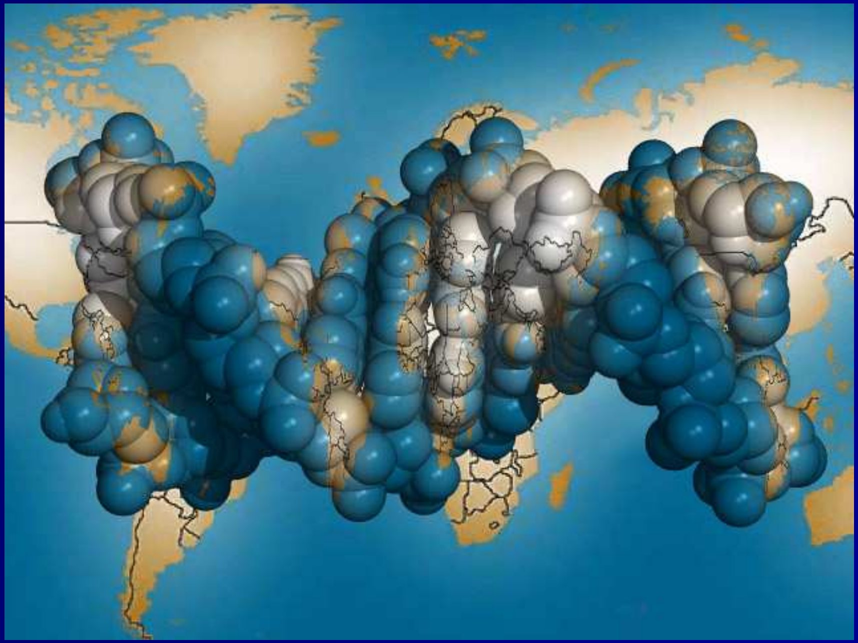
Praktický význam genomickej selekcie holsteinského plemena



Katedra genetiky a plemenárskej biológie, SPU v Nitre

Juraj Candrák

Praktický význam genomickej selekcie holsteinského plemena

Genetické hodnotenie

Genetika

Kvantitatívna genetika

Genomika

Praktický význam genomickej selekcie holsteinského plemena

- **Odhad plemenných hodnôt**

- Výber kvalitných zvierat ako rodičov nasledujúcej generácie potomkov

Aktuálna situácia – budúcnosť

- Zohľadnenie **genomických** informácií pri genetickom hodnotení (pri odhade plemenných hodnôt)

Praktický význam genomickej selekcie holsteinského plemena

- Mlieková úžitkovosť
- Somatické bunky
- Exteriér
- Plodnosť
- Dlhovekosť
- Obtiažnosť pôrodov
- Temperament
- Zdravie

? chovateľ - majiteľ - distribútor - podnikateľ - finančník - špekulant ?

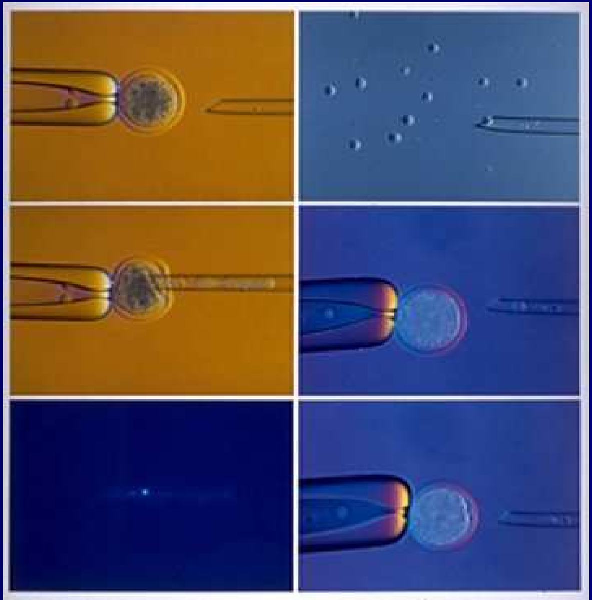
Praktický význam genomickej selekcie holsteinského plemena

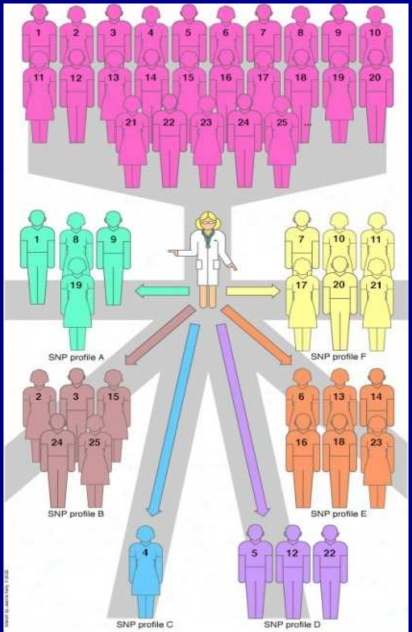
. . . kvantitatívna genetika . . .
Quantitative Trait Locus

- Diabetes Mellitus[3]
- Cancer[3]
- Epilepsy
- Glaucoma
- Hypertension
- Ischaemic heart disease
- Manic depression
- Schizophrenia

. . . a čo tak alergie . . .

P = G + E





Human Genome Project

P = G + E

Human Genome Project

PREČO ???

U.S. DEPARTMENT OF ENERGY

INTERBULL

http://www.interbull.org/

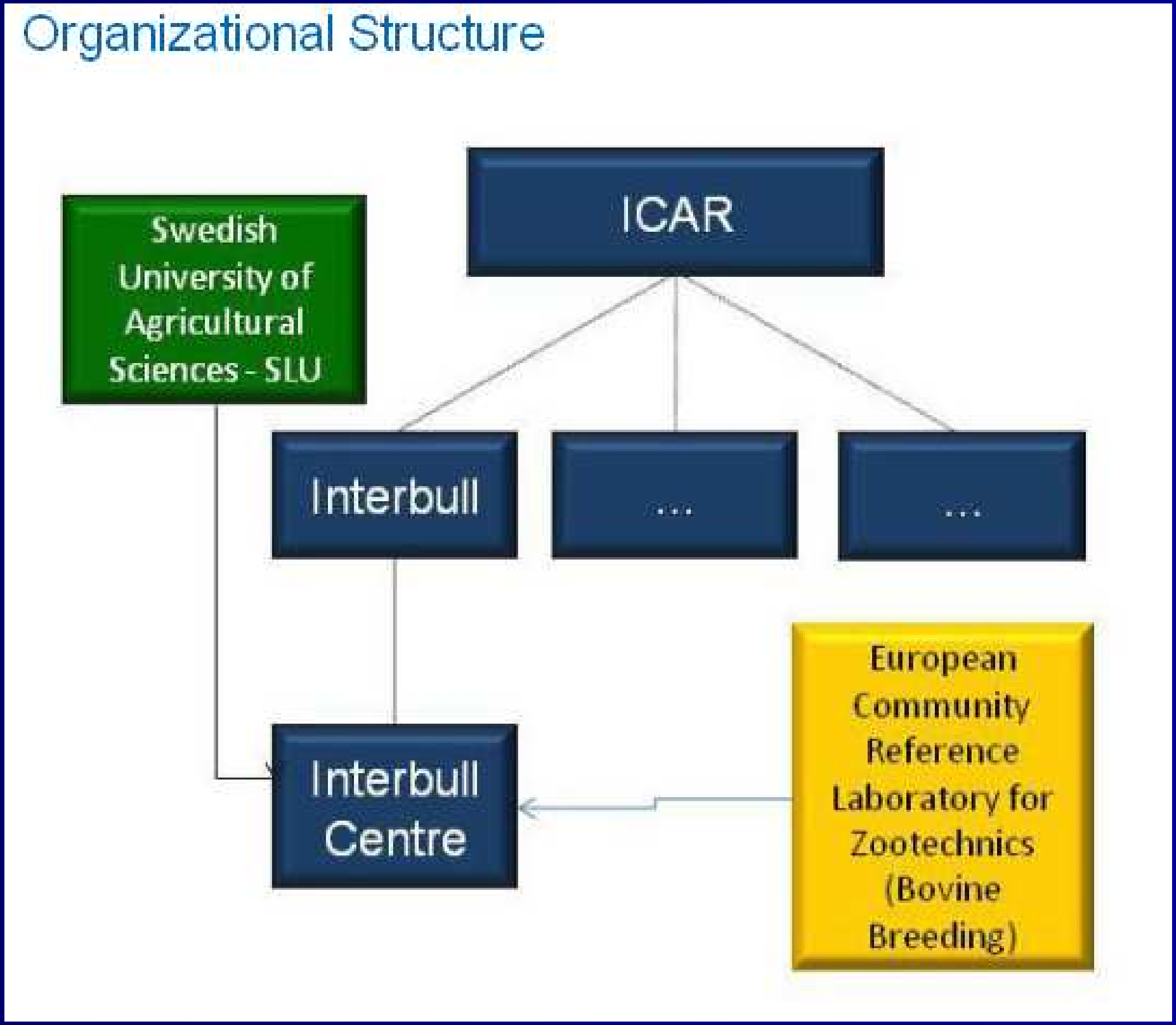
Interbull

Welcome to the International Bull Evaluation Service Official Website. INTERBULL is a sub-committee of the International Committee for Animal Recording (ICAR).

INTERBULL - praktická stránka

Mlieková úžitkovosť
Somatické bunky
Exteriér
Plodnosť
Dlhovekosť
Obtiažnosť pôrodov
Temperament
Zdravie

INTERBULL



Organizational Structure

Swedish University of Agricultural Sciences - SLU

ICAR

Interbull

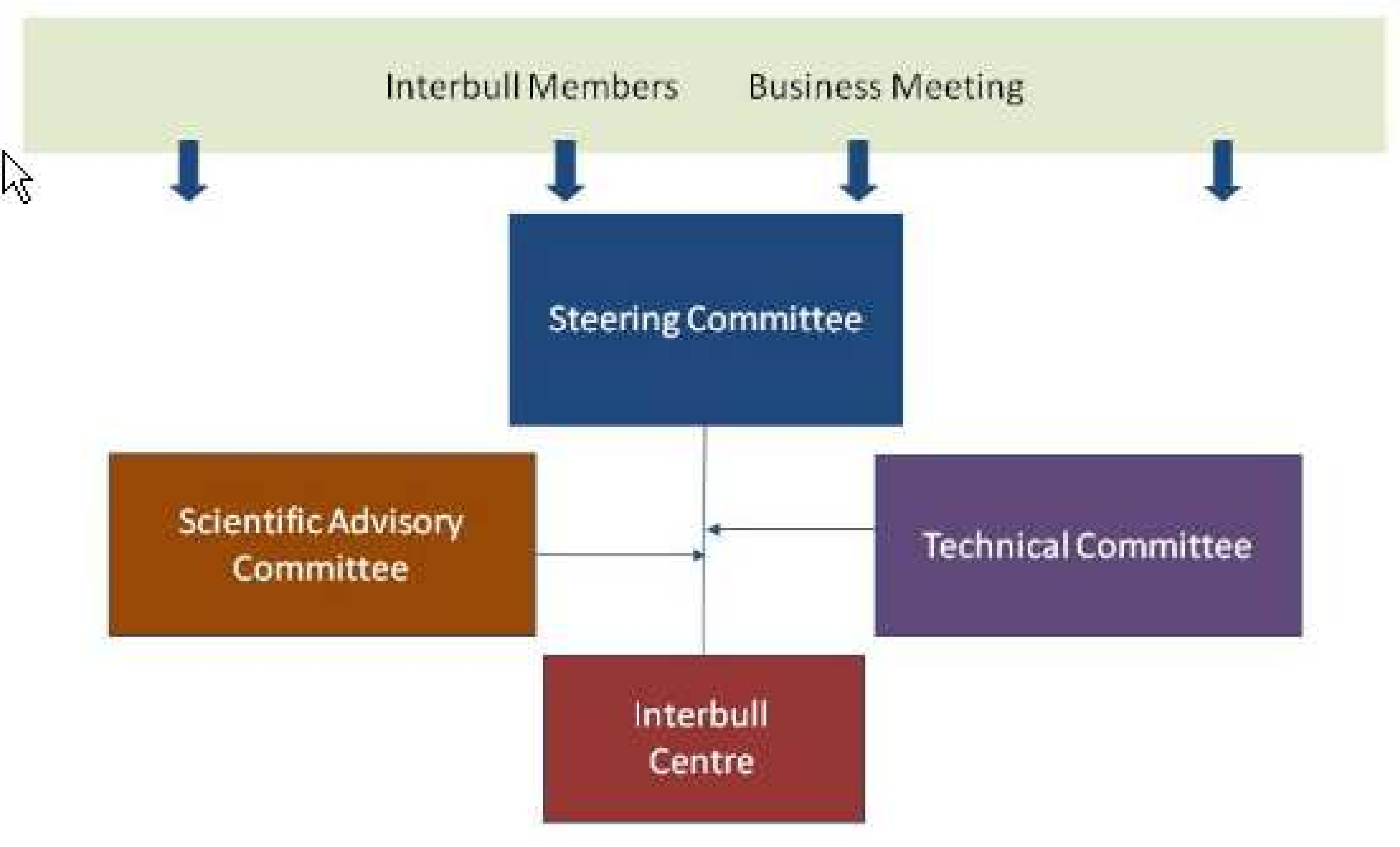
…

…

Interbull Centre

European Community Reference Laboratory for Zootechnics (Bovine Breeding)

INTERBULL



Interbull Members Business Meeting

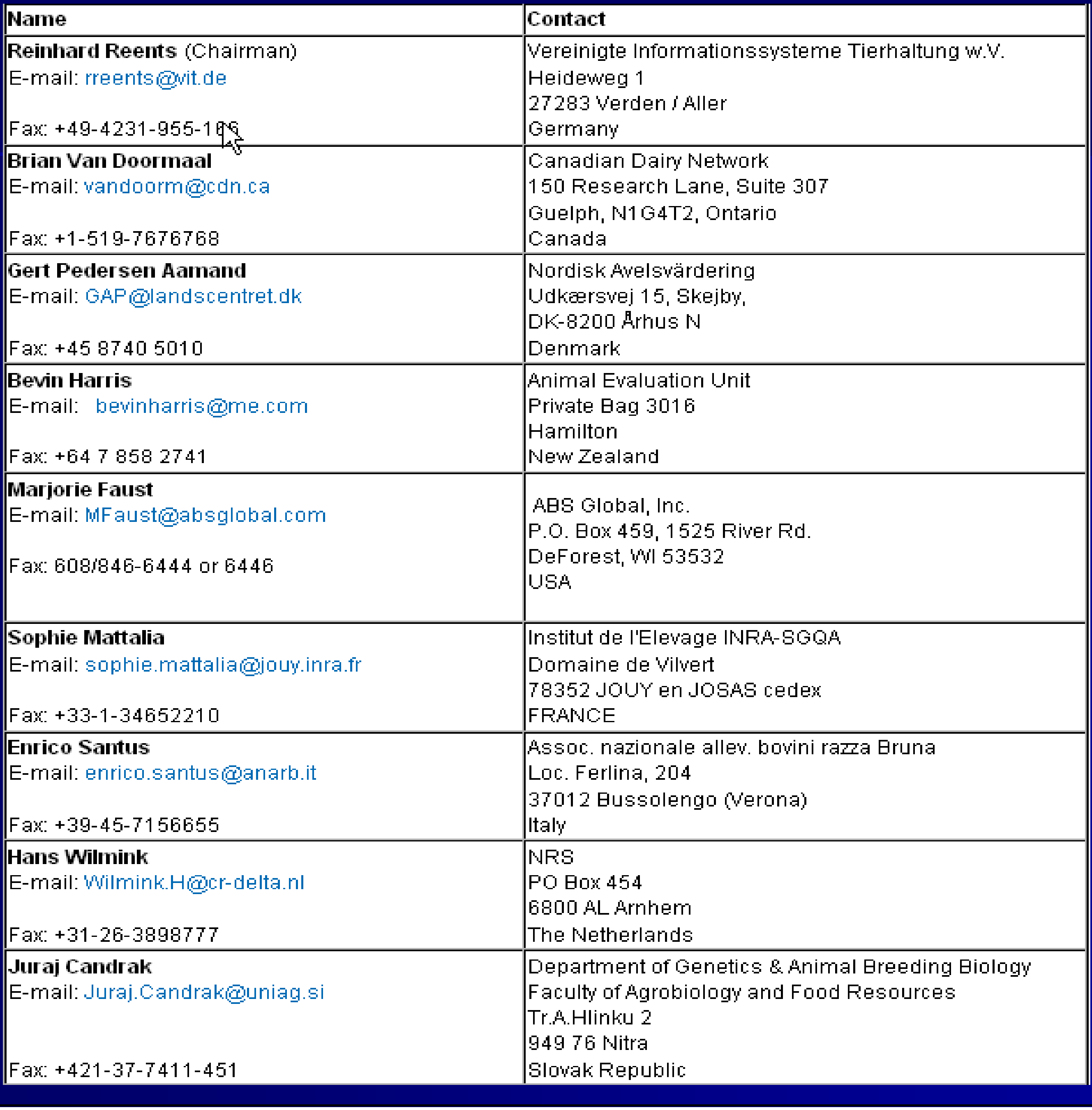
Steering Committee

Scientific Advisory Committee

Technical Committee

Interbull Centre

INTERBULL – steering committee



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Genomika

INTERBULL

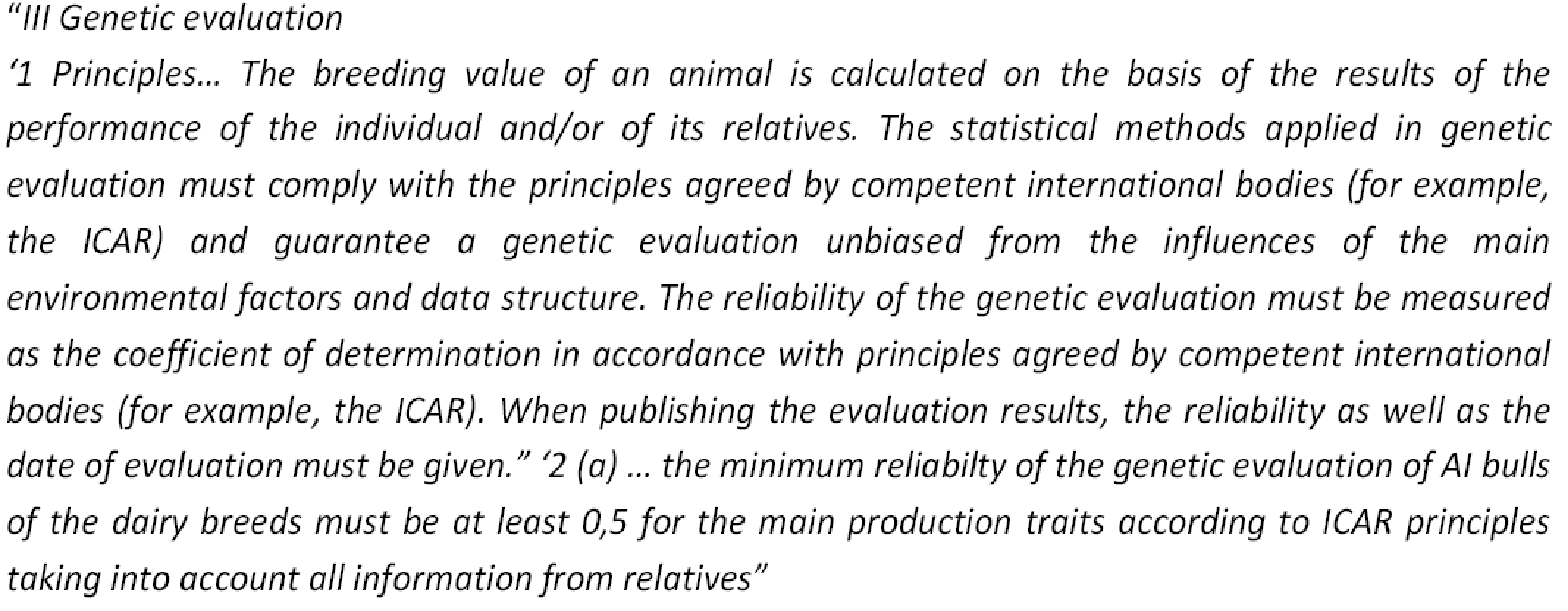
Posúdenie, overenie a vypracovanie návrhu odporúčaní pre možnosti využitia genomických informácií v systémoch genetického hodnotenia HD

Žiadosť o zaslanie genomických informácií

Genomika

EU - nariadenie

European Commission Decision 427 , from June 20th, 2006



"III Genetic evaluation

'1 Principles... The breeding value of an animal is calculated on the basis of the results of the performance of the individual and/or of its relatives. The statistical methods applied in genetic evaluation must comply with the principles agreed by competent international bodies (for example, the ICAR) and guarantee a genetic evaluation unbiased from the influences of the main environmental factors and data structure. The reliability of the genetic evaluation must be measured as the coefficient of determination in accordance with principles agreed by competent international bodies (for example, the ICAR). When publishing the evaluation results, the reliability as well as the date of evaluation must be given." '2 (a) ... the minimum reliabilty of the genetic evaluation of AI bulls of the dairy breeds must be at least 0,5 for the main production traits according to ICAR principles taking into account all information from relatives"

Genomika

INTERBULL

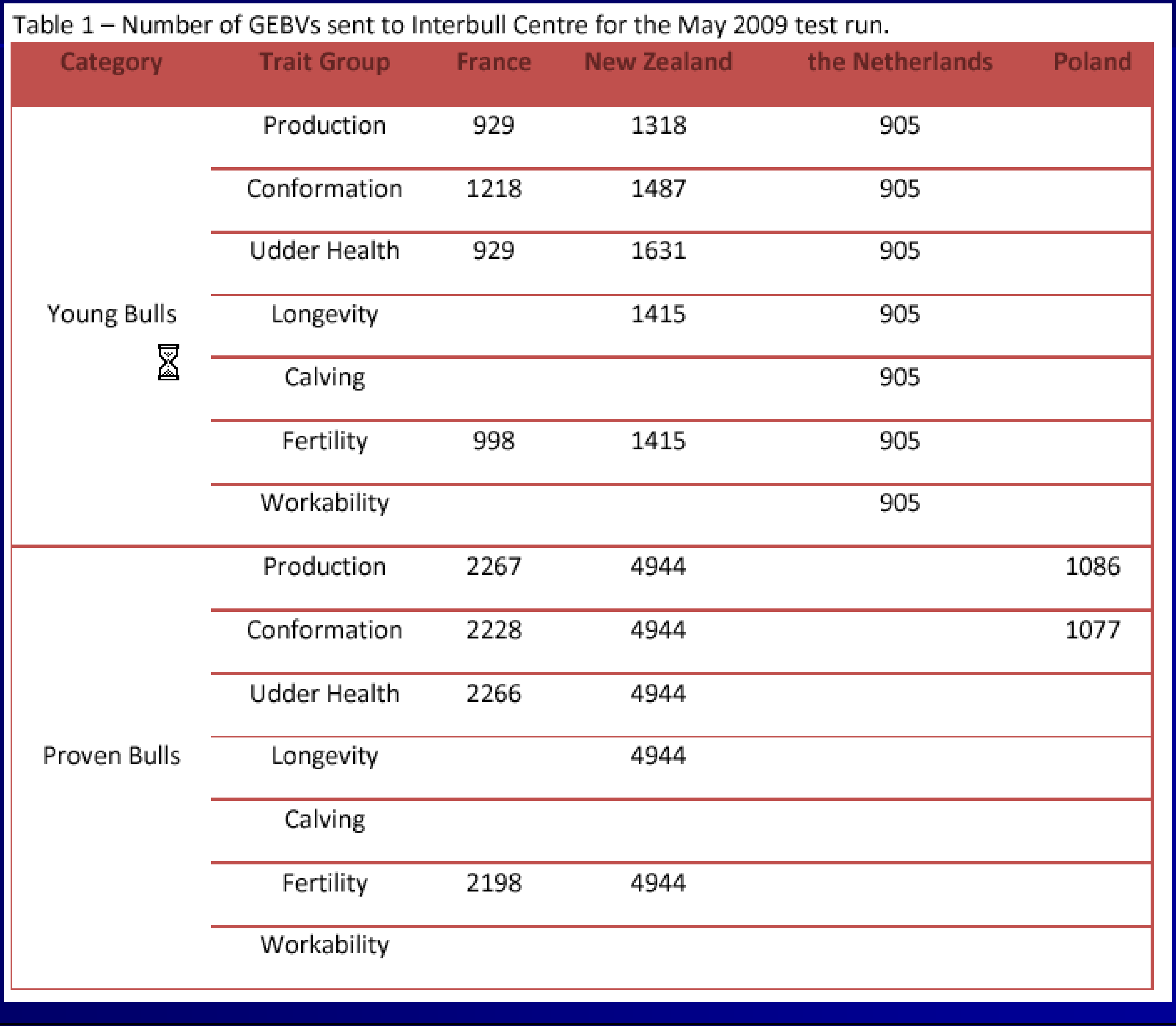


Table 1 – Number of GEBVs sent to Interbull Centre for the May 2009 test run.

Category	Trait Group	France	New Zealand	the Netherlands	Poland
Young Bulls	Production	929	1318	905	
	Conformation	1218	1487	905	
	Udder Health	929	1631	905	
	Longevity		1415	905	
	Calving			905	
	Fertility	998	1415	905	
	Workability			905	
Proven Bulls	Production	2267	4944		1086
	Conformation	2228	4944		1077
	Udder Health	2266	4944		
	Longevity		4944		
	Calving				
	Fertility	2198	4944		
	Workability				

Genomika

INTERBULL

October 26, 2009

INTERBULL PROVISIONAL STRATEGIC PLAN

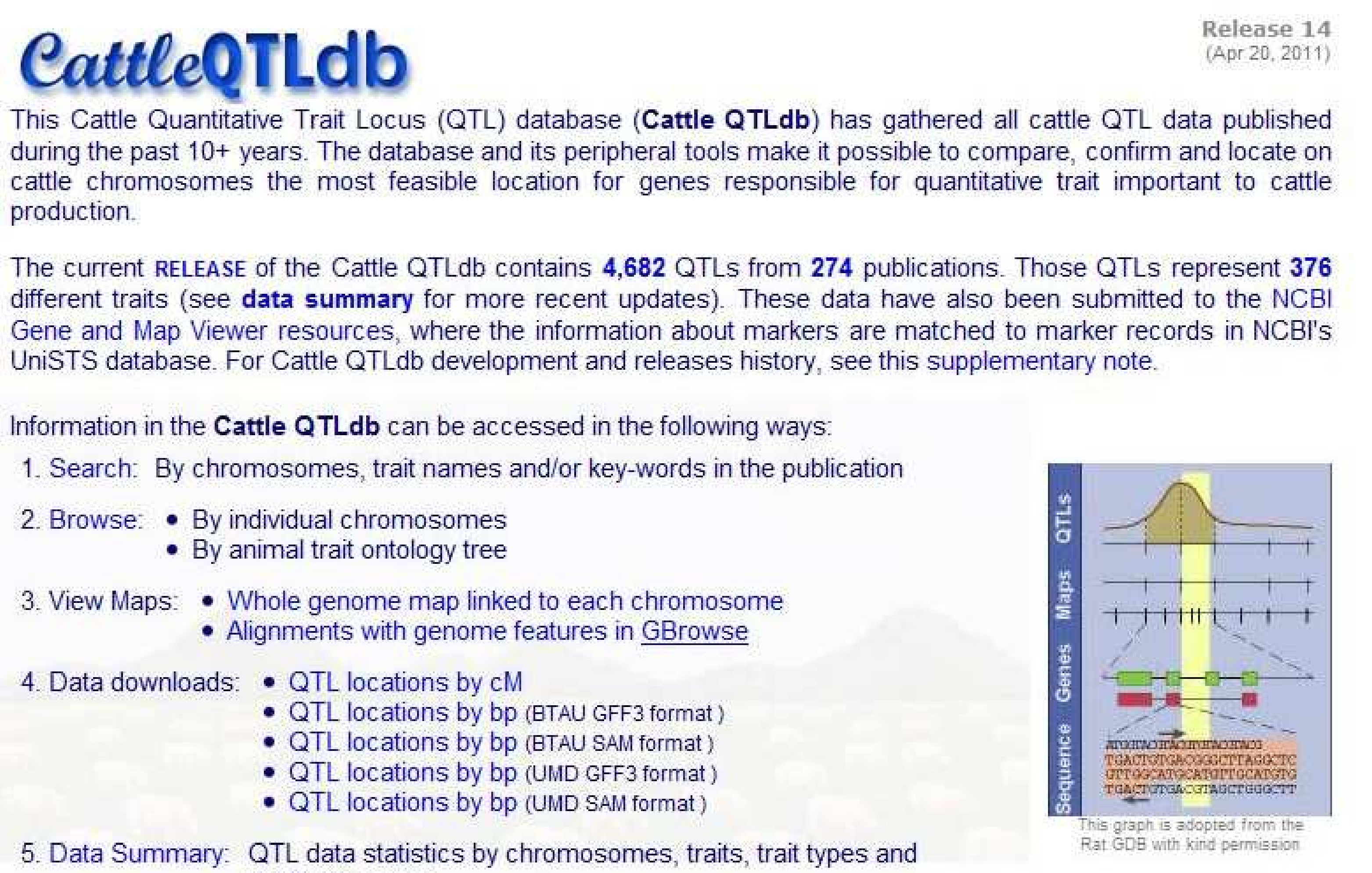
INTERBULL

Genomika

INTERBULL

- presnosť
- nezávislosť
- reálna časová dostupnosť
- transparentnosť
- finančná efektívnosť

P = G + E



Release 14
(Apr 20, 2011)

CattleQTLdb

This Cattle Quantitative Trait Locus (QTL) database (**Cattle QTLdb**) has gathered all cattle QTL data published during the past 10+ years. The database and its peripheral tools make it possible to compare, confirm and locate on cattle chromosomes the most feasible location for genes responsible for quantitative trait important to cattle production.

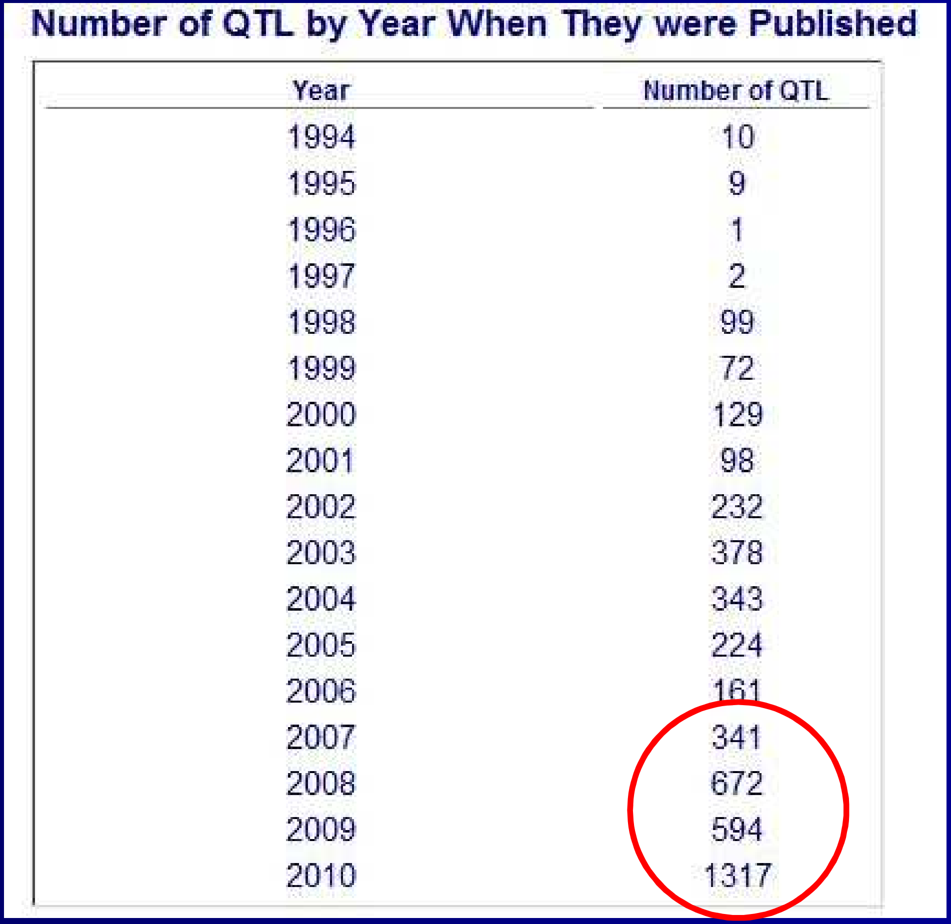
The current RELEASE of the Cattle QTLdb contains **4,682** QTLs from **274** publications. Those QTLs represent **376** different traits (see **data summary** for more recent updates). These data have also been submitted to the NCBI Gene and Map Viewer resources, where the information about markers are matched to marker records in NCBI's UniSTS database. For Cattle QTLdb development and releases history, see this supplementary note.

Information in the **Cattle QTLdb** can be accessed in the following ways:

1. Search: By chromosomes, trait names and/or key-words in the publication
2. Browse:
   - By individual chromosomes
   - By animal trait ontology tree
3. View Maps:
   - Whole genome map linked to each chromosome
   - Alignments with genome features in GBrowse
4. Data downloads:
   - QTL locations by cM
   - QTL locations by bp (BTAU GFF3 format)
   - QTL locations by bp (BTAU SAM format)
   - QTL locations by bp (UMD GFF3 format)
   - QTL locations by bp (UMD SAM format)
5. Data Summary: QTL data statistics by chromosomes, traits, trait types and publication year

This graph is adopted from the Rat GDB with kind permission

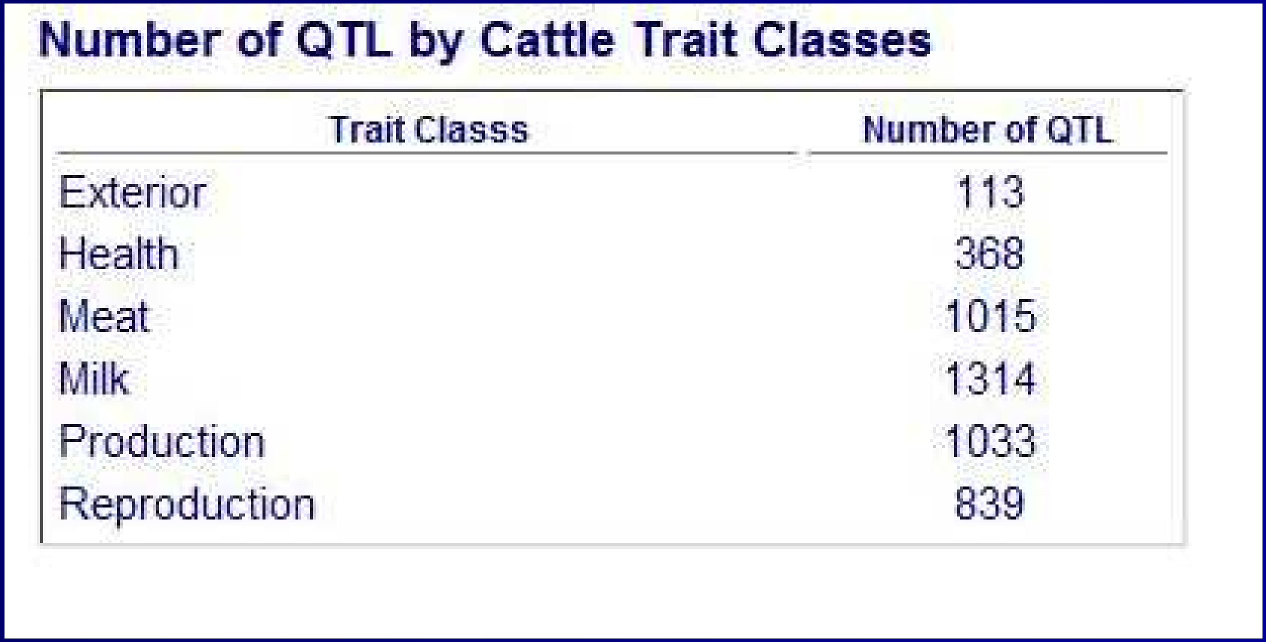
P = G + E



Number of QTL by Year When They were Published

Year	Number of QTL
1994	10
1995	9
1996	1
1997	2
1998	99
1999	72
2000	129
2001	98
2002	232
2003	378
2004	343
2005	224
2006	161
2007	341
2008	672
2009	594
2010	1317

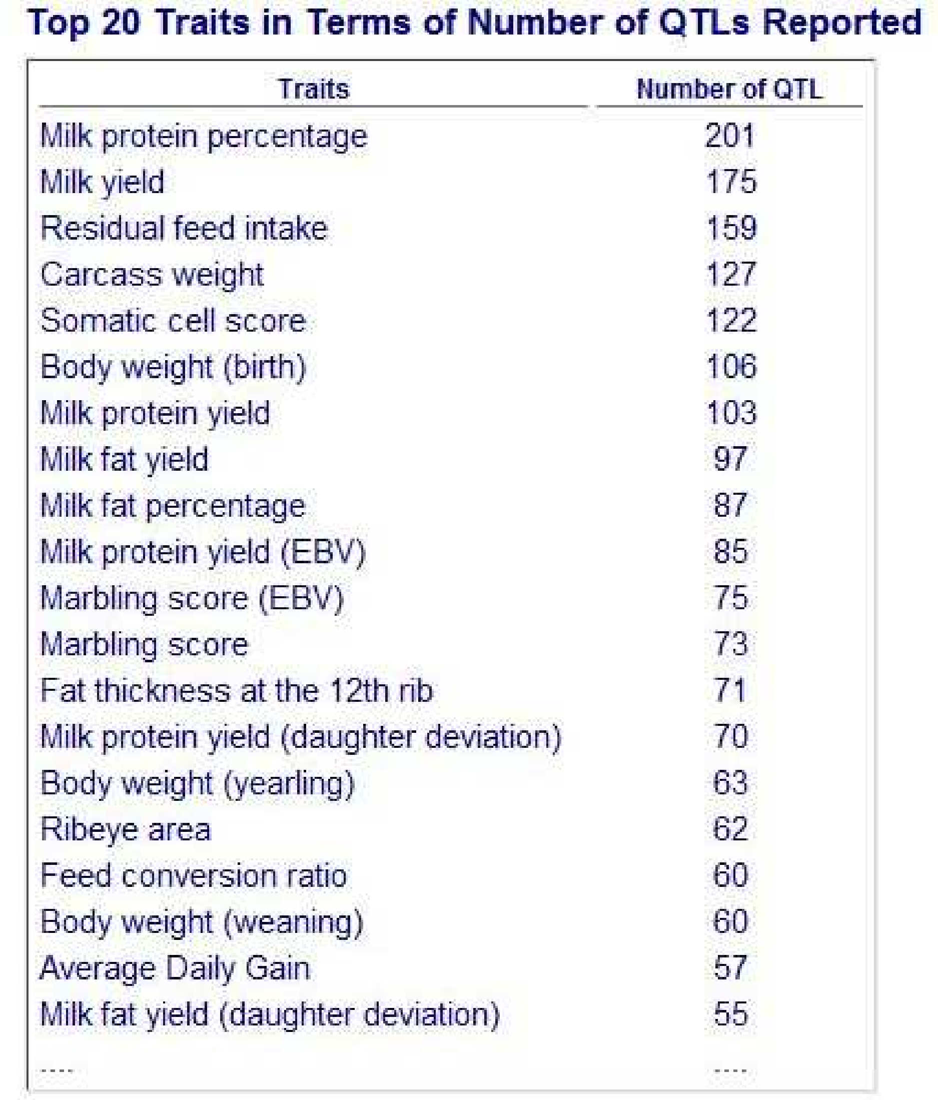
P = G + E



Number of QTL by Cattle Trait Classes

Trait Classs	Number of QTL
Exterior	113
Health	368
Meat	1015
Milk	1314
Production	1033
Reproduction	839

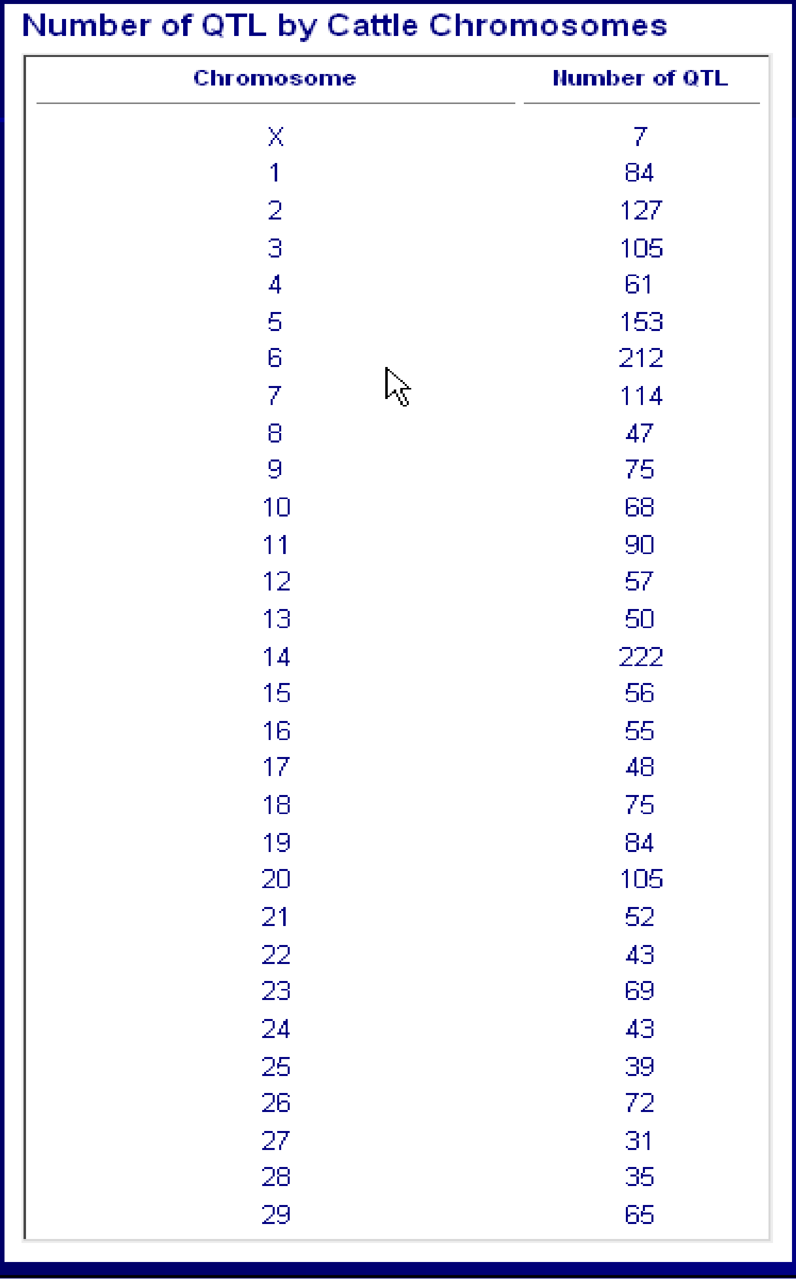
P = G + E



Top 20 Traits in Terms of Number of QTLs Reported

Traits	Number of QTL
Milk protein percentage	201
Milk yield	175
Residual feed intake	159
Carcass weight	127
Somatic cell score	122
Body weight (birth)	106
Milk protein yield	103
Milk fat yield	97
Milk fat percentage	87
Milk protein yield (EBV)	85
Marbling score (EBV)	75
Marbling score	73
Fat thickness at the 12th rib	71
Milk protein yield (daughter deviation)	70
Body weight (yearling)	63
Ribeye area	62
Feed conversion ratio	60
Body weight (weaning)	60
Average Daily Gain	57
Milk fat yield (daughter deviation)	55
....	....

$P = G + E$

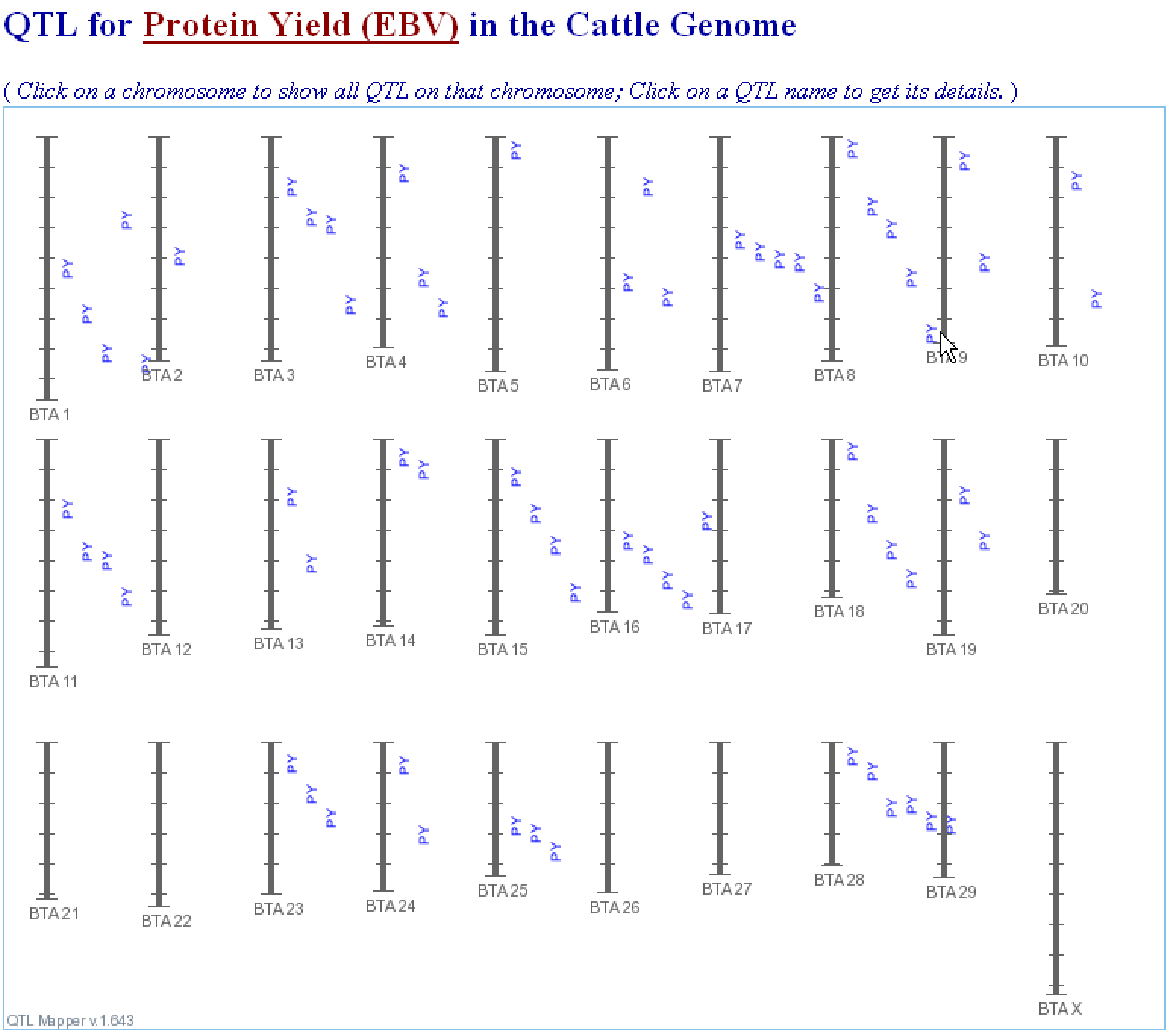


Number of QTL by Cattle Chromosomes

Chromosome	Number of QTL
X	7
1	84
2	127
3	105
4	61
5	153
6	212
7	114
8	47
9	75
10	68
11	90
12	57
13	50
14	222
15	56
16	55
17	48
18	75
19	84
20	105
21	52
22	43
23	69
24	43
25	39
26	72
27	31
28	35
29	65

Chromozóm	počet SNP	%
X	1672	3,14
1	3343	6,28
2	2764	5,19
3	2566	4,82
4	2541	4,77
5	2181	4,10
6	2535	4,76
7	2294	4,31
8	2362	4,44
9	2036	3,82
10	2179	4,09
11	2267	4,26
12	1683	3,16
13	1802	3,38
14	1722	3,23
15	1688	3,17
16	1606	3,02
17	1585	2,98
18	1351	2,54
19	1378	2,59
20	1564	2,94
21	1419	2,66
22	1299	2,44
23	1083	2,03
24	1294	2,43
25	987	1,85
26	1086	2,04
27	977	1,83
28	942	1,77
29	1048	1,97

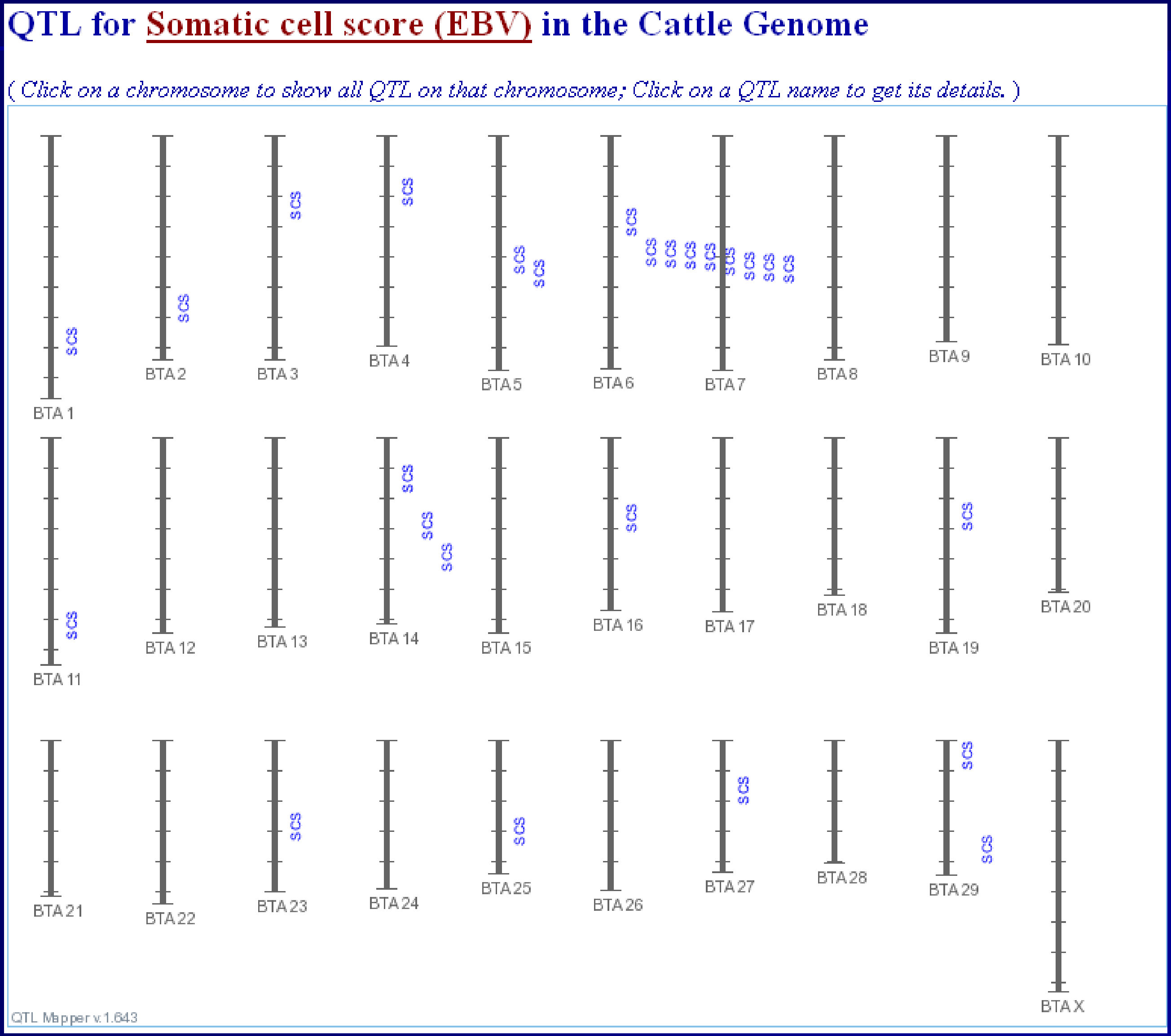
Bielkoviny



QTL for Protein Yield (EBV) in the Cattle Genome

(Click on a chromosome to show all QTL on that chromosome; Click on a QTL name to get its details.)

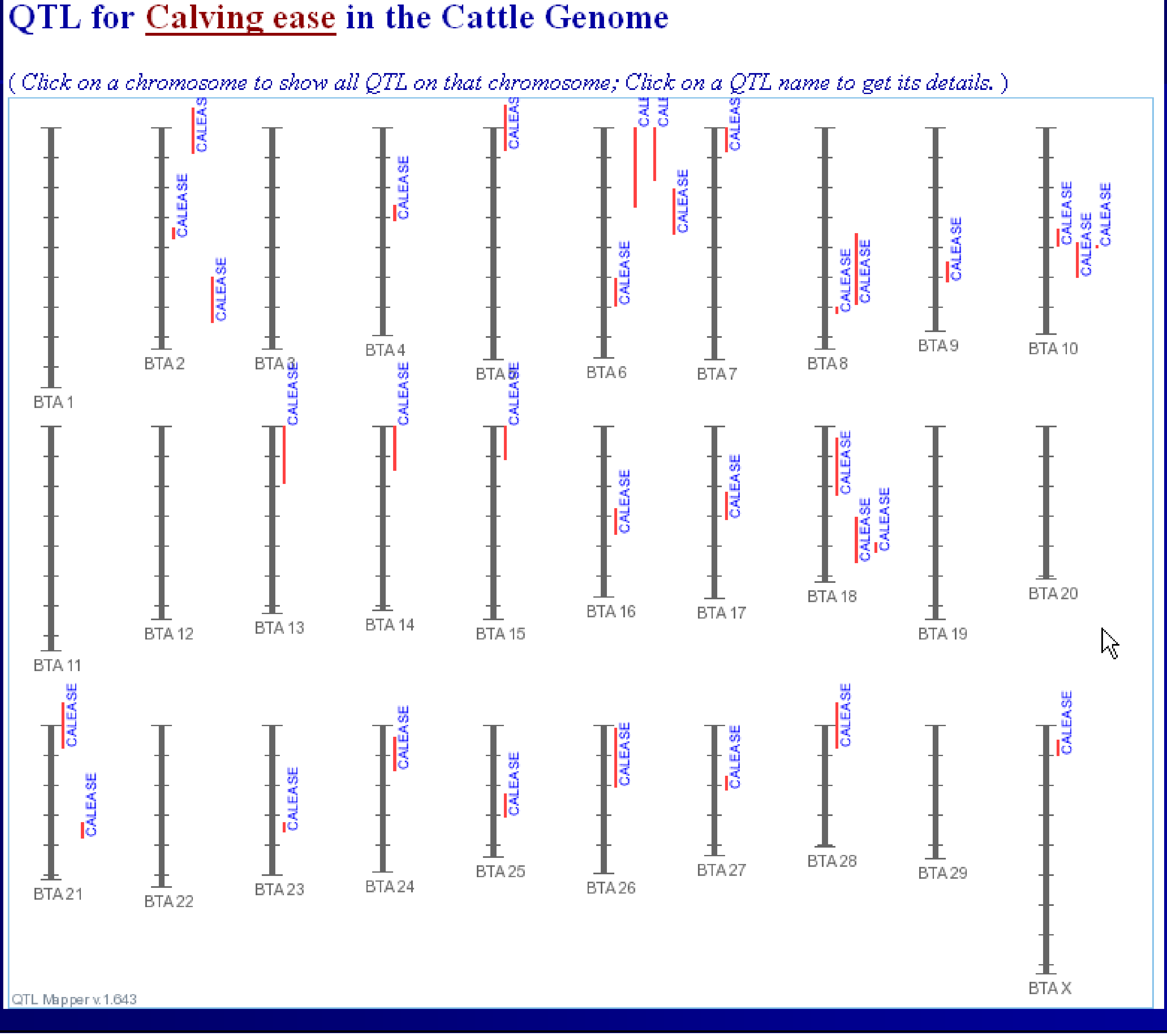
Somatické bunky



QTL for Somatic cell score (EBV) in the Cattle Genome

(Click on a chromosome to show all QTL on that chromosome; Click on a QTL name to get its details.)

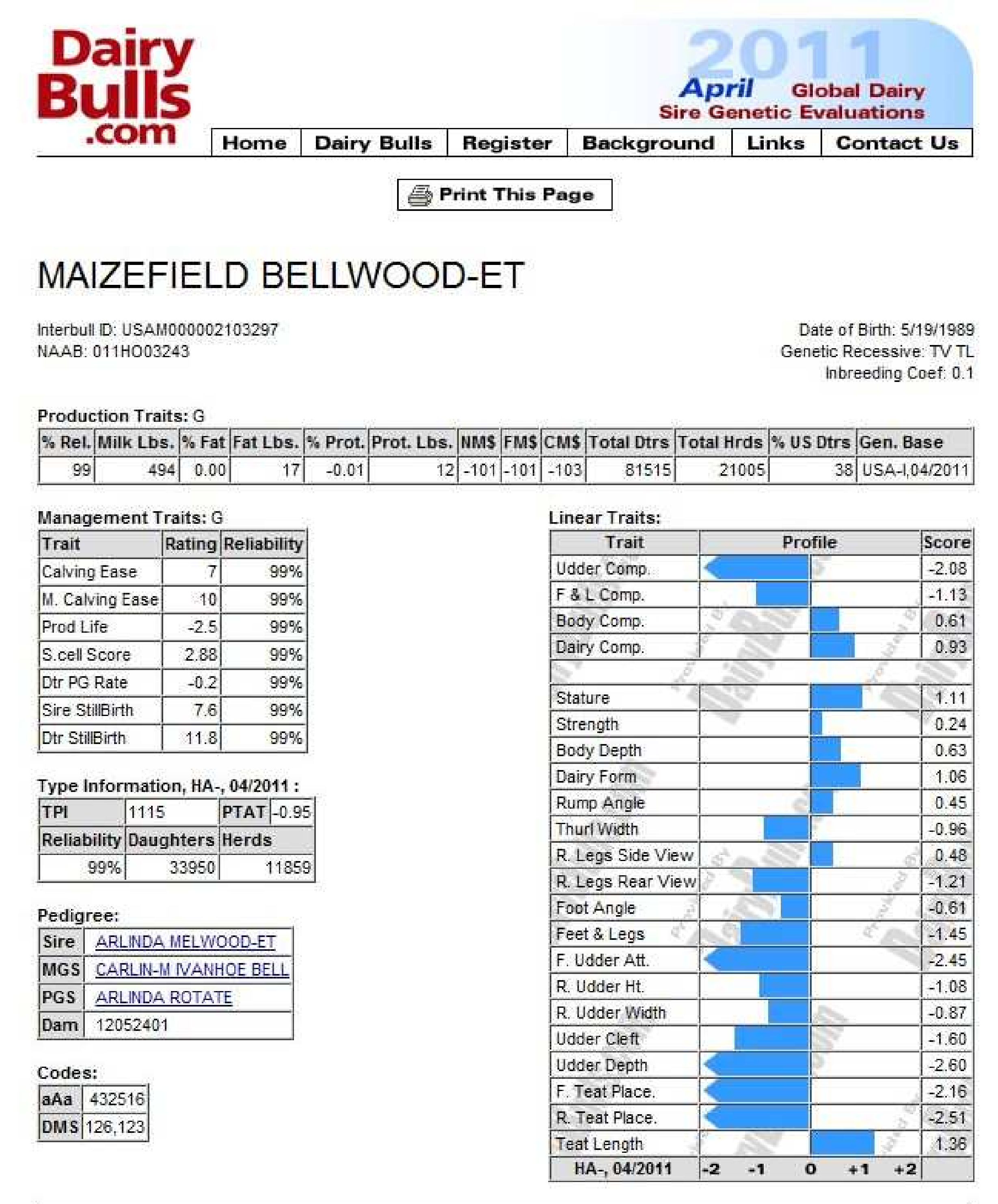
Obtiažnosť telenia



QTL for Calving ease in the Cattle Genome

(Click on a chromosome to show all QTL on that chromosome; Click on a QTL name to get its details.)

QTL Mapper v.1.643



MAIZEFIELD BELLWOOD-ET

Interbull ID: USAM000002103297
NAAB: 011HO03243

Date of Birth: 5/19/1989
Genetic Recessive: TV TL
Inbreeding Coef: 0.1

Production Traits: G

% Rel.	Milk Lbs.	% Fat	Fat Lbs.	% Prot.	Prot. Lbs.	NM$	FM$	CM$	Total Dtrs	Total Hrds	% US Dtrs	Gen. Base
99	494	0.00	17	-0.01	12	-101	-101	-103	81515	21005	38	USA-I,04/2011

Management Traits: G

Trait	Rating	Reliability
Calving Ease	7	99%
M. Calving Ease	10	99%
Prod Life	-2.5	99%
S.cell Score	2.88	99%
Dtr PG Rate	-0.2	99%
Sire StillBirth	7.6	99%
Dtr StillBirth	11.8	99%

Type Information, HA-, 04/2011 :

TPI	1115	**PTAT**	-0.95
Reliability	**Daughters**	**Herds**	
99%	33950	11859	

Pedigree:

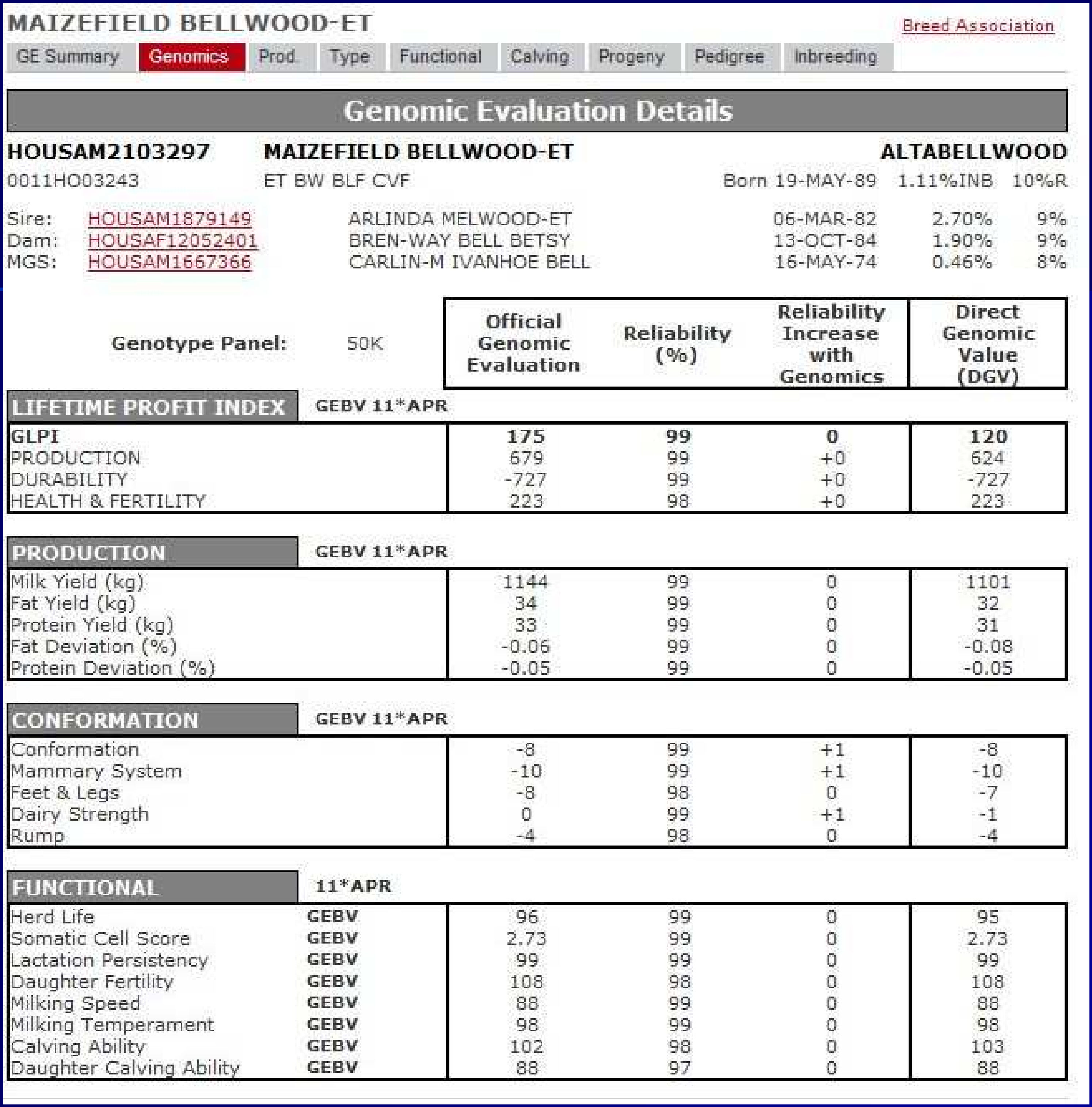
Sire	ARLINDA MELWOOD-ET
MGS	CARLIN-M IVANHOE BELL
PGS	ARLINDA ROTATE
Dam	12052401

Codes:

aAa	432516
DMS	126,123

Linear Traits:

Trait	Profile	Score
Udder Comp.		-2.08
F & L Comp.		-1.13
Body Comp.		0.61
Dairy Comp.		0.93
Stature		1.11
Strength		0.24
Body Depth		0.63
Dairy Form		1.06
Rump Angle		0.45
Thurl Width		-0.96
R. Legs Side View		0.48
R. Legs Rear View		-1.21
Foot Angle		-0.61
Feet & Legs		-1.45
F. Udder Att.		-2.45
R. Udder Ht.		-1.08
R. Udder Width		-0.87
Udder Cleft		-1.60
Udder Depth		-2.60
F. Teat Place.		-2.16
R. Teat Place.		-2.51
Teat Length		1.36
HA-, 04/2011	**-2 -1 0 +1 +2**	



MAIZEFIELD BELLWOOD-ET

Genomic Evaluation Details

HOUSAM2103297 **MAIZEFIELD BELLWOOD-ET** **ALTABELLWOOD**
0011HO03243 ET BW BLF CVF Born 19-MAY-89 1.11%INB 10%R

Sire:	HOUSAM1879149	ARLINDA MELWOOD-ET	06-MAR-82	2.70%	9%
Dam:	HOUSAF12052401	BREN-WAY BELL BETSY	13-OCT-84	1.90%	9%
MGS:	HOUSAM1667366	CARLIN-M IVANHOE BELL	16-MAY-74	0.46%	8%

Genotype Panel: 50K

LIFETIME PROFIT INDEX **GEBV 11*APR**

	Official Genomic Evaluation	Reliability (%)	Reliability Increase with Genomics	Direct Genomic Value (DGV)
GLPI	**175**	**99**	**0**	**120**
PRODUCTION	679	99	+0	624
DURABILITY	-727	99	+0	-727
HEALTH & FERTILITY	223	98	+0	223

PRODUCTION **GEBV 11*APR**

	Official Genomic Evaluation	Reliability (%)	Reliability Increase with Genomics	Direct Genomic Value (DGV)
Milk Yield (kg)	1144	99	0	1101
Fat Yield (kg)	34	99	0	32
Protein Yield (kg)	33	99	0	31
Fat Deviation (%)	-0.06	99	0	-0.08
Protein Deviation (%)	-0.05	99	0	-0.05

CONFORMATION **GEBV 11*APR**

	Official Genomic Evaluation	Reliability (%)	Reliability Increase with Genomics	Direct Genomic Value (DGV)
Conformation	-8	99	+1	-8
Mammary System	-10	99	+1	-10
Feet & Legs	-8	98	0	-7
Dairy Strength	0	99	+1	-1
Rump	-4	98	0	-4

FUNCTIONAL **11*APR**

		Official Genomic Evaluation	Reliability (%)	Reliability Increase with Genomics	Direct Genomic Value (DGV)
Herd Life	**GEBV**	96	99	0	95
Somatic Cell Score	**GEBV**	2.73	99	0	2.73
Lactation Persistency	**GEBV**	99	99	0	99
Daughter Fertility	**GEBV**	108	98	0	108
Milking Speed	**GEBV**	88	99	0	88
Milking Temperament	**GEBV**	98	99	0	98
Calving Ability	**GEBV**	102	98	0	103
Daughter Calving Ability	**GEBV**	88	97	0	88

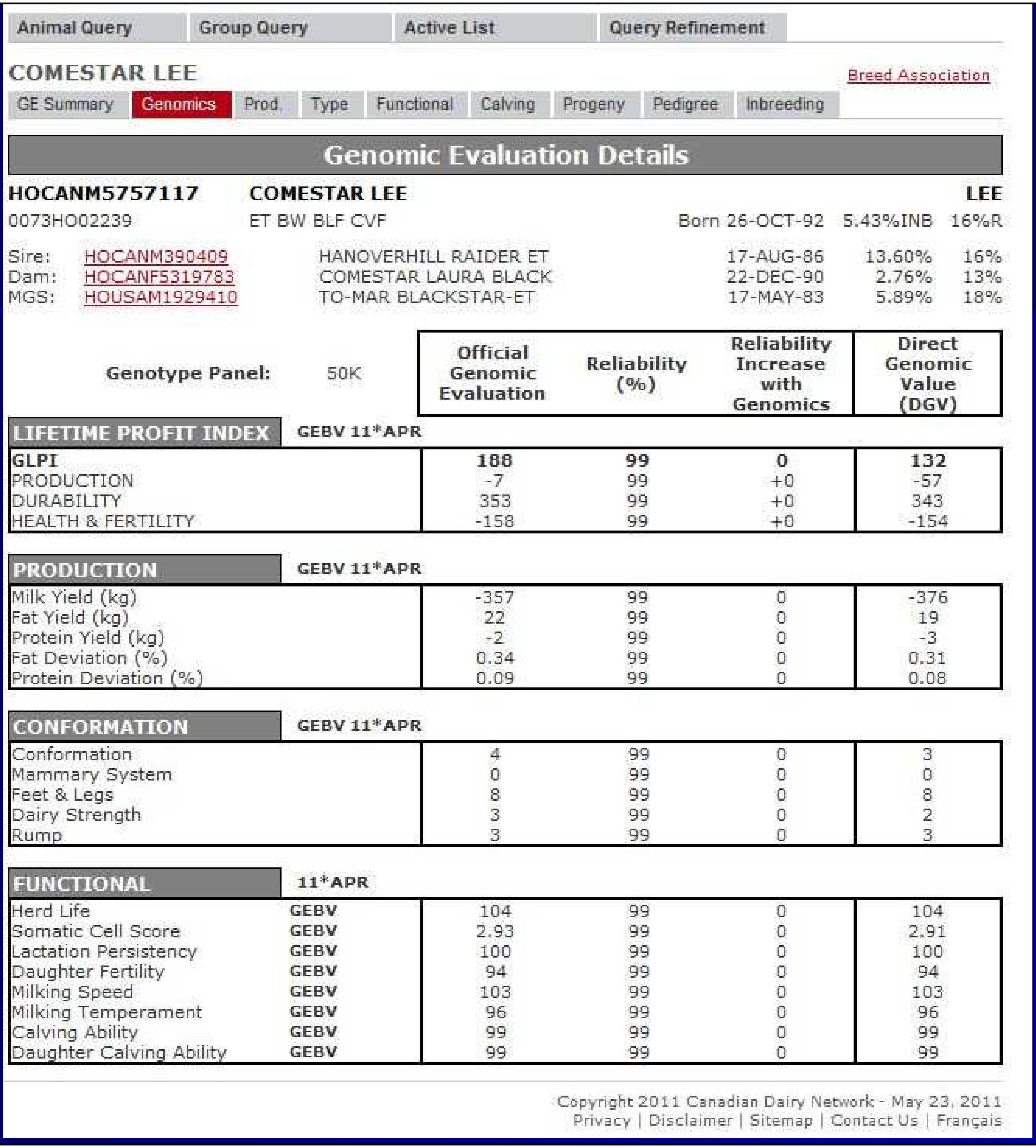
Praktický význam genomickej selekcie holsteinského plemena

Nevyhnutnosť genomických testov preverených býkov

Plemenné hodnoty

Genomické testy

Využitie závislostí pri mladých býkoch



COMESTAR LEE

Genomic Evaluation Details

HOCANM5757117 **COMESTAR LEE** **LEE**

0073HO02239 ET BW BLF CVF Born 26-OCT-92 5.43%INB 16%R

Sire:	HOCANM390409	HANOVERHILL RAIDER ET	17-AUG-86	13.60%	16%
Dam:	HOCANF5319783	COMESTAR LAURA BLACK	22-DEC-90	2.76%	13%
MGS:	HOUSAM1929410	TO-MAR BLACKSTAR-ET	17-MAY-83	5.89%	18%

Genotype Panel: 50K

LIFETIME PROFIT INDEX **GEBV 11*APR**

	Official Genomic Evaluation	Reliability (%)	Reliability Increase with Genomics	Direct Genomic Value (DGV)
GLPI	**188**	**99**	**0**	**132**
PRODUCTION	-7	99	+0	-57
DURABILITY	353	99	+0	343
HEALTH & FERTILITY	-158	99	+0	-154

PRODUCTION **GEBV 11*APR**

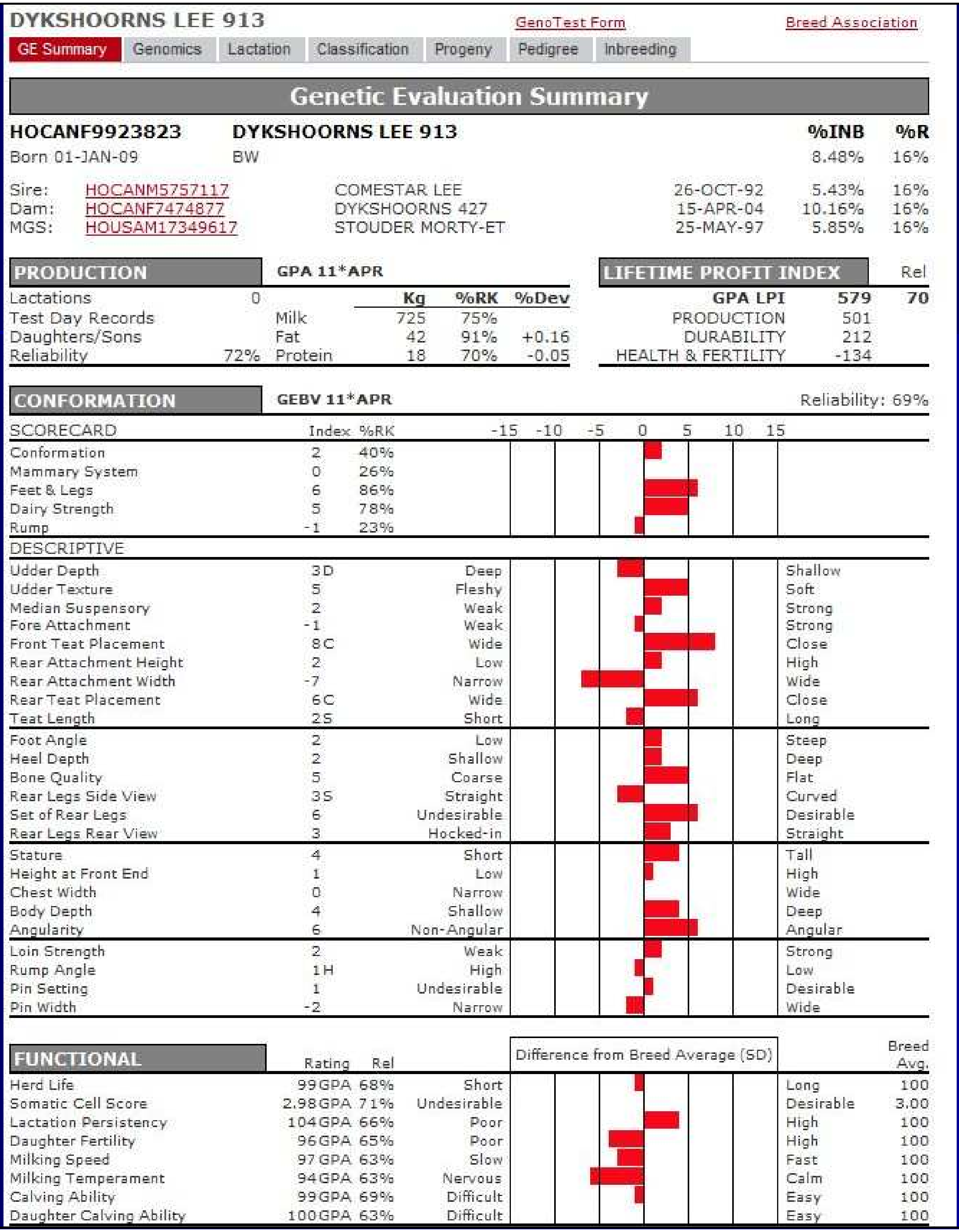
	Official Genomic Evaluation	Reliability (%)	Reliability Increase with Genomics	Direct Genomic Value (DGV)
Milk Yield (kg)	-357	99	0	-376
Fat Yield (kg)	22	99	0	19
Protein Yield (kg)	-2	99	0	-3
Fat Deviation (%)	0.34	99	0	0.31
Protein Deviation (%)	0.09	99	0	0.08

CONFORMATION **GEBV 11*APR**

	Official Genomic Evaluation	Reliability (%)	Reliability Increase with Genomics	Direct Genomic Value (DGV)
Conformation	4	99	0	3
Mammary System	0	99	0	0
Feet & Legs	8	99	0	8
Dairy Strength	3	99	0	2
Rump	3	99	0	3

FUNCTIONAL **11*APR**

		Official Genomic Evaluation	Reliability (%)	Reliability Increase with Genomics	Direct Genomic Value (DGV)
Herd Life	**GEBV**	104	99	0	104
Somatic Cell Score	**GEBV**	2.93	99	0	2.91
Lactation Persistency	**GEBV**	100	99	0	100
Daughter Fertility	**GEBV**	94	99	0	94
Milking Speed	**GEBV**	103	99	0	103
Milking Temperament	**GEBV**	96	99	0	96
Calving Ability	**GEBV**	99	99	0	99
Daughter Calving Ability	**GEBV**	99	99	0	99



DYKSHOORNS LEE 913

GenoTest Form

Breed Association

Genetic Evaluation Summary

HOCANF9923823	**DYKSHOORNS LEE 913**		**%INB**	**%R**
Born 01-JAN-09	BW		8.48%	16%
Sire: HOCANM5757117	COMESTAR LEE	26-OCT-92	5.43%	16%
Dam: HOCANF7474877	DYKSHOORNS 427	15-APR-04	10.16%	16%
MGS: HOUSAM17349617	STOUDER MORTY-ET	25-MAY-97	5.85%	16%

PRODUCTION GPA 11*APR

			Kg	%RK	%Dev
Lactations	0				
Test Day Records		Milk	725	75%	
Daughters/Sons		Fat	42	91%	+0.16
Reliability	72%	Protein	18	70%	-0.05

LIFETIME PROFIT INDEX

		Rel
GPA LPI	**579**	**70**
PRODUCTION	501	
DURABILITY	212	
HEALTH & FERTILITY	-134	

CONFORMATION GEBV 11*APR

Reliability: 69%

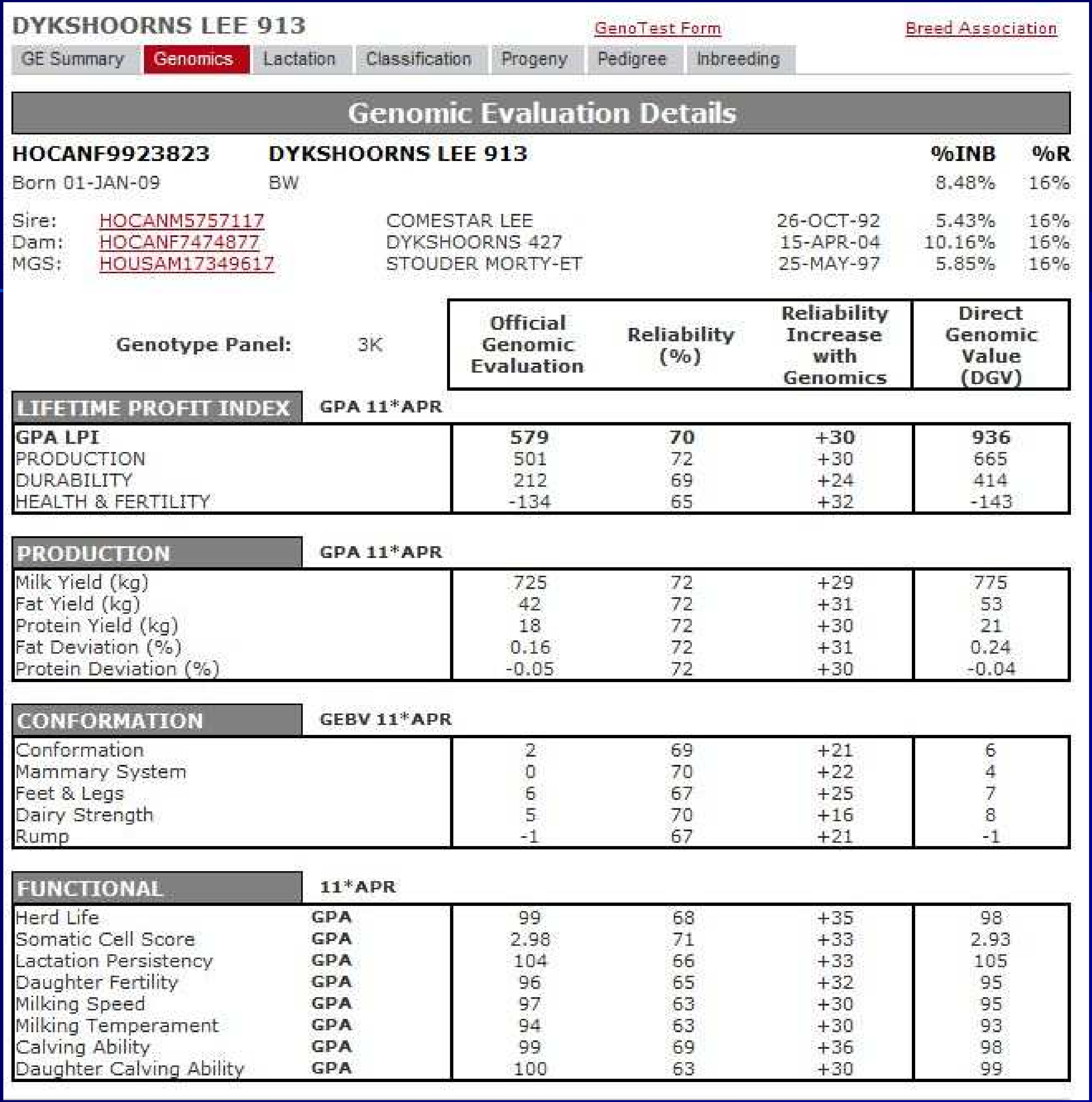
SCORECARD	Index	%RK
Conformation	2	40%
Mammary System	0	26%
Feet & Legs	6	86%
Dairy Strength	5	78%
Rump	-1	23%

DESCRIPTIVE			
Udder Depth	3D	Deep	Shallow
Udder Texture	5	Fleshy	Soft
Median Suspensory	2	Weak	Strong
Fore Attachment	-1	Weak	Strong
Front Teat Placement	8C	Wide	Close
Rear Attachment Height	2	Low	High
Rear Attachment Width	-7	Narrow	Wide
Rear Teat Placement	6C	Wide	Close
Teat Length	2S	Short	Long
Foot Angle	2	Low	Steep
Heel Depth	2	Shallow	Deep
Bone Quality	5	Coarse	Flat
Rear Legs Side View	3S	Straight	Curved
Set of Rear Legs	6	Undesirable	Desirable
Rear Legs Rear View	3	Hocked-in	Straight
Stature	4	Short	Tall
Height at Front End	1	Low	High
Chest Width	0	Narrow	Wide
Body Depth	4	Shallow	Deep
Angularity	6	Non-Angular	Angular
Loin Strength	2	Weak	Strong
Rump Angle	1H	High	Low
Pin Setting	1	Undesirable	Desirable
Pin Width	-2	Narrow	Wide

FUNCTIONAL

Difference from Breed Average (SD)

	Rating	Rel			Breed Avg.
Herd Life	99GPA	68%	Short	Long	100
Somatic Cell Score	2.98GPA	71%	Undesirable	Desirable	3.00
Lactation Persistency	104GPA	66%	Poor	High	100
Daughter Fertility	96GPA	65%	Poor	High	100
Milking Speed	97 GPA	63%	Slow	Fast	100
Milking Temperament	94GPA	63%	Nervous	Calm	100
Calving Ability	99GPA	69%	Difficult	Easy	100
Daughter Calving Ability	100GPA	63%	Difficult	Easy	100



DYKSHOORNS LEE 913

Genomic Evaluation Details

				%INB	%R
HOCANF9923823	**DYKSHOORNS LEE 913**				
Born 01-JAN-09	BW			8.48%	16%
Sire:	HOCANM5757117	COMESTAR LEE	26-OCT-92	5.43%	16%
Dam:	HOCANF7474877	DYKSHOORNS 427	15-APR-04	10.16%	16%
MGS:	HOUSAM17349617	STOUDER MORTY-ET	25-MAY-97	5.85%	16%

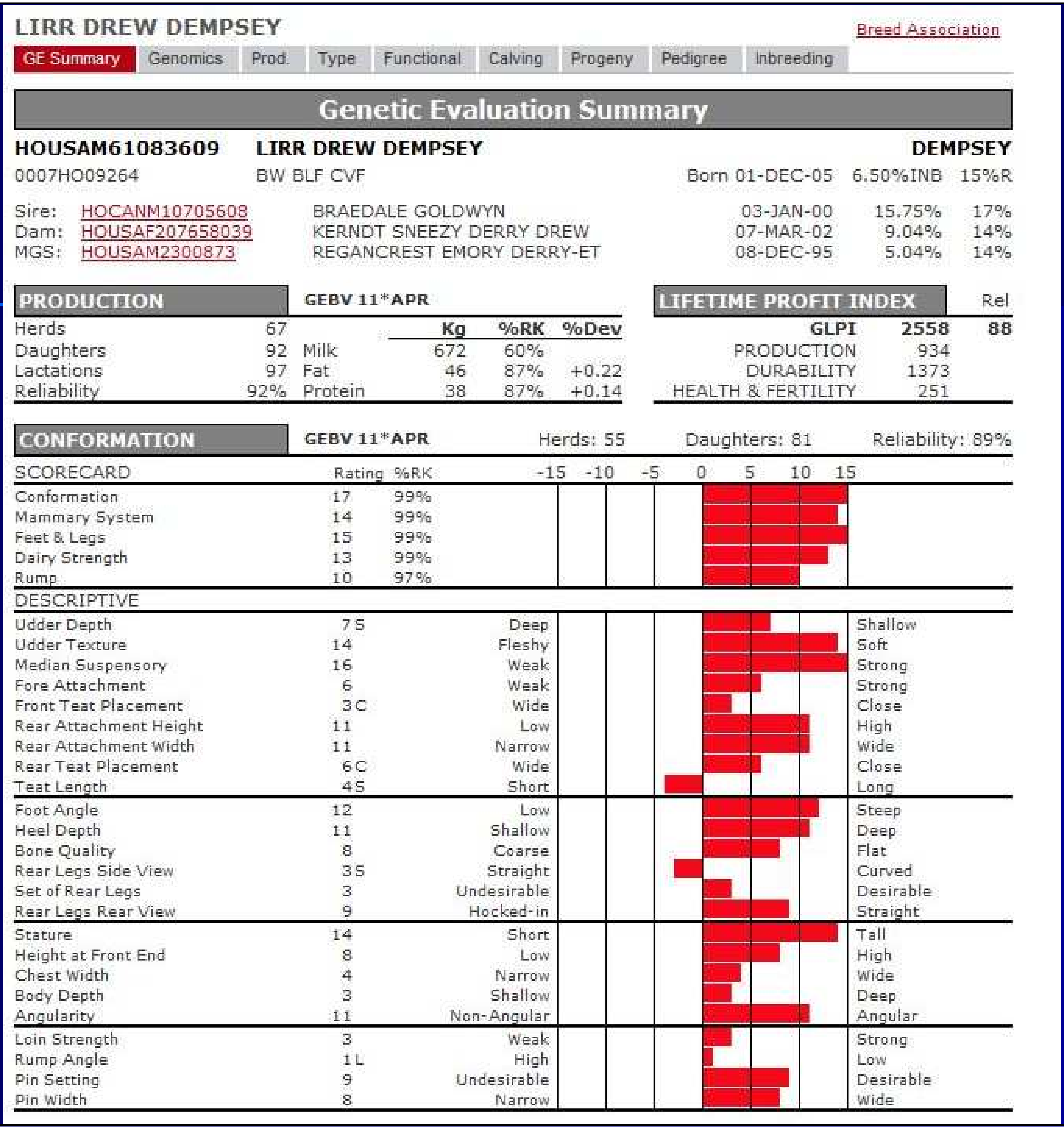
Genotype Panel: 3K

LIFETIME PROFIT INDEX GPA 11*APR	Official Genomic Evaluation	Reliability (%)	Reliability Increase with Genomics	Direct Genomic Value (DGV)
GPA LPI	**579**	**70**	**+30**	**936**
PRODUCTION	501	72	+30	665
DURABILITY	212	69	+24	414
HEALTH & FERTILITY	-134	65	+32	-143

PRODUCTION GPA 11*APR	Official Genomic Evaluation	Reliability (%)	Reliability Increase with Genomics	Direct Genomic Value (DGV)
Milk Yield (kg)	725	72	+29	775
Fat Yield (kg)	42	72	+31	53
Protein Yield (kg)	18	72	+30	21
Fat Deviation (%)	0.16	72	+31	0.24
Protein Deviation (%)	-0.05	72	+30	-0.04

CONFORMATION GEBV 11*APR	Official Genomic Evaluation	Reliability (%)	Reliability Increase with Genomics	Direct Genomic Value (DGV)
Conformation	2	69	+21	6
Mammary System	0	70	+22	4
Feet & Legs	6	67	+25	7
Dairy Strength	5	70	+16	8
Rump	-1	67	+21	-1

FUNCTIONAL	11*APR	Official Genomic Evaluation	Reliability (%)	Reliability Increase with Genomics	Direct Genomic Value (DGV)
Herd Life	GPA	99	68	+35	98
Somatic Cell Score	GPA	2.98	71	+33	2.93
Lactation Persistency	GPA	104	66	+33	105
Daughter Fertility	GPA	96	65	+32	95
Milking Speed	GPA	97	63	+30	95
Milking Temperament	GPA	94	63	+30	93
Calving Ability	GPA	99	69	+36	98
Daughter Calving Ability	GPA	100	63	+30	99



LIRR DREW DEMPSEY

Genetic Evaluation Summary

HOUSAM61083609 **LIRR DREW DEMPSEY** **DEMPSEY**
0007HO09264 BW BLF CVF Born 01-DEC-05 6.50%INB 15%R

Sire:	HOCANM10705608	BRAEDALE GOLDWYN	03-JAN-00	15.75%	17%
Dam:	HOUSAF207658039	KERNDT SNEEZY DERRY DREW	07-MAR-02	9.04%	14%
MGS:	HOUSAM2300873	REGANCREST EMORY DERRY-ET	08-DEC-95	5.04%	14%

PRODUCTION **GEBV 11*APR**

			Kg	%RK	%Dev
Herds	67				
Daughters	92	Milk	672	60%	
Lactations	97	Fat	46	87%	+0.22
Reliability	92%	Protein	38	87%	+0.14

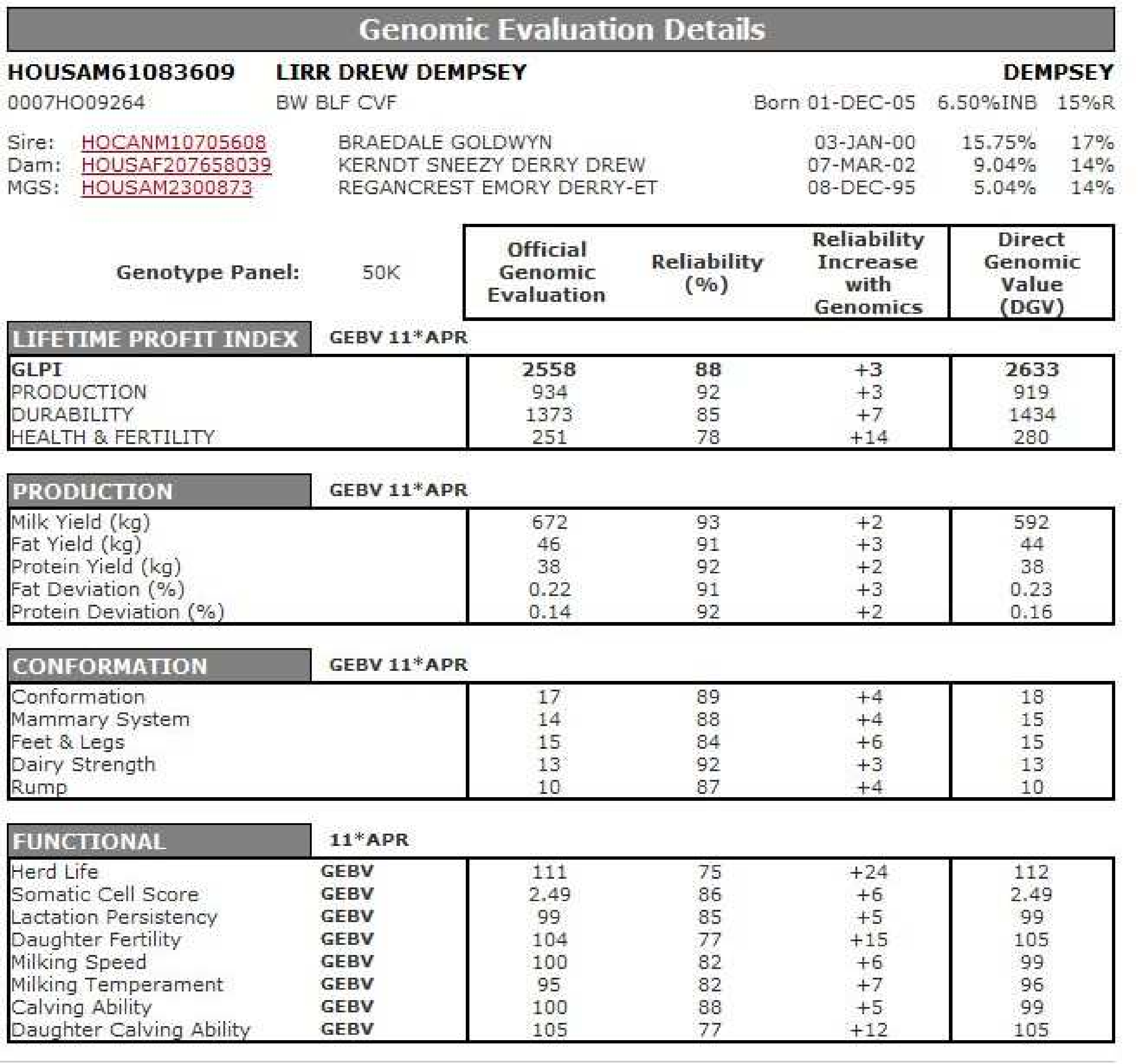
LIFETIME PROFIT INDEX

		Rel
GLPI	2558	88
PRODUCTION	934	
DURABILITY	1373	
HEALTH & FERTILITY	251	

CONFORMATION **GEBV 11*APR** Herds: 55 Daughters: 81 Reliability: 89%

SCORECARD	Rating	%RK
Conformation	17	99%
Mammary System	14	99%
Feet & Legs	15	99%
Dairy Strength	13	99%
Rump	10	97%

DESCRIPTIVE	Rating		
Udder Depth	7 S	Deep	Shallow
Udder Texture	14	Fleshy	Soft
Median Suspensory	16	Weak	Strong
Fore Attachment	6	Weak	Strong
Front Teat Placement	3 C	Wide	Close
Rear Attachment Height	11	Low	High
Rear Attachment Width	11	Narrow	Wide
Rear Teat Placement	6 C	Wide	Close
Teat Length	4 S	Short	Long
Foot Angle	12	Low	Steep
Heel Depth	11	Shallow	Deep
Bone Quality	8	Coarse	Flat
Rear Legs Side View	3 S	Straight	Curved
Set of Rear Legs	3	Undesirable	Desirable
Rear Legs Rear View	9	Hocked-in	Straight
Stature	14	Short	Tall
Height at Front End	8	Low	High
Chest Width	4	Narrow	Wide
Body Depth	3	Shallow	Deep
Angularity	11	Non-Angular	Angular
Loin Strength	3	Weak	Strong
Rump Angle	1 L	High	Low
Pin Setting	9	Undesirable	Desirable
Pin Width	8	Narrow	Wide



Genomic Evaluation Details

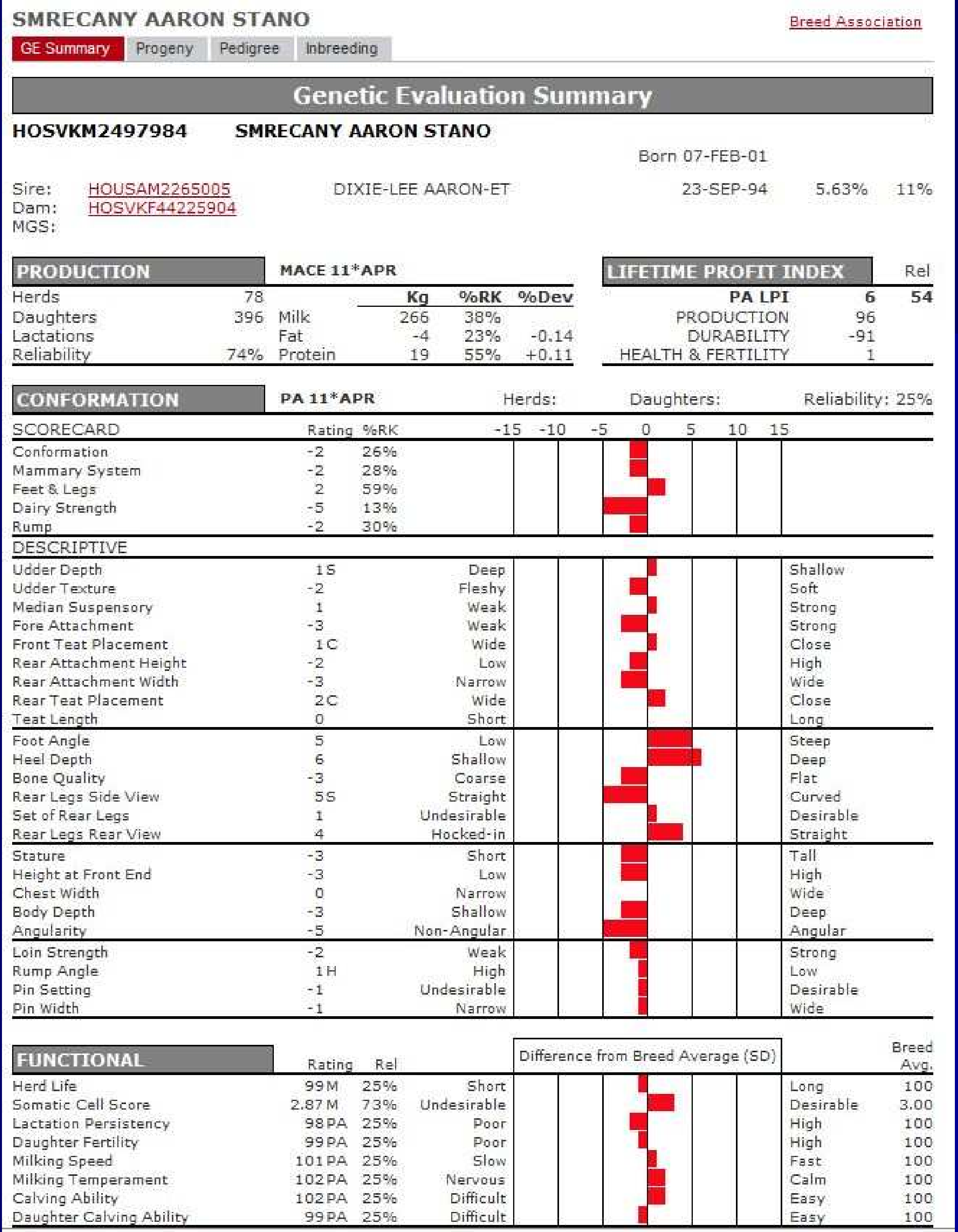
HOUSAM61083609 **LIRR DREW DEMPSEY** **DEMPSEY**

0007HO09264 BW BLF CVF Born 01-DEC-05 6.50%INB 15%R

Sire:	HOCANM10705608	BRAEDALE GOLDWYN	03-JAN-00	15.75%	17%
Dam:	HOUSAF207658039	KERNDT SNEEZY DERRY DREW	07-MAR-02	9.04%	14%
MGS:	HOUSAM2300873	REGANCREST EMORY DERRY-ET	08-DEC-95	5.04%	14%

Genotype Panel: 50K

	Official Genomic Evaluation	Reliability (%)	Reliability Increase with Genomics	Direct Genomic Value (DGV)
LIFETIME PROFIT INDEX GEBV 11*APR				
GLPI	**2558**	**88**	+3	**2633**
PRODUCTION	934	92	+3	919
DURABILITY	1373	85	+7	1434
HEALTH & FERTILITY	251	78	+14	280
PRODUCTION GEBV 11*APR				
Milk Yield (kg)	672	93	+2	592
Fat Yield (kg)	46	91	+3	44
Protein Yield (kg)	38	92	+2	38
Fat Deviation (%)	0.22	91	+3	0.23
Protein Deviation (%)	0.14	92	+2	0.16
CONFORMATION GEBV 11*APR				
Conformation	17	89	+4	18
Mammary System	14	88	+4	15
Feet & Legs	15	84	+6	15
Dairy Strength	13	92	+3	13
Rump	10	87	+4	10
FUNCTIONAL 11*APR				
Herd Life **GEBV**	111	75	+24	112
Somatic Cell Score **GEBV**	2.49	86	+6	2.49
Lactation Persistency **GEBV**	99	85	+5	99
Daughter Fertility **GEBV**	104	77	+15	105
Milking Speed **GEBV**	100	82	+6	99
Milking Temperament **GEBV**	95	82	+7	96
Calving Ability **GEBV**	100	88	+5	99
Daughter Calving Ability **GEBV**	105	77	+12	105



SMRECANY AARON STANO

Genetic Evaluation Summary

HOSVKM2497984 **SMRECANY AARON STANO**

Born 07-FEB-01

Sire:	HOUSAM2265005	DIXIE-LEE AARON-ET	23-SEP-94	5.63%	11%
Dam:	HOSVKF44225904				
MGS:					

PRODUCTION **MACE 11*APR**

			Kg	%RK	%Dev
Herds	78				
Daughters	396	Milk	266	38%	
Lactations		Fat	-4	23%	-0.14
Reliability	74%	Protein	19	55%	+0.11

LIFETIME PROFIT INDEX

		Rel
PA LPI	**6**	**54**
PRODUCTION	96	
DURABILITY	-91	
HEALTH & FERTILITY	1	

CONFORMATION **PA 11*APR** Herds: Daughters: Reliability: 25%

SCORECARD	Rating	%RK
Conformation	-2	26%
Mammary System	-2	28%
Feet & Legs	2	59%
Dairy Strength	-5	13%
Rump	-2	30%

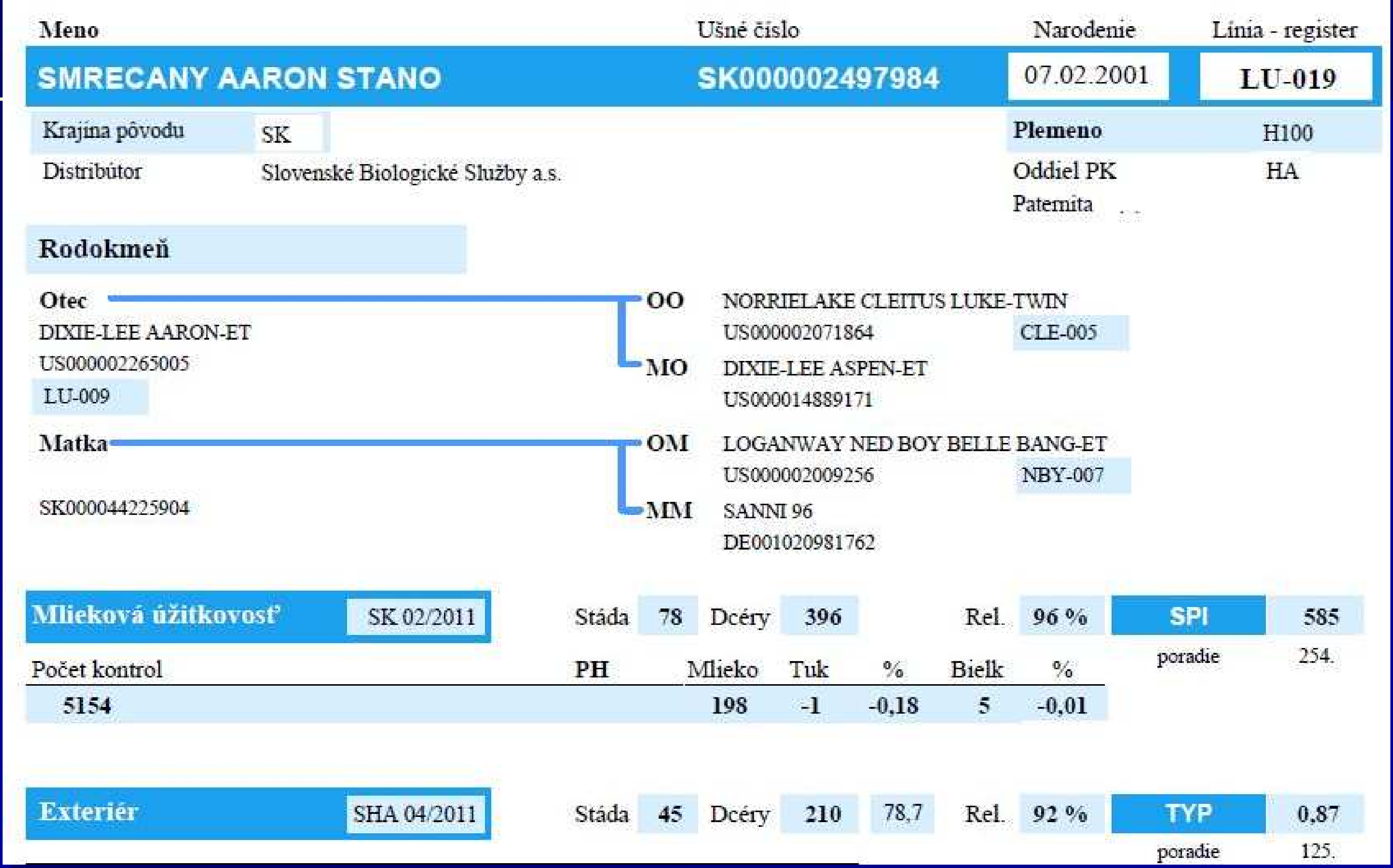
-15 -10 -5 0 5 10 15

DESCRIPTIVE	Rating		
Udder Depth	1 S	Deep	Shallow
Udder Texture	-2	Fleshy	Soft
Median Suspensory	1	Weak	Strong
Fore Attachment	-3	Weak	Strong
Front Teat Placement	1 C	Wide	Close
Rear Attachment Height	-2	Low	High
Rear Attachment Width	-3	Narrow	Wide
Rear Teat Placement	2 C	Wide	Close
Teat Length	0	Short	Long
Foot Angle	5	Low	Steep
Heel Depth	6	Shallow	Deep
Bone Quality	-3	Coarse	Flat
Rear Legs Side View	5 S	Straight	Curved
Set of Rear Legs	1	Undesirable	Desirable
Rear Legs Rear View	4	Hocked-in	Straight
Stature	-3	Short	Tall
Height at Front End	-3	Low	High
Chest Width	0	Narrow	Wide
Body Depth	-3	Shallow	Deep
Angularity	-5	Non-Angular	Angular
Loin Strength	-2	Weak	Strong
Rump Angle	1 H	High	Low
Pin Setting	-1	Undesirable	Desirable
Pin Width	-1	Narrow	Wide

FUNCTIONAL

Difference from Breed Average (SD)

	Rating	Rel			Breed Avg.
Herd Life	99 M	25%	Short	Long	100
Somatic Cell Score	2.87 M	73%	Undesirable	Desirable	3.00
Lactation Persistency	98 PA	25%	Poor	High	100
Daughter Fertility	99 PA	25%	Poor	High	100
Milking Speed	101 PA	25%	Slow	Fast	100
Milking Temperament	102 PA	25%	Nervous	Calm	100
Calving Ability	102 PA	25%	Difficult	Easy	100
Daughter Calving Ability	99 PA	25%	Difficult	Easy	100



Meno	Ušné číslo	Narodenie	Línia - register
SMRECANY AARON STANO	**SK000002497984**	07.02.2001	**LU-019**

Krajina pôvodu	SK	**Plemeno**	H100
Distribútor	Slovenské Biologické Služby a.s.	Oddiel PK	HA
		Paternita	

Rodokmeň

Otec
DIXIE-LEE AARON-ET
US000002265005
LU-009

OO NORRIELAKE CLEITUS LUKE-TWIN
US000002071864 CLE-005

MO DIXIE-LEE ASPEN-ET
US000014889171

Matka
SK000044225904

OM LOGANWAY NED BOY BELLE BANG-ET
US000002009256 NBY-007

MM SANNI 96
DE001020981762

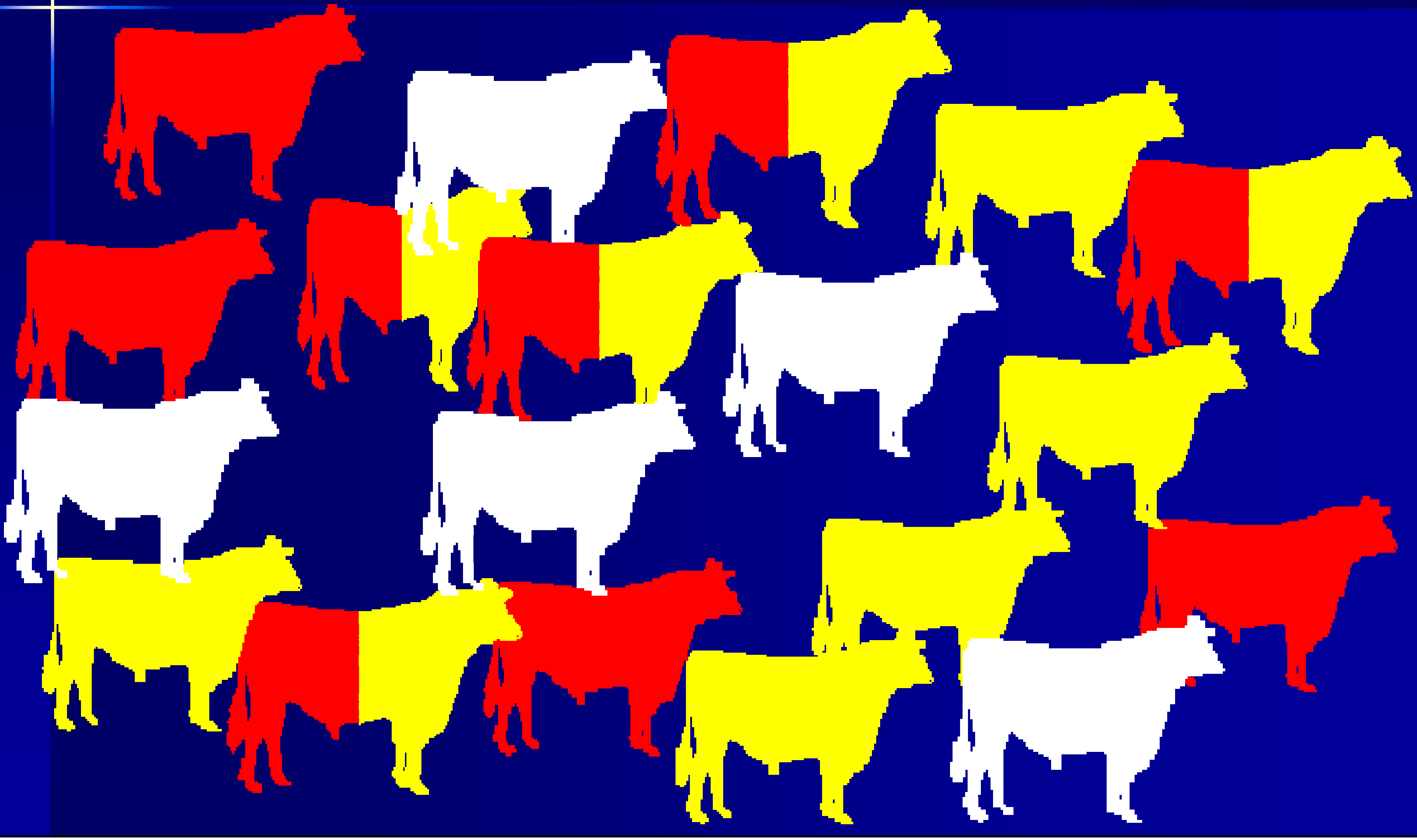
Mlieková úžitkovosť SK 02/2011 | Stáda **78** | Dcéry **396** | Rel. **96 %** | **SPI** **585**
poradie 254.

Počet kontrol	PH	Mlieko	Tuk	%	Bielk	%
5154		**198**	**-1**	**-0,18**	**5**	**-0,01**

Exteriér SHA 04/2011 | Stáda **45** | Dcéry **210** | 78,7 | Rel. **92 %** | **TYP** **0,87**
poradie 125.

Gene Assisted Selection

"DNA Chips"



Genomics - Genomika

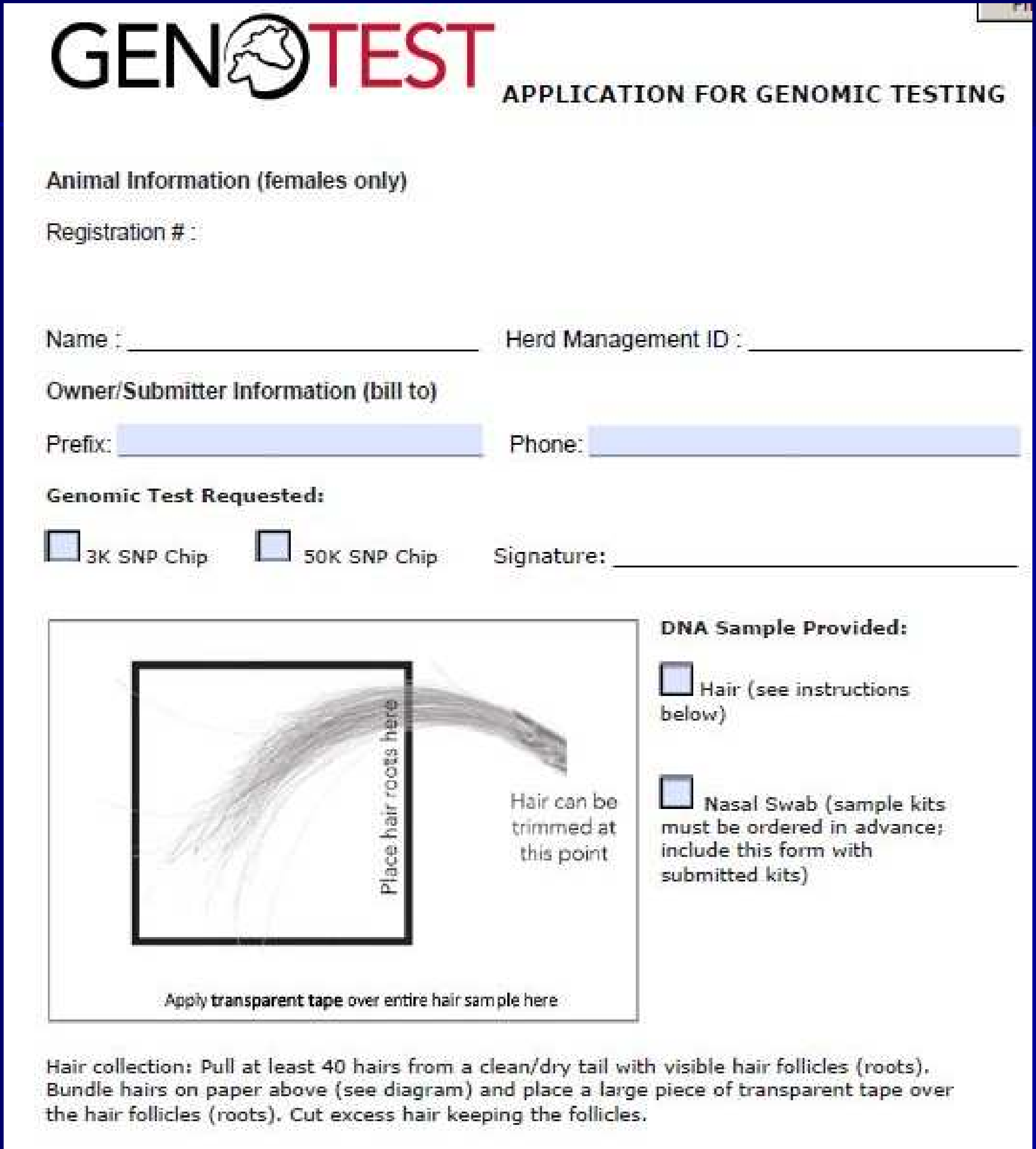
Štruktúrna genomika

Bioinformatika

Funkčná genomika

Zaplať a my dekódujeme Tvoju DNA

Zaplať a my dekódujeme Tvoju DNA



GENOTEST

APPLICATION FOR GENOMIC TESTING

Animal Information (females only)

Registration # :

Name : ______________________ Herd Management ID : ____________________

Owner/Submitter Information (bill to)

Prefix: ______________________ Phone: ____________________

Genomic Test Requested:

☐ 3K SNP Chip ☐ 50K SNP Chip Signature: ____________________

Place hair roots here

Hair can be trimmed at this point

Apply **transparent tape** over entire hair sample here

DNA Sample Provided:

☐ Hair (see instructions below)

☐ Nasal Swab (sample kits must be ordered in advance; include this form with submitted kits)

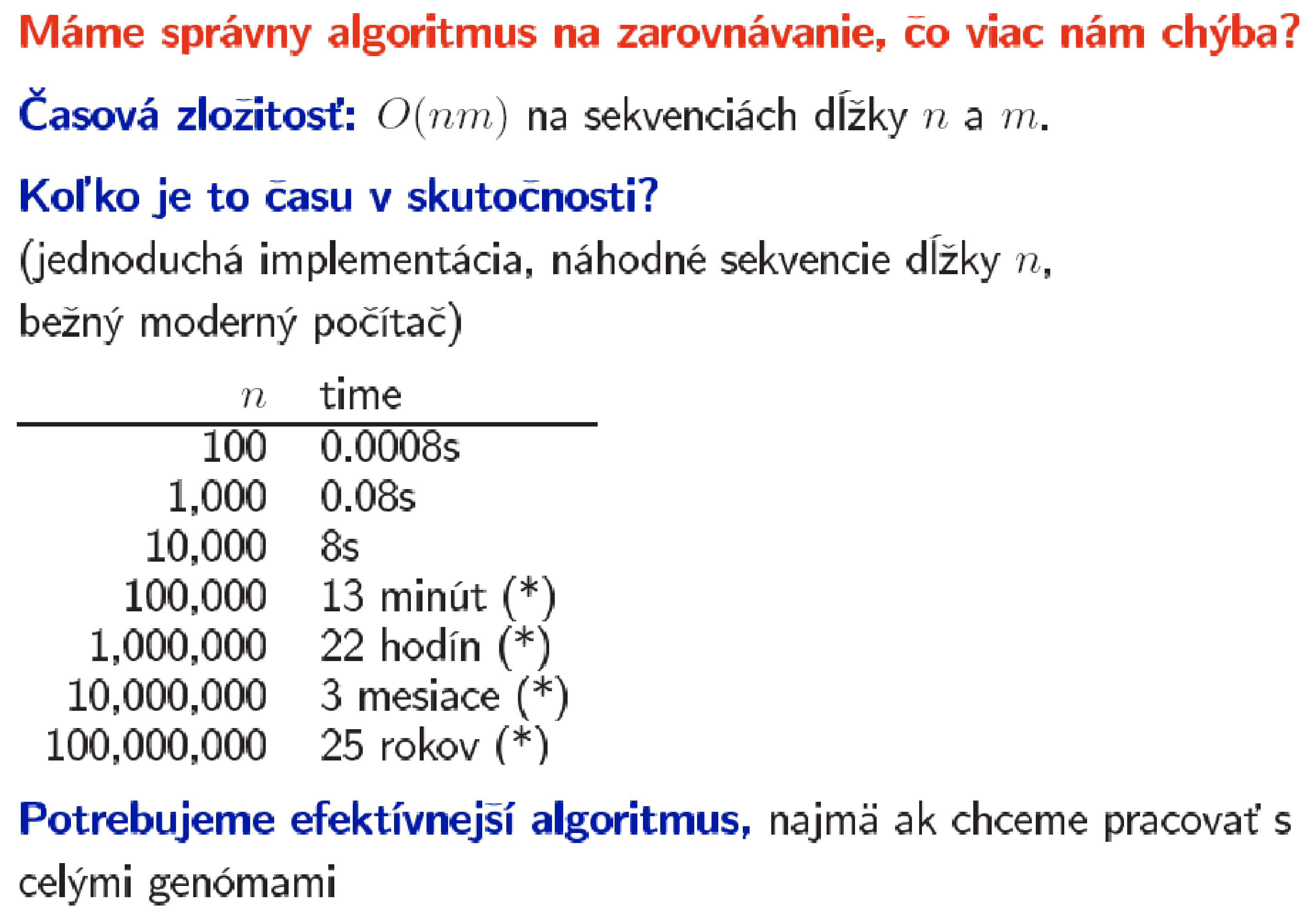
Hair collection: Pull at least 40 hairs from a clean/dry tail with visible hair follicles (roots). Bundle hairs on paper above (see diagram) and place a large piece of transparent tape over the hair follicles (roots). Cut excess hair keeping the follicles.

Genomika

Zložitosť - jednoduchosť problému

Organism type	Organism	Genome size (base pairs)	mass - in pg	Note
Virus	Bacteriophage MS2	3,569	0.00000352	First sequenced RNA-genome[8]
Virus	SV40	5,224		[9]
Virus	Phage Φ-X174	5,386		First sequenced DNA-genome[10]
Virus	Phage λ	48,502		
Bacterium	*Carsonella ruddii*	159,662		Smallest non-viral genome.[12]
Bacterium	*Buchnera aphidicola*	600,000		
Bacterium	*Wigglesworthia glossinidia*	700,000		
Bacterium	*Haemophilus influenzae*	1,830,000		First genome of living organism, July 1995[11]
Bacterium	*Escherichia coli*	4,600,000		[13]
Bacterium	*Solibacter usitatus* (strain Ellin 6076)	9,970,000		Largest known Bacterial genome
Yeast	*Saccharomyces cerevisiae*	12,100,000		[17]
Nematode	*Pratylenchus coffeae*	20,000,000		Smallest animal genome known[19]
Fungus	*Aspergillus nidulans*	30,000,000		
Plant	*Genlisea margaretae*	63,400,000		Smallest recorded flowering plant genome, 2006.[15]
Nematode	*Caenorhabditis elegans*	100,300,000		First multicellular animal genome, December 1998[18]
Insect	*Drosophila melanogaster* (fruit fly)	130,000,000		[20]
Plant	*Arabidopsis thaliana*	157,000,000		First plant genome sequenced, December 2000.[15]
Fish	*Tetraodon nigroviridis* (type of puffer fish)	385,000,000		Smallest vertebrate genome known
Plant	*Populus trichocarpa*	480,000,000		First tree genome, September 2006
Moss	*Physcomitrella patens*	480,000,000		First genome of a bryophyte, January 2008 [16]
Insect	*Bombyx mori* (silk moth)	530,000,000		
Insect	*Apis mellifera* (honey bee)	1,770,000,000		
Mammal	*Homo sapiens*	3,200,000,000		
Plant	*Fritillaria assyrica*	130,000,000,000		
Fish	*Protopterus aethiopicus* (marbled lungfish)	130,000,000,000		Largest vertebrate genome known
Amoeboid	*Polychaos dubium* (*Amoeba dubia*)	670,000,000,000	678.824	Largest known genome.[14]

Zložitosť - jednoduchosť problému



Máme správny algoritmus na zarovnávanie, čo viac nám chýba?

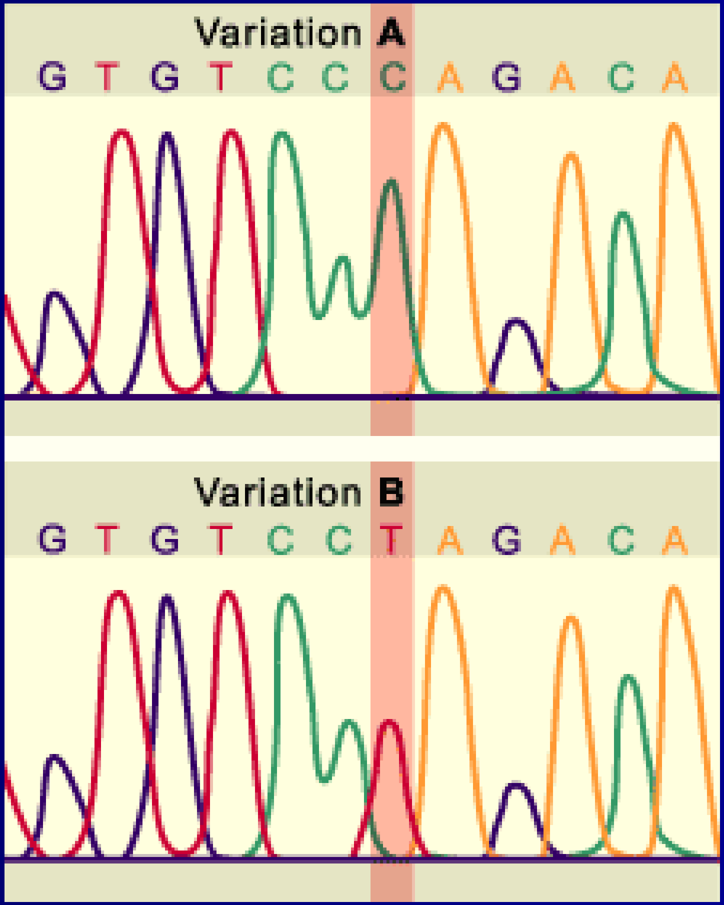
Časová zložitosť: $O(nm)$ na sekvenciách dĺžky n a m.

Koľko je to času v skutočnosti?
(jednoduchá implementácia, náhodné sekvencie dĺžky n,
bežný moderný počítač)

n	time
100	0.0008s
1,000	0.08s
10,000	8s
100,000	13 minút (*)
1,000,000	22 hodín (*)
10,000,000	3 mesiace (*)
100,000,000	25 rokov (*)

Potrebujeme efektívnejší algoritmus, najmä ak chceme pracovať s celými genómami

Genomics - Genomika

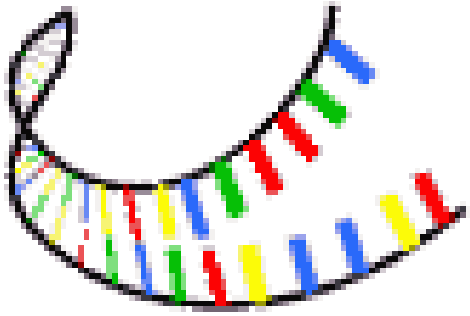


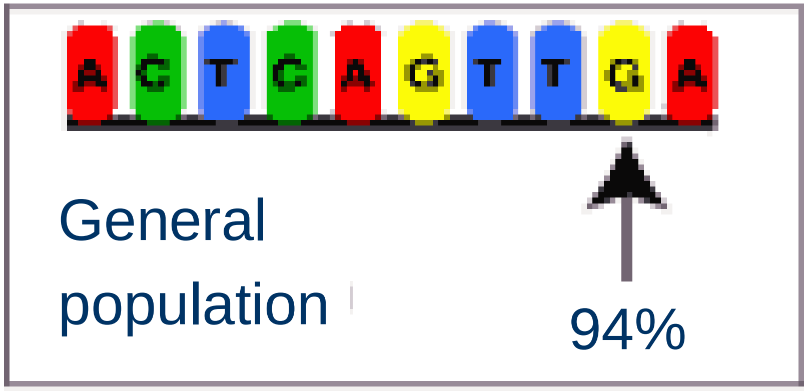
Genetic Markers

- Allow inheritance of a region of the genome to be followed across generations
- Single nucleotide polymorphisms (SNiP) are the markers of the future!
- Need lots!
  - 3 million in the genome
  - 10,000 initial goal

Polymorphism

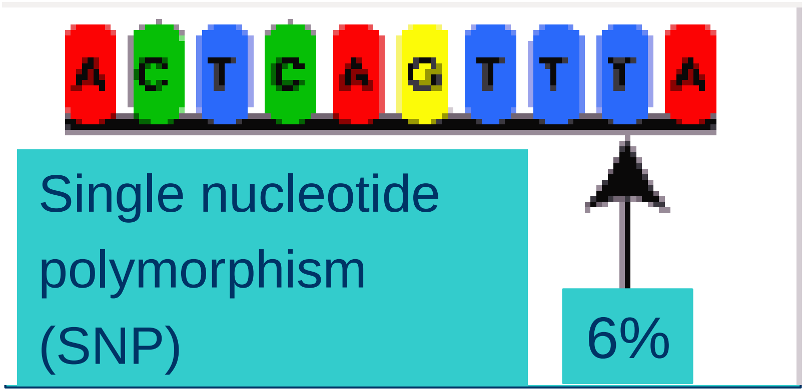
“poly” = many “morph” = form





General population

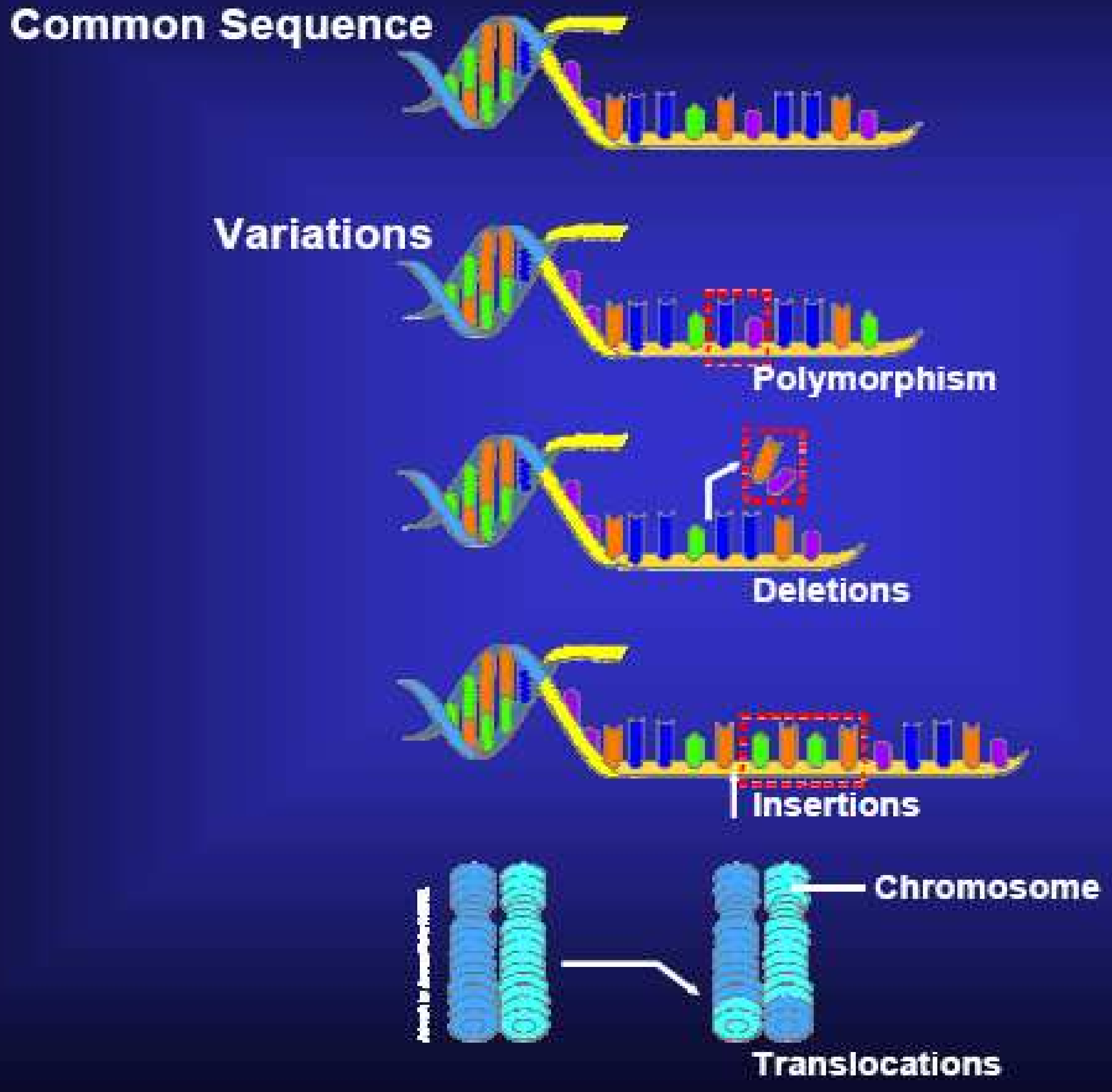
94%



Single nucleotide polymorphism (SNP)

6%

What Is Variation in the Genome?



Common Sequence

Variations

Polymorphism

Deletions

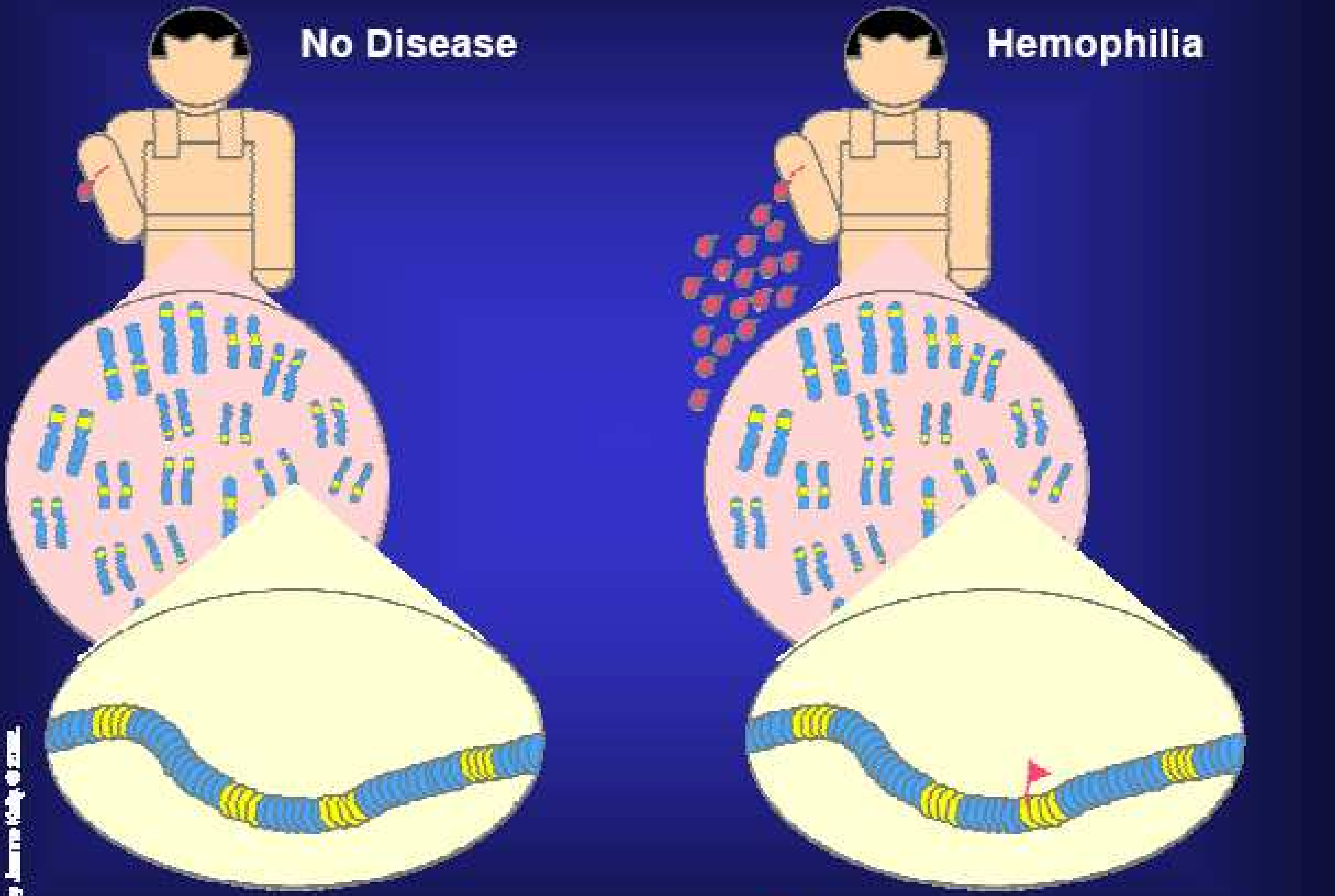
Insertions

Chromosome

Translocations

NATIONAL CANCER INSTITUTE

Variations Causing Harmful Changes



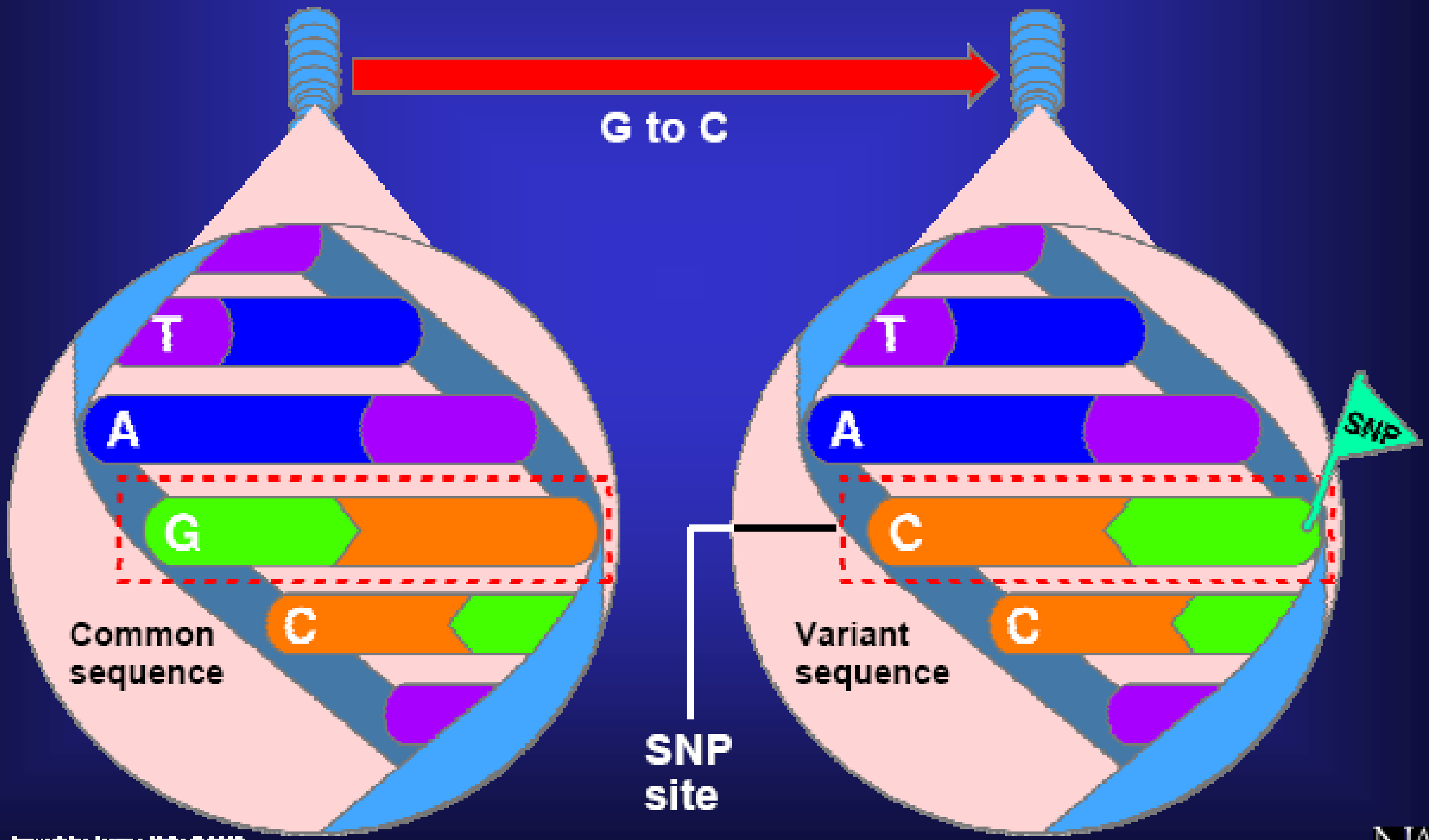
Artwork by Jeanne Kelly © 2002.

No Disease

🚩 = Variation in DNA that causes harmful change

NATIONAL CANCER INSTITUTE

SNPs Are the Most Common Type of Variation



Most of the population

At least 1 percent
of the population

G to C

Common
sequence

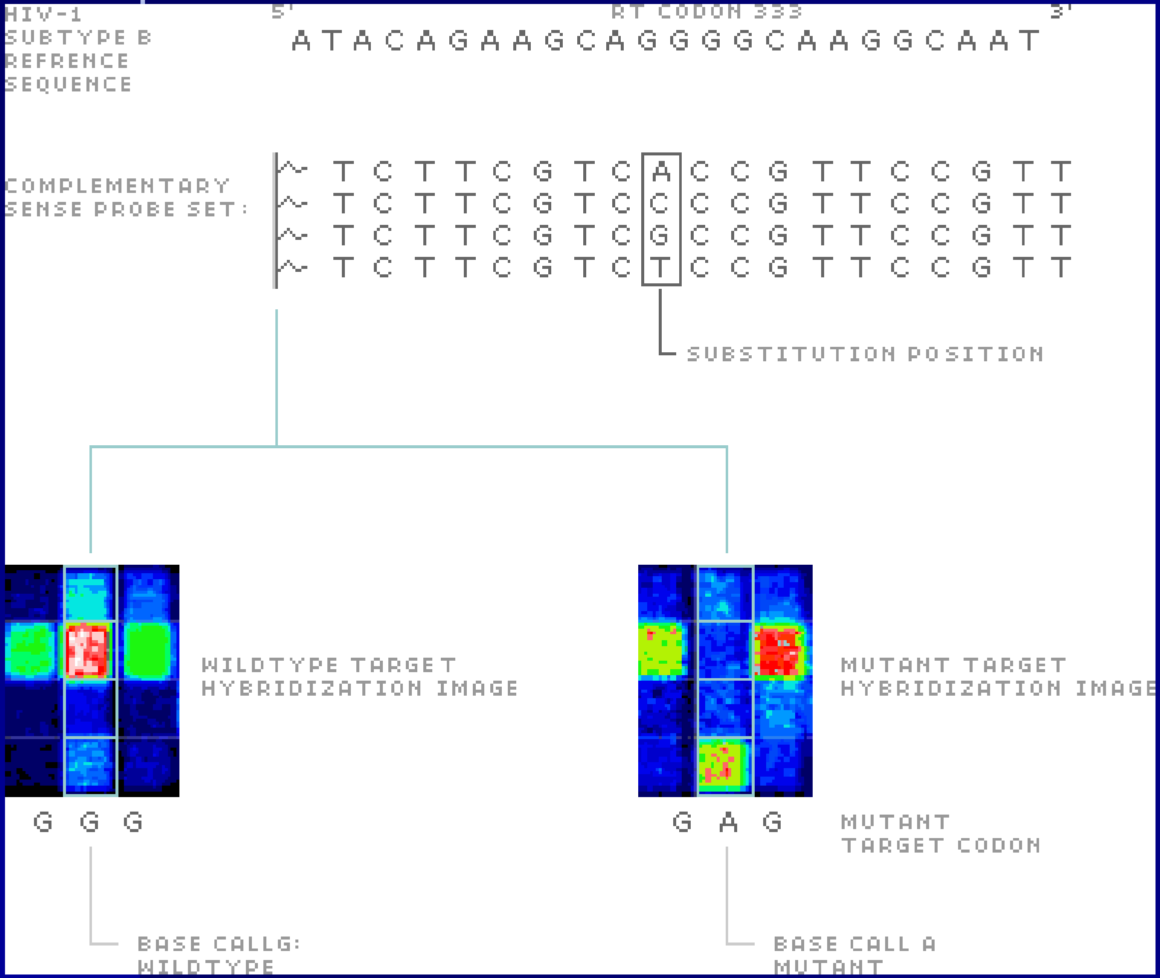
Variant
sequence

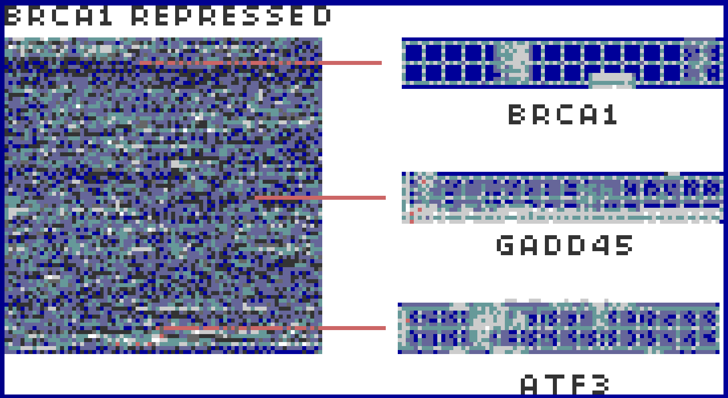
SNP
site

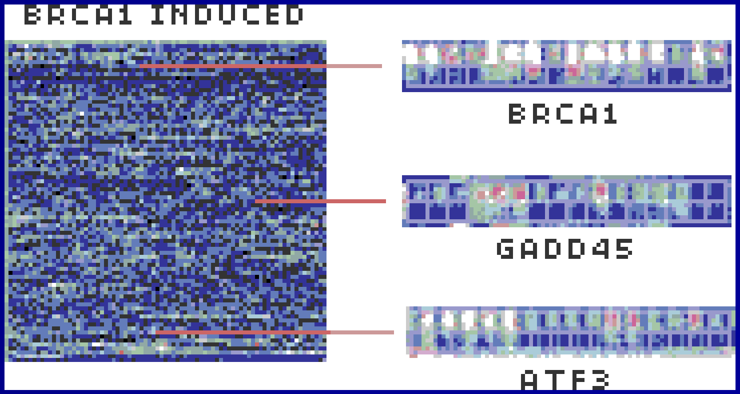
Artwork by Jeanne Kelly © 2002.

NATIONAL
CANCER
INSTITUTE

“DNA Chips”







www.affymetrix.com

Genomika

Moderné prístupy

Genomics

ILLUMINA® SNP GENOTYPING

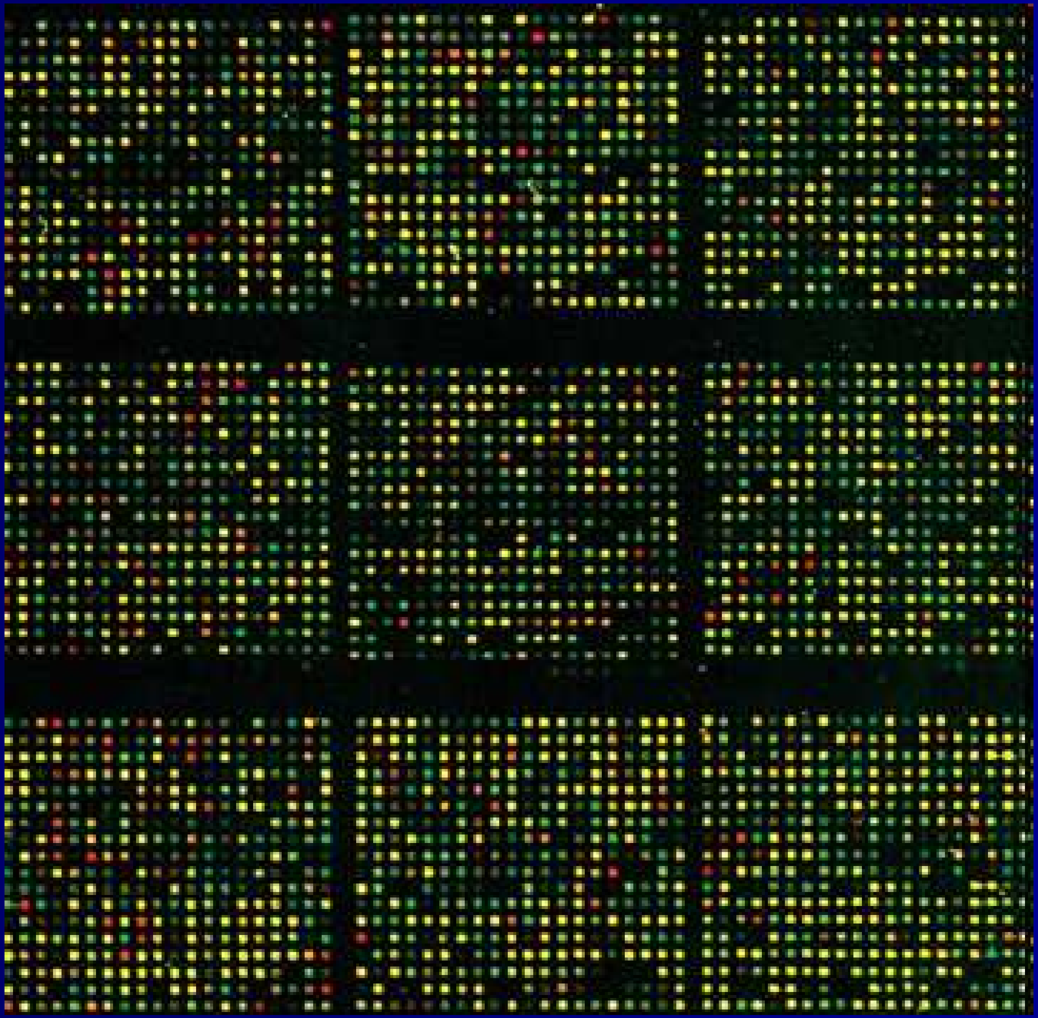
BovineSNP50 Genotyping BeadChip

Developed in collaboration with leading bovine researchers, the BovineSNP50 BeadChip features more than 54,000 evenly spaced SNP probes that span the bovine genome. This 12-sample BeadChip presents a cost-effective and high-quality solution for cattle researchers interested in genome-wide genotyping applications.

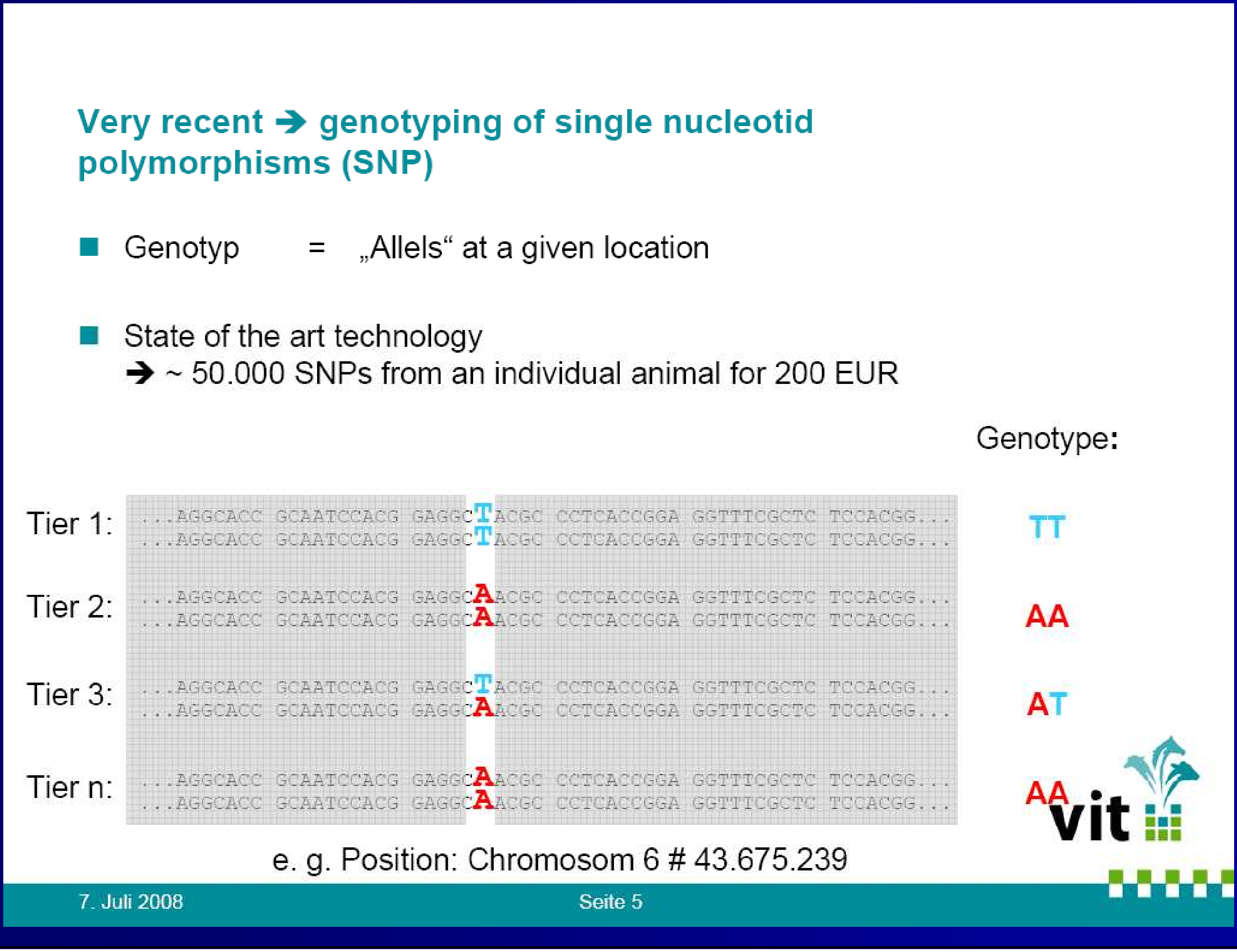
Január 2009

www.illumina.com

Zaplať a my dekódujeme DNA



“DNA Chips”



Very recent ➔ genotyping of single nucleotid polymorphisms (SNP)

- Genotyp = „Allels“ at a given location
- State of the art technology
  ➔ ~ 50.000 SNPs from an individual animal for 200 EUR

Genotype:

Tier 1:
...AGGCACC GCAATCCACG GAGGCTACGC CCTCACCGGA GGTTTCGCTC TCCACGG...
...AGGCACC GCAATCCACG GAGGCTACGC CCTCACCGGA GGTTTCGCTC TCCACGG...
TT

Tier 2:
...AGGCACC GCAATCCACG GAGGCAACGC CCTCACCGGA GGTTTCGCTC TCCACGG...
...AGGCACC GCAATCCACG GAGGCAACGC CCTCACCGGA GGTTTCGCTC TCCACGG...
AA

Tier 3:
...AGGCACC GCAATCCACG GAGGCTACGC CCTCACCGGA GGTTTCGCTC TCCACGG...
...AGGCACC GCAATCCACG GAGGCAACGC CCTCACCGGA GGTTTCGCTC TCCACGG...
AT

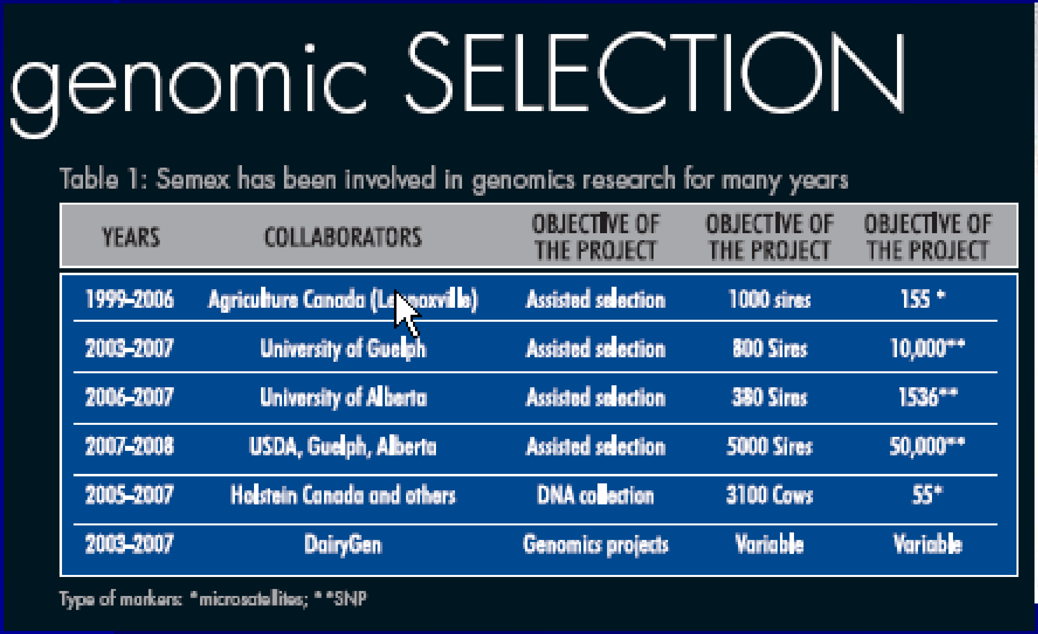
Tier n:
...AGGCACC GCAATCCACG GAGGCAACGC CCTCACCGGA GGTTTCGCTC TCCACGG...
...AGGCACC GCAATCCACG GAGGCAACGC CCTCACCGGA GGTTTCGCTC TCCACGG...
AA

e. g. Position: Chromosom 6 # 43.675.239

Genomika

Praktické prístupy

SEMEX'S GENOMIC PROGRAM genomax



genomic SELECTION

Table 1: Semex has been involved in genomics research for many years

YEARS	COLLABORATORS	OBJECTIVE OF THE PROJECT	OBJECTIVE OF THE PROJECT	OBJECTIVE OF THE PROJECT
1999-2006	Agriculture Canada (Lennoxville)	Assisted selection	1000 sires	155 *
2003-2007	University of Guelph	Assisted selection	800 Sires	10,000**
2006-2007	University of Alberta	Assisted selection	380 Sires	1536**
2007-2008	USDA, Guelph, Alberta	Assisted selection	5000 Sires	50,000**
2005-2007	Holstein Canada and others	DNA collection	3100 Cows	55*
2003-2007	DairyGen	Genomics projects	Variable	Variable

Type of markers: *microsatellites; **SNP

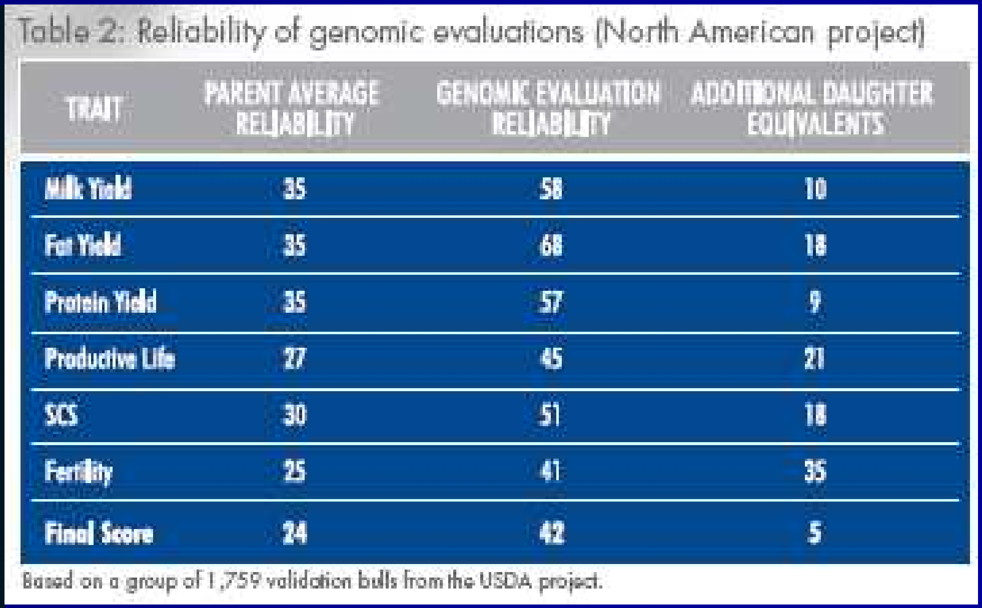


Table 2: Reliability of genomic evaluations (North American project)

TRAIT	PARENT AVERAGE RELIABILITY	GENOMIC EVALUATION RELIABILITY	ADDITIONAL DAUGHTER EQUIVALENTS
Milk Yield	35	58	10
Fat Yield	35	68	18
Protein Yield	35	57	9
Productive Life	27	45	21
SCS	30	51	18
Fertility	25	41	35
Final Score	24	42	5

Based on a group of 1,759 validation bulls from the USDA project.

Genomika

Praktické prístupy

EURO
Genomics
for reliable cattle breeding

UNCEIA, CRV, DHV a VIT, VIKING GENETICS

Genomika

Praktické prístupy

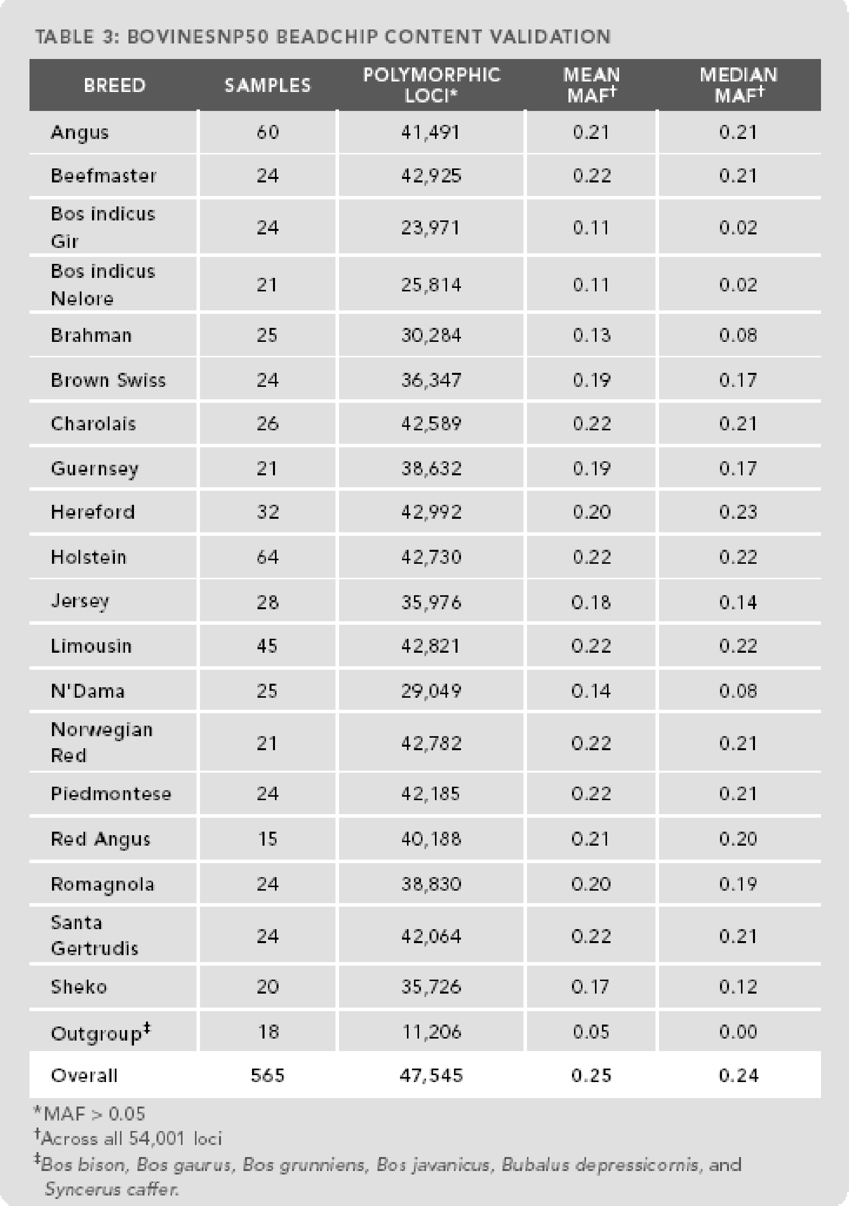


TABLE 3: BOVINESNP50 BEADCHIP CONTENT VALIDATION

BREED	SAMPLES	POLYMORPHIC LOCI*	MEAN MAF[†]	MEDIAN MAF[†]
Angus	60	41,491	0.21	0.21
Beefmaster	24	42,925	0.22	0.21
Bos indicus Gir	24	23,971	0.11	0.02
Bos indicus Nelore	21	25,814	0.11	0.02
Brahman	25	30,284	0.13	0.08
Brown Swiss	24	36,347	0.19	0.17
Charolais	26	42,589	0.22	0.21
Guernsey	21	38,632	0.19	0.17
Hereford	32	42,992	0.20	0.23
Holstein	64	42,730	0.22	0.22
Jersey	28	35,976	0.18	0.14
Limousin	45	42,821	0.22	0.22
N'Dama	25	29,049	0.14	0.08
Norwegian Red	21	42,782	0.22	0.21
Piedmontese	24	42,185	0.22	0.21
Red Angus	15	40,188	0.21	0.20
Romagnola	24	38,830	0.20	0.19
Santa Gertrudis	24	42,064	0.22	0.21
Sheko	20	35,726	0.17	0.12
Outgroup[‡]	18	11,206	0.05	0.00
Overall	565	47,545	0.25	0.24

*MAF > 0.05

[†] Across all 54,001 loci

[‡] *Bos bison, Bos gaurus, Bos grunniens, Bos javanicus, Bubalus depressicornis,* and *Syncerus caffer.*

Genomika

Výhody

Vyššia presnosť plemennej hodnoty (GEBV)
ako presnosť rodokmeňovej PH

Možnosť jej získania
už pri narodení zvieraťa

Možné zmeny v šľachtiteľských programoch
? ? ?

Genomika

Nevýhody

Odhady SNP efektov sa časom menia

Nutnosť vykonávať opakované odhady

Rozdiely medzi plemenami a populáciami

Zmena SNP techniky (počet SNPs)

Možné zmeny v šľachtiteľských programoch

Riziká nesprávnej predselekcie býkov
(Maria Curie efekt)
Patentované gény
DGAT1 (US007537888), GHR (US007407750), ABCG2 (WO2007/002735, PCT/US2006/025117)

Komerčné záujmy

Klasický prístup

0 - narodenie býka
1 - vstup do testu
2 - narodenie dcér
3 - dcéry vstupujú do reprodukcie
4 - prvá laktácia dcér
5 - 6 výsledky testu

(môžeš sa ale pozrieť na moje dcéry)

Genomický prístup

0 - narodenie býka
genomický test

1 - vstup do testu ako preverený býk

(nemôžeš sa pozrieť na moje dcéry)

Praktický význam genomickej selekcie holsteinského plemena

Kto vlastne ušetrí peniaze ? ? ?

Neváhajte a zatepľujte . . .

Vývoj nezastavíš . . . ? ? ?

Ďakujeme za pozornosť

(otec + matka) / 2 = potomok

alebo, niekedy ani nie