
Working group closed meetings

Lunch for ICAR Board, WG SC members

AFTERNOON
Performance recording in small ruminants and camelids

EVENING
ICAR Board + ICAR Secretariat + SC and WG Chairpersons Dinner



One of the sessions will be a managed debate session whereby a number of raconteurs will move throughout the room enticing and stimulating members of the audience to engage in a debate about how ICAR can respond to the future challenges in data collection, use, processing and reporting. This will be preceded by a short presentation by a notable speaker on Big Data in animal improvement and implications for ICAR.

ICAR has traditionally been focused on milk recording simply because that is the dominant service provided by ICAR members. Increasingly, beef, sheep and goat recording is falling under its remit and so all sessions will carry papers relating to all species. There is a specialist session on small ruminants and camelids on Tuesday but papers will feature on all species in all sessions where relevant.

Plenary 1

Legal implications of data provision services

Data is provided by farmers to service providers for a specific purpose. Services are morphing into new and increasingly integrated services and are likely to continue to do so at an increasing rate. The integration will involve data from many sources, from automated equipment, from competing companies, from national databases, from overseas databases. Once data is integrated into a new piece of information new IP is generated. Questions now arise as to the ownership and exploitation rights of the new IP and the equitable distribution of the value arising from that new IP. How is it determined? How is it distributed? How is it protected? How is it exploited? How is it turned into value?

Plenary 2

The future for phenotyping strategies – how will ICAR members exploit the opportunities?

Historically, milk recording has been undertaken by farmers for management purposes and the service provision has evolved to include management reporting to further exploit the value of the collected data. An additional value add has been genetic evaluation. Whilst the system of recording and the manner of reporting differs across countries (and in some cases within country), it is fundamentally the same – management is the reason for milk recording and it is undertaken for purely selfish reasons. The future may be characterised by a different collection model while the requirements remain the same. Farmers may collect more and more data locally using modern techniques of data assimilation such as automatic recording, robotic milkers, motion detectors, calving monitors, web cams, image collection, and temperature detection.

This will have an impact on ICAR approved data collection companies if the equipment manufacturers do not value the certification of ICAR or view it as a barrier to their commercial interests. What if breeding companies pay farmers to collect data for them specifically and pay them to send the data to them rather than send it for central storage? What about the scenario where producer groups break off into those operated by, for example, a veterinary practice? Or a national retailer? What about the scenario whereby data required for genetic evaluations is collected at ICAR approved farms and all other data is collected and handled locally at lower levels of authentication (and cost)? This will significantly reduce the number of farms that require ICAR approval – how can ICAR organisations continue to provide high cost and high value services in these new potential scenarios?

Impact of genomic services on performance recording organisations

Farmers are beginning to consider genotyping females for both management and selection purposes. In some countries genomic testing services are provided by recording companies but in some countries they are also available from additional companies that do not supply performance recording services e.g. Zoetis. How can ICAR members provide additional genotyping services to add value to their existing services and provide a 1-stop shop for farmers? How are current members incorporating genomics services into their service provision? Who are the competitors in this space and how are ICAR members responding to this threat? Apart from genomic services, does genomics make recording of novel phenotypes more important? What opportunities does it create for ICAR Members?

Integrating data to provide added value services - topping up from other data sources

Existing services are produced from data recorded by the recording service. However, there are data items either recorded by other organisations (e.g. service records from AI companies, foot trimmer data, abattoir data, pedigree breed societies) or by automated devices that may or may not make their data freely available. How can ICAR members assimilate additional data to make their services more useful/valuable and thereby cooperate with new service providers? What useful management information can be derived from combining sources of data?

Methods to gather new phenotypes

A recently completed EU project (Optimir) has resulted in many ICAR members now harvesting spectral data from milk analysis machines for the purposes of predicting new and novel phenotypes for both on-farm management and for genetic evaluations. These new phenotypes include fatty acids (saturated / unsaturated), energy balance, ketosis, feed intake, methane emissions, pregnancy status. These potential phenotypes are currently being investigated in a number of countries and the way they can be utilised by farmers are being explored. How will these new phenotypes be used? How will they be standardised and authenticated? What are the issues of using lower accuracy predicted phenotypes in management services and for genetic evaluations? What are the hurdles in bringing the new value to farmers?

Robots, Sensors and ICAR

After many years of promise, it seems that robotics and sensors are finally with us for routine use – or are they? What examples exist of successful implementation of sensors in routine farm use? What are the currently promising technologies that are likely to be in routine use in the next 3 years? What barriers exist to the uptake of new technologies in agriculture? What are the major traits that would benefit most from sensors or robotics? How will ICAR members exploit new sensor technologies? How will ICAR services adapt? What does ICAR need to do to remain relevant in an environment where more and more recording will be undertaken without human intervention?

Performance recording in small ruminants and camelids

The expansion of ICAR activities into species other than dairy cattle seems a logical extension of its accumulated experiences and skills. The principals of applying documented standards to performance recording of any species is established. What are the main issues in performance recording of small ruminants? How can the obstacles to performance recording in extensive farming systems be overcome? How can robotics and sensors be utilised to overcome such obstacles and increase the breadth and depth of recording in small ruminants? How can ICAR standards be implemented in countries with less well developed performance recording infrastructures?

Local Organising Committee

The members of the local organising committee

Chairman: Marco Winters - Head of Genetics, AHDB Dairy
Member: Mike Coffey, Professor of Livestock Informatics, SRUC

Events Executive: Jenna Porch (main contact)
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