



# Genomic selection in breeding program

Jukka Pösö  
Faba/NAV

Elinvoimaa!

# Breeding is selection

- aim: select the genetically superior individuals to produce the next generation
  - genes in offspring are superior than in their parents
    - populations, individual animals
  - repeat generation after generation
- breeding program
  - nationwide plan what traits to improve and how

Bulls:				Cows:			
RDC	HOL	FIC	Traits	RDC	HOL	FIC	Traits
1.00	1.00	0.9	yield	0.91	0.90	1.1	yield
0.28	0.41	0.3	fertility	0.28	0.41		fertility
0.15	0.20		birth	0.15	0.20		birth
0.13	0.22		calving	0.13	0.22		calving
0.35	0.46	0.4	udder health	0.35	0.46	0.3	udder health
0.13	0.15		other diseases	0.13	0.15		other diseases
0.10	0.16		feet and legs	0.10	0.16		feet and legs
0.35	0.24	0.4	udder conformation	0.35	0.24	0.5	udder conformation
0.10	0.11		milkability	0.10	0.11		milkability
0.03	0.04		temperament	0.03	0.04		temperament
0.09	0.15		longevity	0.09	0.15		longevity
0.00	0.08		growth	0.00	0.08		growth
0.05	0.10		claw health	0.05	0.10		claw health

# Correlation between NTM and individual traits

	RDC	Holstein
yield	0.67	0.61
growth	0.05	0.10
fertility	0.17	0.43
birth	0.20	0.30
calving	0.21	0.34
udder health	0.30	0.45
other diseases	0.26	0.49
body	0.06	-0.04
feet and legs	0.18	0.13
udder conformation	0.33	0.33
milkability	0.21	0.12
temperament	0.21	0.00
longevity	0.61	0.71
claw health	0.13	0.17

# Problem in selection

- how to identify the best by their genes?
  - traits are affected by hundreds of genes
  - phenotype is not the same as genotype
  - new techniques: genomic information
    - based on DNA-sample we can **predict** genetic merit

# Breeding value?

- how good are the offspring
  - depends on the genes animal passes on
- always an **estimate** of breeding value
  - accuracy depends on amount of information
- true breeding value remains unknown
  - current methods

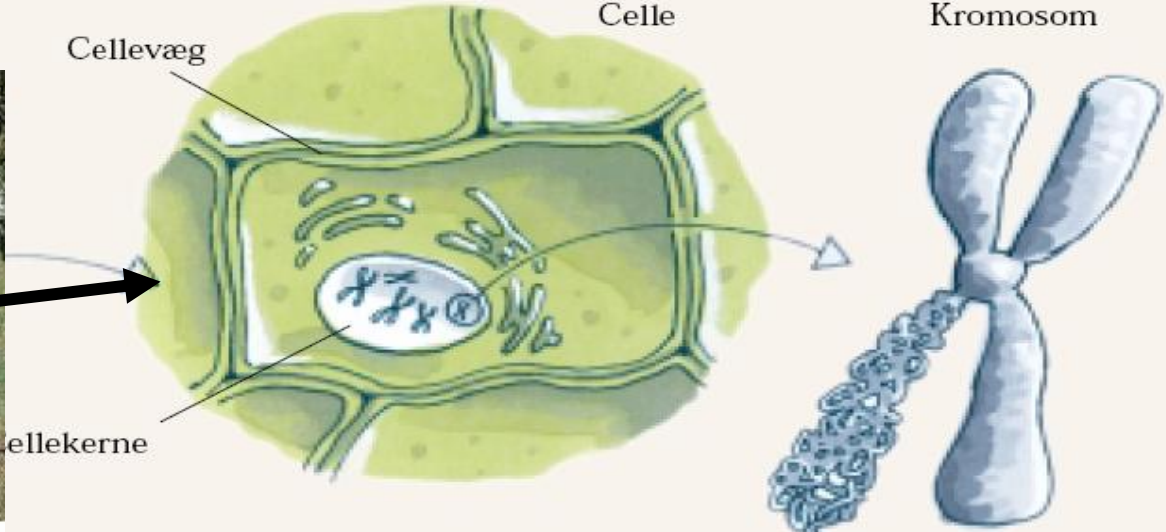
# Traditional breeding value estimation

- large number of observations on animals
  - breeding goal traits, correlated traits
- pedigree information
  - animal model
- distinction of genotype from phenotype
  - heritability,  $h^2$
  - environmental effects
  - BLUP
- EBVs
  - tools to be used in selection

# Hvad er et gen?



provided by Hoard's Dairyman

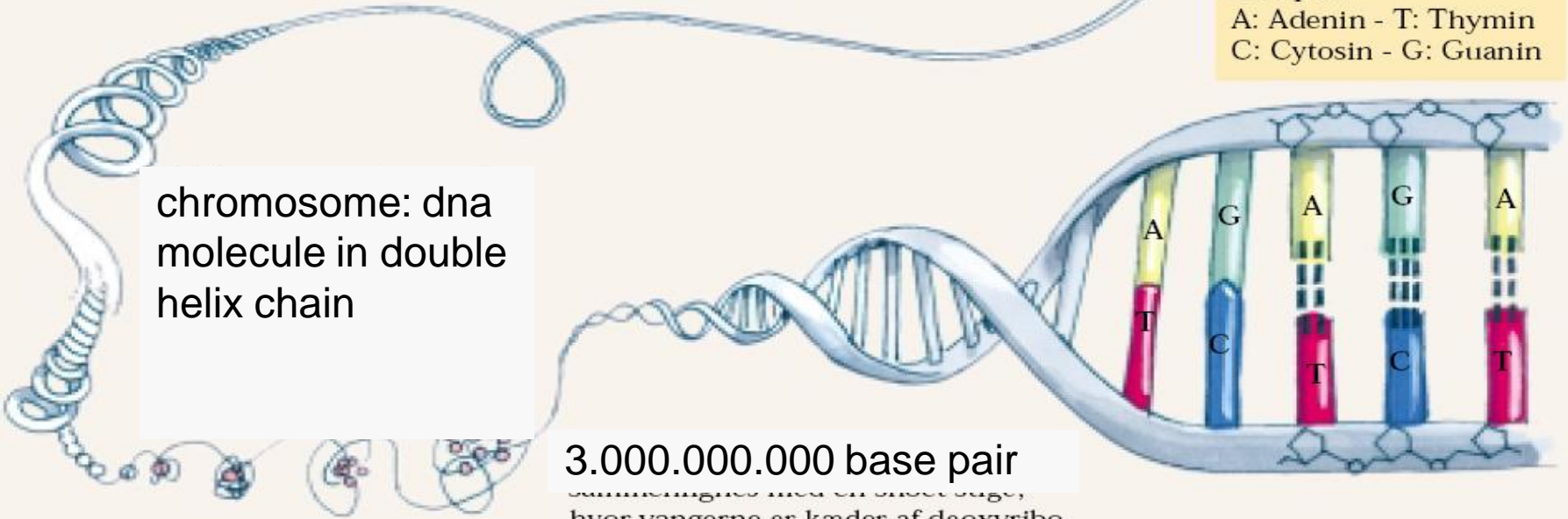


2 x 30 chromosomes in nucleus in each cell

Basepar:  
A: Adenin - T: Thymin  
C: Cytosin - G: Guanin

chromosome: dna molecule in double helix chain

3.000.000.000 base pair  
sammengøres med en sukker søge,  
hvor vangerne er kæder af deoxyribo-  
semolekyler, og trinene er basepar.





Gene 1

Gene 2

ATGACTAGGTCTCGATCGTAGCTATAGGGCTAGCTAGCTAGCTAGGTACCACATATAGATACATC

- gene = sequence of DNA
  - contains codes for protein manufacture
- approximately 20 000 genes, the rest of the DNA (95 %) is irrelevant?

## Gene 1

## Gene 2

Bull 1	ATGACTAGGTCTCGATCGTAGCTATAGGGCTAGCTAGCTAGCTAGGTACCACATATAGATACATC
Bull 2	ATGACTAGGTCTCGATCGTAGCTATAGGGCTAGCTAGCTAGCTAGGTACCACATATAGATACATC
Bull 3	ATGACTAGGTCTCGATCGTCGCTATAGGGCTAGCTAGCTAGCTAGGTACCACATATAGATACATC
Bull 4	ATGACTAGGTCTCGATCGTAGCTATAGGGCTAGCTAGCTAGCTAGGTACCACATATAGATACATC

## Gene 1

## Gene 2

Bull 1	ATGACTAGGTCTCGATCGTAGCTATAGGGCTAGCTAGCTAGCTAGGTACCACATATAGATAACATC
Bull 2	ATGACTAGGTCTCGATCGTAGCTATAGGGCTAGCTAGCTAGCTAGGTACCACATATAGATAACATC
Bull 3	ATGACTAGGTCTCGATCGTCGCTATAGGGCTAGCTAGCTAGCTAGGTACCACATATAGATAACATC
Bull 4	ATGACTAGGTCTCGATCGTAGCTATAGGGCTAGCTAGCTAGCTAGGTACCACATATAGATAACATC

”gene marker” (SNP, single nucleotide polymorphism)  
-millions, some are connected to traits we select for

# Gene 1

bull 1 ATGACTAGGTCTCGATCGTAGCTATAGGGCTAGCT...AGCTAGCTAGG.....GACCACATATAGATA

bull 2 ATGACTAGGTCTCGATCGTAGCTATAGGGCTAGCT...AGCTAGCTAGG.....TACCACATATAGATA

bull 3 ATGACTAGGTCTCGATCGTCGCTATAGGGCTCGCT...TGCTAGCTAGG.....GACCACATATAGATA

bull 4 ATGACTAGGTCTCGATCGTAGCTATAGGGCTAGCT...AGCTAGCTAGG.....TACCACATATAGATA

SNP

EBVs of the animals

- at least 2000 bulls with reliable EBVs based on offspring (reference group)
  - type of SNP (54 000 SNP chip)
  - combine SNP and EBV information
- model that explains which of the SNPs affect the trait in question and how much
  - SNP must be part of the genes or close to them to contain information on trait

# Genomic evaluation

- take a DNA sample (blood, nose secretion)
- typing of SNP
- use the genomic model based on reference group
  - individual SNP effects are summed up
- direct genomic EBV



## VR Maitoahon Turandot Tornado A 45863 C

## Translation of breeding values to phenotypic values

Born: 31.05.2010, Kiuruvesi  
Breeder: Maitoaho Ay  
Color: RV 2

Int.ID: FIN000000045863  
VG

Animal ID: 10175630

Sire: S.Turandot AAA 43576 C  
PGS: L-K.Luuro AAA 40751 C  
PGD: Noheva 1219670.AAA  
Dam: Uhmakas 1272353.AAA  
MGS: Peterslund1213 AAA 43002 C  
MGD: RAKKARI 1264706A  
MGS: K.Kelli AAA 40347 C

Trait	Daughters Reliability
Production	
Functional	
Health	
Conformation	

NTM: 24		23.02.2012				
		80	90	100	110	120
<b>Production</b>	107					
Milk-kg	105					
Fat-%						
Fat-kg	106					
Prot.-%						
Prot.kg	107					
Persistency	non-pers.					persistant
<b>Fertility</b>	117					
<b>Birth</b>	107					
<b>Calving</b>	102					
Still birth sire						
Still birth mgs						
Calving index (sire)						
Calving index (mgs)						
NRR (male fertility)	118					
Growth	96					
<b>Udder health</b>	114					
Cell count						
<b>Milkability</b>	98					
Leakage						
<b>Other treatments</b>	117					
<b>Temperament</b>	86					
Hoofohealth						
<b>Longevity</b>	105	bad				good
<b>Conformation</b>		80	90	100	110	120
Body	102	bad				good
Stature	102	short				tall
Angularity	98	thick				angular
Chest width	109	narrow				wide
Body depth	91	shallow				deep
Topline	98	weak				strong
Rump angle	97	high				low
Rump width	97	narrow				wide
<b>Feet &amp; Legs</b>	101	bad				good
Rear legs rear view	102	hoofs out				parallel
HockQuality	107	coarse				fine
BoneQuality	99	coarse				fine
Rear legs side view	108	straight				curved
Foot angle		low				steep
Hoof angle	99	low				straight

# Benefits from genomics(1)

- first and reliable estimate of BV right after birth (in future before birth)
  - much higher reliability than pedigree index
    - EBVs based on daughters takes 5 years
- selection possible much sooner
  - much higher quality of test bulls
  - less bulls to be tested in field
    - different pedigree
- tool to limit inbreeding
  - only best sons of bull sire in use



## Benefits from genomics (2)

- approximately same reliability in all traits
  - also in low  $h^2$  traits
  - **health, fertility and longevity get more focus**
- reliability the same in females and males
  - stronger selection on females
  - on-farm testing available for farmers
    - heifers/cows to be flushed
  - **health, fertility and longevity get more focus also in females**



faster genetic improvement

# Data is everything!

- recording equally important in the future
  - milk recording, health recording, inseminations, type scoring, hoof trimmings
- large data sets, good quality
- genomic evaluation is dependant on phenotypic information from offspring
  - genomic models need constant updating

# Genomic evaluation in NAV

- increasing reference population size gives higher reliabilities
  - co-operation EURO Genomics and GENO
  - HOL: more than 20 000 bulls
  - RDC: 8000 bulls
- genomic model for all traits
  - including health
- the only genomic model for ayrshire in the world

- genomic selection is a revolutionary tool in animal selection
  - massive impact on breeding programs
- increases reliability and selection pressure especially in females
  - emphasizes health, fertility and longevity
- increases genetic gain
  - rate of inbreeding must be monitored
- genomic selection in Nordic countries seems to be working as expected