THE GLOBAL STANDARD
FOR LIVESTOCK DATA

Section 4 - Guidelines for DNA Technology

Section 4 – DNA Technology

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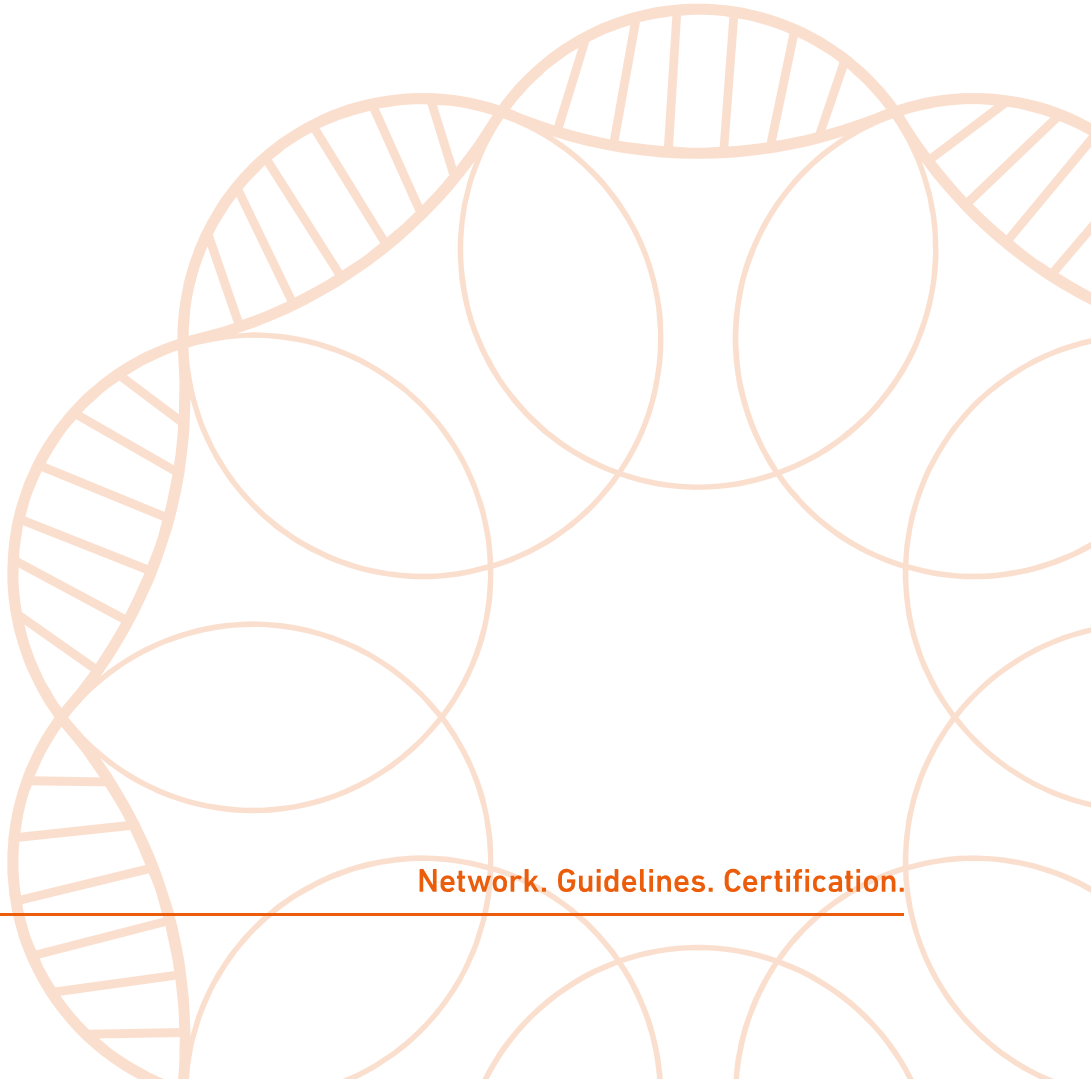

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Change Summary

Date of Change	Nature of Change
August 17	Reformated using new template.
August 17	Table of contents added.
August 17	Heading numbers and heading text edited for clarity and removal of redundant text.
August 17	Annexes replaced by links to relevant Appendices on ICAR website.
August 17	Moved the file to the new template (v2017_08_29)
August 17	Links to ICAR website hidden behind “here”.
September 17	Update version to September, 2017.
September 17	Links to DNA technology websites corrected.
September 17	Link to application forms on ICAR website corrected. Update version to October. Replace links for terminology.
October 17	Hyperlinks have been corrected.
January 18	Comprehensive review and improvements completed by the DNA Working Group.
September 18	Updated and finalized Part 1 and related sections. ICAR Guidelines Template applied. Edits from DNA-WG meeting 25th September. Accept all changes and save as v18.05.
October 18	Prepare and submit for Board approval.
Sept. 2020	List of the ICAR 554 SNP for parentage discovery has been added

1 Molecular Genetics

1.1 Introduction

Advances in molecular biology, especially genomics, provide a new set of information to be incorporated into the animal industry. On one hand, the use of molecular information may contribute to the enhancement of consumers' trust in the ability to monitor and control the animal production chain. On the other hand, molecular information will greatly contribute to the achievement of genetic improvement for animal traits through the use of genomic breeding values, marker assisted selection, gene introgression, heterosis prediction, pedigree validation/prediction, and genetic defect carrier status. In most cases, advantages of using molecular information via genomic evaluations, comes from improved accuracy of animal breeding values, shortened generation intervals, and increased intensity of selection. Even with these advancements there is still a need for research and development in the search for associations between genetic markers and traits of interest, especially as new traits are included in national evaluation indexes. In addition to that, even with the current incorporation of genomic information into national selection schemes, an understanding of gene action, gene interactions, and differential gene expression to avoid negative collateral effects is needed. Cooperation between animal industries and research is required for a successful and beneficial search for genetic information in commercial livestock populations.

1.2 Genetic Markers

Genetic markers are the fundamental molecular tools for genomics, even as the type of marker used has changed. The first genetic marker associations in livestock were reported using blood typing in the 1960s, the technology then moved to microsatellites (MS) in the 1990s and more recently to the use of Single Nucleotide Polymorphism (SNP). SNP and MS are polymorphic DNA sequences (alleles) at a specific locus of a particular chromosome.

1.2.1 Microsatellites

These are segments of DNA containing tandem repeats of simple motifs usually dimers or trimers. These segments are located throughout the genome and normally in non-coding regions. Over time, these regions are subject to the addition or subtraction of tandem repeats, which means that each microsatellite can have from 2 to over 15 unique alleles. Microsatellites are commonly used in many livestock species for parentage validation.

1.2.2 Single Nucleotide Polymorphism (SNP)

SNP are the most common type of genetic variation: each SNP represents a variation in a single nucleotide. There are multitudes of SNP located throughout the genome of every livestock species. For genomics the most informative SNP traditionally are either located in (a) coding regions where different alleles change the structure or function of the encoded protein, or (b) at non-coding regions that are involved in the regulatory function of the gene. For genomic breeding values, SNP that are located in other regions of the genome are also informative as they could be in linkage disequilibrium with alleles that do cause a phenotype change.

One of the big advantages of SNP is their deployment on SNP arrays with a strong parallel processing capacity whereby thousands or hundreds of thousands of SNP can be screened together in a cost-effective and efficient manner across a large number of animals. Currently the largest livestock genotyping labs can process more than 100,000 animals yearly on such arrays. The availability of these large SNP panels is therefore bolstering the search for mutations underlying genetic variation for simple and complex traits. It is also revolutionizing the speed at which trait associated genes or gene regions are being discovered as well as the adoption rate of genomic selection strategies.

1.3 Definitions and Terminology

Table 1 includes a brief overview of terms used in relation to molecular genetics, genomics and/or parentage analysis.

Table 1. Terms used in relation to molecular genetics, genomics and/or parentage analysis.

Term	Definition
Animal identification confirmation	The process by which genomic markers are used to determine if a tissue sample can be excluded as originating from a particular animal.
Genomics	The range of technologies which identify the genetic make-up of an animal at the gene level and the DNA sequences of an animal's genome.
Haplotype	A group of genetic marker alleles that are inherited together from a single parent. The genetic markers are all on the same chromosome and normally comprise a defined segment length on that chromosome.
ICAR accreditation	Recognition by ICAR that an organization has provided sufficient evidence that it follows ICAR's guidelines.
Imputation	The process of filling in an animal's missing genotypes based upon its pedigree and other genetic markers. Normally used for SNP and/or microsatellite imputation from SNP.
MAF	Minor allele frequency.
Maternal-grandsire prediction	The process by which the haplotypes inherited from the dam are used to predict the dam's most likely sire.
Microsatellite	Segment of DNA containing tandem repeats of simple motifs usually dimers or trimers. Also referred to as STR: short-tandem-repeat.
Parentage analysis	The general analysis of genotypes as it relates to parentage and may include parentage verification, parentage discovery, and maternal-grandsire prediction.
Parentage discovery	The process by which a number of potential parents, usually male but also possibly female, of an animal are examined and based on matching genotypes reduced to the most likely sire and/or dam.
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 an animal to determine if one or both are excluded as the parent(s).
QTL	Quantitative Trait Loci. A genomic region that has an impact on a quantitative trait, like height. This region may have a small effect, <0.01%, or large effect, >5%, on the phenotype. A quantitative trait will have multiple QTL spread over the genome.
Sire verification	The same as parentage verification but based on consideration of a recorded sire only.
SNP	Single nucleotide polymorphism: single base change in a DNA sequence.

1.4 Current and Potential Uses of DNA Technologies

1.4.1 Parentage verification and parental assignment

Prior to the emergence of SNP genotyping, parentage verification was the main commercial use of genetic markers. Traditionally, parentage testing was based on the exclusion of relationship (i.e.: sire or dam) when an animal has a genotype inconsistent to a putative relationship. New trends in animal production systems are tending to encourage animal production in larger numbers per farm in response to environmental and production related constraints. In these large settings, multiple animals could be bred or give birth on the same day, which can result in more pedigree recording errors. As the cost of the analysis decreases and the number of genetic markers available increases, breed societies are now able to build up pedigree records using genetic markers to predict the pedigree of calves born in a herd at a given time. This normally requires a prior knowledge of candidate sires and dams for a calf when lower number (<200) of markers are used, but with enough SNP the correct parents can be predicted without prior knowledge being available as long as the parent is also genotyped. The probability of assignment to a correct pair of animals will depend on the number of markers used, number of alleles per loci, the minor allele frequency in the population, the number of parents, and the number of possible matings. The International Society of Animal Genetics (www.isag.us) has species-specific panels recommended of microsatellite and SNP markers for this purpose, which can be accessed via a link such as provided in Appendix 1. Link to SNP markers recommended by ISAG for parentage verification. For cattle, ICAR has developed a set of parentage SNP, ICAR554, which incorporates the ISAG recommended panel and other highly informative SNP. This panel allows for highly accurate parentage validation and discovery while not allowing for accurate imputation to a higher density. Therefore, the ICAR554 panel can be shared among countries and competitors for parentage analysis without fear of others being able to use them to predict genomic breeding values. ICAR and the Interbull Centre collaborate in offering an international genotype exchange service, referred to as GenoEx, which is described further in Chapter 5 specifically for the exchange of SNP genotypes for the purposes of parentage analysis.

1.4.2 Traceability and authentication of animal products offered to consumers

Due to multiple crisis, including BSE outbreaks to ground beef containing horsemeat, and with increased consumer interest in where their food comes from the traceability of meat products is of greater concern to the industry. Traceability is based on the availability of a verification and control system that monitors all relevant details throughout the entire livestock production chain. Since an individual's genetic sequence is unique and does not change, its DNA remains constant from 'conception to consumption'. Therefore, use of genetic markers allows one to match the DNA of an individual at birth to the final product.

Genetic markers for the authentication of animal products for labels of quality related to geographic location and labels of quality related to specific breeds or their crosses are/or will be very useful. However, this requires the establishment of molecular standards or allele frequencies for each breed within a species. A lot of information is coming from studies of genetic diversity among breeds. Genes subject to intense selection in each population are of particular interest. With a large enough set of SNP and genotyped purebred reference animals it is also possible to predict the most likely breed composition of individuals.

1.4.3 Molecular genetic information for marker-assisted selection schemes

Quantitative traits are generally assumed to be controlled by a large number of genes. However, individual genes sometimes account for a significant amount of variation of the trait. Such is the case for the Myostatin gene and double muscling in beef cattle, the DGAT1 gene and milk components in dairy cattle, or the Booroola fecundity gene and ovulation rate

in sheep. Since the genotype of an animal does not change during its lifetime, use of DNA information through the identification of markers linked to QTL with effects on production traits or the identification of a gene itself together with the causative variant is of great interest. Nevertheless, with complex traits there is a growing need of having a sufficiently large marker set to incorporate molecular information for selection decisions. Including genomic information as a selection criterion is of special interest for traits that are difficult and costly to measure and/or are measured late in life. By 2018, >116,000 cattle, >10,000 chicken, >28,000 swine, and >2,000 sheep QTL have been identified that are associated with economically important traits such as health, carcass, milk, fertility, and body conformation. The AnimalQTLdb database housed at the National Animal Genome Research Program contains up to date information on cattle, chicken, horse, pig, trout, and sheep QTL data assembled from published data.

Recording schemes have been collecting information for decades on the most common production traits measured in domestic livestock. There is an ever-increasing volume of information becoming available, but for some traits like meat quality, disease resistance and feed efficiency, those records are very expensive to measure, difficult to obtain, or are performed late in the animal's life. Because of these challenges information for such traits is commonly collected on a reduced number of animals in any given population.

For these challenging, but economically important traits, genetic markers and genomic selection offer significant opportunities for trait selection where it was not economically feasible before. In general, genetic markers and genomics will play an important role for important traits regardless the livestock species. Genomics can also allow us to increase selection intensities since we can predict genomic breeding values on a large number of animals and thus have more candidates for selection.

1.4.4 Disease resistance and genetic defects

Another group of traits with a high potential for the use of molecular data and genomics are those linked to resistance, resilience, and susceptibility to diseases. There are a number of multi-factorial or complex diseases that are the result of the interaction between an animal's genome and environmental components. Disease resistance traits are among the most difficult to include in genetic improvement programs because they require good field measurement of the disease status of the animals and a systematic control of management or environmental conditions that allow for the identification of the environmental influence on the health status of the animal. Infectious diseases depend very much upon environmental factors such as the degree of exposure to the pathogen agent. Thus, if exposure is low, animals will show little variation. Part of the phenotypic differences for resistance may be differences in the degree of challenge. Therefore, if genes or genetic markers linked to resistance are correctly identified, resistant animals will be able to be selected on the base of their genomic information. For many diseases, identification of genes associated with resistance will require experimental conditions to be used. Genetic analysis to identify heterozygous carriers of genetic diseases caused by single, recessive genes are currently in use. Examples in dairy cattle include complex vertebral malformation (CVM), brachyspina (BY), cholesterol deficiency (CD) and several genes, gene regions or haplotypes causing embryo loss or stillbirth in different dairy breeds. In 2018, OMIA (Online Mendelian Inheritance in Animals), listed >770 traits or genetic defects in livestock with a known causative mutation (cattle: 150, sheep: 50, chicken: 44, horse: 44). Including these causative allele or associated haplotypes in a breeding program will allow producers to minimize their risk from genetic defects while maximizing genetic progress from beneficial traits.

1.5 Technical Aspects

1.5.1 DNA collection

Systematic collection of DNA is recommended in several livestock populations. DNA may be obtained from any nuclear cell in the body. Protocols for DNA extraction are now available for blood (white cells), semen, saliva (epithelial cells), hair follicles, muscle, skin, organs (such as liver, spleen etc.). Red blood cells may also be used for poultry as they retain the nuclear body while most other species do not. Small amounts of tissue material are required for routine DNA analysis. However, if there are multiple future uses of an individual's DNA (whole genome sequencing, traceability, causative allele validations, ...), then DNA storage costs, extraction costs, quality, and quantity obtained by different protocols will have to be carefully examined and optimized. Common collection methods include hair follicles, tissue samples (often ear punch) in an enclosed container, blood spots on filter paper, and nasal swabs.

1.5.2 Data collection

A centralised database may be organised in respect to the main uses of the genetic information:

a. Parent verification, assignment, and/or discovery
b. Traceability of meat products
c. Breed identification or breed diversity
d. Qualitative and quantitative traits

Database tables may contain:

a. Animal identification to link to all other information on the animal and its relatives.
b. Number of genetic markers: n
c. Standard name of each marker i (for i= 1, n)
d. Accession number for marker such as the dbSNP ID
e. Alleles for marker i
f. Genomic location of marker i
g. Affect of non-reference allele on the protein
h. Phenotypic affect of the allele
i. Association with other traits

1.5.3 Genomic Quality Control

One of the most important parts of a large genomic database is to ensure that a genotype associated with an individual animal truly belongs to that animal. Most large livestock genomic databases deal with SNP data only so this section will focus quality control for that genomic data type. Both sample and SNP quality control measures are needed, and it is encouraged to develop a system for them early. Sources of errors include producers, laboratory, and A.I. centres.

Recommended genetic quality control measures include the exclusion of a genotype when:

a. Call rate is less than 90% since lower call rates indicate that the accuracy of the remaining genotype could be questionable. The genotype concordance rate is <99% when call rates are below 90%.
b. Deviation from Hardy-Weinberg equilibrium (excluding those that are lethal or strongly selected upon).
c. The SNP constantly has >1% parent-progeny conflicts when the other SNP do not.
d. If the animal's genotype frequency (AA, AB, BB) is <20%.
e. If there are unexpected alleles (eg.: ATCG when expecting AB).

Recommended animal quality control measures include discarding the genotype when:

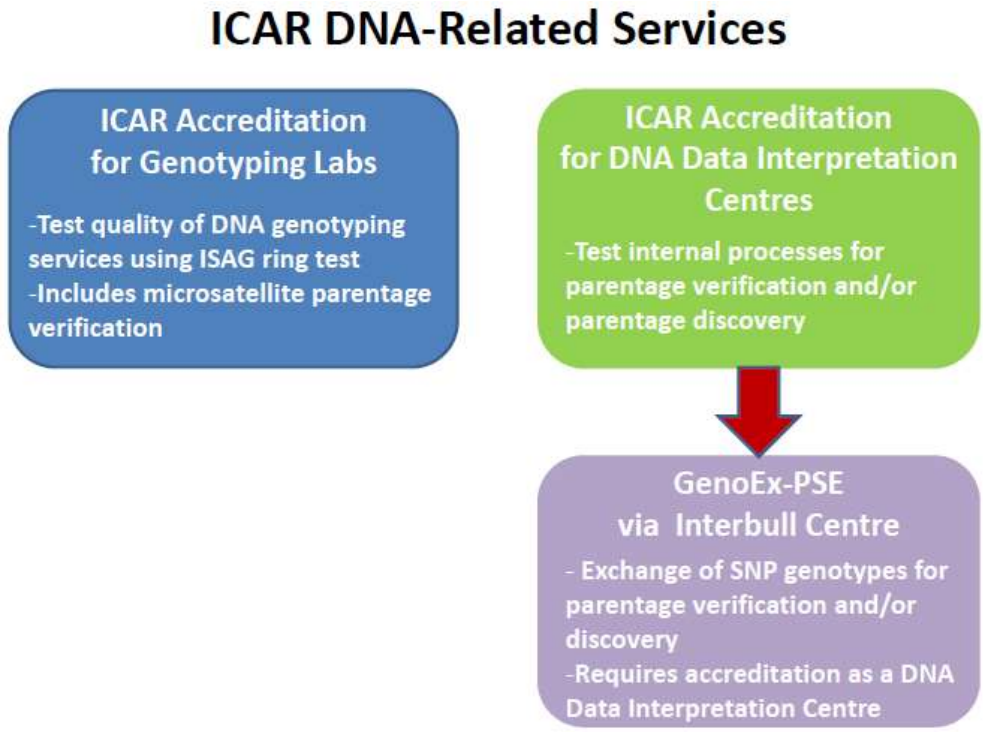
a. The predicted sex from SNP located on chromosome(s) X and/or Y do not match the animal's listed sex.
b. The genotype is >99% identical to another animal who is not its twin.
c. An animal's genotype is <99% identical to its previous genotype.
d. The predicted breed is different from the reported/recorded breed.

For standardization purposes with respect to the nomenclature of genes or loci, a web site is available at: https://www.genenames.org/about/guidelines#genenames and markers at: http://www.HGVS.org/varnomen.

2 ICAR Services Related to DNA Technology

Effective 2018, ICAR offers three services that are related to the use of DNA all of which are linked to parentage analysis in one form or another, as shown in Figure 1. ICAR DNA services., and describing in more detail in the sections below.

Figure 1. ICAR DNA services.



3 ICAR Accreditation of Laboratories Providing DNA Genotyping Services

3.1 Introduction

Considering the need for high quality standards in all uses of molecular data, ICAR has for several years offered an accreditation service based on defined minimum requirements for laboratories providing DNA genotyping services. The basic requirements of this accreditation include proof of the minimum internal management quality assurance standards and participation in an international ring test developed and offered by the International Society for Animal Genetics (ISAG).

In addition, such laboratories generally have been analyzing the resulting genotypes to carry out microsatellite- and/or SNP-based parentage analysis services including either parentage verification or animal identification confirmation. This ICAR accreditation service has previously been used for recognizing the genotyping laboratory as an accredited organization to provide parentage analysis functions without specifically testing the technical accuracy of doing so. Effective 2018, the launch of the SNP-based parentage analysis accreditation service for DNA Data Interpretation Centres has replaced the previous laboratory accreditation for SNP-based parentage verification. In the future, a similar technical process for the accreditation of microsatellite-based parentage analysis may be introduced by ICAR but until such time, the existing process for the accreditation of genotyping laboratories will remain in effect.

The following guidelines for accreditation are provided for microsatellite- and SNP-based genotyping in cattle. Minimum requirements for additional species and other DNA tests may be defined in the future.

3.2 Scope

These guidelines are for the accreditation, by ICAR, of genotyping laboratories that analyze biological samples from cattle using microsatellite- and or SNP-based genotyping, which may be subsequently used for various levels of parentage analysis, genotype imputation, estimation of genomic breeding values and other activities related to genomic selection strategies. This accreditation process also includes parentage verification based on microsatellites. For ICAR accreditation associated with SNP-based parentage verification, genotyping laboratories must apply to ICAR for it parallel service of parentage analysis accreditation for DNA data interpretation centres, as described below.

3.3 ICAR Rules and Guidelines for Accreditation of Genotyping Laboratories

The accreditation process comprises the following steps:

a. Application for accreditation
b. Payment of relevant fee
c. Review of application
d. Granting of accreditation

3.3.1 Application for accreditation

Laboratories requesting accreditation for microsatellite- and/or SNP-based genotyping must apply by downloading and completing the appropriate forms as in Appendix 2. Application form for microsatellite-based parentage verification in cattle, and Appendix 3. Application form for SNP-based parentage verification in cattle respectively and emailing them to the ICAR secretariat (dna@icar.org). The forms must be filled out accurately and completely, providing the necessary documentation as required.

3.3.2 Payment of relevant fee

Along with the completed application form the applicant must also provide full payment of the relevant fee as established by ICAR and given in Appendix 4. ICAR DNA Laboratory Accreditation Service fees.

3.3.3 Review of application

The application will be evaluated by a committee of experts appointed by ICAR that will either:

a. Approve the application
b. Request additional information, or
c. Reject the application

In the case of rejection, the laboratory may make a new submission at least one year after the failed application.

3.3.4 Granting of accreditation

Accreditation will be given for a two-year period.

3.3.5 Renewal of accreditation

At the end of the two-year term, a laboratory can apply for renewal of their accreditation by submitting an application as described in paragraph 3.3.1 above.

3.3.6 Laboratory accreditation

Currently, either ISO17025 or ISO9001 accreditation is mandatory for microsatellite (STR)-based accreditation. Effective the 2020 ICAR call for accreditation of genotyping laboratories, ISO17025 accreditation, or an equivalent accreditation for ensuring quality internal management systems, will be a mandatory requirement for SNP-based accreditation. In addition, effective the 2020 call for accreditation of genotyping laboratories, ISO9001 certification will no longer be acceptable and only ISO17025, or an equivalent accreditation, will be an acceptable level of accreditation to ensure quality internal management systems for microsatellite (STR)-based accreditation.

3.3.7 Participation and performance in ring test

ISAG conducts an international ring (comparison) test of laboratories for both microsatellite- and SNP-based genotyping. The participation in ISAG and performance within these ring tests must be disclosed, and certificates provided, when available. Applicants must also sign a release allowing ISAG to directly disclose their ring test results to ICAR. The participation in at least two ISAG ring tests is a minimum requirement. For the ISAG microsatellite ring test, lab genotyping performance for the official set of 12 ISAG microsatellites must be disclosed. The committee of experts will decide performance thresholds for each ring test with due consideration for the structure of the ring test and the average performance of laboratories in the ring test that year. Only those laboratories achieving Rank 1 status in the annual ISAG ring test shall automatically receive ICAR accreditation as a genotyping laboratory and ICAR accreditation of genotyping laboratories with a lower ring test rank shall be at the discretion of the committee of experts.

3.3.8 Microsatellite markers

The names of all microsatellites typed on all animals (marker set I) and of the additional ones assayed in the case of unresolved parentage (marker set II) must be declared, as well as the number of animals typed in at least the last two years. The minimum requirement for international exchange is the complete set of 12 official ISAG microsatellite markers. To ensure sufficient experience within the lab, analysis of 500 animals per year is set as minimum requirement for microsatellite parentage verification certification.

Appendix 5. ISAG recommended microsatellites for parentage verification in cattle contains the list of microsatellite markers recommended by ISAG and the method for calculating 1 parent and 2 parent exclusion probabilities. The rules for microsatellite-based parentage verification in cattle are described in Appendix 6. Rules for microsatellite-based parentage verification in cattle. Exclusion probability (PE; 2 parents and 1 parent) of each marker and of the complete marker sets must be calculated and provided in the application. The type of population and number of animals (minimum 150) used for computations are to be described. ICAR recommends using Holstein as a reference group when possible. The ICAR committee of experts will evaluate that an appropriate PE is reached for accreditation, on the basis of the population analyzed.

3.3.9 SNP markers

The name of all SNP genotyped on all animals (marker set I) and of the additional markers assayed in the case of unresolved parentage (marker set II) must be declared, as well as the number of animals genotyped in at least the last two years. It is a minimum requirement to

use at least 95 SNP from the set recommended by ISAG (see Appendix 7. ISAG recommended SNP markers for parentage verification in cattle) on all animals genotyped.

3.3.10 Marker nomenclature

Nomenclature of markers must be described. ISAG nomenclature is required for the official ISAG 12 marker set as well as for the ISAG SNP marker set.

4 Accreditation of Organisations Performing SNP-Based Parentage Analysis

4.1 Introduction

With the advent of SNP genotyping, the function of DNA genotyping as a laboratory activity can be separated from the functions of performing parentage verification and parentage discovery. Consequently, ICAR has established a separate accreditation for applying the results of SNP-based genotyping, which may be undertaken by laboratories, breed association societies, genetic evaluation centres and any other organization involved in parentage verification and/or the data processing of SNP genotypes.

Parentage verification and discovery are concerned with using the results that are delivered by the laboratories from DNA genotyping and require SNP genotypes for the animal itself, its recorded parents and other possible parents in the case of parentage discovery. Organizations undertaking this function may be service providers between laboratories that ICAR has accredited for microsatellite- and or SNP-based DNA genotyping and end users that may include breed societies, breeding companies, breeders and commercial farmers.

Service providers could use different laboratories for different breeds and/or species. Considering the importance of animal identification and parentage verification in animal recording, ICAR has decided to define the minimum requirements for using the results of DNA genotyping, and other information, for the purpose of:

a. Parentage verification
b. Parentage discovery, and
c. Animal identification confirmation

The purpose of these guidelines is to provide a basis for the accreditation of processes used by organizations that use SNP genotypes in cattle. Minimum requirements for additional species and other DNA analyses may be defined in the future.

4.2 Scope

These guidelines are for the accreditation, by ICAR, of organizations that use the results of SNP-based tests for parentage analysis in cattle, which includes parentage verification, parentage discovery and/or animal identification confirmation.

4.3 Accreditation of Organizations Performing Parentage Analysis

The ICAR accreditation process comprises the following steps:

a. Application for accreditation
b. Payment of relevant fee
c. Review of application
d. Technical processing of test data files

e. Granting of accreditation

4.3.1 Application

Organizations carrying out SNP-based parentage analysis and requesting ICAR accreditation as a DNA Data Interpretation Centre must apply by downloading and completing the appropriate form included below as Appendix 8. Application form for organizations seeking ICAR parentage analysis accreditation for DNA data interpretation centres. This form must be filled out accurately and completely, providing necessary documentation as required, and submitted to ICAR with payment of the appropriate fee.

4.3.2 Review of application

The application will first be reviewed internally by ICAR for its completeness and additional details may be requested as needed. ICAR administration will also confirm receipt of the applicable fee.

4.3.3 Technical processing of test files

The applicant organization will receive a set of data files from ICAR through the Interbull Centre, for processing using its existing procedures for carrying out the level of parentage analysis for which the applicant is seeking ICAR accreditation as a DNA Data Interpretation Centre. A detailed description of this step is described in the Applicant's Guide for ICAR Parentage Analysis Accreditation for DNA Data Interpretation Centres included below as Appendix 9. Applicant's Guide for ICAR Parentage Analysis Accreditation for DNA Data Interpretation Centres. In order for the applicant to be successful in obtaining the requested ICAR accreditation, it's procedures for conducting parentage analysis must exactly follow the ICAR Guidelines for Parentage Verification and Parentage Discovery Based on SNP Genotypes, which is also included below in Appendix 10. ICAR Guidelines for Parentage Verification and Parentage Discovery Based on SNP Genotypes. The list of SNP to be used for either parentage verification or parentage discovery are available in Appendix 11. List of SNP to be used for either parentage verification or parentage discovery. Once the applicant has completed its internal parentage analysis procedures based on the accreditation test files it received, it must send a data file of results back to the Interbull Centre. A maximum time period for 90 calendar days will be allowed for the applicant to submit acceptable files of results back to the Interbull Centre.

4.3.4 Granting of accreditation

Once the Interbull Centre receives the file of parentage analysis results from the applicant, it will complete the technical review and determine if the applicant has successfully completed the accreditation or not. The Interbull Centre shall inform ICAR of the results and ICAR shall issue a formal notification to the applicant. In the event the applicant was not successful in receiving ICAR accreditation, the applicant may initiate a new request for accreditation by completing and submitting the appropriate forms and providing payment of the applicable fee, as outlined above.

5 Genotype Exchange Service - GenoEx-PSE

Effective 2018, ICAR has made available a genotype exchange service for parentage analysis, GenoEx-PSE, offered through the Interbull Centre. The main goal of this service is to facilitate the international exchange of SNP genotypes such that approved service users can carry out parentage analysis services at a national level in an efficient manner. The GenoEx-PSE database system and user interface has been developed to allow for the exchange of SNP genotypes for either parentage verification or parentage discovery based on the list of SNP

provided in Appendix 11. List of SNP to be used for either parentage verification or parentage discovery.

In order for an organization to qualify as a service user for GenoEx-PSE, it must first receive ICAR accreditation as a DNA data interpretation centre. The level of such ICAR accreditation (i.e.: for SNP-based parentage verification alone or for both SNP-based parentage verification and discovery) shall determine the highest level of SNP that may be exchanged via the GenoEx-PSE service. For detail associated with this ICAR service, refer to the GenoEx-PSE web site at www.GenoEx.org.

6 LIST OF APPENDICIES

6.1 Appendix 1. Link to SNP markers recommended by ISAG for parentage verification

http://www.isag.us/Docs/Cattle-SNP-ISAG-core-additional-panel-2013.xlsx

6.2 Appendix 2. Application form for microsatellite-based parentage verification in cattle

Please refer here on the ICAR website for the Application Form for accreditation of microsatellite-based parentage verification in cattle.

6.3 Appendix 3. Application form for SNP-based parentage verification in cattle

Please refer here on the ICAR website for the Application form for accreditation of SNP-based parentage verification in cattle.

6.4 Appendix 4. ICAR DNA Laboratory Accreditation Service fees

Please refer here on the ICAR website for DNA testing accreditation services fees.

6.5 Appendix 5. ISAG recommended microsatellites for parentage verification in cattle

Please refer here on the ICAR website for the list of ISAG recommended microsatellites for parentage verification in cattle. The method of calculation is described here.

6.6 Appendix 6. Rules for microsatellite-based parentage verification in cattle

Please refer here on the ICAR website for the rules for microsatellite-based parentage verification in cattle.

6.7 Appendix 7. ISAG recommended SNP markers for parentage verification in cattle

Please refer here on the ICAR website for the ISAG recommended SNP markers for parentage verification in cattle.

6.8 Appendix 8. Application form for organizations seeking ICAR parentage analysis accreditation for DNA data interpretation centres

Please refer here on the ICAR website for the application form for organizations seeking ICAR accreditation status as a DNA data interpretation centre.

6.9 Appendix 9. Applicant's Guide for ICAR Parentage Analysis Accreditation for DNA Data Interpretation Centres

Please refer here on the ICAR website for the Applicant's Guide for ICAR Parentage Analysis Accreditation for DNA Data Interpretation Centres.

6.10 Appendix 10. ICAR Guidelines for Parentage Verification and Parentage Discovery Based on SNP Genotypes

Please refer here on the ICAR website for the ICAR Guidelines for Parentage Verification and Parentage Discovery Based on SNP Genotypes.

6.11 Appendix 11. List of SNP to be used for either parentage verification or parentage discovery

Please refer here on the ICAR website for the list of SNP to be used for either parentage verification or parentage discovery.

6.12 Appendix 12: List of the ICAR 554 SNP List for Parentage Discovery

Please refer here on the ICAR website for the list of the ICAR 554 SNP for parentage discovery