

Changes implemented in the past 2 years

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Areas with recent changes

- Fee management
- Grandsire discovery
- Initial BBR
- Update herd reason code via FixPed
- Cross reference when both IDs have genotypes

Fee management

- Single nomination per animal-requester
 - Where there are multiple genotypes per animal, the group name and fee code are forced to be current
 - Group name and fee code not stored with genotype thus avoiding possible conflict
- Sample ID no longer part of nomination
 - Not possible due to multiple genotypes for a requester-animal
 - Sample ID no longer backup ID for genotype
- Nominators required to plan for new nominators for customers if discontinue

Grandsire discovery

- Discovery by haplotype method for both MGS & PGS
 - Determined as part of weekly evaluation
- When pedigree grandsire is discovered grandsire, unlikely designation removed
 - Previously done only for MGS where sire was confirmed
- To provide possible grandsires before weekly, web query added to search among ~17,000 bulls with recent progeny or grandprogeny for them
- PVR reports a maximum of 3 possible MGS

Consequences of Grandsire changes

- Discovery is by haplotype method which is more accurate than SNP-at-a-time
- Extends automatic removal on unlikely designation to PGS and MGS where sire not verified when discovered GS = pedigree GS
- Must rely on web query if discovered grandsire needed before weekly evaluation

Initial BBR – Use of breed SNP ended

- As genotype is loaded, an approximate BBR is calculated
 - Uses only SNP on the chip to avoid imputation
 - Genotypes with $BBR \geq 85$ initially assigned to purebred processing in weekly. If imputation based $BBR < 90$, moved to XX processing
- Wrong breed error now based on $BBR \geq 85$ for breed that is not the breed of the ID
 - For breed XX, if sire breed was stored previously and matches breed of $\max(BBR)$, no error
- Non genomic breed error based on breed of ID except XX where the breed of sire is checked
- Breed SNP no longer used

Initial BBR calculation benefits

- More accurate assignment of genotypes to crossbred calculation
- Provides more accurate wrong breed error determination
- Eliminates need to explain/understand breed SNP
- Determination of breed of evaluation for XX standardized

Update of herd reason code via FixPed

- An unlikely MGS designation often is eliminated by blanking the dam
- Often the dam is the basis for qualifying for a specific fee code
- A herd reason code can specify the animal's presence in a herd
- A format 1G record can both blank the dam and set the herd reason code
- FixFmt1 in the genotype query was modified to create format 1G records to do both

Cross reference of IDs – both with genotypes

- Requires that sire, dam, and birth date match
- There must be an error indicating that the 2 genotypes are identical
- There are 2 steps
 - One genotype is assigned to the internal ID (animal key) of the other
 - A normal cross reference is run
- The genotype reassignment is done during one of the twice daily updates
- This process is not immediate, and the preferred ID may not be the one intended, so results must be checked

Under construction

- Reducting time to process new genotypes
- Faster application of updates to genotypes
- Adding genomic ancestors

Loading and updating of genotypes

- This is a time-consuming process because:
 - The time to compare each genotype with all others consumes an increasing amount of time as the number of genotypes increases
 - The comparison is repeated when there is a change in pedigree that might create or remove a conflict

Faster loading and updating of genotypes

- The solution currently being developed includes:
 - To speed the comparisons, a set of 3552 SNP present on most chips has been selected and ordered so that, for most genotypes, after checking the first 96 the genotype can be excluded as being a parent, progeny or identical
 - To speed updates, the identity of all genotype pairs that are similar enough that they could be a parent-progeny pair or identical are stored so the update process only needs to check them

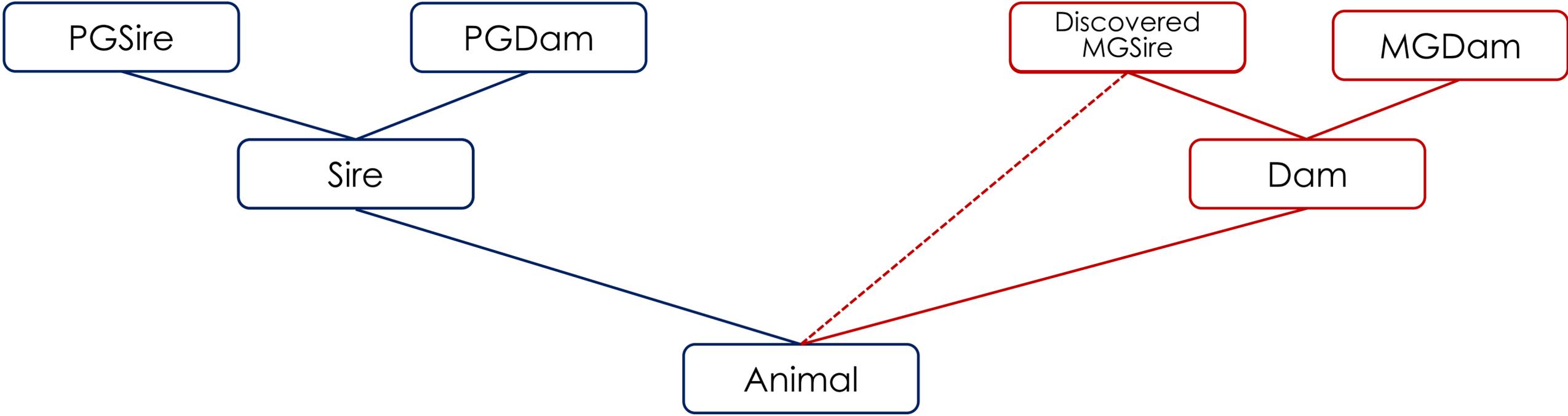
Reducing start up time

- Reliance on 4K genotypes for discovering close relatives may enable removing genotypes from the initialization file enabling faster start up
- Relying on database access for data as needed may enable elimination of the initialization file.

Adding discovered ancestors

- The process that provides discovered grandsires also discovers MGGS
- Accuracy of genomic evaluations can be improved by adding these discovered ancestors to the pedigree
- Where the dam ID is known, but no pedigree was provided, CDCB adds the discovered MGS as her sire
- To add an MGS or MGGS when the dam or granddam is unknown we can construct IDs to enable these IDs to be added
- We have developed a way to reject a discovered MGS or MGGS

Dam known, sire unknown, discovered MGS stored as Dam's Sire



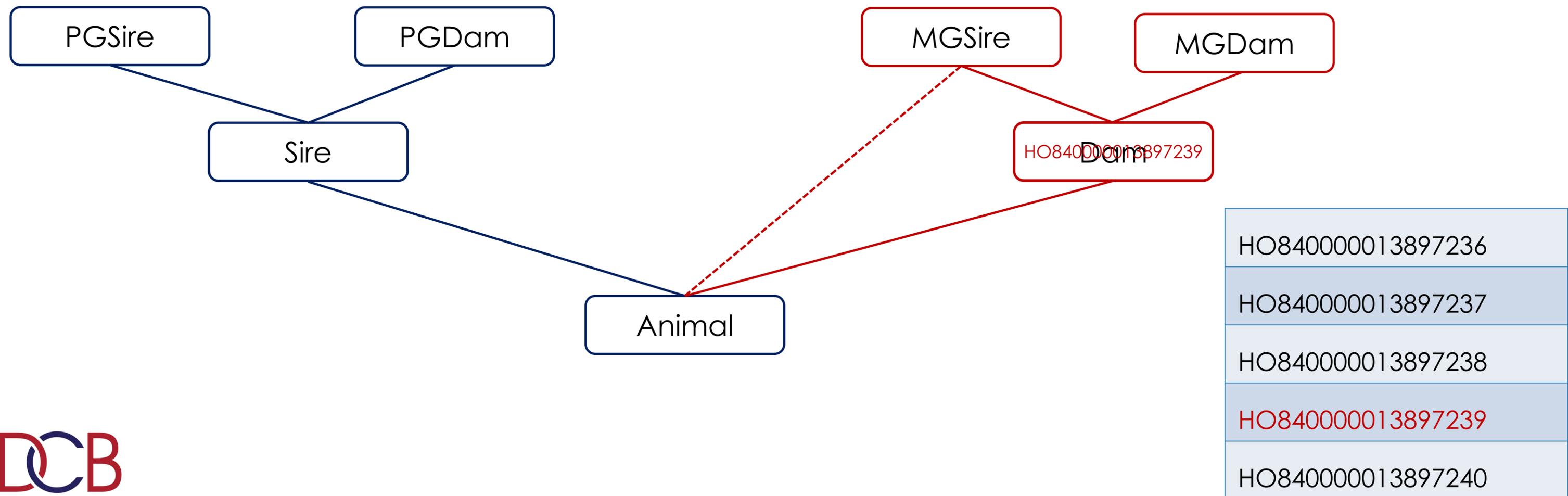
Spec	Sex	Animal	Sire	Dam	Xref									
0	F	HOCAN000013897236	H0840003010353429											
Birth		Animal Name	GrpName	PI	US	RSN	ProcDate	Src	Type	Ver	MBC	Reg	Stat	Disp
2004070E		Dam of JEUSA000067119068					20210408	A	P	0	1			

Known Dam

Discovered MGS



Dam unknown; Dam suggested based on herd, sire, and calving date



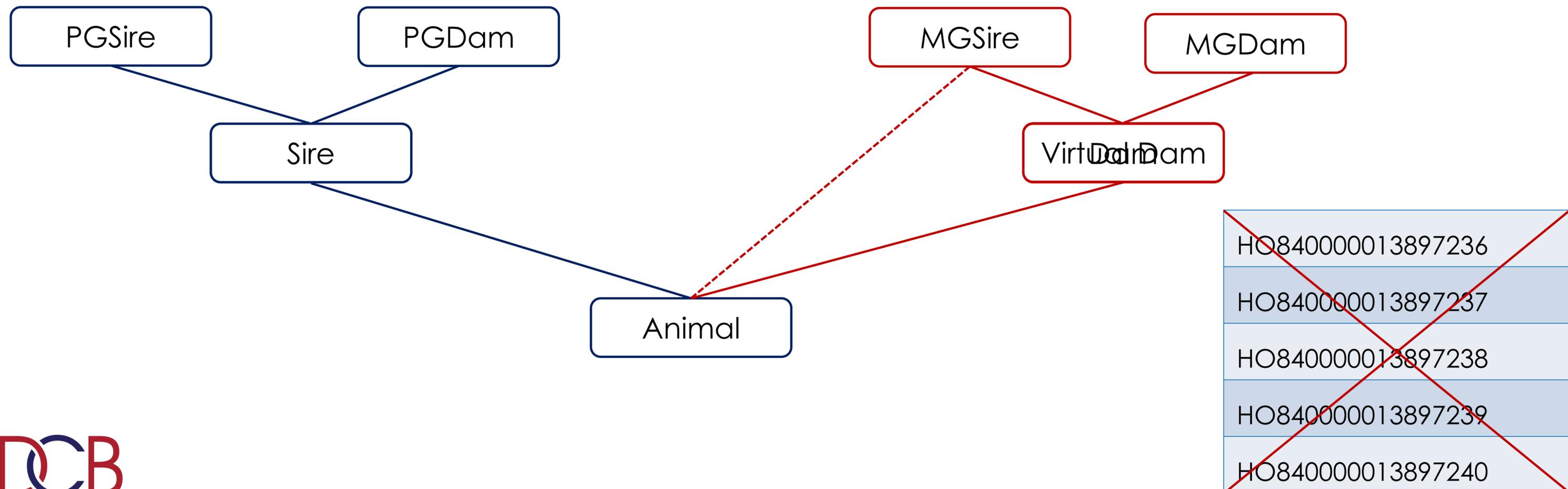
Spec	Sex	Animal	Sire	Dam	Xref
0	F	HOCAN000013897236	H0840003010353429	H0840000013897239	

Birth	Animal Name	GrpName	PI	US	RSN	ProcDate	Src	Type	Ver	MBC	Reg	Stat	Disp
2004070						20210408	A	P	0	1			



Dam suggested based on herd, sire, and calving date

Dam unknown; Dam ID constructed, and pedigree created with discovered MGS as sire



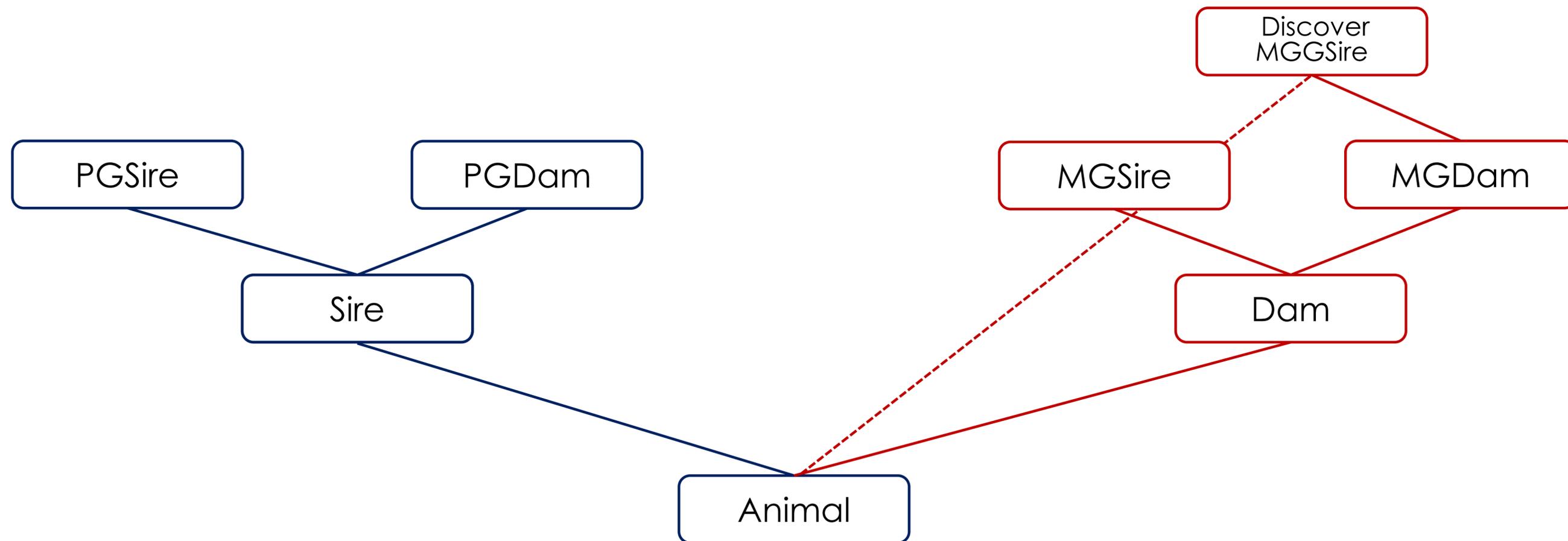
Spec	Sex	Animal	Sire	Dam	Xref
0	F	JEUSA000067119068	JEUSA0000000663363	JEUSADAM048222671	

Birth	Animal Name	GrpName	PI	US	RSN	ProcDate	Src	Type	Ver	MBC	Reg	Stat
20051231	YOSEMITE QUEST MANDATE	F19068				20210408	A	P	0	2		HR



Virtual Dam

MGD known, discovered MGGs added as her sire



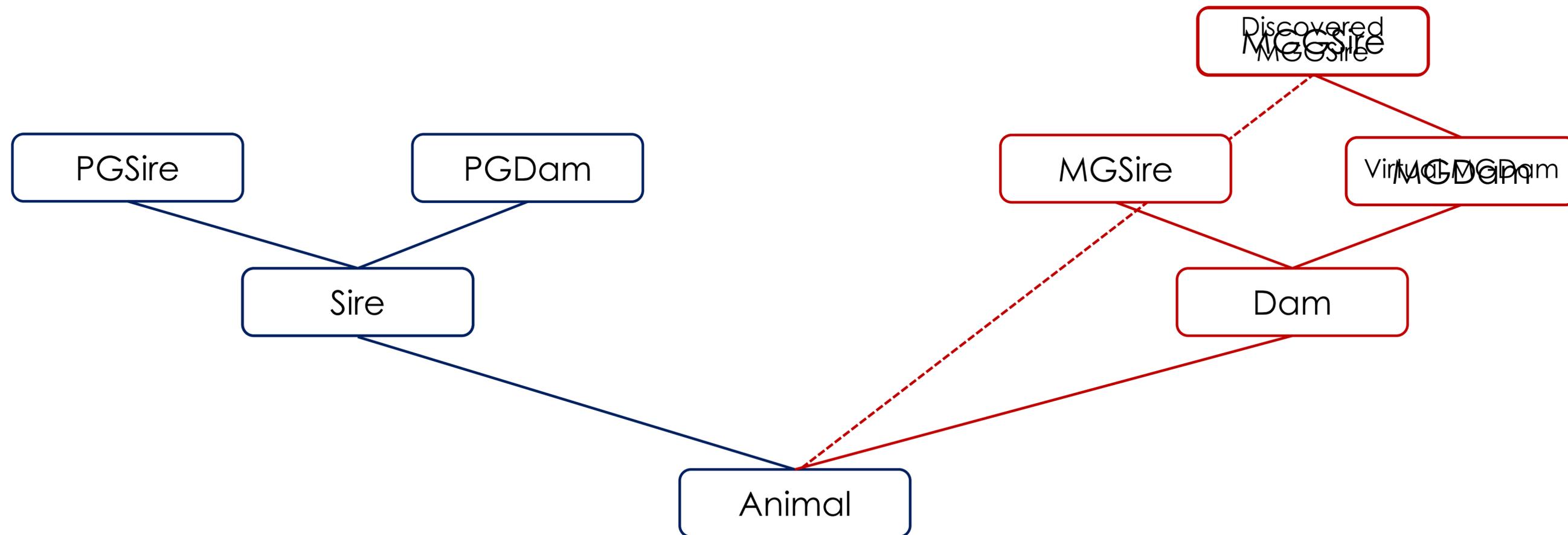
Spec	Sex	Animal	Sire	Dam	Xref
0	F	HOCAN000013897236	JEUSA000110587444		

Birth	Animal Name	GrpName	PI	US	RSN	ProcDate	Src	Type	Ver	MBC	Reg	Stat	Disp
2004070						20210408	A	P	0	1			

MGDam

Discovered MGGS

MGD unknown MGD ID constructed, and pedigree created with discovered MGGS as sire



Spec	Sex	Animal	Sire	Dam	Xref
0	F	JEUSAMGD048222671	JEUSA000000651068		

Birth	Animal Name	GrpName	PI	US	RSN	ProcDate	Src	Type	Ver	MBC
Reg Stat Disp										
2003010E MGD of	JEUSA000067119068					20210408	A	P	0	1

Constructed MGDam

Discovered MGGsire

Proposal

- Discovered MGS added to pedigree of known dam automatically except for B source where source is notified and is expected to submit update, or a record to reject the sire
- Constructed IDs when needed added to pedigree of genotyped animal or its dam
 - pedigree record for constructed ID added with the discovered MGS/MGGS as sire
- Notification of discovered dam sent to source

Counts from genotypes - animals born 2020

Group	Number
Discovered MGS	85,929
Discovered MGGS	112,915
Constructed Dam ID	71,424
Sire added for known Dam	8,775
Discovered dam	4,017
Constructed MGD ID	51,370
Sire added for Known MGD	4,916