THE GLOBAL STANDARD FOR LIVESTOCK DATA

DNA Working Group Webinar Meeting
Friday, 19 May 2017

(15h00 Paris time)

AGENDA

1. Call to Order - Brian Van Doormaal

2. Roll Call of Participants

3. Review of Agenda

4. Summary of Previous Meeting held 21 April 2017 (Attachment)

5. ICAR Accreditation for DNA Data Interpretation Centres

    5.1 ISAG Feedback Re: ICAR Guidelines for Parentage Verification and Parentage Discovery (Attachment)
    5.2 Analysis of Test Files for ICAR Accreditation

6. New Technologies

    6.1 New Affymetrix 50K chip
    6.2 Others for WG Information and/or Consideration

7. Next Meeting - Tuesday, June 13 in Edinburgh, Scotland (Attachment)

    7.1 Recommended/Requested Agenda Topics

8. Adjournment

DNA WG Meeting Notes
21 April 2017 at 15.00 (Paris time)

1. Call to Order

   Chair Brian Van Doormaal called the meeting to order and welcomed all present.

2. Roll Call of Participants

   Brian Van Doormaal (Chair), Andre Eggen, Suzanne Harding, Dariusz Kamola, Sandra Kipp, Nilesh Nayee, Raffaele Mazza, Matthew McClure, Romy Morrin-O'Donnell, Ezequiel Nicolazzi and Cesare Mosconi from ICAR.

   Apologies were received from Carine Megneaud and Wim van Haeringen.

3. Review of Agenda

   Following a review of the proposed agenda, no items were added so it was accepted as circulated.

4. Notes of Previous Meeting held 30 March 2017 and Business Arising

   Brian explained that member participation at the last meeting was more limited, due to various reasons, so topics were discussed but essentially no decisions were taken so those same topics are on this meeting agenda. No corrections to the minutes were noted so they were accepted as circulated.

   In terms of business arising from the last meeting, Brian provided some clarification regarding the new service that Interbull is planning to introduce later this year, which is the exchange of results for "Genetic Trait" testing. Interbull has started by using three countries, namely Germany, Netherlands and the UK, to help submit date for testing the developed exchange system and plans to have the topic discussed at the next Interbull Business Meeting in Tallinn, Estonia in late August. Data files could be submitted as part of the September 2017 test run and then officially introduced by Interbull effective the December 2017 MACE/GMACE release. Discussion ensued to clarify that this service would likely start with the Holstein breed and other dairy breeds if the respective World Federation made such a request to Interbull and it could also include beef breeds if there is interest. Also, the service would only include those genetic traits for which there is a gene test recognized by the World Federation for the respective breed, which means that haplotype analysis results are excluded. Suzanne mentioned that she was recently appointed by ICAR as the new chair of the Breed Associations WG and this topic is one where there would be some overlap in terms of role with this DNA WG, which could clearly have a technical advisory/input role to the Breed Associations WG. Some discussion also took place about whether gene tests for beta casein (ie. A1/A2) would be included and it was clarified that this is not currently the case. It was also noted that kappa casein testing falls in a similar category of genetic test. Matt added that there are more sophisticated tests available for some of these, such as A1A2 that are more accurate than looking at the single A1/A2 allele.

   Action: Romy, Matt and Raffaele agreed to collaborate to draft a background document to describe this issue and to make recommendations for committee consideration at the next meeting in May or at the meeting in June at the latest.

5. Call for ICAR Accreditation of Genetic Laboratories for Parentage Verification

   The email and draft call circulated by Cesare was discussed and accepted for sending out as soon as possible noting that results would be reviewed at the meeting in Edinburgh.

6. ICAR Accreditation for DNA Data Interpretation Centres

6.1 Draft ICAR Guidelines for Parentage Verification and Parentage Discovery

Brian explained that he had drafted the document provided as background after first circulating it to Matt and Romy for input, given their expertise and involvement with ISAG. In order for the ICAR accreditation to work properly, the ISAG guidelines for parentage verification needed to be reviewed and clarified to ensure consistent results by all organizations. In addition, no international guidelines for parentage discovery currently exist so they need to be developed.

While the testing process for ICAR accreditation must be clear and lead to consistent results, any given organization may still end up using additional SNP for parentage verification and/or discovery when offering services at a national level.

Currently, the ICAR accreditation services allow an applicant to apply for parentage verification based on the ISAG 200 SNP and parentage discovery based on the approved list of 554 SNP that will be included in the GenoEx-PSE exchange. Brian asked input from WG members as to whether a third level of application should be introduced by ICAR, which would be for parentage verification based on only the ISAG 100 core SNP, since various organizations are currently providing such services.

Agreed: It was agreed that ICAR should not introduce a parentage verification accreditation level based only on the 100 core SNP of ISAG since a higher minimum number of SNP should be encouraged as the international standard.

Brian went through each of the recommended revised steps for carrying out parentage verification and discovery as described in the document. For the table under parentage verification that lists the four current SNP recommended to be excluded from among the list of ISAG 200 SNP, it was agreed that such a table should be provided as an annex attached to the guidelines. A similar table could be added as an annex for listing SNP to be excluded for parentage discovery. This approach would allow for an easier management of changes to such lists without making any changes to the guidelines.

Agreed: It was agreed that lists of SNP to be excluded for parentage verification and/or discovery be included as an annex to the guidelines document.

In terms of process for determining any SNP to be included in such annex for exclusion, the DNA WG would be responsible, on behalf of ICAR, for making such decisions but welcome recommendations and input from ISAG. It is understood that decisions to exclude must be science-based and ideally with evidence of problems demonstrated and/or supported by multiple organizations with experience in parentage analysis.

Discussion ensued regarding the file format of genotypes for carrying out parentage analysis and Brian mentioned that the GenoEx-PSE service to be offered by Interbull has defined file layouts in both AB and TOP format. Interbull will require a process for translating from one format to another but it was clarified that this would need the correct manifest to be able to do so. In any event, the process for carrying out ICAR accreditation as a DNA Data Interpretation Centre must allow the applicant to use genotypes in either AB or TOP format.

Action: Brian to modify the document and provide to WG members.

Action: Brian contact various organizations involved with the GenoEx-PSE Expert Group and/or the DNA WG to request submission of SNP among the list of 554 for parentage discovery for which they have evidence and/or reasons for exclusion.

Action: Romy forward the revised document and recommendations to ISAG for reaction and input.

6.2 Analysis of Test Data Files

Brian, Sandra, Matt and Ezequiel (via George Wiggans) are involved with using the ICAR accreditation test files to make sure that they are appropriate for potential applicants. The revised guidelines can now be applied and results should be identical for each country.

6.3 Draft ICAR Accreditation Application Form

Brian summarized the discussion from the previous meeting noting that the only point requiring further action is the fee structure outlined on page 4. ICAR set the fee at 300 Euro per application and is planning to require a biannual renewal. After some discussion, including the option of moving the renewal frequency to every three years, it was agreed that the ICAR proposal was reasonable as is.

7. Status of GenoEx-PSE Service

Interbull staff have experienced various delays in terms of development of the GenoEx-PSE software and database. Most recently, some technical issues arose that require involvement of BC Platforms as the software provider. The ultimate goal is still to have the software available for testing in advance of the ICAR meetings in Edinburgh but official service commencement not likely prior to the Interbull meetings in late August. For the GenoEx-PSE service contract, ICAR and Interbull agreed to change it from the 3-party agreement presented in Chile in October to a 2-party agreement between the Service User and the Interbull Centre.

8. Future Meetings

The next meeting was reaffirmed for 19 May at 15h00 Paris time. For the face-to-face meeting in Edinburgh on Tuesday, June 13, all meeting participants confirmed their intent to attend, with the exception of Nilesh Nayee.

9. Adjournment

The meeting was duly adjourned at 17h00 Paris time.

Recommended Guidelines for Parentage Verification and Parentage Discovery Based on SNP Genotypes

Prepared by: DNA Working Group

Purpose

In 2017, ICAR will commence offering two new services related to the use of SNP genotypes for dairy and beef cattle. The first is the **Geno**type **Ex**change **P**arentage **S**NP **E**xchange (GenoEx-PSE) Service, which allows countries to exchange SNP genotypes for the purpose of offering parentage analysis services to specific breed populations at the national level. The second is the service of ICAR Accreditation for Data Interpretation Centres, which allows organizations wishing to carry out parentage analysis services to be accredited by an independent third party. Organizations wishing to be a service user of GenoEx-PSE must first receive the ICAR Accreditation for Data Interpretation Centres.

In July 2012, the International Society for Animal Genetics (ISAG) approved standards for genotyping laboratories to conduct parentage verification. These *"Guidelines for cattle parentage verification based on SNP markers"* were based on carrying out parentage verification using a set of 200 recommended SNP, with 100 considered as core SNP and a second set of 100 as backup SNP.

The purpose of this document is two-fold:

1. Revise the existing ISAG guidelines for conducting parentage verification in dairy and beef cattle using the 200 SNP recommended by ISAG, and

2. Establish new guidelines for conducting parentage discovery based on the SNP included for this purpose in the GenoEx-PSE genotype exchange service, which initially totals 554.

Principles

When carrying out parentage analysis, which includes parentage verification and/or parentage discovery, the following underlying principles should be considered:

- A consistent set of SNP must be defined for use by all organizations for international recognition of parentage analysis accreditation and for the subsequent delivery of "certified" parentage information.

- Each animal involved in the parentage analysis process (i.e.: animal and each potential parent) must have a SNP genotype available for which a minimum proportion of the defined set of SNP have been called and are available. When establishing such minimum requirements consideration should be given to the inclusion of the defined SNP on various genotyping chips used widely in the population of animals being considered.

- While it is understood that only informative SNP (i.e.: SNP whereby the animal and the parent in question are both homozygous) provide useful information for parentage analysis, it is more practical that guidelines are based on the total number of SNP available for the animal and parent(s) in question. Roughly speaking, about one-third of available SNP for parentage analysis are informative but this proportion depends on the average minor allele frequency of the included SNP within the population of animals being considered.

Parentage Verification

The current ISAG guidelines for parentage verification in cattle are based on a set of 100 core SNP and then a second set of another 100 backup SNP. The guidelines outline a possible two-step process whereby results from the 100 core SNP may be used to either deem the status as "Parentage Accepted" or "Parentage Excluded" and only when this first status is "Parentage Doubtful" does the analysis continue using the second group of 100 backup SNP. This second step of the parentage verification process may then result in a final status of "Parentage Accepted" or "Parentage Excluded". In the event that a second result of "Parentage Doubtful" arises, and new samples and/or genotypes for the animals involved have been processed and the customer cannot identify any other possible parents, the recorded parentage would still be deemed as "Parentage Accepted".

Given the current state of knowledge and experience with using SNP genotypes for parentage verification, the following modifications to the existing ISAG guidelines are recommended:

1. Upon approval by the ICAR DNA Working Group, specific individual SNP included in the current group of 200 SNP recommended by ISAG for parentage verification in cattle, may be deemed inappropriate for inclusion. This reduction in the total set of SNP to be used would be applied by all organizations receiving ICAR Accreditation for Data Interpretation Centres. Annex 1 attached lists the SNP that have shown to cause problems for parent verification and are recommended for exclusion from the original list of 200 recommended by ISAG for parentage verification. On an ongoing basis ISAG may identify other problematic SNP from various chip platforms and technologies for inclusion in Annex 1 upon final approval by the ICAR DNA Working Group.

2. Given the improved accuracy of parentage verification achieved by the inclusion of more SNP, the current two-step process should be replaced by a single analysis based on the full set of approximately 200 SNP for parentage verification, excluding those in Annex 1.

3. The required minimums in terms of number of SNP, as outlined in the current ISAG guidelines, must be scaled to reflect the total number of SNP to be used for parentage verification analysis. For example, if the total number of SNP from those recommended by ISAG, is reduced from 200 to 195, then the minimum number of SNP available in the profile of each animal and potential parent must be scaled to 185 (from the current minimum of 95/100).

4. For assigning the parentage verification status according to the number of SNP conflicts found, the revised recommended rules are the following:

   Step 1: Conduct a separate verification for each combination of the animal with its recorded sire and/or dam with a SNP genotype. The informative SNP are those for which the animal and reported parent are both homozygous and a conflict is considered when they are each homozygous for a different allele for any informative SNP. Based on the minimum criteria of 185 SNP available for the animal and each parent, the minimum number of common SNP available for verifying each animal-parent combination is 175.

   For this step, the following rules apply for assigning the parentage verification status:

   - Number of mismatches/SNP conflicts: 0 - 2 => Parentage Accepted
   - Number of mismatches/SNP conflicts: 3 - 5 => Parentage Doubtful
   - Number of mismatches/SNP conflicts: >5 => Parentage Excluded

   Step 2: In the case that both sire and dam have a status of "Parentage Accepted" from Step 1, verify that the combination of those parents is acceptable. In this case the informative SNP are those for which both verified parents are homozygous and the progeny is heterozygous. A conflict exists when the parents are homozygous for the same allele at any informative SNP while the progeny is heterozygous. In this case, the minimum number of common SNP available is 165.

For this step, the following rules apply for confirming the parentage verification status for the combination of verified parents:

- Number of mismatches/SNP conflicts: 0 - 3 => Parentage Accepted
- Number of mismatches/SNP conflicts: 4 - 7 => Parentage Doubtful
- Number of mismatches/SNP conflicts: >7 => Parentage Excluded

5. For animals with only one parent genotyped, only those animal-parent combinations achieving the status of "Parentage Accepted" from Step 1 would qualify for the organization to issue an official confirmation of parentage for that parent. For animals with both parents genotyped, only those animals achieving the status of "Parentage Accepted" from Step 2 would qualify for the organization to issue an official confirmation of parentage including both parents.

6. As an added service for those organizations receiving ICAR accreditation to carry out parentage discovery, the process outlined below could be applied to all animals for which the parentage verification result was either "Parentage Doubtful" or "Parentage Excluded" in either Step or Step 2 above.

Parentage Discovery

No international guidelines currently exist for organizations to carry out parentage discovery even though most, if not all, genetic evaluation service providers have developed such processes internally. As with parentage verification, the accuracy of parentage discovery is improved as the number of SNP included increases. For the GenoEx-PSE service, a list totalling 554 SNP have been defined for the genotype exchanges involving service users that have been accredited by ICAR for this level of parentage analysis and have agreed to upload these SNP to the GenoEx-PSE database at the Interbull Centre, which is the requirement for downloading the same. These 554 SNP include the 200 SNP recommended by ISAG for parentage verification in cattle as well as an additional group of 354 SNP. In addition to the 200 SNP for parentage verification another 75 for parentage discovery are spread across chromosomes 1 to 29 while the remaining 279 SNP were selected from only ten chromosomes, specifically 1, 2, 3, 5, 7, 8, 11, 13, 19 and 21. This strategy for SNP selection was adopted to reduce the accuracy of genotype imputation and genomic predictions in the event that a GenoEx-PSE service users attempts to use the exchanged genotype in this manner even though it is clearly prohibited as outlined in the GenoEx-PSE Service Agreement.

To be consistent with the principles and revised guidelines for parentage verification outlined above, the following are recommended guidelines for parentage discovery:

1. The ICAR DNA Working Group may, from time to time, identify and approve SNP, from among those included in the GenoEx-PSE service, that must be excluded for carrying out parentage discovery, which are listed in Annex 2 attached. Any such SNP would include those approved for exclusion for parentage verification and may also include other SNP once there is sufficient reason to do so.

2. Organizations carrying out parentage discovery services must implement quality assurance procedures that ensure the following:
    - That a discovered parent is older than the animal and, in fact, not an offspring
    - That a discovered parent is of the appropriate sex such that sires are male and dams are female
    - That genetically identical animals are pre-identified such that a discovered parent is reported as any one of the genetically identical siblings

3. Based on a recent assessment of SNP lists associated with various SNP chips used internationally to genotype dairy and/or beef cattle, each chip has at least 500 in common with the 554 SNP recommended for parentage discovery. Given possible call rates of genotypes for the animal and any potential parent to be discovered, it is recommended that each genotype included in such an analysis have a minimum of 450 of the 554 SNP available in order to conduct parentage discovery.

4. Given that genotyping SNP chips actively being used in cattle populations globally have a varying number of the 554 SNP defined for inclusion in the GenoEx-PSE service, parentage discovery results must be based on a percentage of SNP available between the animal and any potential parent being considered. The following is recommended for assigning the parent discovery status:

   Step 1: In separate processes, attempt to discover either the sire (i.e.: male older than animal with fewest conflicts) or dam (i.e.: female older than animal with fewest conflicts) of the animal based on SNP genotypes available. Based on the minimum criteria for each SNP genotype to be included, as outlined in point 3 above, a minimum number of common SNP between the animal and each parent will be 350.

   For this step, the following rules apply for assigning the status of each parent discovered:

   - Percentage of common SNP with a conflict: 0 to <1.0% => Parent Discovered
   - Percentage of common SNP with a conflict: 1.0 to <3.0% => Parent Doubtful
   - Percentage of common SNP with a conflict:: ≥3.0% => Parent Excluded

   Step 2: In the case that an animal has both a sire and dam with a successful status of "Parent Discovered" from Step 1, this parent combination must also be verified.

   For this step, the following rules apply for assigning the status of the combination of parents discovered:

   - Percentage of common SNP with a conflict: 0 to <1.5% => Parents Discovered
   - Percentage of common SNP with a conflict: 1.5 to <4.0% => Parents Doubtful
   - Percentage of common SNP with a conflict:: ≥4.0% => Parents Excluded

5. For animals with only one parent with the status of "Parent Discovered" in Step 1, only that animal-parent combination would qualify for the organization to issue an official confirmation of parentage for that parent. For animals with both parents with the status of "Parent Discovered" in Step 1, only those animals achieving the status of "Parents Discovered" from Step 2 would qualify for the organization to issue an official confirmation of parentage with the status of "Parentage Accepted" for both parents.

ANNEX 1: SNP Among the ISAG 200 to be Excluded from Parentage Verification for ICAR Accreditation

SNP Name (Illumina Bead Chips)	ISAG Group	Reason for Exclusion
ARS-USMARC-Parent-DQ837645-rs29015870	Core	Clustering issues*
ARS-BGFL-NGS-76191	Backup	Clustering issues*
BTA-100621-no-rs	Backup	Clustering issues*
ARS-BFGL-NGS-99210	Backup	Tri-allelic**

* - McClure et al. (2015)
** - Based on sequence validation to be specifically problematic with bead chips

SNP associated with other chip platforms and/or technologies may be added over time.

ANNEX 2: SNP Included in GenoEx-PSE to be Excluded from Parentage Discovery for ICAR Accreditation

SNP Name (Illumina Bead Chips)	ISAG Group	Reason for Exclusion
ARS-USMARC-Parent-DQ837645-rs29015870	Core	Clustering issues*
ARS-BGFL-NGS-76191	Backup	Clustering issues*
BTA-100621-no-rs	Backup	Clustering issues*
ARS-BFGL-NGS-99210	Backup	Tri-allelic**

* - McClure et al. (2015)
** - Based on sequence validation to be specifically problematic with bead chips

SNP associated with other chip platforms and/or technologies may be added over time.

Event Programme

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

SUNDAY 11 JUNE 2017

MORNING	
08:30-12:30	ICAR Board meeting
12:30 – 13:30	Lunch for ICAR Board and Chairpersons
AFTERNOON	
13:30-17:30	ICAR Board and Chairpersons meeting
EVENING	
TBC	ICAR Board and Secretariat, SC and WG Chairpersons dinner (Invitation only)

MONDAY 12 JUNE 2017

MORNING	
08:30-12:30	Training workshops for ICAR Auditors
12:30-13:30	Lunch for ICAR Board, WG & SC members
AFTERNOON	
13:30-18:00	Forum for ICAR Auditors
13:30-17:30	Interbeef Technical group meeting (closed)
13:30-18:00	Functional Traits working group meeting (closed)
13:30-18:00	Recording and Sampling Devices working group meeting (closed)
13:30-18:00	Sheep, Goat and Camelid working group meeting (closed)

TUESDAY 13 JUNE 2017

MORNING	
08:30-12:30	Joint workshops for ICAR – Interbeef members (closed)
09:00-13:00	Dairy Cattle Milk Recording working group meeting (closed)
09:00-13:00	Conformation Recording working group meeting (closed)
09:00-13:00	Recording Sampling Devices working group meeting (closed)
09:00-13:00	Animal Identification sub-committee meeting (closed)
09:00-13:00	Global Reach working group meeting (closed)
09:00-13:00	Artificial Insemination and RT working group (closed)
09:00-13:00	Functional Traits working group meeting (closed)
12:30 – 14:00	Lunch for ICAR Board, WG and SC members

AFTERNOON	
13:30-17:30	Interbeef working group meeting (closed)
14:00-18:00	Joint GDMI and Feed and Gas working group meeting (closed)
14:00-18:00	DNA working group meeting (closed)
14:00-18:00	Animal Data Exchange working group meeting (by invitation)
14:00-18:00	Animal Identification sub-committee meeting (closed)
14:30-17:00	Sensor Devices Task-force meeting (closed)
14:00-18:00	Functional Traits working group meeting continued (closed)
16:00-18:00	Milk Analyses sub-committee meeting (closed)

WEDNESDAY 14 JUNE 2017

MORNING	
08:30 – 09:30	Main conference assembly
09:30 – 10:30	Local host welcome talk
11:00 – 12:00	Plenary 1 - Legal implications of data provision services
12:30 – 13:30	Lunch for all ICAR attendees
AFTERNOON	
13:30 – 15:00	Robots, Sensors and ICAR
16:00 – 18:00	Manufacturers' showcase
EVENING	
19:30 – 22:00	Opening reception at Edinburgh Castle

THURSDAY 15 JUNE 2017

MORNING	
08:30 – 09:00	Plenary 2 - The future of ICAR under alternative phenotyping strategies
09:00 – 10:00	Debate with audience participation on Plenary 2 topic
10:30 – 12:00	Integrating data to provide added value services - topping up from other data sources
12:00 – 13:00	Lunch for all ICAR attendees
AFTERNOON	
13:30 – 15:00	Impact of genomic services on milk recording organisations
15:45 – 17:30	Methods to gather new phenotypes
	Update from Interbeef day
17:30 – 18:00	Wrap up: conclusions and next steps in ICAR
EVENING	
19:00-00:00	Gala dinner at Mansfield Traquair (Ticketed event)

FRIDAY 16 JUNE 2017

ALL DAY	Technical tours (TBC)

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.

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?

Preliminary Programme
Data protection aspects by merging cattle data of various origins ***C. Egger-Danner[1]**, M. Mayerhofer[1], M. Koblmüller[2], J. Perner[3], R. Janacek[4], G. Schoder[5], F. Gstöttinger[6], R. Weissensteiner[1], B. Fürst-Waltl[7], M. Schagerl[8], H. Eder[9], E. D*
A computerized consent management tool for breeders: why, how? ***Balvay B[1]***
A Central Database for the Australian Dairy Industry ***S. Jenkins[1],** T. Francis[1]*
Smart Dairy Farming 3.0: multiplying innovations on the farmyard ***B. van 't Land, G. Smeenk, H. Lucas, A. Lamers***

Session 1: 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?

Preliminary Programme
Automating the dairy farmer? Understanding the barriers to uptake and use of precision technology in dairy systems. ***D. A. McConnell***
Use of daily robotic progesterone data for improving fertility traits in Finnish Ayrshire ***J. Häggman***[1], *J.M. Christensen*[2] *& J. Juga*[3]
Collecting milking speed data as part of official milk recording. ***R.H. Fourdraine***[1], *H.A. Adams*[2] *& A.D. Coburn*[3]
Objective Carcass Measurement to Improve Lean Meat Yield and Eating Quality in Australian Beef, Sheep and Pork ***D.J. Brown***[1,5], *D.W. Pethick*[2,5], *P. McGilchrist*[2,5], *C.K. Ruberg*[3,5] ,*W.S Pitchford*[4,5], *R. Apps*[3,5] *& G.E. Gardner*[2,5]
Towards a robust protocol for enteric methane measurements using a hand held Laser Methane Detector in Ruminants ***ThiphaineBruder***[1], *Benoit Rouille*[1], *Tianhai Yan*[2] *&* ***Mizeck G.G. Chagunda***[3]
Sharing data through an API platform - API AGRO. ***Erik Rehben*** [1], *Béatrice Balvay* [2], *Theo Paul Haezebrouck* [3]

Session 2: Manufacturers Showcase and Applications

Preliminary Programme
Milk sample carry over in the field – identifying and resolving the challenges ***Justin Frankfort***
Practical Considerations to Reduce Carry-Over in Design of Recording & Sampling Devices
Addressing the Effect of Known Carry-Over in DHI Milk Samples when Conducting PCR and ELISA Testing in the Laboratory
The new CombiFoss™ 7 DC – Differential Somatic Cell Count and other Advancements in Milk Testing ***D. Schwarz***
Employing high resolution big data for predictive modelling in precision dairy farming ***G. Katz***[1]
Evaluation of a new qPCR test to specify reasons for total bacterial count in bulk tank milk ***S. Sigurdsson***[1], *L.T. Olesen*[2], *A. Pedersen*[3] *and* ***J. Katholm***[4]

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?

Preliminary Programme
Delivering Value-Added Services to a Diverse Customer Base ***A.D. Coburn***
Agrimetrics Data Platform; Harnessing and merging big data ***D. Flanders[1]*** *& M. Coffey[2]*
OPEN DISCUSSION

Session 3: 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?

Preliminary Programme
Predict, Prescribe, Perform: integrating traditional and new data sources to enable Smart Herd Management *S. van der Beek, H.M. Knijn, D. Zouari*
The DataGene Herd Test Dashboard *T.Francis[1], M.Humphris[2], R.Morris[2], T.Sargent[1] & R.Shephard[2]*
Genetic evaluation for claw health traits as part of the integrated system for health monitoring in German Holstein dairy cattle *K. F. **Stock**[1], R. Schafberg[2], V. Müller-Rätz[2] & F. Reinhardt[1]*
National dairy cattle health recording web application in the Czech Republic *A. Svitakova[1], E. Kasna[1], S. Slosarkova[2], P. Fleischer[2], L. Zavadilova[1], S. Stanek[1] & D. Lipovsky[3]*
Cow Own Worth – synergising data to provide a new tool to aid in culling decisions in seasonal dairy herds *M.M. Kelleher[1], D.P. Berry[2], P.R. Amer[3], A. Cromie[1] & R. Evans[1]*
Association between milk fatty acids in early lactation and subsequent reproductive performance of modern high-yielding dairy cows *S. Jorjong[1], G. Opsomer[2], J. Chen[3], A. T. M. van Knegsel[4], B. Kemp[5], **V. Fievez[6]***

Session 4: 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?

Preliminary Programme
Possible principles for breed association models in the genomics era, with reference to beef cattle and sheep breeds

***R.G. Banks*[1]**
Data collection methods used in the Beef Data and Genomics Programme (BDGP) and the development of Restful API's for recording herd data ***Craig Vigors***
A Star Tech, The Final Front-MIR: Estimated breeding values for mid-infrared derived predictions of energy traits in dairy cows. ***S Smith*[1], *V. Hicks*[2], *M. Coffey*[1], *M. Winters*[3] & *E Wall*[1]**
Implementation of genomic selection in small populations – Croatian case ***M. Špehar*[1], Z. Ivkić[1], M. Dražić[1], Z. Barać[1]**
Designing a reference population to accelerate genetic gains for novel traits in Canadian Holstein ***F. Miglior*[1,2], *L. Brito*[2], *P. Martin*[2], *J. Jamrozik*[1,2], *F. S. Schenkel*[2], *A. Canovas*[2], *X. Zhao, and C. F. Baes*[2]**
INTERBEEF Update

Session 5: 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?

Preliminary Programme
Prediction of energy status of dairy cows using MIR milk spectra ***C. Grelet*[1], *A. Vanlierde*[1], *M. Salavati, M*[2]. *Hostens*[3], *L. Foldager*[4], *F. Dehareng*[1] & *GplusE Consortium*[5]**
Body weight prediction and genetic parameter estimation based on type traits in Italian Holstein cows ***R. Finocchiaro*[1],** Johannes B.C.H.M. van Kaam[1], M.Marusi[1] & M. Cassandro[2]
Lactose in milk – How can lactose concentration data be beneficial in management and breeding? ***Peter Løvendahl*[1],** *Martin Riis Weisbjerg*[2]*
Individual methane prediction from milk MIR spectra, across multiple breeds, lactation stages, parities and country-specific dairy farming systems ***Vanlierde A.*[1], Gengler N.[2,3], Soyeurt H.[2,3], Martin C. [4], Lewis E.[5], Grandl F.[6], Kreuzer M.[7], Kuhla B.[8], Lund P.[9], Ferris C.[10], Bertozzi C.[11] & Dehareng F. [1]**
Targeted combination of estimated breeding values for lower accuracy mid-infrared biomarkers increases their usefulness in genetic evaluation of dairy cattle ***N. Gengler1* & *GplusE Consortium*[2]**
Genetic analyses of ketosis and a newly developed risk indicator in Fleckvieh, Braunvieh and German Holstein

H. Hamann[1], A. Werner[2], L. Dale[3], **P. Herold**[4]

Collection and Use of New Phenotypes in Germany

Thomas Hauck

Effectiveness of mid infrared spectroscopy to predict milk phosphorus content

M. Gelé[1], *L. Brun-Lafleur*[1], *A. Boudon*[2], *P. Gaignon*[2], *T. Le Mouël*[2] *& C. Hurtaud*[2]

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