

Data Conflict Resolution

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2024 CDCB Nominators and Laboratories Workshop

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Goals for this presentation

For users of the CDCB database to understand:

1. Where to find both pedigree and genomic conflicts
2. How incorrect pedigree data can cause genomic conflicts
3. How to troubleshoot when pedigree fixes for genomic conflicts fail

Pedigree Errors

Genomic Conflicts

Preventing an
evaluation

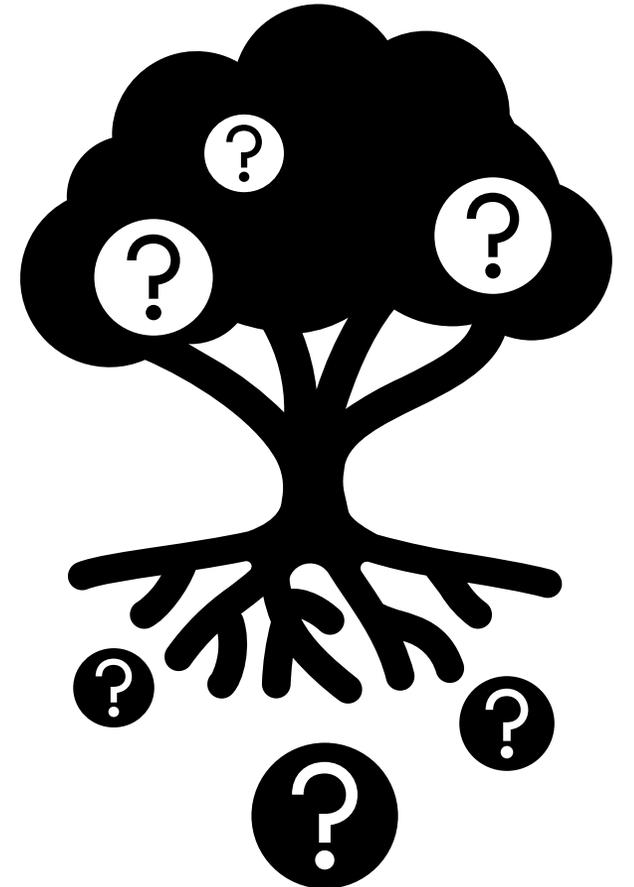


From the CDCB Evaluations Presentation...

- A Usable genotype (Use=Y) is a genotype that:
 1. Has passed quality control checks
 2. Does not have a sex conflict with the animal's pedigree
 3. Does not have genomic conflicts with close relatives that make the animal's pedigree appear unreliable

Pedigree Errors and Genomic Conflicts

- Genotype determines animals X, Y, and Z are all related, but who was born first?
- Relies on accurate pedigree birth dates, multi-birth codes (MBCs), and parentage



Pedigree Errors and Genomic Conflicts

- Pedigree data can come from many sources:

You are here



Code	Description
B	Breed Associations (USA and CAN) and CDDR exchange partners (bulls only)
N/R/I	NAAB, any nominator (except breed associations), Interbull and International pedigree without regular pedigree update
D	Dairy Records Processing Center (DRPC)
H	Pedigree provided in a health record from a National Association of Animal Breeders (NAAB) source
C	CDCB internal use only
A	CDCB

Pedigree Errors and Genomic Conflicts

- Other phenotypic data such as breeding, calving, and lactation data provided by DRPCs can interact with pedigrees
- Pedigree, phenotypic, and genotypic data should all agree



Processing of Pedigrees

- Pedigrees submitted by nominators CDCB via FTP or WebConnect arrive in Format 1 or Format 1G records
- General Format 1 structure (first 99 bytes):

0FH0840003282837717H0840003218556317H0840003149596913

20240307B20240321P01399000000

https://redmine.uscdcb.com/projects/cdcb-customer-service/wiki/Format_1

Processing of Pedigrees

General Format 1 structure (first 99 bytes):

FH0840003282837717H0840003218556317H0840003149596913 20240307B20240321P01399000000

Byte Position(s): 2

Definition: Sex Code

Example: F

Other information: F = Female, M = Male

Processing of Pedigrees

General Format 1 structure (first 99 bytes):

0FH0840003282837717H0840003218556317H0840003149596913 20240307B20240321P01399000000

Byte Position(s): 3–19

Definition: Animal ID

Example: H0840003282837717

Other information: Breed Code (3–4)

Country Code (5–7)

Unique 12–byte ID (8–19)

Processing of Pedigrees

General Format 1 structure (first 99 bytes):

0FH0840003282837717 H0840003218556317 H0840003149596913 20240307B20240321P01399000000

Byte Position(s): 20–36

Definition: Sire ID

Example: H0840003218556317

Other information: Breed Code (20–21)

Country Code (22–24)

Unique 12-byte ID (25–36)

Processing of Pedigrees

General Format 1 structure (first 99 bytes):

0FH0840003282837717H0840003218556317H0840003149596913

20240307B20240321P01399000000

Byte Position(s): 37–53

Definition: Dam ID

Example: H0840003149596913

Other information: Breed Code (37–38)

Country Code (39–41)

Unique 12-byte ID (42–53)

Processing of Pedigrees

General Format 1 structure (first 99 bytes):

0FH0840003282837717H0840003218556317H0840003149596913 20240307B20240321P01399000000

Byte Position(s): 54–70

Definition: Cross-reference

Example: Blank

Other information: Breed Code (54–55)

Country Code (56–58)

Unique 12-byte ID (59–70)

Processing of Pedigrees

General Format 1 structure (first 99 bytes):

0FH0840003282837717H0840003218556317H0840003149596913

20240307B20240321P01399000000

Byte Position(s): 71–78

Definition: Birth Date

Example: 20240307

Other information: YYYYMMDD format

Processing of Pedigrees

General Format 1 structure (first 99 bytes):

0FH0840003282837717H0840003218556317H0840003149596913

20240307B20240321P01399000000

Byte Position(s): 91

Definition: MBC

Example: 3

Other information: Valid values 1–6

Processing of Pedigrees

- The ID of the animal is checked:
 - Novel IDs create new internal keys
 - Existing IDs checked against existing CDCB pedigree
- Pedigree parentage is checked with birth date and MBC so that it makes sense in the context of “available data”

Processing of Pedigrees

- Examples of other potentially “Available data” are
 - Birth dates of parents
 - Breeding and lactation data of the dam
 - Birth dates and MBCs of siblings
 - Existence of other pedigrees with identical parentage and birth date information

Processing of Pedigrees

- Outcomes of pedigree processing:
 - Pedigree is successfully stored/updated – no errors returned
 - Incoming pedigree does not agree with available data parts, of it were “changed” to store the pedigree
 - For existing IDs, updates to pedigrees may be “rejected” if there are too many differences

Processing of Pedigrees

- Outcomes of pedigree processing:
 - In some instances you will be “notified” if pedigrees are stored in an unusual way
 - Ex. Two IDs/animals being merged because an submitted pedigree had identical parentage and birth date information
- Notices, changes, and rejections reported in error files

Where to find Pedigree Errors

- FTP files: files processed from previous dates are zipped in YYYYMMDD.zip
 - X.1EX – Pedigree errors Format 1 files
 - notify_VAL.X – Nomination verifications, Y or N
 - notify_ERR.X – Pedigree errors generated from 1G, presented in a human-readable format

Errors in a 1E file:

0FH0840003265894046H0840003213001120H0840003224851225
20220621 D

20230322B20240307P0110000000840003265894046

000N2Jc

Errors in a notify file:

Rejected fmt 1 record for F H0840003265894046 -- 840003265894046

Sire	Dam	Xref	Birth
H0840003213001120	H0840003224851225		20230322

Source	ProcDate	Type	Verr	MBC	Reg	Stat	filename
B	20240307	P	0	1		00	20240307.1N

Code	Dsp	Reason	ID	Date	Herd	Source
2Jc	N	SS <> Sire		20220621		D



QUERIES

SEARCH FOR

Cattle

Goat

Animal ID (17 bytes)/ Animal ID + Sex Code (18 bytes)

Found 1/1 result sets

INPUT:

- Animal ID (17 bytes): Breed, Country Code, and ID Number.
- Animal ID + Sex Code (18 bytes): Breed, Country Code, Sex Code, and ID Number. (may be omitted leading zeros)

E.g.

- Animal ID (17 bytes): JEUSA000118662185
- Animal ID + Sex Code (18 bytes): HO124F000007890183 or HO124F7890183

Maximum 50 items/once

Over 50 items: [Data Exchange](#)

HO840003265894046

Run Query

Clear

HO840003265894046

Q Search

HO840003265894046

Requested ID Searches

HO840003265894046 ✖

ID/Pedigree

Evaluation

Genotype

Progeny

Errors

Lactations

Animal

Preferred ID: HO840003265894046
Name:
DOB: 2023-03-22
Sex: F
[Multi-Birth Code:](#) 1
[ID Source Code:](#) B
[Pedigree Source Code:](#) B

Sire

ID: [HO840003213001120](#)
Name: PEAK PENDULUM-ET
DOB: 2020-03-16
[Source Code:](#) B
Genotyped: Yes

Dam

ID: [HO840003224851225](#)
Name: DONLEY LANDMINE LORELEI
DOB: 2021-03-21
[Source Code:](#) B
Genotyped: Yes

Error Information

Requested ID Searches

HO840003282837717 ✖

[Pedigree Source Code:](#) B

ID: [HO840003149596913](#)
Name: COLDSPRINGS SPLENDID 10898
DOB: 2018-09-07
[Source Code:](#) B
Genotyped: Yes

Error Information



No Error Information Found!

1 result(s) found!

Dashboard

Q Search

HO840003265894046

Requested ID Searches

HO840003265894046 ✕

ID/Pedigree

Evaluation

Genotype

Progeny

Errors

Lactations

Animal

Preferred ID: HO840003265894046
Name:
DOB: 2023-03-22
Sex: F
[Multi-Birth Code:](#) 1
[ID Source Code:](#) B
[Pedigree Source Code:](#) B

Sire

ID: [HO840003213001120](#)
Name: PEAK PENDULUM-ET
DOB: 2020-03-16
[Source Code:](#) B
Genotyped: Yes

Dam

ID: [HO840003224851225](#)
Name: DONLEY LANDMINE LORELEI
DOB: 2021-03-21
[Source Code:](#) B
Genotyped: Yes

Error Information

Select All

Pedigree (fmt-1)

Lactation (fmt-4)

Reproduction (fmt-5)

Health (fmt-6)

Apply

Clear

Requested ID Searches

HO840003265894046

Error Information

Select All Pedigree (fmt-1) Lactation (fmt-4) Reproduction (fmt-5) Health (fmt-6)

Apply

Clear

▼ Pedigree (fmt-1) | 1 Source File

▼ Errors in File 20240307.1N

Error Code	Disposition Code	Description	ID
2jc	Notified	Input sire differs with master file service sire.	

Sire	Dam	Cross Reference	DOB	Source Code	Processing Date	Record Type	Verification Code
HO840003213001120	HO840003224851225		2023-03-22	B	2024-03-07	P	0

1 result(s) found!

Dashboard



*Will show the most recent format 1 submission errors – does not show previously submitted errors

The Council of Dairy Cattle Breeding

queries.uscdcb.com/formats/geterr.cfm?ecode_in=2J#StartBody

Error Documentation

Home / Error Documentation

WebConnect has launched and is officially open to all collaborators.
 Visit WebConnect at : <https://webconnect.uscdcb.com> .

Master File Service Sire Discrepancy

Code	Description	Action	Returned Data	Updated
2Ja	Input sire differs with master file service sire. Service sire will be updated.	Change	Corrected service sire identification	04/14/2004
2Jb	Input sire differs with master file service sire. Input sire is unknown.	Notify		04/14/2004
2Jc	Input sire differs with master file service sire.	Notify		04/27/2010
2Jd	Input sire differs with master file service sire, and input birthdate differs from master file cow calving date	Notify		04/27/2010

- Error Codes
- Complete Error Lists
 - CSV/Excel
 - Tab Separated
- 0 General Record
- 1 Animal Identification
- 2 Sire Identification
 - 2A Obvious Unknown Sire
 - 2B Obvious Misidentification
 - 2C Unusual Identification
 - 2D Invalid Format
 - 2E Invalid Format
 - 2F Miscellaneous
 - 2G Master File Pedigree Discrepancy
 - 2H Master File Pedigree Discrepancy
 - 2I Master File Pedigree Discrepancy
 - 2J Master File Service Sire Discrepancy

HO840003265894046 ✖

Error Information

 Select All Pedigree (fmt-1) Lactation (fmt-4) Reproduction (fmt-5) Health (fmt-6)[Apply](#)[Clear](#)

▼ Pedigree (fmt-1) | 1 Source File

▼ Errors in File 20240307.1N

Error Code	Disposition Code	Description	ID
2jc	Notified	Input sire differs with master file service sire.	

Sire	Dam	Cross Reference	DOB	Source Code	Processing Date	Record Type	Verification Code
HO840003213001120	HO840003224851225		2023-03-22	B	2024-03-07	P	0

1 result(s) found!

Looking at Pedigree Errors

- Disposition Code: Designation of the error
- Notify or N, an information notice, record accepted
- Change or C, information was changed by CDCB system, record continued down pipeline
- Rejected or R, part or all of the record was rejected

Error Information

Select All Pedigree (fmt-1) Lactation (fmt-4) Reproduction (fmt-5) Health (fmt-6)

Apply

Clear



▼ Pedigree (fmt-1) | 1 Source File

▼ Errors in File 20240307.1N

Description	ID	Herd	Source Code	Date
Input sire differs with master file service sire.			D	2022-06-21



Sire	Dam	Cross Reference	DOB	Source Code	Processing Date	Record Type	Verification Code
HO840003213001120	HO840003224851225		2023-03-22	B	2024-03-07	P	0

Looking at Pedigree Errors

- ID usually indicates the ID of the animal in conflict
- Herd can indicate the herd code in conflict*
- Source indicates the source of the data in conflict
- Date usually indicates the Date in conflict

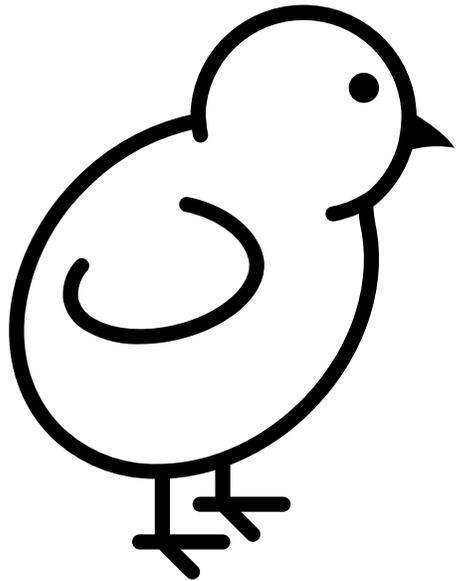
*Not usually relevant for Format 1 submissions

Processing Genotypes

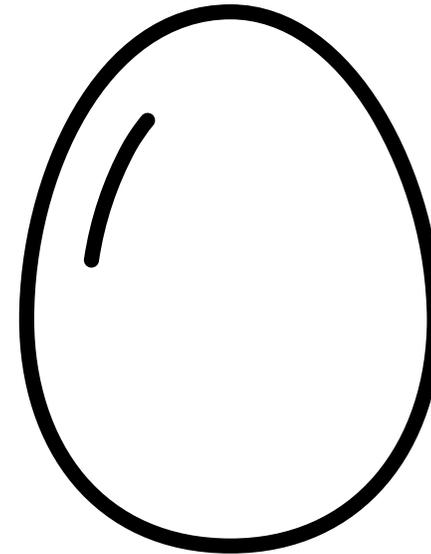
- When genotypes are loaded they are pre-assigned to an animal with a pedigree at CDCB already
- After genotype passes quality checks, it is checked against:
 1. Known Pedigree Relatives
 2. Known Clones
 3. And *then* new relationships are discovered



Pedigree Errors



vs



Genomic Conflicts

Where to find Genomic Errors

- Genomic errors that are generated when a batch is loaded:

\$LAB.batchname.\$NOM.zip containing

\$NOM_Genomic_Errors.csv

- Genomic errors from -o jobs can be found after processing if animals were reprocessed:

\$NOM_Genomic_Errors_YYYYMMDD.csv

Where to find Genomic Errors

Contents of a \$NOM_Genomic_Errors.csv:

Requester_ID, ID18, Sample_ID, Animal_Name, Error_code, Error, Other_ID, Other_Name, Source, Use_Ind, Load_Date

Nominator, HO840F003260134350, Sample123, N3_Sire_conflict, HO840M003223868846, OCD GAMEDAY FRAMPTON-ET, N, N, 20240726

When her genotype was loaded, animal

HO840F003260134350 had an N3 Sire Conflict found



QUERIES

SEARCH FOR

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Goat

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HO840003265894046

Run Query

Clear

HO840003265894046

Q Search

HO840003282837717

ID/Pedigree

Evaluation

Genotype

Progeny

Errors

Lactations

Requested ID Searches

HO840003282837717

Evaluation Breed: HO - Holstein

Animal

Preferred ID: HO840003282837717
Name: COLDSPRINGS JEWEL
14624-ET
DOB: 2024-03-07
Sex: F
[Multi-Birth Code:](#) 3
[ID Source Code:](#) B
[Pedigree Source Code:](#) B
[Blend Code:](#) S

Sire

ID: [HO840003218556317](#)
Name: SIEMERS RZ PAZZLE 34954-ET
DOB: 2021-02-09
[Source Code:](#) B
Genotyped: Yes

Dam

ID: [HO840003149596913](#)
Name: COLDSPRINGS SPLENDID
10898
DOB: 2018-09-07
[Source Code:](#) B
Genotyped: Yes

Maternal Grand sire

ID: [HOUSA000074024998](#)
Name: PINE-TREE SPLENDID-P-ET
DOB: 2015-08-05
[Source Code:](#) B
Genotyped: Yes

[Does the animal qualify for a genomic evaluation?](#)

Q Search

Requested ID Searches
HOCHNF23HIYX211250

Genotype Confirmations, Conflicts, and Other Close Relatives

MGS Info PGS Info Show All

Sample ID: US401315248 - Barcode & Position: 208052550076 R15C04 - Usability Indicator: N

Genotype Confirmations		
Confirmation Type	Confirmed Genotype	
	Barcode & Position	Confirmed I
No records available.		

Genotype Conflicts					
Pedigree Change	Conflict Type		Conflicting Genotype		
	Message	Code	Barcode & Position	Conflicting ID	USE
	Discovered missing sire	OO	201389730198 R03C02	HO840003142181103.[M]	

<< < 1 > >> 1 - 1 of 1 items

Fix_FMT1

Other Close Relatives					
Relative ID	Relative Barcode & Position	USE	SNP		
			Compared	Same	Conflicts
No records available.					



00

- **Full text of the error** : 00 - Discovered missing sire
- **Meaning** : No sire is indicated in the pedigree, but the CDCB system discovered the missing sire. This process is based on identifying bulls with few [Mendelian inheritance conflicts](#)] with the animal. If, after consulting with the customer, the discovered sire is accepted, then pedigree information must be updated as indicated in [corrections to pedigree](#).
- **Correction** : Either accepting the discovered sire in the genotype query or submitting format 1 with the correct sire will add the discovered sire to the pedigree.

01

- **Full text of the error** : 01 - Discovered missing dam
- **Meaning** : No dam is indicated in the pedigree, but the CDCB system discovered the missing dam. This process is based on identifying cows with few [Mendelian inheritance conflicts](#) with the animal. If, after consulting with the customer, the discovered dam is accepted, then pedigree information must be updated as indicated in [corrections to pedigree](#).
- **Correction** : Either accepting the discovered dam in the genotype query or submitting format 1 with the correct dam will add the dam to the pedigree.

02

- **Full text of the error** : 02 - Duplicate genotype identified
- **Meaning** : Identical genotypes are assigned to two different animals with different parents and there is not a clone record established for the animal pair.
- **Correction** : There are a few scenarios that can cause this error to occur:
 1. If the two animals are not related, and would not reasonably have identical genotypes: investigate the genotypes and reassign or withdraw the genotype incorrectly assigned if possible.
 2. If the animal is a clone, split embryo, or identical twin: Clone records can be automatically applied if they meet the conditions described in [Dealing with clone records](#). However, if they are not applied automatically, you can create them as outlined in [Dealing with clone records](#). Before applying clone records, make sure that the pedigree sire and dam are the same for the pair, animals have the same sex, and that the MBC and birth date given to the animals makes sense. For example:
 - For identical twins: the birth date should be the same and the MBC will be 2 for both animals.
 - For an animal that is a clone of another live animal: the clone should have a MBC of 5 and is younger than the DNA ID animal.
 - For animals that were born from split embryos: both animals should have a MBC of 4.
 3. If the animal is not a clone, but actually one animal that was genotyped under two IDs: Both of the genotypes should be under one animal ID, and the two IDs should be cross-referenced or should be removed if the ID is invalid.
Follow these steps carefully:
 1. Move genotypes so that both are under 1 Animal ID
 2. Make sure both IDs have matching pedigrees: Sire, Dam, DOB
 3. Create a cross-reference between the two IDs, submitting the preferred ID in positions 3-19 in the Format 1 **OR delete the invalid ID** .
 4. If the genotypes belong to an embryo/live animal pair: Normally, embryos are merged with their live animal pair automatically, as described here [Embryo and live animal merging process](#). However, a duplicate error could occur if a discrepancy in the pedigrees of the pair (different sire/dam, incorrect MBC applied) prevents them from merging. In the case that you have an embryo/live animal pair that did not merge correctly, please open a ticket on Redmine.

03 (Obsolete)

- **Full text of the error** : 03 - Discovered non-pedigree parent-progeny relationship
- **Meaning** : Based on low Mendelian inheritance conflicts the genotypes appear to be parent and progeny. Indication of progeny or sire/dam is determined based on birth date and sex code from each animal's existing pedigree information.
- **Correction** : If after consulting with the customer, a discovered sire/dam is agreed to, then pedigree information must be updated. The pedigree update can be performed by either accepting the discovered sire/dam in the genotype query[Fix_FMT1] or submitting a [Format 1](#) with the discovered sire/dam. This error has been replaced by T1, T2, and T3 errors.

04

- **Full text of the error** : 04 - Change useable genotype to not useable
- **Meaning** : The sire/dam has not been indicated as the progeny's parent but was discovered to be the progeny's parent through his/her genotype. The sire/dam's genotype is still usable. The progeny should have the sire/dam designated as unreported/discovered sire/dam. The progeny's genotype will not be usable until its parentage is corrected.
- **Correction** : If an animal's nominator also nominated the progeny, they must add the sire/dam as parent to make the progeny's genotype usable.

05

Q Search

Requested ID Searches

HOCHNF23HIYX211250 ✕

Genotype Confirmations, Conflicts, and Other Close Relatives

[MGS Info](#) [PGS Info](#) [Show All](#)

Sample ID: US401315248 - Barcode & Position: 208052550076 R15C04 - Usability Indicator: N

Genotype Confirmations		
Confirmation Type	Confirmed Genotype	
	Barcode & Position	Confirmed I
No records available.		

Genotype Conflicts					
Pedigree Change	Conflict Type		Conflicting Genotype		
	Message	Code	Barcode & Position	Conflicting ID	USE
	Discovered missing sire	OO	201389730198 R03C02	HO840003142181103.[M]	

1 - 1 of 1 items

[Fix_FMT1](#)

Other Close Relatives					
Relative ID	Relative Barcode & Position	USE	SNP		
			Compared	Same	Conflicts
No records available.					



Submitting a Fix_FMT1 via WebConnect

FMT1 ✕

1 Update Information **2** Review Changes and Submit

FMT1 Records

Sex	Animal	Sire	Dam	Cross Reference/Clone	DOB	Source Code	Mod Date	Rec Type	Ped Verif	Rec Ver	MBC	HRC	Reg Stat	Name
Current CDCB pedigree data ←														
F	HOUSA00031WFH6958				20240522	N	20240628	P	2	1	1	U		
Genotype based suggestion ← Suggestion are based on genotypes and other data such as current sire/dam/animal pedigree birthdates, sample labeling, etc..														
F	HOUSA00031WFH6958	HO840003223868608			20240522	N	20240716	P	2	1	1	U		
User Input ←														
F	HOUSA00031WFH6958	<input type="text" value="HO840003223868608"/>	<input type="text"/>	<input type="text"/>	<input type="text" value="2024-05-22"/>	N	20240716	P	2	1	<input type="text" value="1"/>	<input type="text" value="U"/>		<input type="text"/>

Submitting a Fix_FMT1 via WebConnect

FMT1 ✕

1 Update Information 2 Review Changes and Submit

FMT1 Records

Sex	Animal	Sire	Dam	Cross Reference/Clone	DOB	Source Code	Mod Date	Rec Type	Ped Verif	Rec Ver	MBC	HRC	Reg Stat	Name	R
Current CDCB pedigree data															
F	HOUSA00031WFH6958				20240522	N	20240628	P	2	1	1	U			
Genotype based suggestion Suggestion are based on genotypes and other data such as current sire/dam/animal pedigree birthdates, sample labeling, etc..															
F	HOUSA00031WFH6958	HO840003223868608			20240522	N	20240716	P	2	1	1	U			
User Input															
F	HOUSA00031WFH6958	HO840003223868608			20240522	N	20240716	P	2	1	1	U			

[Back](#) [Submit](#)

Submitting a Fix_FMT1 via WebConnect

- Limitations with Fix_FMT1:
 - Fix_FMT1 can only submit one change at a time
 - WebConnect is limited for the record types that can be submitted to resolve genomic conflicts

Submitting Fixes via FTP

General Format 1 structure (first 99 bytes):

0FH0840003282837717H0840003218556317H0840003149596913

20240307B20240321P01399000000

Byte Position(s): 88

Definition: Format Record Type

Example: P

Other information: 

Code	Description
X	Cross-reference record
P	Pedigree record
C	Clone record
L	Lactation data
R	Re-identification only
B	Reproductive record
D	Delete animal pedigree record
G	Genomic record
H	Health record
N	Delete clone record
Y	Delete cross-reference record

Can ALL be
submitted via
Format 1 in the FTP:

Code	Description
X	Cross-reference record
P	Pedigree record
C	Clone record
L	Lactation data
R	Re-identification only
B	Reproductive record
D	Delete animal pedigree record
G	Genomic record
H	Health record
N	Delete clone record
Y	Delete cross-reference record

Can't be submitted
via WebConnect:

Code	Description
X	Cross-reference record
P	Pedigree record
C	Clone record
L	Lactation data
R	Re-identification only
B	Reproductive record
D	Delete animal pedigree record
G	Genomic record
H	Health record
N	Delete clone record
Y	Delete cross-reference record



Submitting Fixes via FTP

General Format 1 structure (first 99 bytes):

0FH0840003282837717H0840003218556317H0840003149596913

20240307B20240321P01399000000

Byte Position(s): 89

Definition: Verification Code

Example: 0

Other information: Can be used in certain cases to “verify” sent information is correct

Submitting Fixes via Format 1

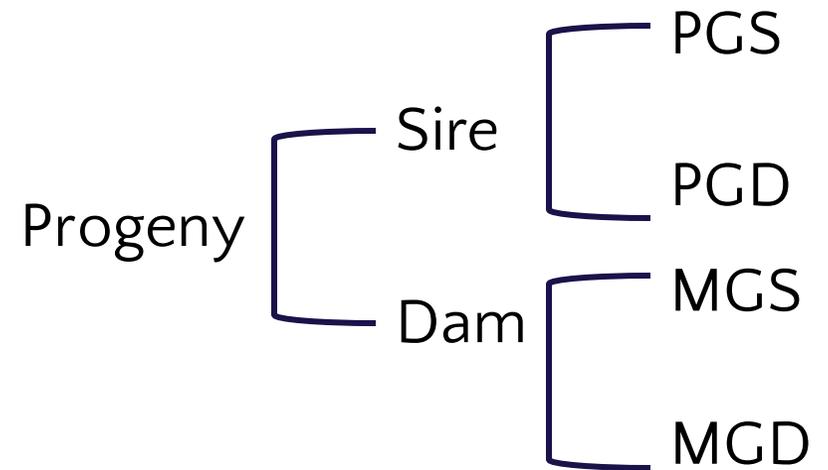
- Reminder: Can only make one change to the pedigree per record
- Can submit multiple records for one animal to make gradual changes to a pedigree

Submitting Fixes via Format 1

- Some changes require verification codes to go through, outlined in these wiki pages:
- Corrections to Pedigrees: https://redmine.uscdcb.com/projects/cdcb-customer-service/wiki/Corrections_to_pedigree
- Birth Date Rules: https://redmine.uscdcb.com/projects/cdcb-customer-service/wiki/Birth_Date_Rules

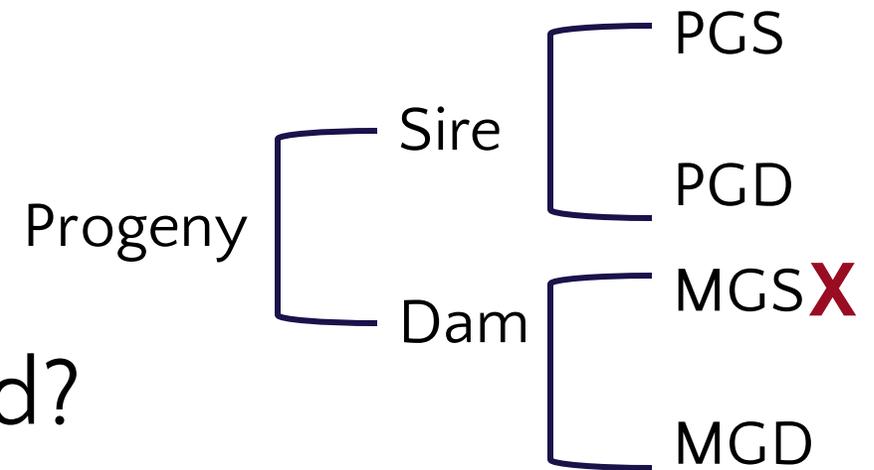
Correcting Pedigree/Genomic Conflicts

- Common Genomic Errors that may require more complex pedigree fixes:
 - O6: MGS Unlikely
 - P2: Non-pedigree Relative Close Birth
 - O2: Duplicate/N9: Discovered Clones



O6: MGS Unlikely

- The MGS has been found Unlikely
- Can be resolved by correcting the dam's sire OR Blanking the dam



- But what if the dam is confirmed?

[MGS Info](#) [PGS Info](#) [Show All](#)

Sample ID: AF05523950 - Barcode & Position: 208160590004 R19C03 - Usability Indicator: Y

Genotype Confirmations		
Confirmation Type	Confirmed Genotype	
	Barcode & Position	Confirmed ID
Sire	203253140011 R23C01	JE840003200210433 [M]
Sire	203359330123 R16C03	JE840003200210433 [M]
Sire	203665660007 R11C01	JE840003200210433 [M]
Dam	208025910022 R12C02	JE840003248901399 [F]

<< < 1 > >> 1 - 4 of 4 items

Genotype Conflicts					
Pedigree Change	Conflict Type		Conflicting Genotype		
	Message	Code	Barcode & Position	Conflicting ID	USE
	MGS is unlikely	O6	203665660037 R04C01	JE840003203116924 [M]	Y

<< < 1 > >> 1 - 1 of 1 items

Other Close Relatives					
Relative ID	Relative Barcode & Position	USE	SNP		
			Compared	Same	Conflicts
No records available.					

Error Information

Select All Pedigree (fmt-1) Lactation (fmt-4) Reproduction (fmt-5) Health (fmt-6)

Apply

Clear



▼ Pedigree (fmt-1) | 1 Source File

▼ Errors in File 20240717.1G.

Error Code	Disposition Code	Description	ID	Herd	Source Code
3Gq	Changed	The dam identification number has been confirmed with a genotype. The dam identification was not changed.	<u>JE840003248901399</u>		N

Sire	Dam	Cross Reference	DOB	Source Code	Processing Date	Record Type	Verification Code	Multi-Birth Code	Registr Status
JE840003200210433			2024-06-05	N	2024-07-17	P	2	1	



[MGS Info](#)

[MGS Info](#)

[Show All](#)

Sample ID: AF05523950 - Barcode & Position: 208160590004 R19C03 - Usability Indicator: Y

Genotype Confirmations		
Confirmation Type	Confirmed Genotype	
	Barcode & Position	Confirmed ID
Sire	203253140011 R23C01	JE840003200210433 [M]
Sire	203359330123 R16C03	JE840003200210433 [M]
Sire	203665660007 R11C01	JE840003200210433 [M]
Dam	208025910022 R12C02	JE840003248901399 [F]

<< < 1 > >> 1 - 4 of 4 items

Genotype Conflicts					
Pedigree Change	Conflict Type		Conflicting Genotype		
	Message	Code	Barcode & Position	Conflicting ID	USE
	MGS is unlikely	O6	203665660037 R04C01	JE840003203116924 [M]	Y

<< < 1 > >> 1 - 1 of 1 items

Other Close Relatives					
Relative ID	Relative Barcode & Position	USE	SNP		
			Compared	Same	Conflicts
No records available.					

Sample ID: AF05523950 - Barcode & Position: 208160590004 R19C03 - Usability Indicator: Y

Maternal Grand Sire Information ✕

Information:

'Unlikely' grandsire indicates that (at time of processing) a genotype associated with the pedigree grandsire, is NOT likely to be the grandsire of genotype associated with the subject animal.

Reasons for this include, but may not be limited to:

- 1) Any of the genotypes could be associated with the wrong animal.

[GenoMove](#)

- 2) The Dam indicated in the Animals pedigree could be wrong.

Check genotype errors for suggestions, or

[Clear Dam Using Fix_FMT1](#)

- 3) The grandsire indicated in the Dams pedigree could be wrong.

[Change_MGS via FMT1 for the Dam](#)

Detection:

MGS candidates based on [percentage of matching haplotypes](#).

(Higher is better, 50% would be surprisingly high.)

JE840003211412088 (50.4 %)

Genotype	USE
03116924 [M]	Y

1 - 1 of 1 items

[MGS Info](#) [PGS Info](#) [Show All](#)

Sample ID: AF05523950 - Barcode & Position: 208160590004 R19C03 - Usability Indicator: Y

Genotype Confirmations		
Confirmation Type	Confirmed Genotype	
	Barcode & Position	Confirmed ID
Sire	203253140011 R23C01	JE840003200210433 [M]
Sire	203359330123 R16C03	JE840003200210433 [M]
Sire	203665660007 R11C01	JE840003200210433 [M]
Dam	208025910022 R12C02	JE840003248901399 [F]

<< < 1 > >> 1 - 4 of 4 items

Genotype Conflicts					
Pedigree Change	Conflict Type		Conflicting Genotype		
	Message	Code	Barcode & Position	Conflicting ID	USE
	MGS is unlikely	O6	203665660037 R04C01	JE840003203116924 [M]	Y

<< < 1 > >> 1 - 1 of 1 items

Other Close Relatives					
Relative ID	Relative Barcode & Position	USE	SNP		
			Compared	Same	Conflicts
No records available.					

Genotype Confirmations		
Confirmation Type	Confirmed Genotype	
	Barcode & Position	Confirmed ID
Progeny	208160590004 R19C03	JE840003283626313 [F]

<< < 1 > >> 1 - 1 of 1 items

Genotype Conflicts					
Pedigree Change	Conflict Type		Conflicting Genotype		
	Message	Code	Barcode & Position	Conflicting ID	USE
	Sire conflict	N3	203665660037 R04C01	JE840003203116924 [M]	Y
	Dam conflict	N4	203718610082 R13C03	JEUSA000067846430 [F]	Y
	Discovered sire	T2	204304290011 R08C02	JE840003211412088 [M]	Y
	PGS is unlikely	O7	201094570009 R05C02	JEUSA000119755026 [M]	Y

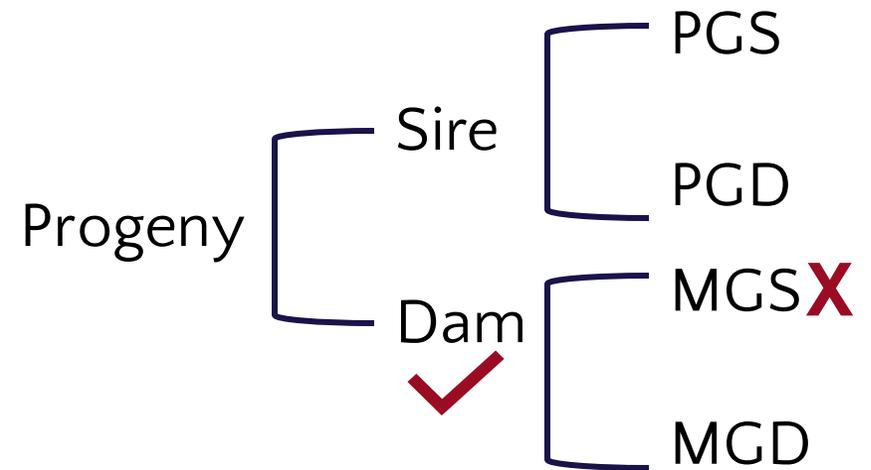
<< < 1 > >> 1 - 4 of 4 items

[Fix_FMT1](#)

Other Close Relatives					
Relative ID	Relative Barcode & Position	USE	SNP		
			Compared	Same	Conflicts
No records available.					

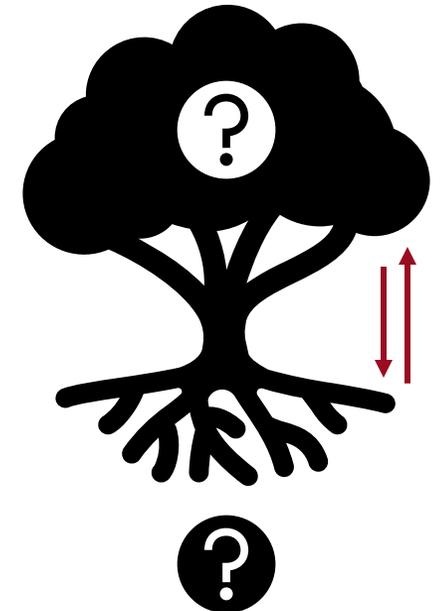
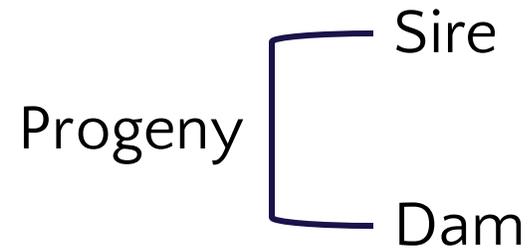
O6: MGS Unlikely

- If the dam is confirmed, investigate the dam's pedigree
 - If the dam's pedigree requires corrections, they will need to be resolved for the Progeny to receive an evaluation



P2: Non-pedigree Relative Close Birth

- A Parent-Progeny relationship has been identified, but the birth dates are too close
 - Birth Date of Parent Incorrect
 - Birth Date of Progeny Incorrect
 - MBC of Progeny Incorrect



P2: Non-pedigree Relative Close Birth

Multiple birth code	
Code	Description
1	Single
2	Multiple birth (Fraternal or identical twins, not from embryo transfer. Twins share the same genomic and gestational dam)
3	Birth from embryo transfer
4	Split embryo (artificially or naturally after embryo implantation)
5	Clone from nuclear transfer
6	Embryo pedigree (implantation date stored as birth date)

P2: Non-pedigree Relative Close Birth

MBC does change the threshold for the number of days between parent and progeny birth dates:

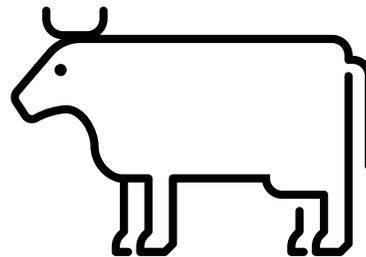
- MBC=1, birth >548 days from parents, 457-548 days with verification
- MBC=3, birth >304 days from dam birth date with verification
- MBC=6, implant date within 60 days of dam birth date



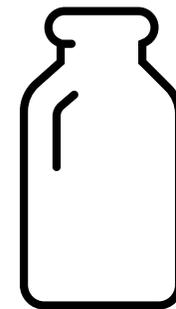
Birth Date Rules: https://redmine.uscdcb.com/projects/cdcb-customer-service/wiki/Birth_Date_Rules

P2: Non-pedigree Relative Close Birth

- General Rule: Birth date can only be changed by 90 days at a time – may require multiple records
- If an animal has progeny or lactation data, the new birth date must agree



Before



P2: Non-pedigree Relative Close Birth

- If you are unable to move the birth date to the confirmed birth date – Don't Panic Check the Errors!
- Likely there is lactation data or another animal in conflict preventing the change

Evaluation Breed: HO – Holstein

Animal

Preferred ID: HO840003287672539
 Name:
 DOB: 2022-12-14
 Sex: F
[Multi-Birth Code:](#) 3
[ID Source Code:](#) N
[Pedigree Source Code:](#) N
[Blend Code:](#) S

[Does the animal qualify for a genomic evaluation?](#)

Indicator: N

Genotype Conflicts					
Pedigree Change	Conflict Type		Conflicting Genotype		
	Message	Code	Barcode & Position	Conflicting ID	USE
	Non-pedigree relative close birth	P2	205785660017 R01C01	HO840003242205975 [M]	Y
	Non-pedigree relative close birth	P2	206451120112 R09C03	HO840003255309314 [E]	Y

1 – 2 of 2 items

Other Close Relatives			
USE	SNP		
	Compared	Same	Conflicts
No records available.			

P2: Non-pedigree Relative Close Birth

456 days

Potential Progeny

ID: HO840F003287672539

Birth Date: 2022-12-14

MBC: 3

164 days

Potential Sire

ID: HO840003242205975

Birth Date: 2021-09-14

MBC: 3

Potential Dam

ID: HO840003255309314

Birth Date: 2022-07-03

MBC: 3

Error Information

Select All Pedigree (fmt-1) Lactation (fmt-4) Reproduction (fmt-5) Health (fmt-6) Apply Clear

▼ Pedigree (fmt-1) | 1 Source File

▼ Errors in File 20240609.1G1

Error Code	Disposition Code		ID	Herd	Source Code
5Db	<u>Changed</u>				
3Gi	<u>Changed</u>	Input dam			

AI Sire pedigrees are very accurate



Sire	Dam	Cross Reference	DOB	Source Code	Processing Date	Record Type	Verification Code	Multi-Birth Code	Regis Stat
HO840003242205975	HO840003255309314		2022-12-14	N	2024-06-09	P	2	3	

Investigate the dam

Dam

HO840003255309314

ID/Pedigree

Evaluation

Genotype

Evaluation Breed: HO - Holstein

Animal

Preferred ID: HO840003255309314

Name:

DOB: 2022-07-03

Sex: F

[Multi-Birth Code:](#) 3

[ID Source Code:](#) N

[Pedigree Source Code:](#) N

[Blend Code:](#) S

Genotype Confirmations

Confirmation Type	Confirmed Genotype	
	Barcode & Position	Confirmed ID
Sire	203985940012 R06C02	HO840003210133059 [M]
Sire	204049080017 R22C01	HO840003210133059 [M]
Dam	204825110071 R03C03	HO840003215219123 [F]
Progeny	208261530110 R11C04	HO840003256639063 [F]
Progeny	208418910119 R07C01	HO840003271726362 [F]
Progeny	208418920121 R21C02	HO840003284942319 [F]

Dam also has other confirmed progeny

Progeny	Sex	DOB
HO840003256639063	F	2024-03-26
HO840003284942319	F	2024-05-07
HO840003271726362	F	2024-05-11
HO840003291040494	F	2024-07-01

Evaluation Breed: HO - Holstein

Animal

Preferred ID: HO840003287672539

Name:

DOB: 2022-12-14

Sex: F

[Multi-Birth Code:](#) 3

[ID Source Code:](#) N

[Pedigree Source Code:](#) N

[Blend Code:](#) S

Birth Date of the potential progeny is most likely incorrect



Indicator: N

Genotype Conflicts					
Pedigree Change	Conflict Type		Conflicting Genotype		
	Message	Code	Barcode & Position	Conflicting ID	USE
				05975 [M]	Y
	Non-pedigree relative close birth	P2	206451120112 R09C03	HO840003255309314 [E]	Y

<< < 1 > >> 1 - 2 of 2 items

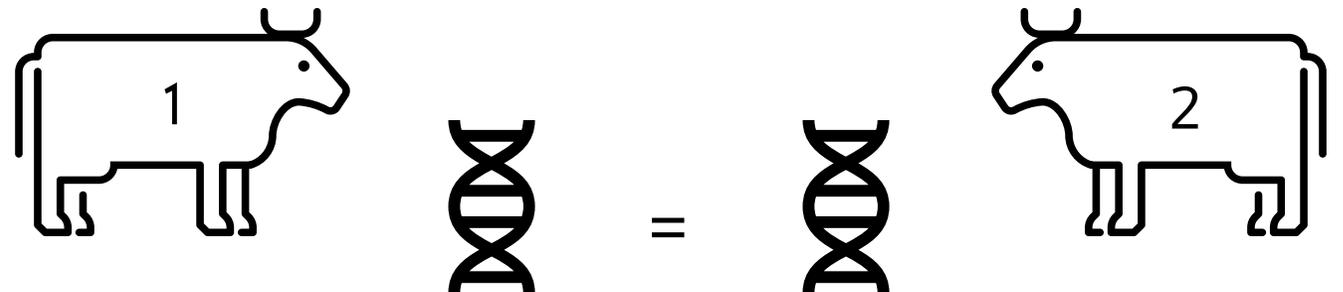
Other Close Relatives			
USE	SNP		
	Compared	Same	Conflicts
No records available.			

[Does the animal qualify for a genomic evaluation?](#)



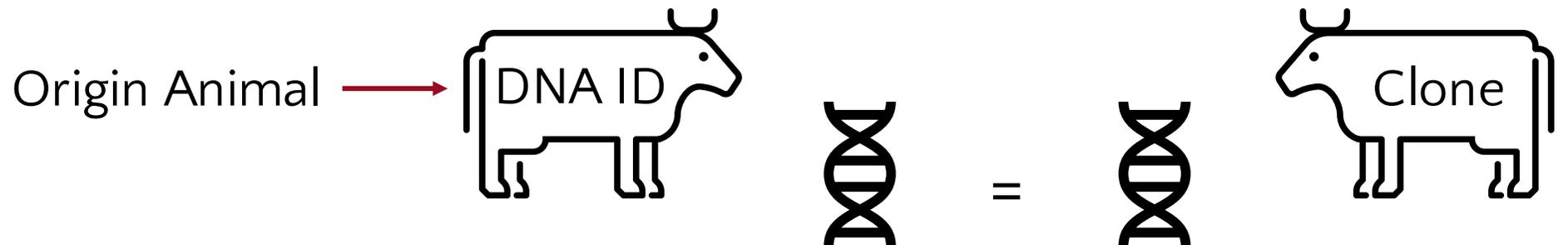
O2: Duplicate/N9: Discovered Clones

- O2: Duplicate; two identical genotypes are assigned to animals with different pedigree parentage
- N9: Discovered Clones; two identical genotypes are assigned to animals with similar pedigrees and no clone record has been established



O2: Duplicate/N9: Discovered Clones

- At CDCB, clone records/relationships do not always indicate animals resulting from cloning
- Having a clone record in the database means that the two animals share identical DNA



O2: Duplicate/N9: Discovered Clones

- Examples of animals that would have a clonal relationship at CDCB:
 - Identical twins: both animals with $MBC=2$ and same birth date
 - Animals resulting from embryo transfer split in vitro or in utero: both animals with $MBC=4$, birth dates expected to be close
 - An origin animal and its clone: origin animal can have any MBC and clone would have $MBC=5$. Origin animal is logically older

O2: Duplicate/N9: Discovered Clones

- Because clone's have identical DNA we expect that their pedigrees:
 1. Have the same parentage
 2. Have MBCs that would spawn animals with identical DNA
 3. Have birth dates that logically make sense with the assigned MBCs

O2: Duplicate/N9: Discovered Clones

- Before trying to create a clone record consider:
 - Is this one animal tested under two different IDs?
 - Is one of the genotypes incorrectly assigned to a different ID?
 - Why wasn't a clone record created automatically?

O2: Duplicate/N9: Discovered Clones

- For an in depth explanation of the situations where clone records are automatically applied see:

- Dealing with Clone Records:

https://redmine.uscdcb.com/projects/cdcb-customer-service/wiki/Dealing_with_clone_records

Conclusions

- Pedigree conflicts are very closely related to genomic conflicts
- If you are having problems fixing a genomic conflict, check the errors returning on the pedigree
- If you need help investigating an in-depth conflict, please open a ticket on Redmine for CDCB help!

Thank you for your attention!