

Council on Dairy Cattle Breeding CDCB web queries

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New Fee Codes in Nomination APP

Here we see a return from the new FEE function in the Nomination APP.

This new function in the Nomination APP uses Nomination Date and/or Scan Date.

If either of these is before 2019-04-03, you are subject to the original Fee Schedule.

Otherwise, the user input is checked for a proper Fee and Group/Herd ID based on the New Fee Schedule.

The output in the pink message box alerts us that the Fee and Group/Herd ID are invalid.

If the suggested values are acceptable changing the input form to match and clicking the submit again, should produce a valid nomination.

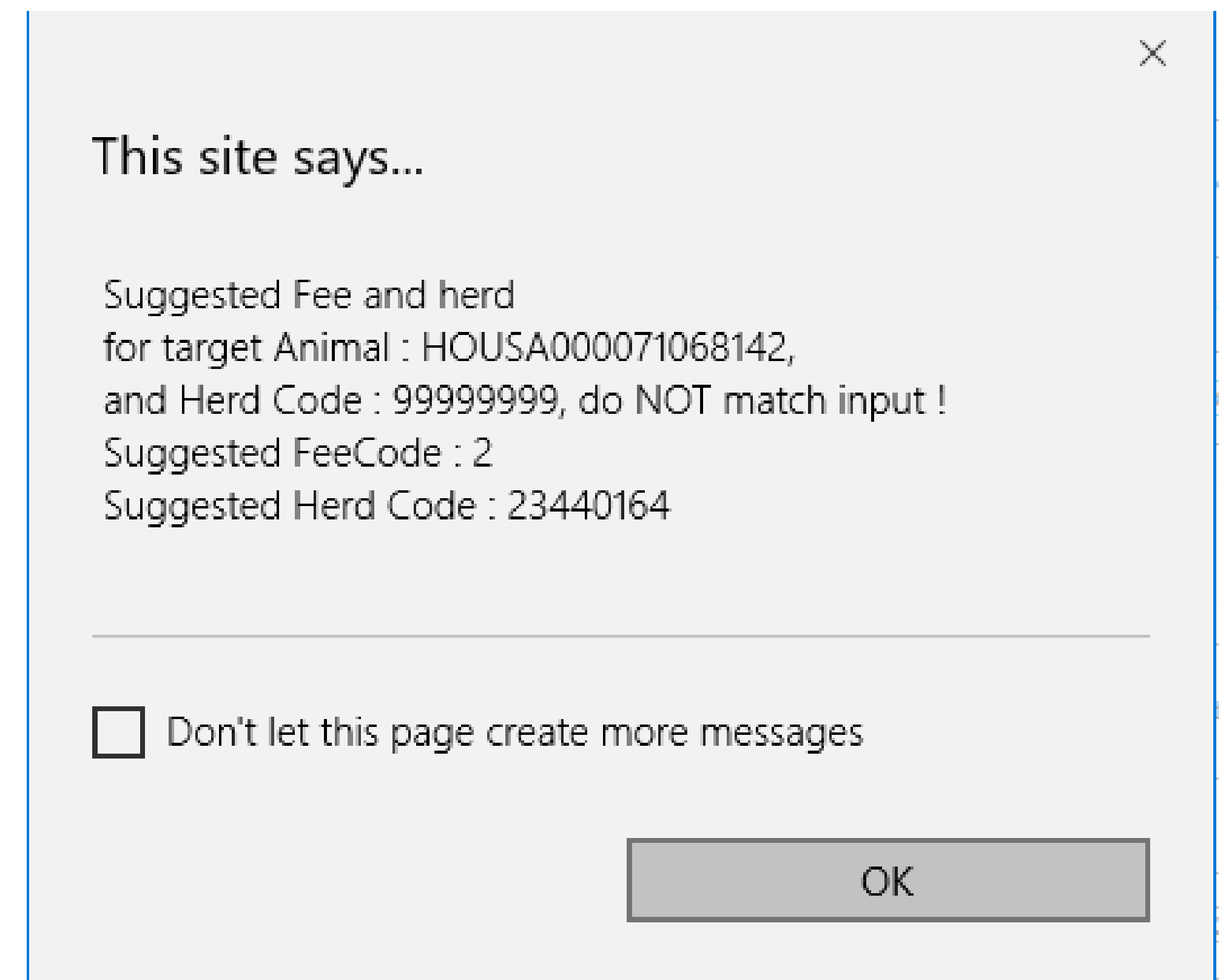
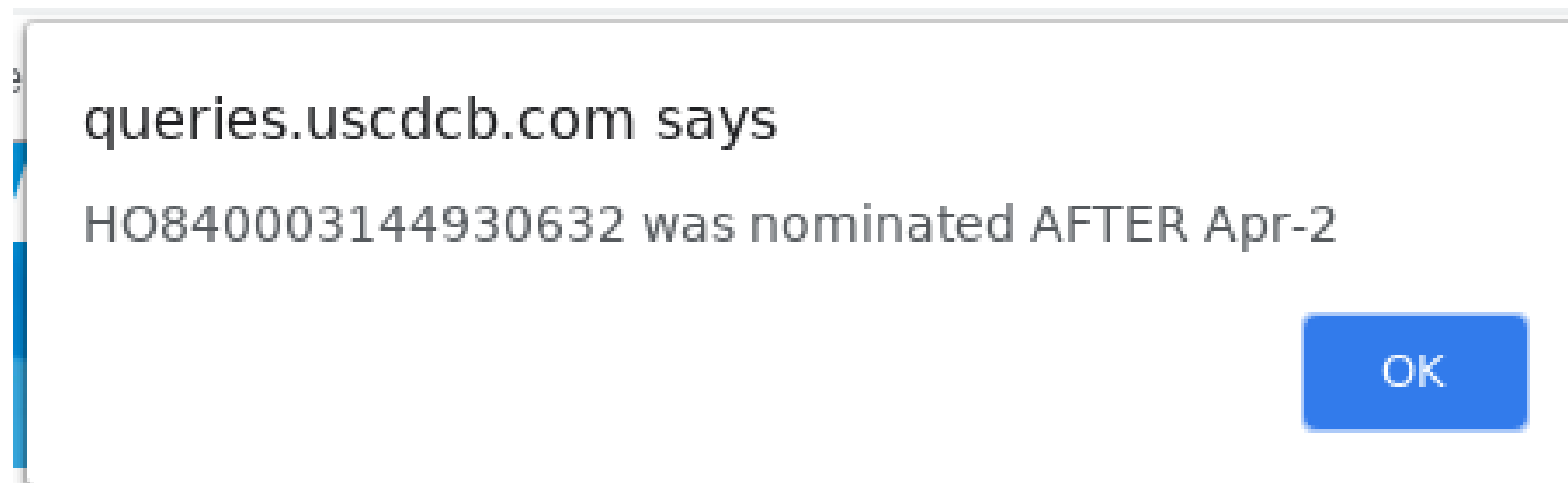
User Input		Sex	Anim_ID	NAAB ID	Name		Sire_ID	Dam_ID	Birth Date	MBC	SRC
HOUSA000071068142		M	HOUSA000071068142		VER-NAN MAYFIELD RUDY-ET		HOUSA000069473980	HOUSA000066879821	2013-02-12	3	B
Nom Date	Scan Date	Rec.	PI	Sample ID	Sold	Nom. ID	Stud	Group / Herd ID	Fee	HRC	Record Actions
2013-02-28	2013-03-19	S	N ▾	HAU0791867A-01	\$=>	HO ▾	0	35370953	1 ▾	▾	<--- Submit Changes
2013-03-21		N	N ▾	HOUSAM000071068142		Select ▾	14		1 ▾	▾	<--- Submit Changes <<--- Delete This Nomination
Click here to toggle display of 'NEW Nomination' form.											
TBD	TBD	NEW	N ▾	FrankTEST		AIPL ▾		99999999	1 ▾	▾	<--- Add This NEW Record
Suggested Fee and Herd Code do NOT match input ! Suggested FeeCode : 2 Suggested Herd Code : 23440164											

New Fee Codes in Genotype Move/Swap APP

The Genotype Move/Swap APP uses similar logic to do the same job.

A major difference though is, since you are moving a genotype (not a nomination), the dates used are Scan Date of the subject genotype, and the earliest Nomination Date; for your Requester ID; for the destination animal.

As output you should see alert dialogs that should inform you of its decisions.



Changes to Genotype Query (or Status APP)

NEW

Animal: HOUSA000065480924 Sex Code: F Eval Breed: HO

Sample ID	Bar Code	Pos.	Chip Name	Use Ind	Pend	Fee Code	Confirmations and Errors	PO	Sire Stat	Dam Stat	No. Prog	Tissue Source	Lab	Req.
4031713	5645094038	R06C04	3K	N <input type="button" value="withdraw"/>		O	<input type="button" value="↑"/>	N	2	2	0	B	GSek	Zoetis

Genotype Confirmations

No displayable confirmation records.

Genotype Conflicts

Pedigree	Conflict Type		Conflicting Genotype			
	Message	Code	Barcode	Position	Conflicting ID	USE
Changed	Sire conflict	N3	6909979044	R05C01	HOCAN000005470579 [M]	Y
	Dam conflict	N4	4482490190	B	HOUSA000060114675 [F]	Y
	MGS is unlikely	O6	1992267206	I	HOCAN000005319769 [M]	Y
	Discovered Sire	O3	9221302048	R12C02	HOUSA000207189287 [M]	Y

Animal: HOUSA000065480924 Sex Code: F Eval Breed: HO
 MGS: Unlikely PGS: Likely/Unknown

OLD

Sample ID	Bar Code	Pos.	Chip Name	Use Ind	Pend	Fee Code	Confirmations and Errors	PO	Sire Stat	Dam Stat	No. Prog	Tissue Source	Lab	Req.	Scan Date	Eval Use Date	SNP_read	Breed SNP Conflicts
4031713	5645094038	R06C04	3K	N <input type="button" value="withdraw"/>		O	<input type="button" value="↑"/>	N	2	2	0	B	GSek	Zoetis	2010-11-19		2882	0

Genotype Confirmations				Genotype Conflicts						
confirmation type	Barcode	Position	confirmed genotype Confirm ID	conflict type		conflicting genotype				
				Message	Code	Barcode	Position	Conflicting ID	USE	
				Dam conflict	N4	4482490190	B	HOUSA000060114675 [F]	Y	
				Sire conflict	N3	6909979044	R05C01	HOCAN000005470579 [M]	Y	
				MGS is unlikely	O6	1992267206	I	HOCAN000005319769 [M]	Y	
				Discovered non-pedigree parent-progeny relationship	O3	9221302048	R12C02	HOUSA000207189287 [M]	Y	

Error Segment Reocrd

ERR_SEGMENT_RECORD processing date : 20160209 14:06:08		Other Genotype		
Error Code	Message	Animal ID	Barcode	Position
O6	MGS is unlikely (unlikely MGS = HOCAN000005319769).	HOCAN000005319769	1992267206	I

Changes to Genotype Query (cnt..)

The 'Pend' column now includes several more specific indicators.

[BLANK] = no pending records were detected

Pending Web_FMT1s, these are normally processed every **5 min**:

PA = pending pedigree CHANGE (Web_FMT1) on the subject animal detected a FMT1 submitted through the web that has not been processed yet

PS = pending pedigree CHANGE (Web_FMT1) on the sire detected a FMT1 submitted through the web that has not been processed yet

PD = pending pedigree CHANGE (Web_FMT1) on the dam detected a FMT1 submitted through the web that has not been processed yet

Pending genotype reprocessing/changes, this are normally processed **twice a day**:

R = pending ReProcessing request

These are caused by a change in the pedigree of the subject animal or a pedigree/genotype change of a closely related animal.

U = pending genotype CHANGE

a change in the supporting values of this genotype (aka: Requester ID, Fee Code, Parentage Only, Sample ID, etc.)

M = pending a Genotype MOVE request

a move request is pending for the subject genotype

Changes to Genotype Query (cnt..)

Genotype request processing (and therefore clearing of errors) is typically only done twice a day, but the FMT1 {pedigree changes} are run far more frequently.

This causes lag between a pedigree fix and the removal of a given error.

This is why we now have the 'Pedigree Changed' column in the Genotype Conflicts table.

This column alerts you that a pedigree change has been processed that will affect the given error, when the genotypes are processed again.

This column can also contain a clickable question mark (?), that can provide additional information about the error.

Get Foreign (fixed)

If nominating an animal CDCB does not already have in the database, you are provided a link to Get_Foreign. This APP will attempt to pull pedigree data from several CDCB colaborators. This APP has been busted for a while as it is very resource intensive.

Get_Foreign has been fixed, but now it only allows one request per IP address to be processed at a time.

THANK YOU FOR YOUR ATTENTION