ICAR SNP-Based Parentage Analysis Certification for DNA Data Interpretation Centres

- Applicant's Guide -

Revised October 2025

Overview

This document serves as a guide for organizations that apply to ICAR for its Parentage Analysis Certification for DNA Data Interpretation Centres. In brief, the following are the steps of this ICAR certification service:

1. Applicant completes the required forms available on the ICAR web site and submits them to ICAR along with payment of the required fee established by ICAR. The applicant may choose to apply for certification for SNP-based Parentage Verification alone or certification for both Parentage Verification and Parentage Discovery, which are conducted separately and sequentially.

2. ICAR will handle the administration of the application process and once completed, ICAR will inform the Interbull Centre to proceed with the technical component of the certification process.

3. Interbull Centre sends by email this Applicant's Guide and the various data files to the contact person provided by the applicant.

   3.1 For **Parentage Verification** certification, these data files include (see Section 1 below on pages 2 to 5):
   a) Animal Genotypes based on the SNP approved by ICAR for Parentage Verification (≈200).
   b) Pedigree information for animals in the genotype file and potential ancestors.
   c) Summary file of Parentage Verification analysis results that must be achieved by the applicant to be successful for ICAR certification.

   3.2 For **Parentage Discovery** certification, these data files include (see Section 2 below starting on page 6):
   a) Animal genotypes based on the SNP approved by ICAR for Parentage Discovery (≈554).
   b) Pedigree information for animals in the genotype file and potential ancestors.
   c) Parentage Verification Results file that is a reduced version of the Animal Genotypes file that only includes animals to be included in the Parentage Discovery analysis.
   d) Discovery Groups Summary file with the Parentage Discovery analysis results that must be achieved by the applicant to be successful for ICAR certification.

4. Applicant receives the certification test files from the Interbull Centre and processes them using internal parentage analysis software. This software must strictly follow the ***ICAR Guidelines for Parentage Verification and Parentage Discovery Based on SNP Genotypes***, as posted on the ICAR web site, in order to successfully pass the requested ICAR certification.

5. Within 90 days from receiving the certification test files from the Interbull Centre, the applicant must send by email to the Interbull Centre, the detailed Results or Discovery Results file derived from applying its internal parentage analysis software. Failure to respect the 90-day time period will result in ICAR notification of an unsuccessful certification status and the applicant has the option to reapply by initiating step 1 described above at any point in time. Within the 90-day time period, the applicant may submit the detailed Results or Discovery Results file up to three times

for first applications and up to two times for renewal applications to resolve any errors and/or issues that may arise during the certification process.

6. Interbull Centre will compare the applicant's Results file or Discovery Results file to the correct answer file associated with the certification test files sent to the applicant. An exact match of results is required, including respecting the defined file layouts outlined in this document, to achieve a successful status for receiving the associated ICAR certificate.

7. Interbull Centre will communicate the Pass or Fail status of the applicant's Results file or Discovery Results file directly to the applicant, while also informing ICAR. As soon as possible thereafter, ICAR administration will issue the proper correspondence to the applicant. In the event of a successful status, ICAR will provide the appropriate SNP-Based Parentage Analysis certificate for DNA Data Interpretation Centres and the date of that certificate shall serve as the anniversary date for the specific parentage analysis certification from ICAR. All such certifications must be renewed, with payment, every two years within the 3-month period prior to the anniversary date of the ICAR certificate. In the event of a successful renewal, the existing certification shall be extended for an additional two years from the anniversary date. In the event the applicant was not successful in receiving the ICAR certification, the applicant may reapply by initiating step 1 described above at any point in time. In the event that the applicant's ICAR certification period has lapsed without a successful renewal in advance of the end of the 2-year period from the anniversary date, the applicant may reapply by initiating step 1 described above at any point in time and a new anniversary date will be designated at the time when ICAR issues a new successful certificate.

File Names and Description

As outlined above, the process for obtaining ICAR Parentage Analysis Certification for DNA Data Interpretation Centres involves the applicant receiving data files from the Interbull Centre and returning a file with results from carrying out the parentage analysis using their internal procedures. The following is a more comprehensive description of the data files involved.

Data Files Received by the Applicant

For each applicant, Interbull Centre provides a unique set of data files for testing the parentage analysis procedures developed and used internally by the applicant. Each set of files includes a unique 5-digit numerical value, expressed as XXXXX in the file names presented below. As much as possible, the file formats used for this certification process follow field descriptions and formats used for other services provided through the Interbull Centre. Similar types of files are involved for Parentage Verification and Parentage Discovery but they are described in separate sections below in this document.

Section 1: Data Files for Parentage Verification

For Parentage Verification certification, there are three files involved that are provided to the applicant:

a) Animal Genotypes (genotype_verifyAB_XXXXX.csv)

The .csv file of genotypes follows the same format as one of the genotype exchange file formats to be used by the GenoEx-PSE service (File 704_AB format) as described below. For applicants that prefer to receive the genotype file in the File 704_TOP format), you are asked to contact the Interbull Centre.

Field Name	Size	Example	Description
Record Type	6 or 7 (fixed)	704-AB (or 704-TOP)	Alphanumeric
Animal ID - Breed Code	3 (fixed)	BSW	Alpha
Animal ID - Nation Code	3 (fixed)	AUS	Alphanumeric (USA, 840, CAN, GBR, FRA, DEU, ...)
Animal ID - Sex Code	1 (fixed)	M	Alpha (M or F)
Animal ID - Registration	18 (maximum)	A1234567890	Alphanumeric
SNP Name	70 (maximum)	ARS-BFGL-NGS-104897	Alphanumeric
Allele 1	1 (fixed)	A/B or A/C/G/T	Alpha
Allele 2	1 (fixed)	A/B or A/C/G/T	Alpha

b) Pedigree (ped_verify_XXXXX.csv)

The file of pedigree data follows the same format as used by Interbull for distributing pedigree information to its customers (pedig_BBB.csv, where BBB refers to the Interbull 3-character breed code). For this ICAR certification process, the following layout and description is used.

Field Name	Size	Example	Description
Animal ID (note 1)	19 (fixed)	XXXZZZF001234567890	Alphanumeric
Sire ID (note 1)	19 (fixed)	XXXZZZM002345678901	Alphanumeric (filled as 0000000000000000000 when unknown)
Dam ID (note 1)	19 (fixed)	XXXZZZF003456789012	Alphanumeric (filled as 0000000000000000000 when unknown)
Animal's Birth Date	8 (fixed)	YYYYMMDD	Numeric
Animal Name	Variable		Always blank
Verification Status	1 (fixed)	U	Always filled as U
Sending Country	3 (fixed)	ZZZ	Always filled as ZZZ

Note 1: First six characters for "Breed" and "Country of Registration" are filled with fictitious values of XXX and ZZZ, respectively.

In essence, the applicant may choose to only use the first four fields included in this comma delimited .csv file and ignore the last three fields. Note that within the Animal ID field, the sex of the animal (i.e.: M or F as character 7), as well as the Animal's Birth Date, are important content that is required for conducting correct Parentage Verification analysis, including the minimum age difference of 517 days (i.e.: 17 months) between an animal and any qualifying parent.

The Pedigree file includes a single record for each of the approximately 15,000 animals, of which approximately 4,000 represent the animals/progeny of interest and the remainder are potential parents of those animals. The progeny/animals of importance for this ICAR Certification are those that have an Animal ID beginning with either XXXZZZF00142 for females or XXXZZZM00142 for males, and these animals must all be included in the Results file to be returned by the applicant to the Interbull Centre.

For Parentage Verification certification, the Animal Genotype file will have up to 200 records (i.e.: one for each called SNP) for each animal in the Pedigree file, which means a maximum total of 3 million records.

c) Summary (summary_XXXXX.csv)

The ICAR certification for Parentage Verification tests 22 distinct cases, as outlined in the following table, depending on the result found for verifying the recorded sire, dam and mating combination involving the trio of animal, sire and dam. Specific to the genotype and pedigree files provided to the applicant, the counts of N1, N2, ..., N22 are provided in the Summary file to enable the applicant to know for certain when they have not yet passed the certification process. Note that the 22 cases tested by this ICAR certification process represent a selected subset of all possible cases that should be handled internally by the applicant for parentage analysis. When the internal parentage analysis procedures applied by the applicant have correctly applied the ICAR Guidelines, then the Results file (see below) should provide counts that match exactly those in the Summary file.

Case No.	Sire Conclusion	Dam Conclusion	Mating Conclusion	Count
1	Sire_Accepted	Dam_Accepted	Mating_Accepted	N1
2	Sire_Accepted	Dam_Accepted	Mating_Doubtful	N2
3	Sire_Accepted	Dam_Accepted	Mating_Excluded	N3
4	Sire_Doubtful	Dam_Accepted	Not_Checked	N4
5	Sire_Excluded	Dam_Accepted	Not_Checked	N5
6	Sire_Accepted	Dam_Doubtful	Not_Checked	N6
7	Sire_Accepted	Dam_Excluded	Not_Checked	N7
8	Sire_Doubtful	Dam_Doubtful	Not_Checked	N8
9	Sire_Doubtful	Dam_Excluded	Not_Checked	N9
10	Sire_Excluded	Dam_Doubtful	Not_Checked	N10
11	Sire_Excluded	Dam_Excluded	Not_Checked	N11
12	Sire_Unknown	Dam_Accepted	Not_Checked	N12
13	Sire_Accepted	Dam_Unknown	Not_Checked	N13
14	Low_Call	Low_Call	Not_Checked	N14
15	Low_Call	Dam_Accepted	Not_Checked	N15
16	Low_Call	Dam_Doubtful	Not_Checked	N16
17	Low_Call	Dam_Excluded	Not_Checked	N17
18	Sire_Accepted	Low_Call	Not_Checked	N18
19	Sire_Doubtful	Low_Call	Not_Checked	N19
20	Sire_Excluded	Low_Call	Not_Checked	N20
21	Sire_Not_Genotyped	Dam_Accepted	Not_Checked	N21
22	Sire_Accepted	Dam_Not_Genotyped	Not_Checked	N22

Note that Case 14 represents the situation when the genotype for the animal itself has too low of a call rate to be used for parentage analysis, so the conclusion of Low_Call is assigned for both the Sire and Dam and the Mating is therefore not checked.

In general, the Mating Conclusion is always Not_Checked except for cases whereby both the Sire Conclusion is Sire_Accepted and the Dam Conclusion is Dam_Accepted (i.e.: cases 1, 2 and 3).

Parentage Verification Results File to be Returned by the Applicant to the Interbull Centre

Once the applicant obtains output from their internal parentage analysis procedures for which the counts exactly match those for each case included in the Summary file, then the applicant should create and send a detailed Results file back to the Interbull Centre. **This file must be a comma (,) delimited .csv file respecting the naming structure as follows**:

results_XXXXX.csv

where XXXXX refers to the same 5-digit numerical value included in the data file provided to the applicant by the Interbull Centre.

The content of the Results file should respect the file layout described below and only include those animals (≈4,000) in the genotype file that have the numerical portion of their Animal ID (Animal ID - Unique Number) starting with "00142".

Field #	Field Name	Size	Example	Description
1	Animal ID - Breed Code	3 (fixed)	XXX	Always XXX
2	Animal ID - Nation Code	3 (fixed)	ZZZ	Always ZZZ
3	Animal ID - Sex Code	1 (fixed)	F	Always F or M
4	Animal ID - Unique Number	12 (fixed)	001426789012	Numeric and must start with 00142
5	No. Usable SNP - Animal	3 (maximum)	190	Count of usable SNP in the Animal's genotype
6	No. Usable SNP - Sire	3 (maximum)	196	Count of usable SNP in the Sire's genotype
7	No. Usable SNP - Dam	3 (maximum)	192	Count of usable SNP in the Dam's genotype
8	Sire Conclusion	Variable	Sire_Accepted	Must be assigned as listed in the Summary file table above under "Sire Conclusion"
9	Dam Conclusion	Variable	Dam_Excluded	Must be assigned as listed in the Summary file table above under "Dam Conclusion"
10	Mating Conclusion	Variable	Not_Checked	Must be assigned as listed in the Summary file table above under "Mating Conclusion"
11	No. SNP Conflicts - Sire[1]	3 (maximum)	5	Count of the number of SNP in conflict between the Animal and the recorded Sire
12	No. SNP Conflicts - Dam[2]	3 (maximum)	4	Count of the number of SNP in conflict between the Animal and the recorded Dam
13	No. SNP Conflicts - Mating[3]	3 (maximum)	5	Count of the number of SNP in conflict when considering the mating of the recorded Sire and Dam as the parents of the Animal
14	Case Number	2 (maximum)	8	Fill in with the appropriate Case No. as described in Summary file section above

Note 1: Field 11: No. SNP Conflicts - Sire must be blank when Sire Conclusion has a result of Low_Call.
Note 2: Field 12: No. SNP Conflicts - Dam must be blank when Dam Conclusion has a result of Low_Call.
Note 3: Field 13: No. SNP Conflicts - Mating must be blank when Mating Conclusion has a result of Not_Checked.

For sake of clarity, the following are examples of correct records with required fields having a value and the three fields associated with No. SNP Conflicts having missing values when appropriate:

XXX,ZZZ,M,00142xxxxxxx,187,192,0,Sire_Accepted,Dam_Not_Genotyped,Not_Checked,0,,,22
XXX,ZZZ,F,00142xxxxxxx,195,195,192,Sire_Doubtful,Dam_Accepted,Not_Checked,5,0,,4
XXX,ZZZ,M,00142xxxxxxx,194,195,195,Sire_Accepted,Dam_Accepted,Mating_Doubtful,0,0,4,2
XXX,ZZZ,F,00142xxxxxxx,179,195,195,Low_Call,Low_Call,Not_Checked,,,,14

Section 2: Data Files for Parentage Discovery

For Parentage Discovery certification, the applicant must first be successful in completing the processing of test files for Parentage Verification as outlined in Section 1 above. Applicants may start the Parentage Discovery certification using either of the following two options:

Option A: The applicant uses the two raw data files provided as input into internal processes for conducting Parentage Discovery. These two files are identical in nature and format as the two input files provided for Parentage Verification certification as described below. It is important to note, however, that all animals for which the Sire Conclusion is Sire_Accepted, the Dam Conclusion is Dam_Accepted and the Mating Conclusion is Mating_Accepted from the Parentage Verification analysis (i.e.: Case 1 animals in the table on page 4) are therefore excluded from the subsequent Parentage Discovery processing.

a) Animal Genotypes (genotype_discoveryAB_XXXXX.csv)

The .csv file of genotypes follows the same format as one of the genotype exchange file formats to be used by the GenoEx-PSE service (File 704_AB format) as described below. For applicants that prefer to receive the genotype file in the File 704_TOP format, you are asked to contact the Interbull Centre.

Field Name	Size	Example	Description
Record Type	6 or 7 (fixed)	704-AB (or 704-TOP)	Alphanumeric
Animal ID - Breed Code	3 (fixed)	BSW	Alpha
Animal ID - Nation Code	3 (fixed)	AUS	Alphanumeric (USA, 840, CAN, GBR, FRA, DEU, ...)
Animal ID - Sex Code	1 (fixed)	M	Alpha (M or F)
Animal ID - Registration	18 (maximum)	A1234567890	Alphanumeric
SNP Name	70 (maximum)	ARS-BFGL-NGS-104897	Alphanumeric
Allele 1	1 (fixed)	A/B or A/C/G/T	Alpha
Allele 2	1 (fixed)	A/B or A/C/G/T	Alpha

Note: Since the maximum number of possible SNP used for Parentage Discovery is 554 per animal, and this file includes roughly 5,000 to 5,500 animals, it includes between 2.5 and 3 million records and has a file size between 135 and 155 MB.

b) Pedigree (ped_discovery_XXXXX.csv)
The file of pedigree data follows the same format as used by Interbull for distributing pedigree information to its customers (pedig_BBB.csv, where BBB refers to the Interbull 3-character breed code). For this ICAR certification process, the following layout and description is used.

Field Name	Size	Example	Description
Animal ID (note 1)	19 (fixed)	XXXZZZF001234567890	Alphanumeric
Sire ID (note 1)	19 (fixed)	XXXZZZM002345678901	Alphanumeric (filled as 0000000000000000000 when unknown)
Dam ID (note 1)	19 (fixed)	XXXZZZF003456789012	Alphanumeric (filled as 0000000000000000000 when unknown)
Animal's Birth Date	8 (fixed)	YYYYMMDD	Numeric
Animal Name	Variable		Always blank
Verification Status	1 (fixed)	U	Always filled as U
Sending Country	3 (fixed)	ZZZ	Always filled as ZZZ

Note 1: First six characters for "Breed" and "Country of Registration" are filled with fictitious values of XXX and ZZZ, respectively.

In essence, the applicant may choose to only use the first four fields included in this comma delimited .csv file and ignore the last three fields. Note that within the Animal ID field, the sex of the animal (i.e.: M or F as character 7), as well as the Animal's Birth Date, are important content that is required for conducting correct parentage analysis, especially for Parentage Discovery, including the minimum age difference of 517 days (i.e.: 17 months) between an animal and any qualifying parent.

The Pedigree file includes a single record for approximately 10,000 animals, of which approximately 5,000 to 5,500 represent the animals/progeny of interest and the remainder are potential parents of those animals. The progeny/animals of importance for this ICAR Certification are those that have an Animal ID beginning with either XXXZZZF00142 for females or XXXZZZM00142 for males, and these animals must all be included in the Results Discovery file to be returned by the applicant to the Interbull Centre.

Option B: The applicant uses the Parentage Verification Results file (results_short_verify_XXXXX.csv) that is provided with the raw data files as input for the Parentage Discovery portion of its internal processes.

The first step in the process of Parentage Discovery is to consider any parentage information (i.e.: sire and/or dam) in the test data provided and conduct the ICAR-approved procedures for Parentage Verification. Applicants interested in ICAR certification for Parentage Discovery must first be successful at passing the process for ICAR certification for Parentage Verification. In the test files provided for Parentage Discovery, only animals not successful in the Parentage Verification step should be considered, which requires the Sire, Dam and Mating conclusions to have been “Accepted” (corresponding to Case 1 in Summary table). Any other result of the Parentage Verification process for any of these three tests would mean the animal is included in the subsequent step of Parentage Discovery processing. The Parentage Verification Results file provided to the applicant provides the opportunity to confirm that this part of the testing procedure has be completed successfully.

This file provides basic information listing the analysis conclusions for verifying the sire, dam and mating combination based on the parentage data available and the following layout and description is used.

Field Name	Size	Example	Description
Animal ID (note 1)	19 (fixed)	XXXZZZF001234567890	Alphanumeric
Sire ID (note 1)	19 (fixed)	XXXZZZM002345678901	Alphanumeric (filled as 0000000000000000000 when unknown)
Dam ID (note 1)	19 (fixed)	XXXZZZF003456789012	Alphanumeric (filled as 0000000000000000000 when unknown)
Sire Conclusion	Variable	Sire_Accepted	Must be assigned as listed under "Sire Conclusion" in the Summary file table provided in Section 1.
Dam Conclusion	Variable	Dam_Excluded	Must be assigned as listed under "Dam Conclusion" in the Summary file table provided in Section 1.
Mating Conclusion	Variable	Not Checked	Must be assigned as listed under "Mating Conclusion" in the Summary file table provided in Section 1.

Note 1: First six characters for "Breed" and "Country of Registration" are filled with fictitious values of XXX and ZZZ, respectively.

This file includes a single record for each of the roughly 5,000 to 5,500 animals with an Animal ID beginning with either XXXZZZF00142 for females or XXXZZZM00142 for males.

The analysis required for Parentage Discovery is more complex compared to that for Parentage Verification and several different situations may arise, which must all be handled correctly. The following table provides an overview of the various cases that are tested within the Parentage Discovery process. For both sire and dam, in addition to the outcome of Verified from Parentage Discovery, the possible conclusions from Parentage Discovery are Discovered, Possible or Not Discovered. The cells represent the various outcomes that can arise when testing the sire and dam mating combination for which possible conclusions are Confirmed, Possible, Excluded or Not Checked. **Note that it is not guaranteed that all possible combinations will appear in every test data set since some combinations are rarer**.

		Conclusion for DAM			
		Verified	**Discovered**	**Possible**	**Not Discovered**
Conclusion for SIRE	**Verified**	Confirmed Possible Excluded Not Checked	Confirmed Possible Excluded Not Checked	Confirmed Possible Excluded Not Checked	Not Checked
	Discovered	Confirmed Possible Excluded Not Checked	Confirmed Possible Excluded Not Checked	Confirmed Possible Excluded Not Checked	Not Checked
	Possible	Confirmed Possible Excluded Not Checked	Confirmed Possible Excluded Not Checked	Confirmed Possible Excluded Not Checked	Not Checked
	Not Discovered	Not Checked	Not Checked	Not Checked	Not Checked

To be clear in terminology, for the ICAR Certification process, the following vocabulary and associated definitions are used:

Analysis of Parents (Sire or Dam)	
Conclusion	**Description**
Verified	The parent was provided in the pedigree and passed the pedigree verification process with “Accepted” status.
Discovered	The parent that does not match the parent in the pedigree was found meeting the criteria for Discovered.
Situation 1	The parent listed in the pedigree was not verified (due to low call or genotyping error) but was accepted using the 554 SNP included for Parentage Discovery.
Situation 2	There was no sire/dam provided in the pedigree file but a sire/dam was discovered during Parentage Discovery.
Situation 3	The sire/dam in the provided pedigree file failed Parentage Verification or was not genotyped and a different sire/dam was found during Parentage Discovery processing that met the criteria for being discovered.
Possible	A possible parent was found but it does not meet the criteria for Discovered.
Situation 1	The sire/dam provided in the pedigree file was not verified or discovered but could not be excluded.
Situation 2	There was no sire/dam provided in the pedigree file and a possible sire/dam was found.
Situation 3	The sire/dam in the provided pedigree file failed verification or was not genotyped and a different sire/dam was found that met the criteria for parentage possible.
Not Discovered	No parent was found meeting the criteria for Discovered or Possible.
Situation 1	There was no sire/dam provided in the pedigree file and no sire/dam was discovered.
Situation 2	The sire/dam in the provided pedigree file failed verification and no sire/dam was discovered.
Situation 3	The sire/dam in the provided pedigree was not genotyped and no sire/dam was discovered.

c) Discovery Groups Summary (summary_discovery _XXXXX.csv)

Similar to the Summary file that is involved with the Parentage Verification certification process, the Discovery Groups Summary file provides the applicant with a count of animals associated with each possible outcome from the discovery step. This file includes a row for each of the possible combinations of Sire Conclusion, Dam Conclusion and Mating Conclusion presented in the previous table above that exist in the data set. This file provides the applicant with an overall idea of whether the Parentage Discovery procedures obtained the expected results since the count of animals for each combination of Sire, Dam and Mating conclusions must be exactly met. The following table shows the content of this file and includes various rows that may appear in each certification test file, noting that not all test files will have all 43 possible combinations represented.

Sire Conclusion	Dam Conclusion	Mating Conclusion	Count
Sire_Discovered	Dam_Discovered	Mating_Confirmed	N1
Sire_Discovered	Dam_Discovered	Mating_Excluded	N2
Sire_Discovered	Dam_Discovered	Mating_Not_Checked	N3
Sire_Discovered	Dam_Discovered	Mating_Possible	N4
Sire_Discovered	Dam_Not_Discovered	Mating_Not_Checked	N5
Sire_Discovered	Dam_Possible	Mating_Confirmed	N6
Sire_Discovered	Dam_Possible	Mating_Excluded	N7
Sire_Discovered	Dam_Possible	Mating_Not_Checked	N8
Sire_Discovered	Dam_Possible	Mating_Possible	N9
Sire_Discovered	Dam_Verified	Mating_Confirmed	N10
Sire_Discovered	Dam_Verified	Mating_Excluded	N11
Sire_Discovered	Dam_Verified	Mating_Not_Checked	N12
Sire_Discovered	Dam_Verified	Mating_Possible	N13
Sire_Not_Discovered	Dam_Discovered	Mating_Not_Checked	N14
Sire_Not_Discovered	Dam_Not_Discovered	Mating_Not_Checked	N15
Sire_Not_Discovered	Dam_Possible	Mating_Not_Checked	N16
Sire_Not_Discovered	Dam_Verified	Mating_Not_Checked	N17
Sire_Possible	Dam_Discovered	Mating_Confirmed	N18
Sire_Possible	Dam_Discovered	Mating_Excluded	N19
Sire_Possible	Dam_Discovered	Mating_Not_Checked	N20
Sire_Possible	Dam_Discovered	Mating_Possible	N21
Sire_Possible	Dam_Not_Discovered	Mating_Not_Checked	N22
Sire_Possible	Dam_Possible	Mating_Confirmed	N23
Sire_Possible	Dam_Possible	Mating_Excluded	N24
Sire_Possible	Dam_Possible	Mating_Not_Checked	N25
Sire_Possible	Dam_Possible	Mating_Possible	N26
Sire_Possible	Dam_Verified	Mating_Confirmed	N27
Sire_Possible	Dam_Verified	Mating_Excluded	N28
Sire_Possible	Dam_Verified	Mating_Not_Checked	N29
Sire_Possible	Dam_Verified	Mating_Possible	N30
Sire_Verified	Dam_Discovered	Mating_Confirmed	N31
Sire_Verified	Dam_Discovered	Mating_Excluded	N32
Sire_Verified	Dam_Discovered	Mating_Not_Checked	N33
Sire_Verified	Dam_Discovered	Mating_Possible	N34
Sire_Verified	Dam_Not_Discovered	Mating_Not_Checked	N35
Sire_Verified	Dam_Possible	Mating_Confirmed	N36

Sire_Verified	Dam_Possible	Mating_Excluded	N37
Sire_Verified	Dam_Possible	Mating_Not_Checked	N38
Sire_Verified	Dam_Possible	Mating_Possible	N39
Sire_Verified	Dam_Verified	Mating_Confirmed	N40
Sire_Verified	Dam_Verified	Mating_Excluded	N41
Sire_Verified	Dam_Verified	Mating_Not_Checked	N42
Sire_Verified	Dam_Verified	Mating_Possible	N43

Parentage Discovery Results File to be Returned by the Applicant to the Interbull Centre

Once the applicant obtains output from their internal parentage analysis procedures for which the counts exactly match those for each case included in the Discovery Groups Summary file, then the applicant should create and send a detailed Results Discovery file back to the Interbull Centre. **This file must be a comma (,) delimited .csv file respecting the naming structure as follows**:

results_discovery_XXXXX.csv

where XXXXX refers to the same 5-digit numerical value included in the data file provided to the applicant by the Interbull Centre.

The content of the Results Discovery file should respect the file layout described below and only include a subset of the approximately 5,000 to 5,500 animals in the Animal Genotypes file that have the numerical portion of their Animal ID (Animal ID - Unique Number) starting with "00142" and were included for the parentage discovery analysis.

Field #	Field Name	Size	Example	Description
1	Animal ID	19 (fixed)	XXXZZZF001234567890	Alphanumeric
2	Sire ID	19 (fixed)	XXXZZZM002345678901	Alphanumeric (filled as 0000000000000000000 when Sire is not discovered)
3	No. Conflicts – Sire[1]	3 (maximum)	1	Count of informative SNP with a conflict between the Animal and the Discovery Sire (blank if Sire is not discovered)
4	% Conflicts – Sire[1]	3 (maximum)	0.20	Numeric and rounded to two digits after the decimal (blank if Sire is not discovered)
5	No. Common SNP – Sire[1]	3 (maximum)	508	Count of common SNP to the genotype of the Discovery Sire (blank if Sire is not discovered)
6	Dam ID	19 (fixed)	XXXZZZF003456789012	Alphanumeric (filled as 0000000000000000000 when Dam is not discovered)
7	No. Conflicts – Dam[2]	3 (maximum)	0	Count of informative SNP with a conflict between the Animal and the Discovery Dam (blank if Dam is not discovered)
8	% Conflicts - Dam[2]	3 (maximum)	0.00	Numeric and rounded to two digits after the decimal (blank if Dam is not discovered)
9	No. Common SNP - Dam[2]	3 (maximum)	509	Count of common SNP to the genotype of the Discovery Dam (blank if Dam is not discovered)
10	No. Possible Sires	2 (maximum)	1	Numeric (0 if Sire is not discovered)
11	No. Possible Dams	2 (maximum)	1	Numeric (0 if Dam is not discovered)
12	No. Conflicts – Matings[3]	2 (maximum)	1	Count of informative SNP with a conflict among the trio of the Animal and the combination of the Discovery Sire and

				Discovery Dam (blank if Sire and/or Dam are not discovered)
13	% Conflicts - Mating[3]	3 (maximum)	0.21	Numeric and rounded to two digits after the decimal (blank if Sire and/or Dam are not discovered)
14	No. Common SNP - Mating[3]	3 (maximum)	471	Count of common SNP for the genotypes of the trio involving Animal, Discovery Sire and Discovery Dam (blank if Sire and/or Dam are not discovered)
15	Sire Conclusion	Variable	Sire_Verified	Must be assigned as listed in the Discovery Groups Summary table above under "Sire Conclusion"
16	Dam Conclusion	Variable	Dam_Discovered	Must be assigned as listed in the Discovery Groups Summary table above under "Dam Conclusion"
17	Mating Conclusion	Variable	Mating_Confirmed	Must be assigned as listed in the Discovery Groups Summary table above under "Mating Conclusion"
18	Identical Animal	1 (fixed)	I or N	"I" indicates that the Animal has an identical animal in the test file
19	Identical Sire	1 (fixed)	I or N	"I" indicates that the Discovery Sire has an identical animal in the test file
20	Identical Dam	1 (fixed)	I or N	"I" indicates that the Discovery Dam has an identical animal in the test file

Note 1: Fields 3, 4 and 5 must be blank when Sire Conclusion has a result of Not_Discovered.
Note 2: Fields 7, 8 and 9 must be blank when Dam Conclusion has a result of Not_Discovered.
Note 3: Fields 12, 13 and 14 must be blank when Mating Conclusion has a result of Mating_Not_Checked.

For fields 4, 8 and 13, which include the % Conflicts for Sire, Dam and Mating respectively, the calculated value to be included in the file must be rounded to two digits after the decimal. As an example, in the case whereby there are 3 conflicts out of 480 common SNP, the final value for % Conflicts is .63 (i.e.: 3/480 x 100 = .625, which is rounded to .63).

The last three columns of this file contain information as to whether the Animal, Sire or Dam has a genetically identical animal. I – when a genetically identical animal has been found, N – when no genetically identical animal has been found. For ICAR parentage analysis certification services, any pair or group of animals should be considered as genetically identical when their genotypes have ≤ 2% differences among the common set of SNP that were successfully called in their genotypes, regardless of the number of common SNPs between the animals. For Parentage Verification, which is currently based on 195 SNP, this means no more than 3 called SNP in common that are not the same and for Parentage Discovery, which is currently based on 549 SNP, this means no more than 10 called SNP in common that are not the same.

For cases whereby any of the Sire or Dam has been found to have one or more genetically identical animals in the test data file, the Results Discovery file must include multiple output records for the Animal. For example, if a candidate dam is genetically identical to another animal, both of these animals should be listed as candidate dams, in separate lines, as long as both qualify as a potential dam with regards to minimum number of common SNPs and/or maximum percent conflict with the offspring. In this case, the records included in the Results Discovery file must be listed in ascending order of the % Conflicts field for the Sire (Field 4 above) or Dam (Field 8 above) with the genetically identical animal. If needed, a secondary sort for listing such records would be the No. Common SNP field for the Sire (Field 5 above) or Dam (Field 9 above), in descending order.

For verified parents, the parentage conclusion from the Verification step (Sire Verified/Dam Verified) is maintained. The number of common SNPs and percentage of conflicts from the Parentage Discovery SNP panel must be included in the result, even when the number of common SNPs is <400 or the percentage of conflicts is >2%. For cases where any of the Sire or Dam is Verified, no alternative Sire or Dam to the one Verified should be presented, also in the cases where the Verified Sire or Dam is genetically identical to another animal in the test file.

In certain cases, it is possible for an animal to have multiple records in the Results Discovery file as more than one Sire or Dam might be Discovered or Possible, even if they are not involved with any case of Sire or Dam having a genetically identical animal in the test data set. In these cases, all alternative Sires or Dams should be printed, in separate lines. The exception to this rule is if both Sire and Dam is Discovered, alternatively one is Discovered and the other is Verified, and Mating Conclusion is Mating_Confirmed, then only this line should be printed.

When multiple records are included, they should be listed in descending order of the Mating Conclusion such that Mating_Possible ranks higher than Mating_Excluded, which ranks higher than Mating_Not_Checked

For sake of clarity, the following are examples of correct records with required fields having a value, and the various fields associated with Sire, Dam or Mating SNP having missing values when appropriate, as indicated by sequences of commas when in .csv file format

XXXZZZF001420070912,XXXZZZM001421281280,0,0.00,480,XXXZZZF001424406656,0,0.00,485,1,1,0,0.00,427,Sire_Discovered,Dam_Discovered,Mating_Confirmed,N,N,N

XXXZZZF001420086272,XXXZZZM001421601024,0,0.00,406,XXXZZZF001420971008,0,0.00,449,2,1,,,,Sire_Discovered,Dam_Discovered,Mating_Not_Checked,N,I,N
XXXZZZF001420086272,XXXZZZM001426439424,6,1.30,462,XXXZZZF001420971008,0,0.00,449,2,1,,,,Sire_Possible,Dam_Discovered,Mating_Not_Checked,N,I,N

XXXZZZF001421823488,0000000000000000000,,,,XXXZZZF001425097600,0,0.00,481,0,1,,,,Sire_Not_Discovered,Dam_Discovered,Mating_Not_Checked,N,N,N

XXXZZZF001424070400,XXXZZZM001422103936,4,1.01,398,XXXZZZF001426792576,6,1.46,411,1,1,,,,Sire_Verified,Dam_Possible,Mating_Not_Checked,N,N,N

Section 3: Assessment of Certification Results

Once the Results file for Parentage Verification or the Results Discovery file for Parentage Discovery is sent by the applicant to the Interbull Centre, it will be compared, record by record, to the correct answer key associated with the specific set of certification test files originally sent to the applicant. Only in the event that this comparison yields identical results will ICAR subsequently grant a successful certification for the associated level of parentage analysis. If this is not the outcome, further options available to the applicant are described in the Overview section of this document. If desired, the applicant may request to receive from the Interbull Centre the correct answer key for the Results file or the Results Discovery file, which would help identify the specific areas that need improvement for achieving a successful outcome if the applicant decided to subsequently re-apply for the ICAR Parentage Analysis Certification for DNA Data Interpretation Centres.