Genotyping and procedure for validation of pedigree

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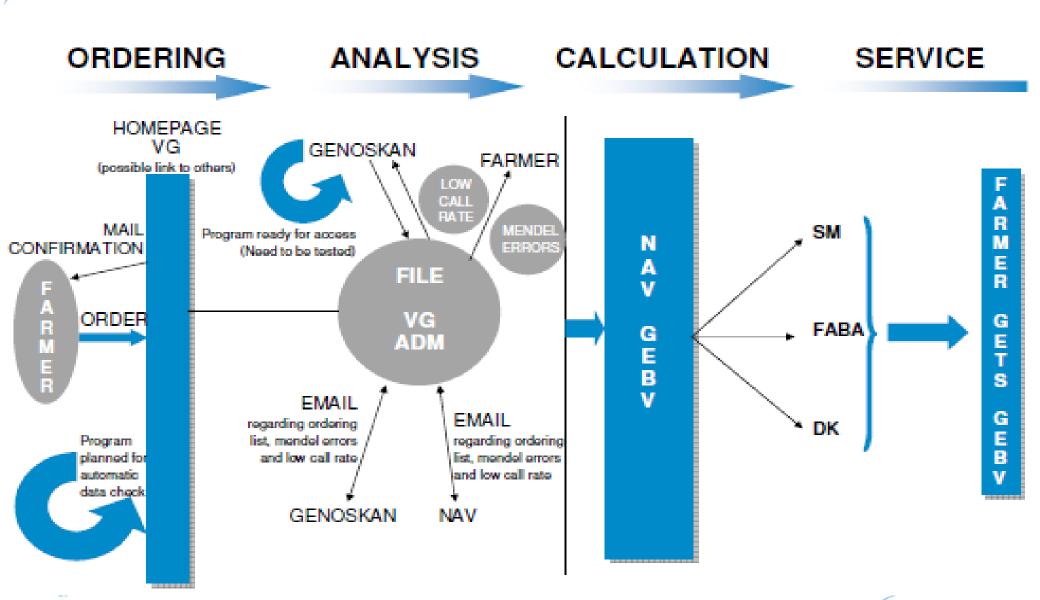
Number of genotypes animals

	RDC	Holstein	Jersey
54K Males (candidates)	3444	5338	862
54 K Females	1818	3181	550
Reference population	4519	4.798 (DSF) +18394 (EG)	1132
Total	9756	13616	2404

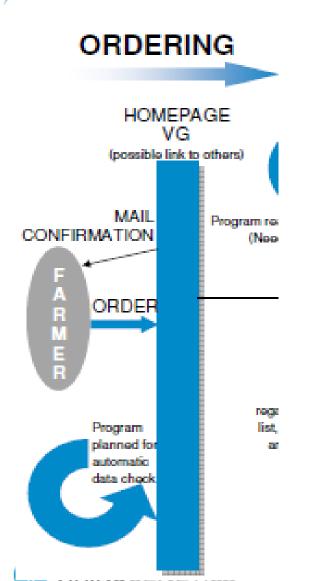
	RDC	Holstein	Jersey
770K Males	754	578	400 in process



Flow chart



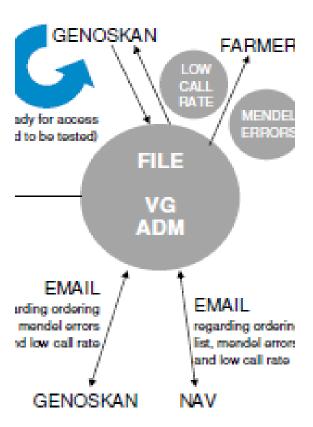
Flow chart - Ordering



- Farmer order females at homepage
 - Genoskan sends TSU
- VG order bulls internally and send letter and sample kit to farmer about wish to test bull calf
- Labels with ID and barcode are produced for samples
- All VG orders are collected in VG and send to Genoskan

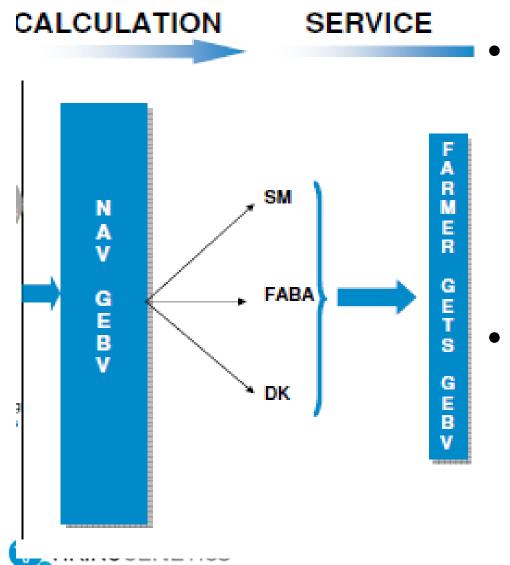
Flow chart - Analysis

ANALYSIS



- All samples are sent to Genoskan
- All sample ids are sent to NAV for id check
- List from Genoskan with missing animals
- List from Genoskan with animals that have low call rate
- List from NAV with Mendel Errors

Flow chart – calculation and service



- NAV calculates and sends GEBV to national databases that distrubutes GEBV's of females and males older than 20 months
- NAV sends bullcalfs younger that 20 months and females to VG for selection

Pedigree control and SNP based parenting

Check of Sample ID

Mendel Error Check

Check of retyped animals

Check of Sample ID

- A list of Sample IDs in ID-nor format is recieved from VG, when samples are sent to GenoSkan for genotyping.
- A lookup of sample ID-nor in an updated version of the NAV-pedigree file is performed
- ✓ If match, sample ID-nor is accepted





Mendel Error Check

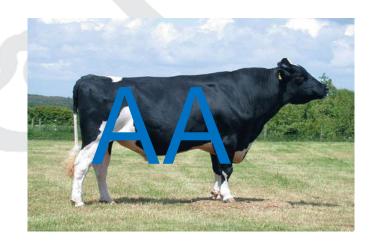
- If one or both parents are genotyped, Mendel Error Check can be performed
 - Parents from DFS and EuroGenomics/GENO are used
- Mendel Error Check is done by using PLINK
 - Incorporated in BC|SNPmax
- Mendel Error Check is performed at chromosom 20



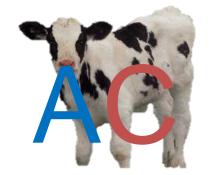


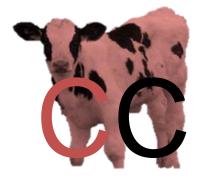
Principle behind Mendel Error Check











Mendel Error Check 1 parent genotyped

- PLINK can only scan full trios
- If only one parent is genotyped a parent dummy genotype is created
 - Parent dummy genotype = offspring genotype
- Only "homozygote" Mendel Errors between genotyped parent and offspring is counted





Mendel Error Check 1 parent genotyped

Sire

A..G..C..A..C..C..A..A..T..C C..G..A..T..G..C..A..C..A..C

Homologous chromosomes

Offspring





Mendel Error Check 2 parents genotyped

Sire

Homologous chromosomes

Offspring

Dam





Mendel Error Check 2 parrents genotyped

Sire

Homologous chromosomes

Offspring

Dam

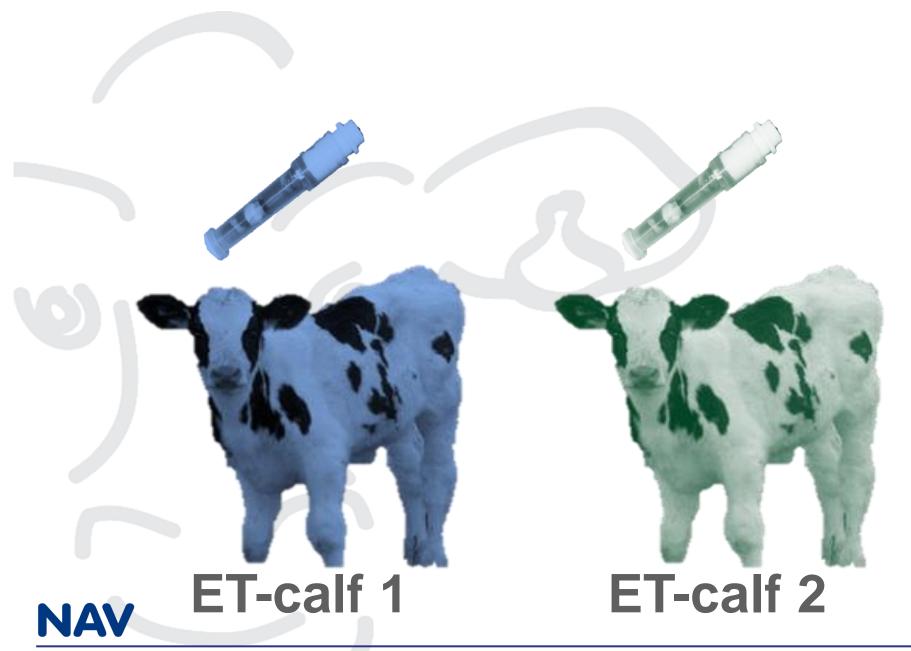




Mendel Error Results

- Mendel Errors may result from:
 - True pedigree error
 - Wrong animal sampled
 - Switch of samples by technician/laboratory/me
- Do not include animals with Mendel Errors in genomic evaluation
 - Genotypes are saved in separate table
- List of Mendel Error animals is sent to VG
- NAV Mendel Test is <u>no</u> official Parentage Test







Check of retyped animals

- Selected bulls, GenVikPLUS bulls, are retyped to avoid erroneous GEBVs
- The new genotype is compared with the old genotype for all common SNPs
- Clear separation of OK and erroneous retypings

NAV VG is infomed about check-result of retyping



Handling of low call rate (VG)

 DNA samples collected are tissue(DK) and nose swaps (FIN and SV)

- Low Call rate

 New samples from animals
 - Denmark, new tissue sample
 - Sweden and Finland, Hair sample

Reason for new sample is possible twin reaction



Handling of Mendel errors (VG)

- Mendel Errors
 - Message to owner
 - Owner orders parentage test if animal still interesting for him or VG
 - Owner informs VG when parentalship is verified →
 Animal enters next evaluation

