Genomics – A New Era for Cattle Breeding.

ICBF & Teagasc Genomics Conference.

Killeshin Hotel Portlaoise.

14th November 2012.

Objective of conference.

- An opportunity to understand genomics, from the basic concepts through to it’s role in parentage identification and future genetic improvement programs.

Session 1. Genomics & parentage identification (10 am – 1 pm)

- Chair: Gerard Brickley, beef farmer and herdbook representative on board of ICBF.
- Introduction to animal breeding, including genomics – Dr. Sinead McParland, Teagasc.
- Genomics and parentage verification – Dr. Matt McClure, US Department of Agriculture.
- Developing a customised chip for Ireland – Dr. Mike Mullen, Teagasc.
- Implementation of genomic services – Mary McCarthy, ICBF and Dr John Flynn, Weatherby's Ireland.
- Role of genomics in Irish dairy and beef breeding programs (Part 1) – Dr. Andrew Cromie, ICBF.
- Discussion.

Session 2. Genomics & genetic improvement (2-5 pm).

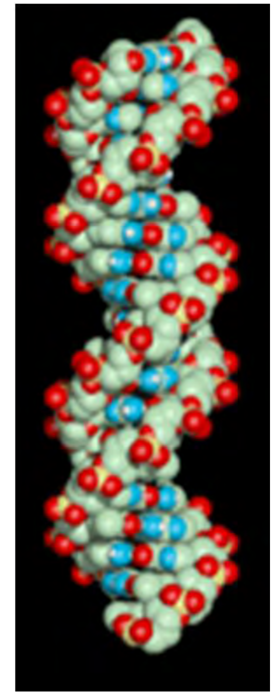
- Chair: John O’Sullivan, dairy farmer and chairman of board of ICBF.
- Role of genomics in Irish dairy and beef breeding programs (Part 2) – Dr. Andrew Cromie, ICBF.
- Developments in beef genomics – Dr. Donagh Berry, Teagasc
- Developments in dairy genomics – Dr. Francis Kearney, ICBF
- Where next for genomics and cattle breeding – Dr. Matt McClure, US Department of Agriculture.
- Discussion.

Introduction to Animal Breeding & Genomics

Sinead McParland
Teagasc, Moorepark, Ireland

Sinead.McParland@teagasc.ie

Overview

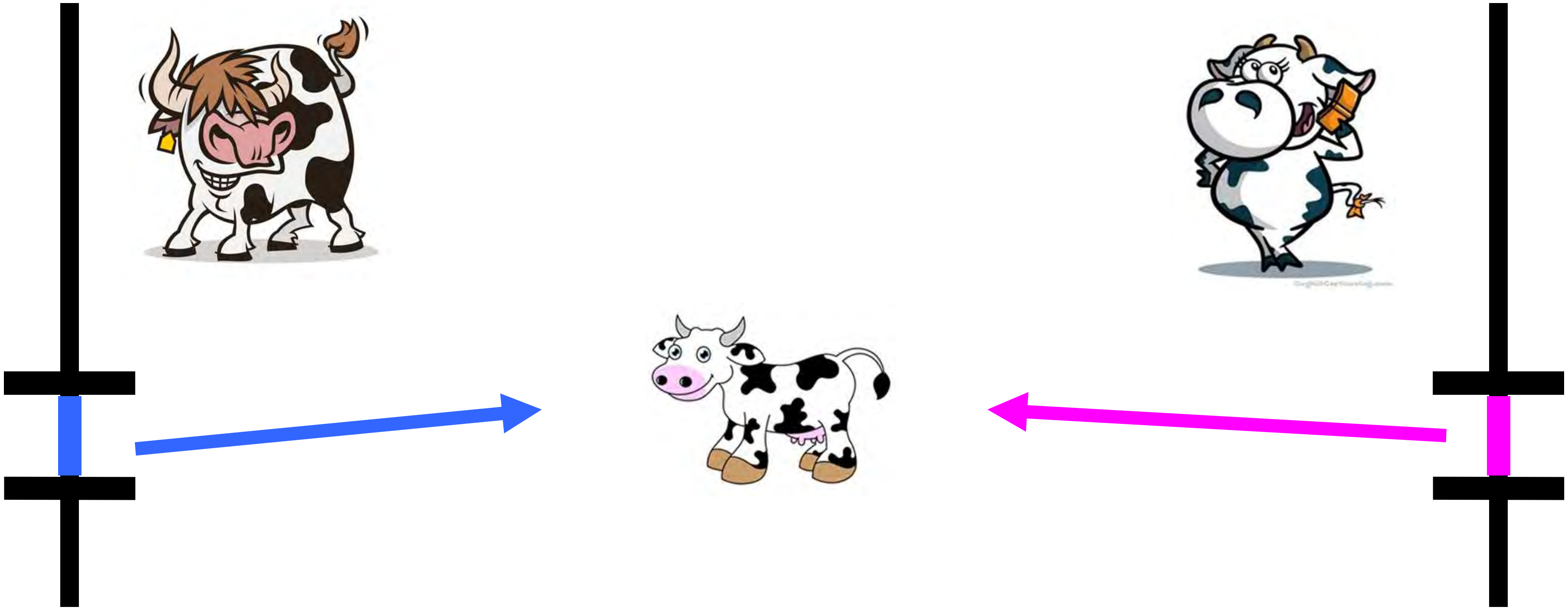


- Changes to traditional animal breeding

- Using DNA in animal breeding
  - Microsatellites
  - SNPs
  - A method to reduce cost of genomic testing
  - Can SNP information replace microsatellites?

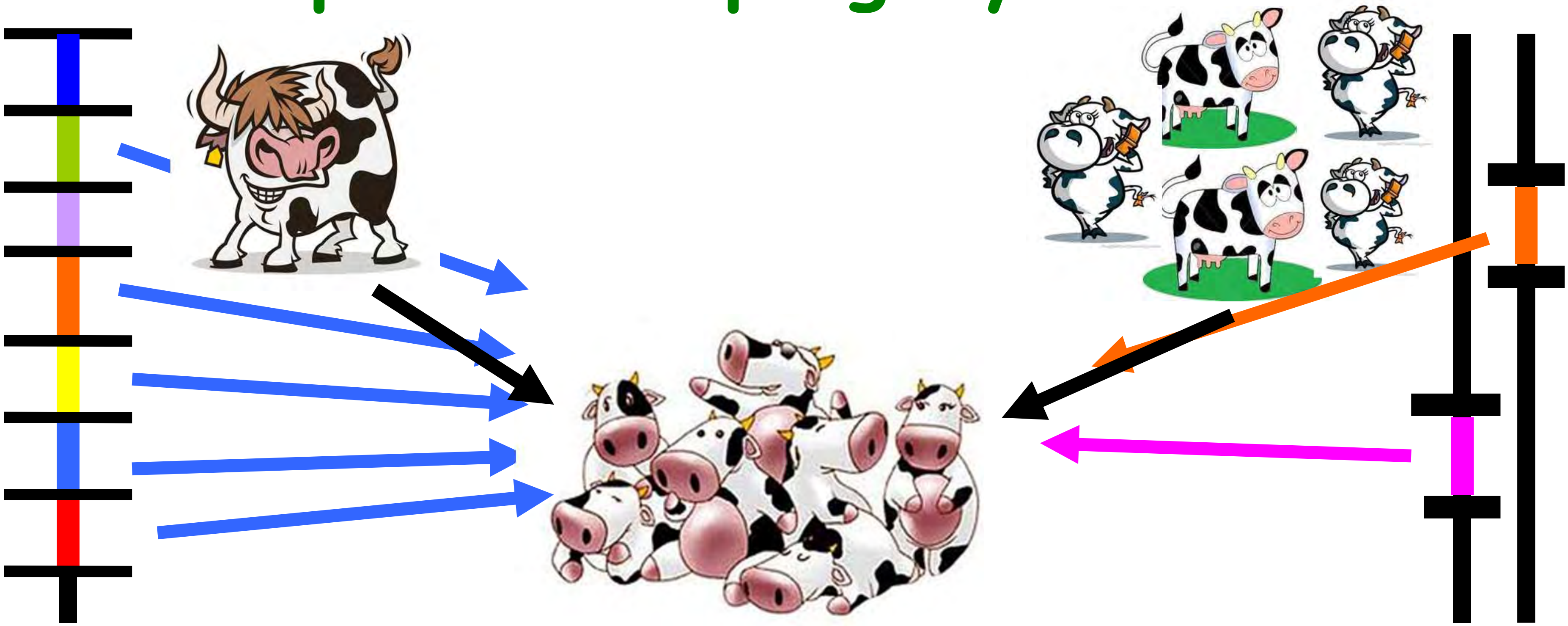
- Some terms to help you through today!!

Traditional Animal Breeding



- Calf produces 500 kg milk solids & 400 day CI
- Bull EBI reliability 30%

Bull completes his progeny test



- Bull has 100 daughters milking
- More of his DNA expressed in the population
- Bull reliability for milk ~80%

Using technology of today

- At birth we know about parts of the calf DNA
- Calf BV reliability increases to ~ 50%
  - Equivalent of 15 daughters milking

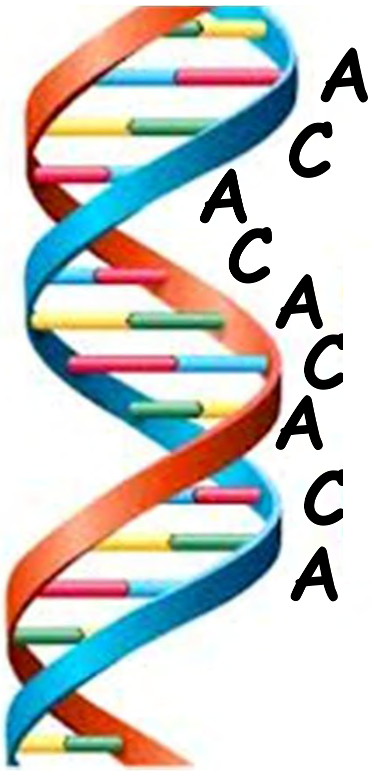
DNA - From the tip of your nose to the tops of your toes!!

DNA is the same in every cell of your body and doesn't change throughout your life

How do we use this DNA information?

Microsatellites

- Short repeats of DNA sequence



- Caused by mutations and subsequently passed to progeny
- Used for parentage verification

…GTCCGTACACACACTTATCAA…

What is a SNP?

- 99.9% of human DNA is identical – most of the differences are in the form of SNPs

… ACGTACGTCAATGACTTTTACGTAT…

… ACGTACGACAATGACTTTTACGTAT…

- Single Nucleotide ~~Polymorphism~~ Change

How do SNPs relate to performance?

- The cattle genome has ~ 3 billion nucleotides
- Scientists have discovered ~ 40 million SNPs

- At a SNP locus different variants are present
  - Different variants have different associations with performance

SNP effect on performance

SNP	Var	Milk	Beef
1	A	+5	-0.6
1	G	+20	-0.4
2	A	12.3	-0.6
2	T	-14.46	+20.2
⋮	⋮	⋮	⋮
n	A	+25	+5.2

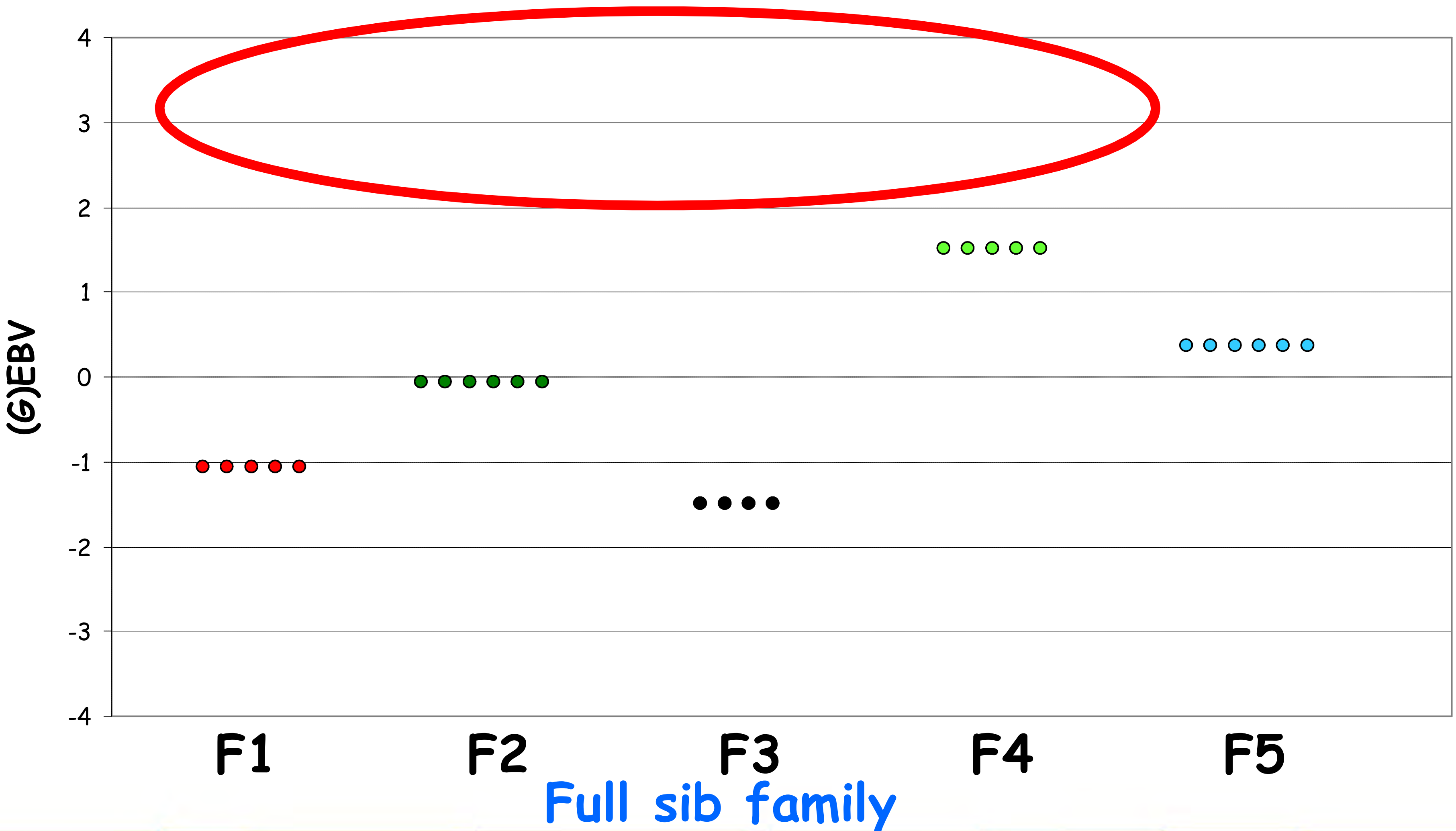
Genomic selection

- Increase accuracy of selection at a younger age

- Traditionally used parental information
  - Progeny = ½ mother + ½ father DNA
  - Progeny = average of mother & father BVs
  - Assumed full sibs were identical

- Available SNP information can be used to supplement the traditional approach
  - See difference in full-sibs at birth

Indentifying Mendelian sampling term



Why not 100% accurate?

- Phenotypes / performance are typically affected by more than one gene
  - Up to 80% of human stature attributable to genetics – no major gene found to date
- Genes may influence more than one phenotype / performance
- Genes interact with one another
- Genes interact with the environment

Cost of sequencing has decreased

But we don't need to know about EVERY piece of DNA in the body

cing

Applied Biosciences (2004)
$15,000,000

Illumina (2011)
$15,000

Different SNP platforms (levels of DNA information) available

54,609 SNPs

50k chip

IMPUTE

6,909 SNPs

BovineLD

777,962 SNPs

High Density chip

Imputation

Sire

…..TCACCGCTGAG…..

…..CAGATAGGATT…..

…..??G??????A??….

…..??T??????T??…..

Offspring

Imputation

Sire

.....TCACCGCTGAG.....

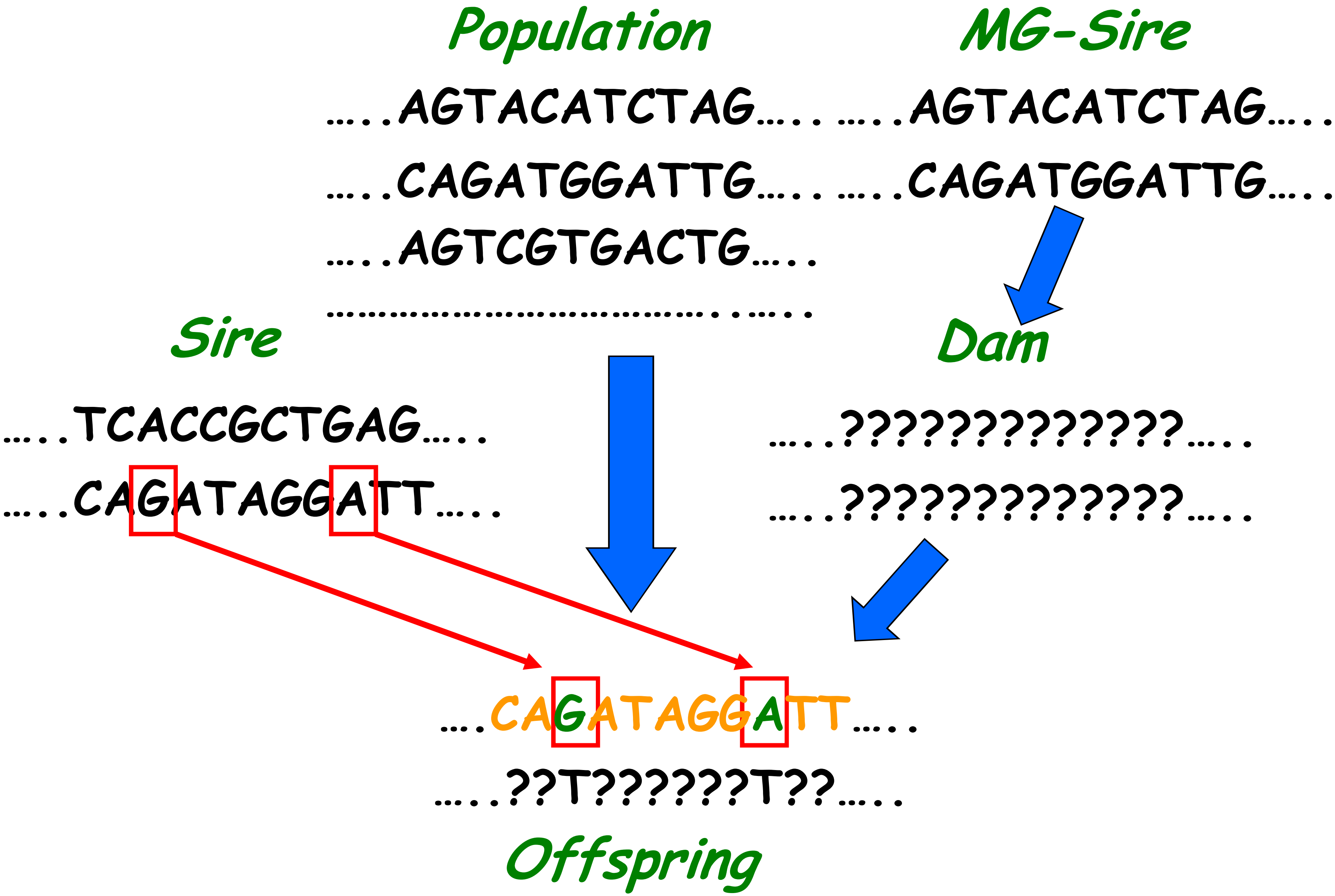
.....CAGATAGGATT.....

....CAGATAGGATT.....

.....??T??????T??.....

Offspring

Imputation



Population
…..AGTACATCTAG…..
…..CAGATGGATTG…..
…..AGTCGTGACTG…..
MG-Sire
…..AGTACATCTAG…..
…..CAGATGGATTG…..
Sire
…..TCACCGCTGAG…..
…..CAGATAGGATT…..
Dam
…..?????????????…..
…..?????????????…..
…..CAGATAGGATT…..
…..??T??????T??…..
Offspring

Imputation

Population	*MG-Sire*
…..AGTACATCTAG…..	…..AGTACATCTAG…..
…..CAGATGGATTG…..	…..CAGATGGATTG…..

…..TC …..

…..CA …..

Accuracy

Sire is known – 99%

No sire or MGS – 98%

….CAGATAGGATT…..

….AGTACATCTAG…..

Offspring

Parentage

Sire

…...TCACCGCTGAG…...

…...CA$\boxed{G}$ATAGG$\boxed{A}$TT…...

…...??$\boxed{G}$??????$\boxed{A}$??….

…...??T??????T??…...

Offspring

Parentage

Database

Sire 1 …..TCGGGCTGTG…..

Sire 2 …..CAGATAGGATT…..

Sire 3 …..TCACCGCTGAG…..

Sire 4 …..CAAATAGGCTT…..

Sire

…..TCACCGCTGAG…..

…..CA$\boxed{G}$ATAGG$\boxed{A}$TT…..

…..??$\boxed{A}$??????$\boxed{C}$??….

…..??T??????T??…..

Offspring

Parentage

Database

80% of parentage errors corrected using this method

….CA**A**ATAGG**C**TT…..

…..??T??????T??…..

Offspring

What options are available?

Illumina

6,909 (LD)

54,609 (50k)

777,962 (HD)

LD + additional selected SNPs (LD+)

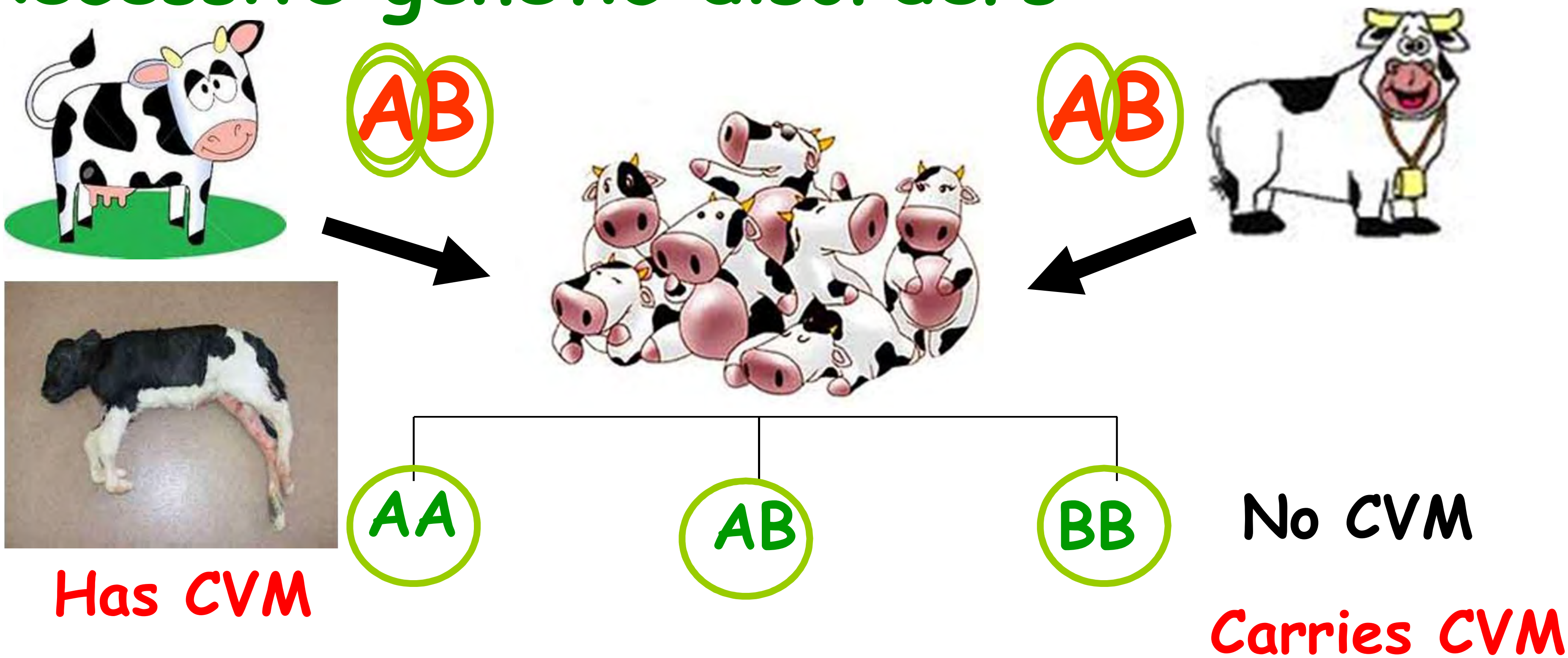
Affymetrix

608,874 (BOS1)

50,000 (customised)

- can work across species

Recessive genetic disorders

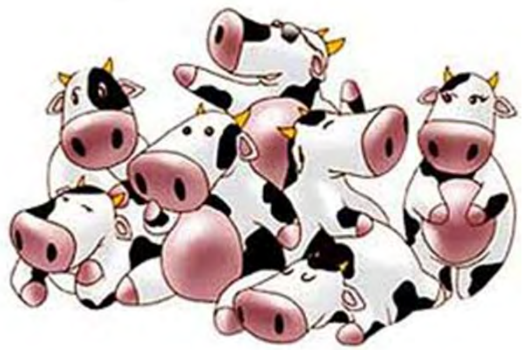


- Non-CVM allele (B) expressed whenever present
- CVM Allele is recessive "hidden" when with non-CVM

Screen for CVM through genotyping

AB

BB



~~AA~~

BB No CVM

AB Carries CVM

- Customised chip will identify "carriers" of genetic recessive disorders
- Choose NOT to mate 2 carriers of CVM

To Conclude

- Differences seen between individuals of a species are mostly due to SNPs
- We can relate SNP variants to performance
    - Genomic selection
- SNP information can also be used to predict parentage accurately
- Imputation is a method to accurately predict SNP variants present cheaper than traditionally
- Customised chips to be developed for Ireland

Thank you
for your attention

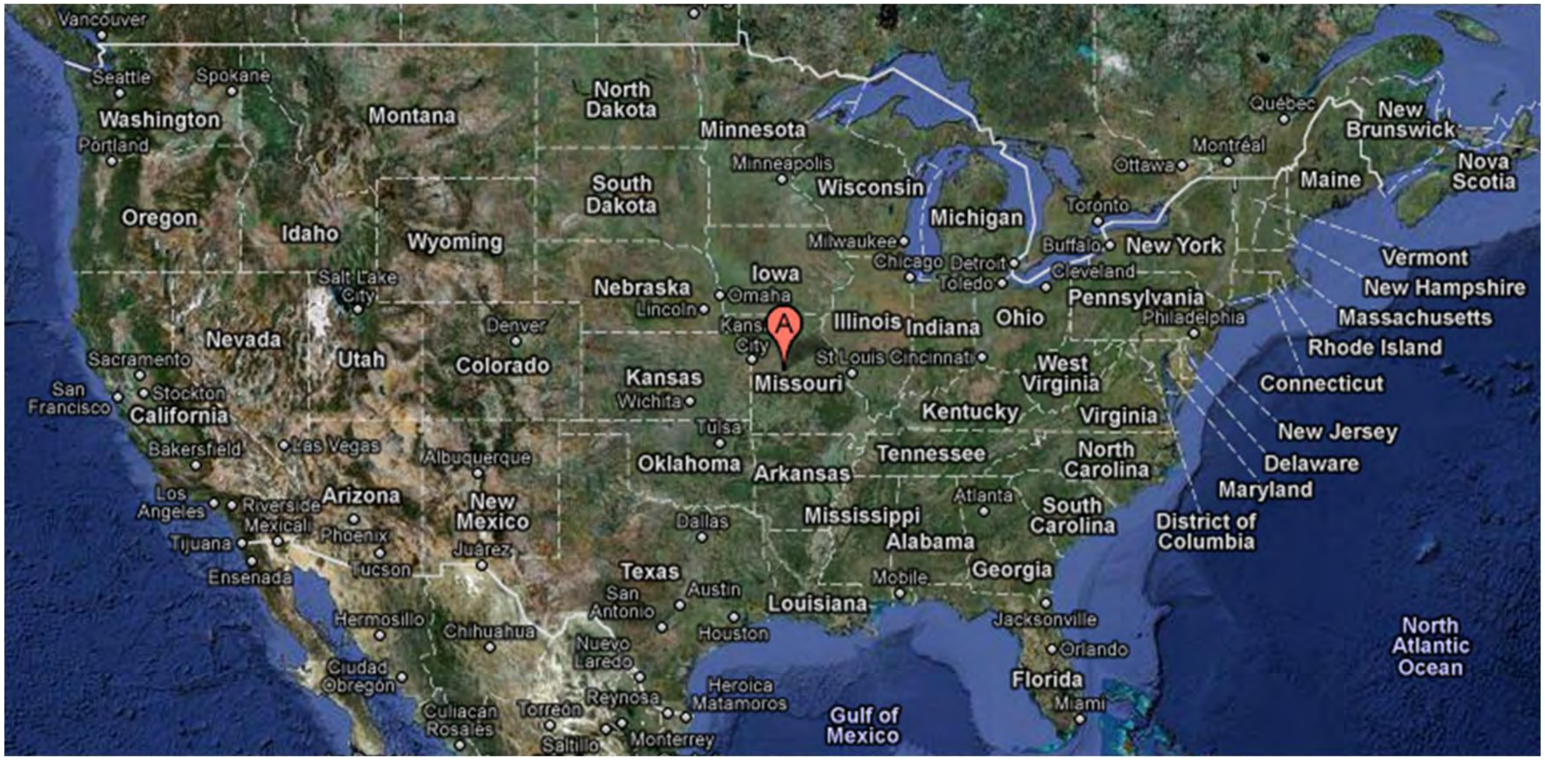
Genomic Advances in Parentage Verification

Matthew McClure[1], Tad Sonstegard[1*], George Wiggans[2],

Alison Van Eenennaam[3], Kristina Weber[3], Cecilia Penedo[4], Curt Van Tassell[1]

[1] USDA-Agriculture Research Service, Bovine Functional Genomics Lab, Beltsville, MD, USA
[2] USDA-ARS, Animal Improvement Program Lab, Beltsville, MD, USA
[3] UC Davis, Department of Animal Science, Davis, CA, USA
[4] UC Davis, School of Veterinary Medicine, Davis, CA, USA

Background


Vancouver
Seattle
Spokane
Washington
Portland
Montana
North Dakota
Minnesota
Minneapolis
Wisconsin
South Dakota
Oregon
Idaho
Wyoming
Michigan
Milwaukee
Chicago
Detroit
Toledo
Cleveland
Buffalo
New York
Toronto
Ottawa
Montréal
Québec
New Brunswick
Nova Scotia
Maine
Vermont
New Hampshire
Massachusetts
Rhode Island
Connecticut
New Jersey
Delaware
Maryland
District of Columbia
Salt Lake City
Nebraska
Lincoln
Omaha
Iowa
Illinois
Indiana
Ohio
Pennsylvania
Philadelphia
Nevada
Utah
Denver
Colorado
Kansas City
St Louis
Cincinnati
West Virginia
Virginia
Sacramento
San Francisco
Stockton
California
Kansas
Wichita
Missouri
Kentucky
Bakersfield
Las Vegas
Albuquerque
Tulsa
Oklahoma
Arkansas
Tennessee
North Carolina
Los Angeles
Riverside
Mexicali
Arizona
Phoenix
New Mexico
Dallas
Mississippi
Atlanta
South Carolina
Tijuana
Juárez
Alabama
Ensenada
Tucson
Texas
Mobile
Georgia
San Antonio
Austin
Louisiana
Jacksonville
Hermosillo
Chihuahua
Houston
Orlando
Nuevo Laredo
North Atlantic Ocean
Ciudad Obregón
Heroica Matamoros
Florida
Reynosa
Miami
Culiacán Rosales
Torreón
Gulf of Mexico
Saltillo
Monterrey

U.S. Department of Agriculture, Agriculture Research Service

USDA's chief scientific research agency

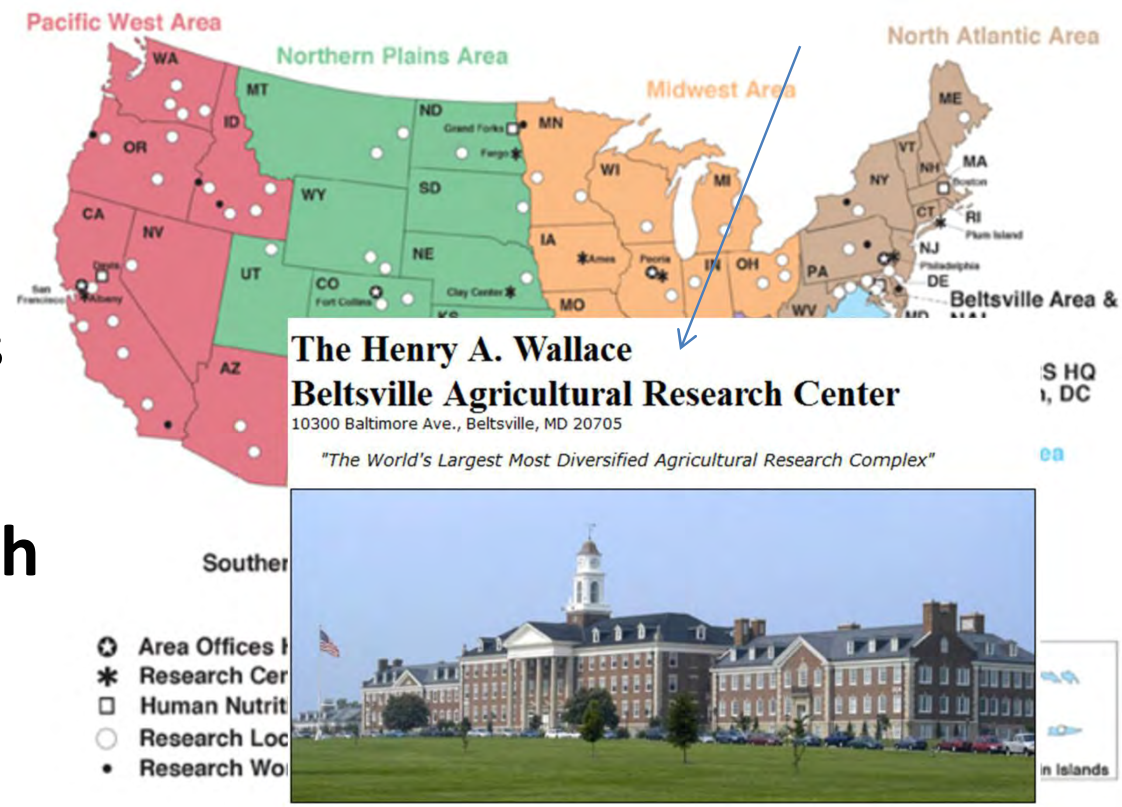
20 National Programs

850 research projects

2,200 scientists

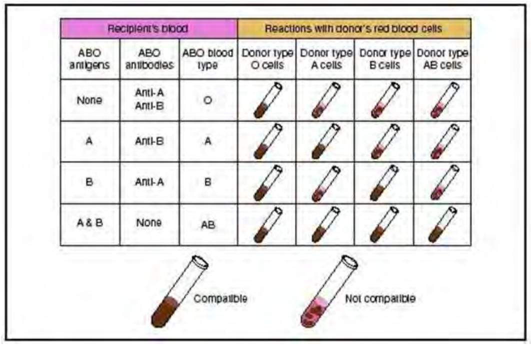
100 US research locations

Farm to Table Research

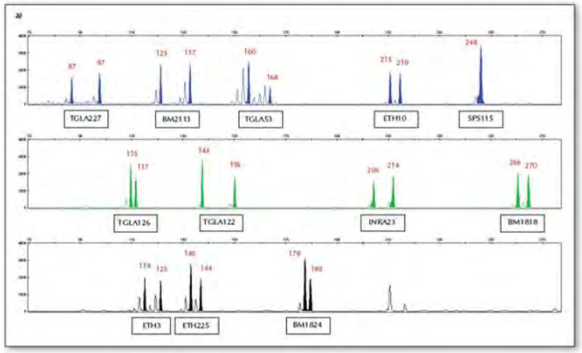


Parentage Verification

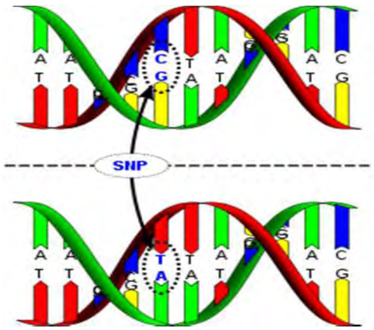
<1990's

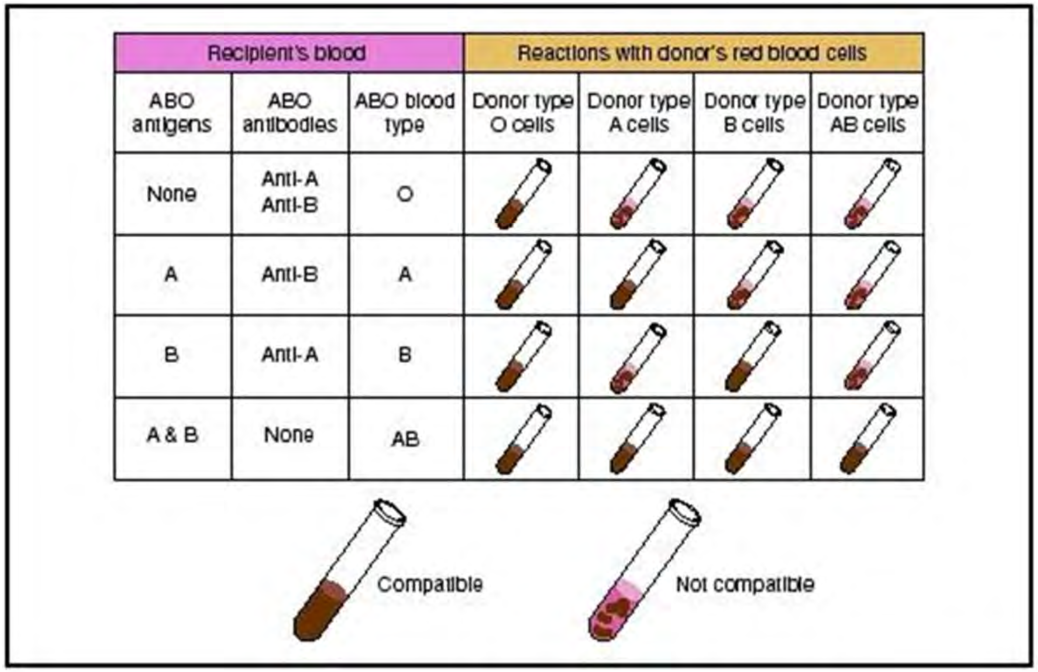


Present



Future

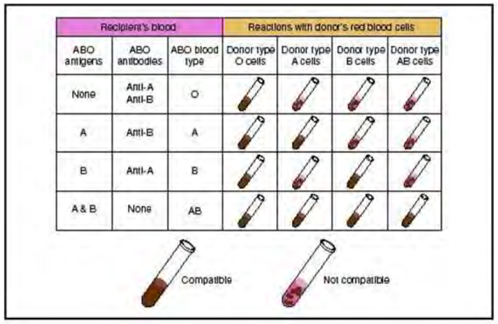




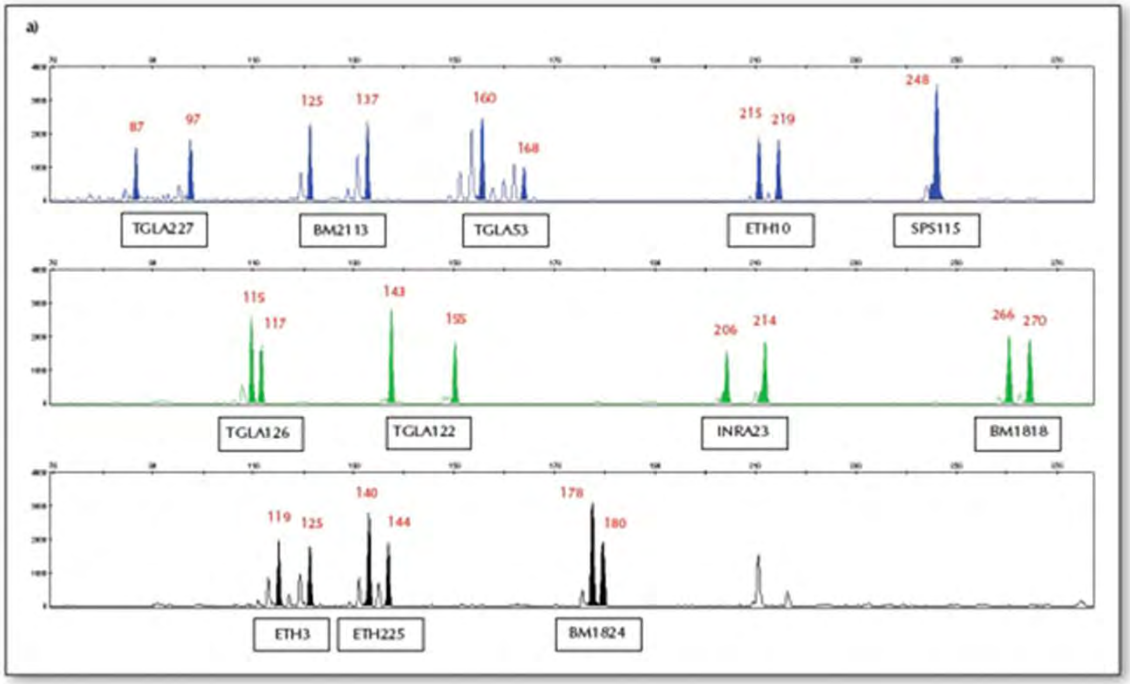
Blood Typing >1990's

Used to detect genetic variations in blood groups and protein types

Required fresh blood samples



Microsatellite Markers 1990’s-present

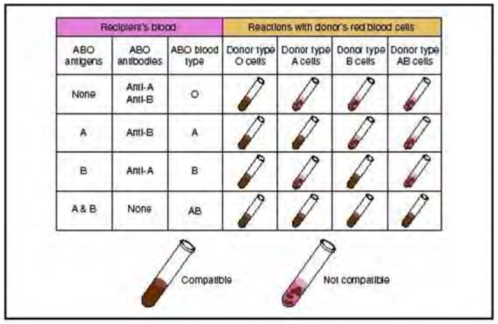


Used to detect genetic variations in bi-nucleotide repeats

DNA could be obtained from any tissue

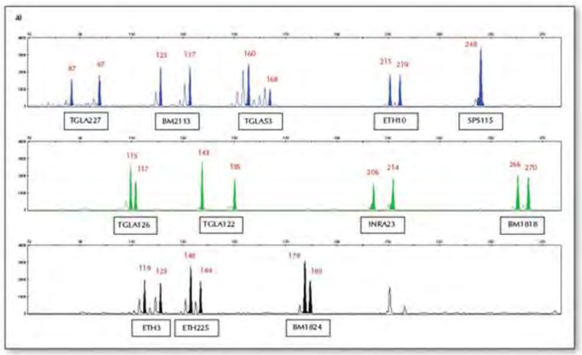
Difficulty in multiplexing, scoring, automation

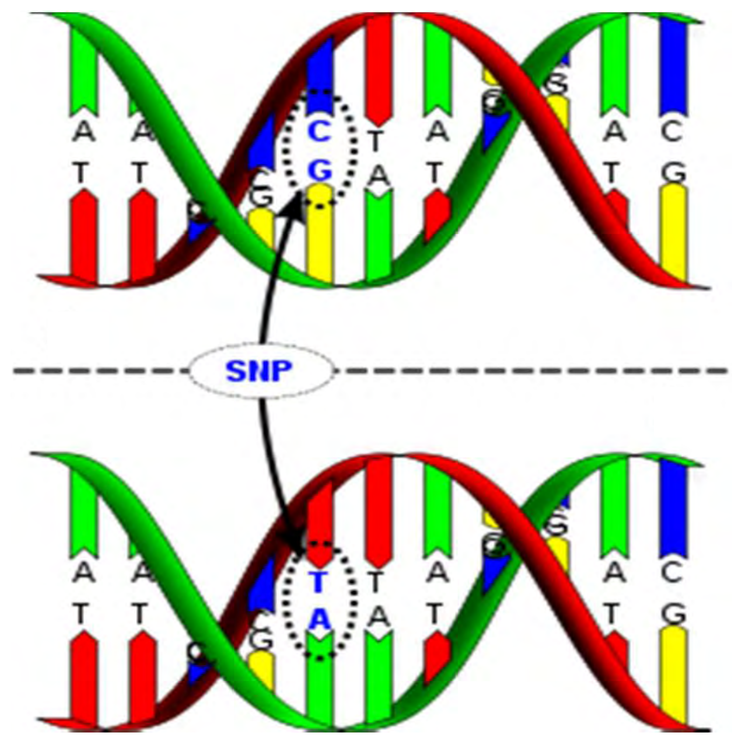
Single Nucleotide Polymorphisms
2010-present



Recipient's blood			Reactions with donor's red blood cells			
ABO antigens	ABO antibodies	ABO blood type	Donor type O cells	Donor type A cells	Donor type B cells	Donor type AB cells
None	Anti-A Anti-B	O				
A	Anti-B	A				
B	Anti-A	B				
A & B	None	AB				

Compatible Not compatible



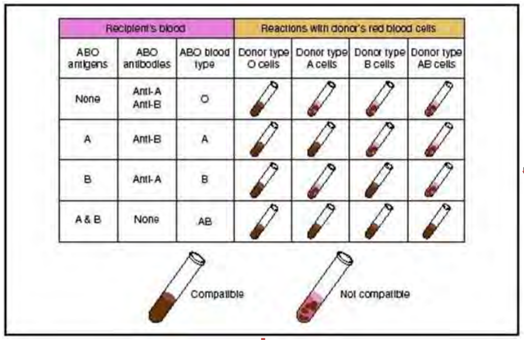


Used to detect bi-allelic polymorphisms

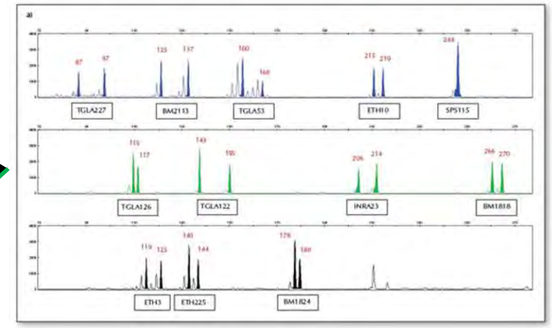
DNA could be obtained from any tissue

Ease of multiplexing, scoring, automation

Traditional Technology Transfer

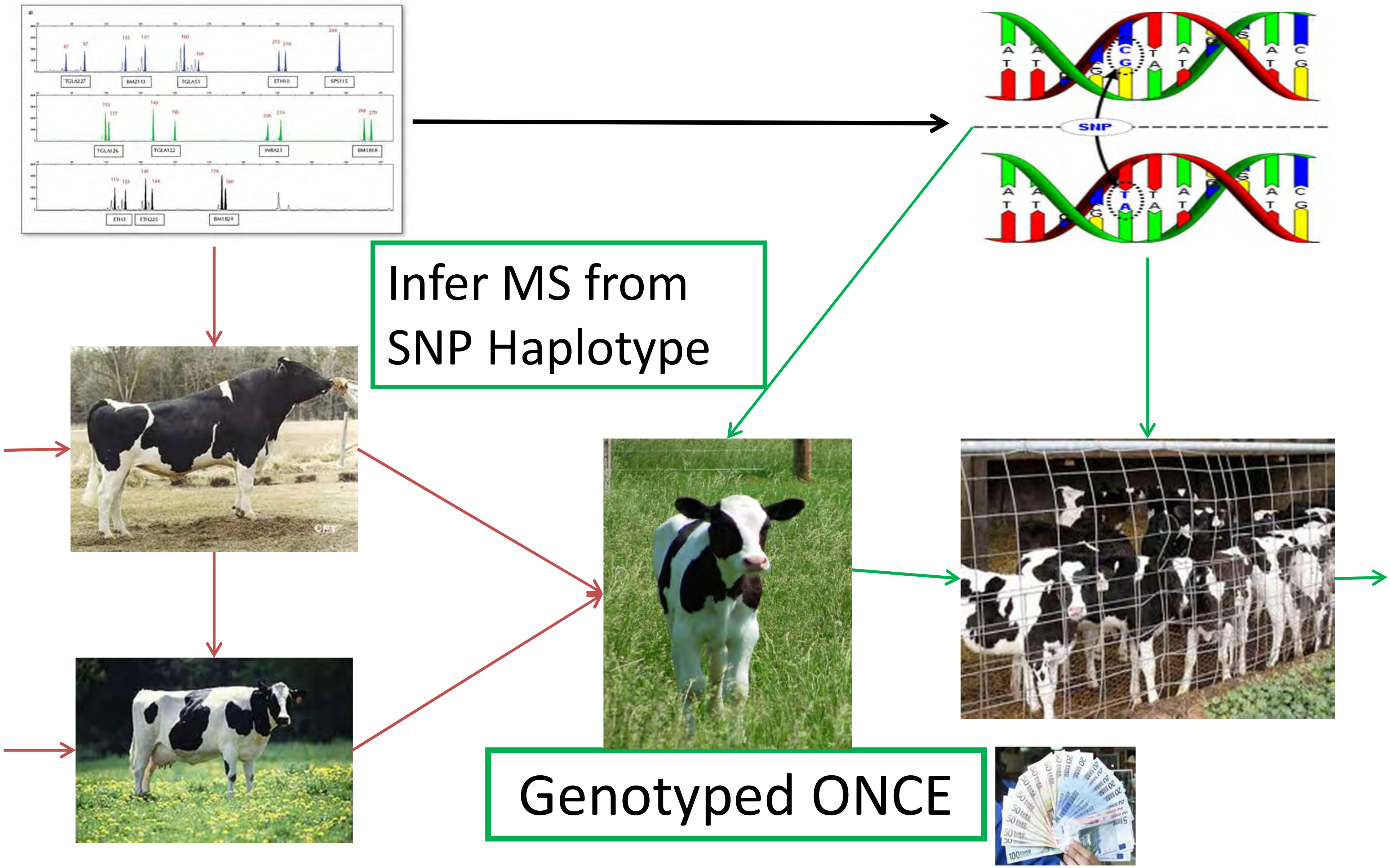


Recipient's blood			Reactions with donor's red blood cells			
ABO antigens	ABO antibodies	ABO blood type	Donor type O cells	Donor type A cells	Donor type B cells	Donor type AB cells
None	Anti-A Anti-B	O				
A	Anti-B	A				
B	Anti-A	B				
A & B	None	AB				

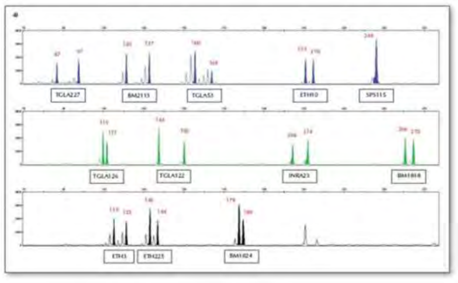


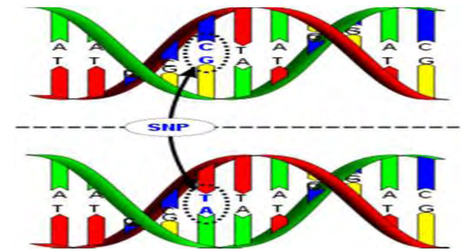
Genotyped TWICE $$

Technology Transfer via Imputation



Technology Transfer via Imputation



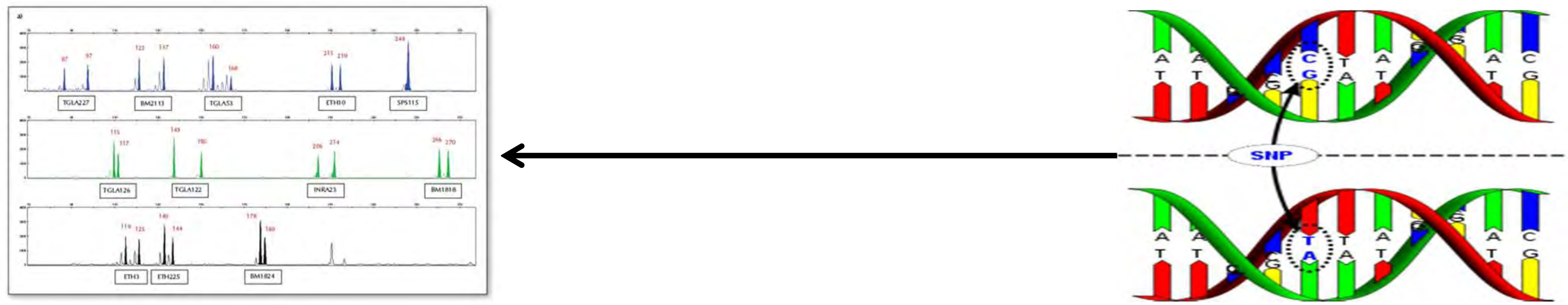


B	A	A	A	262	B	A	A	B	B
A	B	A	A	260	B	A	B	B	B

A	B	A	A	B	A	B	B
A	B	B	B	A	B	B	A

A	B	A	B	266	B	A	B	A	A
A	B	A	B	264	B	A	A	B	A

Impute ISAG cattle MS alleles from SNP



BM1818	INRA023
BM1824	SPS115
BM2113	TGLA122
ETH10	TGLA126
ETH225	TGLA227
ETH3	TGLA53

Method

347 cattle with ISAG MS and Illumina HDSNP data

Brown Swiss= 33

Holstein= 250

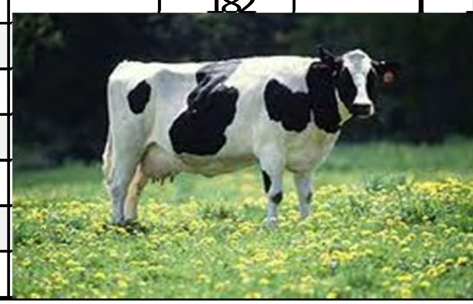
Guernsey= 16

Jersey= 48

SNP haplotype to MS allele

BM1824	Imputated Allele				
Haplotype	Brown Swiss	Guernesy	Holstein	Jersey	Overall
BABBAABBAAAABBBAABABABBBABBBAAAB	178	178	178	178	178
BAABAABBAAAABBBAABABABBBABBBAAAB					178
BBBBAABBAAAABBBAABABABBBABBBAAAB					178
BABBAABBAAAABBBAABABABBBAABBBBAB	178				178
BABBAABBAAAABBBAABABABBBABBBAABA	178				178
BAABBAABBAAABBBAABABABABABBBAAAB					178
BAABABABBAAABBAABAABABBBABAAAABA					180
BAABABABBAAABBAABAABABBBABBBAAAB					180
AABBAABBBAAABBAABAABABBBABBBAAAB					
AAAABAAABBABBAAABAABABABABAAAAAB					
AAAABAAABBABBAAABAABABABABAAAABA					
AAAABAAABBABBAAABAABABABABAAAAAA			182		182
BAABBAABBBABBBAABBABABABABABAAAA			182		182
AAAABAAABBABBAAABAABABABABABAAAA					182
BABBAABBAABAABBBBBBABAAAABABBBBBAB					182
BAAABABBAABAABBBBBBABAAAABABBBBBAB					188
BAABAABBAABAABBBBBBABAAAABABBBBBAB					_188
AABBAABBAABAABBBBBBABAAAABABBBBBAB	188				188
AAAABABBAABAABBBBBBABAAAABABBBBBAB	188				_190

B	A	A	A	262	B	A	A	B	B
A	B	A	A	260	B	A	B	B	B



A	B	A	B	266	B	A	B	A	A
A	B	A	B	264	B	A	A	B	A

SNP haplotype to MS allele

BM1824	Imputated Allele				
Haplotype	Brown Swiss	Guernesy	Holstein	Jersey	Overall
BABBAABBAAAABBBAABABABBBABBBAAAB	178	178	178	178	178
BAABAABBAAAABBBAABABABBBABBBAAAB			178		178
BBBBAABBAAAABBBAABABABBBABBBAAAB			178		178
BABBAABBAAAABBBAABABABBBAABBBBAB	178				178
BABBAABBAAAABBBAABABABBBABBBAABA	178				178
BAABBAABBAAABBBAABABABABABBBAAAB		178			178
BAABABABBAAABBAABAABABBBABAAAABA			180		180
BAABABABBAAABBAABAABABBBABBBAAAB			180		180
AABBAABBBAAABBAABAABABBBABBBAAAB				180	180
AAAABAAABBABBAAABAABABABABAAAAAB	180	180			180
AAAABAAABBABBAAABAABABABABAAAABA	182	182	182	182	182
AAAABAAABBABBAAABAABABABABAAAAAA			182		182
BAABBAABBBABBBAABBABABABABABAAAA			182		182
AAAABAAABBABBAAABAABABABABABAAAA				182	182
BABBAABBAABAABBBBBBABAAABABBBBAB		182			182
BAAABABBAABAABBBBBBABAAABABBBBAB			188		188
BAABAABBAABAABBBBBBABAAABABBBBAB		182	188		182_188
AABBAABBAABAABBBBBBABAAABABBBBAB	188			188	188
AAAABABBAABAABBBBBBABAAABABBBBAB	188	188	188_190	188_190	188_190

17% MS-SNP haplotypes identical across ≥2 breeds

Validate

Cattle with SNP and MS on self or parent

Brown Swiss= 71

Guernsey= 60

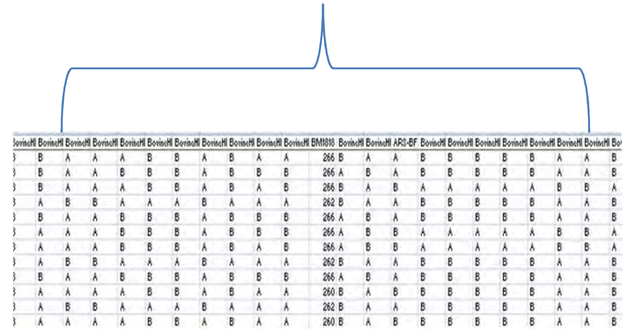
Holstein= 1110

Jersey= 60

Validate

Phase, impute, check

Phased Haplotype



The secret origin of cheese wiz

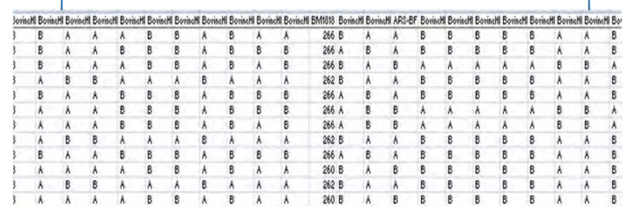
Validate

Phase, impute, check

316 SNP

BEAGLE

Phased Haplotype



BM1824	Imputated Allele				
Haplotype	Brown Swiss	Guernesy	Holstein	Jersey	Overall
BABBAABBAAAABBBAABABABBBABBBAAAB	178	178	178	178	178
BAABAABBAAAABBBAABABABBBABBBAAAB			178		178
BBBBAABBAAAABBBAABABABBBABBBAAAB			178		178
BABBAABBAAAABBBAABABABBBAABBBBAB	178				178
BABBAABBAAAABBBAABABABBBABBBAABA	178				178
BAABBAABBAAABBBAABABABABABBBAAAB		178			178
BAABABABBAAABBAABAABABBBABAAAABA			180		180
BAABABABBAAABBAABAABABBBABBBAAAB			180		180
AABBAABBBAAABBAABAABABBBABBBAAAB				180	180
AAAABAAABBABBAAABAABABABABAAAAAB	180	180			180
AAAABAAABBABBAAABAABABABABAAAABA	182	182	182	182	182
AAAABAAABBABBAAABAABABABABAAAAAA			182		182
BAABBAABBBABBBAABBABABABABABAAAA			182		182
AAAABAAABBABBAAABAABABABABABAAAA				182	182
BABBAABBAABAABBBBBBABAAABABBBBAB		182			182
BAAABABBAABAABBBBBBABAAABABBBBAB			188		188
BAABAABBAABAABBBBBBABAAABABBBBAB		182	188		182_188
AABBAABBAABAABBBBBBABAAABABBBBAB	188			188	188
AAAABABBAABAABBBBBBABAAABABBBBAB	188	188	188_190	188_190	188_190

Validate

Phase, impute, check

316 SNP

BEAGLE

Phased Haplotype

BM1824	Imputated Allele				
Haplotype	Brown Swiss	Guernesy	Holstein	Jersey	Overall
BABBAABBAAAABBBAABABABBBABBBAAAB	178	178	178	178	178
BAABAABBAAAABBBAABABABBBABBBAAAB			178		178
BBBBAABBAAAABBBAABABABBBABBBAAAB			178		178
BABBAABBAAAABBBAABABABBBAABBBBAB	178				178
BABBAABBAAAABBBAABABABBBABBBAABA	178				178
BAABBAABBAAABBBAABABABABABBBAAAB		178			178
BAABABABBAAABBAABAABABBBABAAAABA			180		180
BAABABABBAAABBAABAABABBBABBBAAAB			180		180
AABBAABBBAAABBAABAABABBBABBBAAAB				180	180
AAAABAAABBABBAAABAABABABABAAAAAB	180	180			180
AAAABAAABBABBAAABAABABABABAAAABA	182	182	182	182	182
AAAABAAABBABBAAABAABABABABAAAAAA			182		182
BAABBAABBBABBBAABBABABABABABAAAA			182		182
AAAABAAABBABBAAABAABABABABABAAAA				182	182
BABBAABBAABAABBBBBBABAAABABBBBAB		182			182
BAAABABBAABAABBBBBBABAAABABBBBAB			188		188
BAABAABBAABAABBBBBBABAAABABBBBAB		182	188		182_188
AABBAABBAABAABBBBBBABAAABABBBBAB	188			188	188
AAAABABBAABAABBBBBBABAAABABBBBAB	188	188	188_190	188_190	188_190

BM1824
178/180

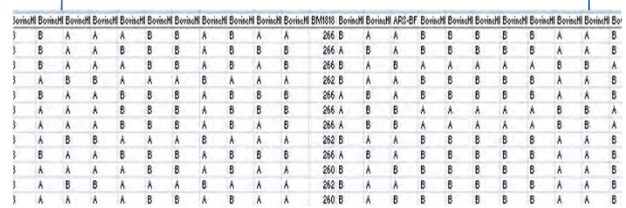
Validate

Phase, impute, check

316 SNP

BEAGLE

Phased Haplotype



>94% Two imputed alleles

>99% Parentage verified

BM1824

178/180

BM1824	Imputated Allele				
Haplotype	Brown Swiss	Guernesy	Holstein	Jersey	Overall
BABBAABBAAAABBBAABABABBBABBBAAAB	178	178	178	178	178
BAABAABBAAAABBBAABABABBBABBBAAAB			178		178
BBBBAABBAAAABBBAABABABBBABBBAAAB			178		178
BABBAABBAAAABBBAABABABBBAABBBBAB	178				178
BABBAABBAA	178				178
BAABBAABBA					
BAABABABBA					
BAABABABBA					
AABBAABBBA					
AAAABAAABB					
AAAABAAABB					
AAAABAAABB					
BAABBAABBB					
AAAABAAABB					
BABBAABBAA					
BAAABABBAA					
BAABAABBAA					
AABBAABBAA					
AAAABABBAA					

frontiers in GENETICS

ORIGINAL RESEARCH ARTICLE
published: 14 August 2012
doi: 10.3389/fgene.2012.00140

Imputation of microsatellite alleles from dense SNP genotypes for parental verification

Matthew McClure[1], Tad Sonstegard[1], George Wiggans[2] and Curtis P Van Tassell[1]*

[1] Bovine Functional Genomics Lab, United States Department of Agriculture, Agriculture Research Service, Beltsville, MD, USA
[2] Animal Improvement Program Lab, United States Department of Agriculture, Agriculture Research Service, Beltsville, MD, USA

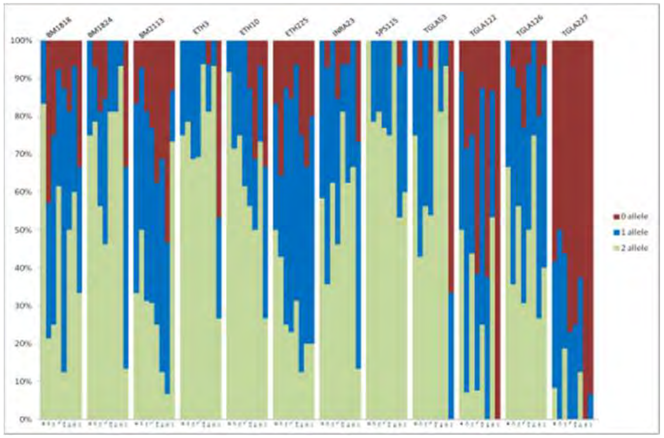
GENESEEK
a Neogen® Company

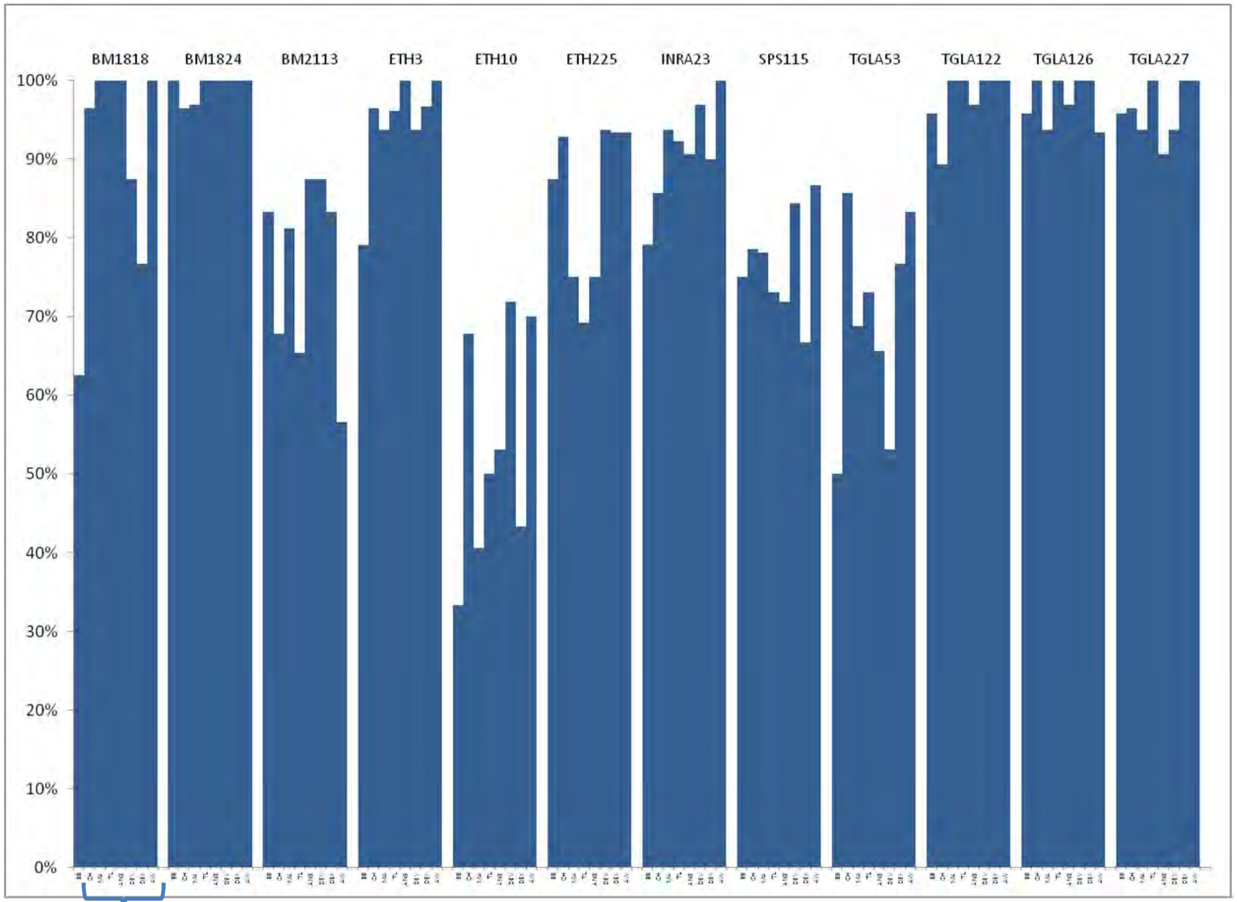
Beef Application????

- GeneSeek

- 8 beef breeds: 116 animals
  - Belgian Blue (12)
  - Charolais (14)
  - Maine-Anjou (16)
  - Texas Longhorn (13)
  - Angus (15)
  - Devon (16)
  - Dexter (15)
  - Ankole-Watusi (15)

Validation with DAIRY table





Order: Belgian Blue, Charolais, Maine-Anjou, Texas Longhorn, Angus, Devon, Dexter, Ankole

>71% imputed alleles

~46% 2 alleles

~31% 1 allele

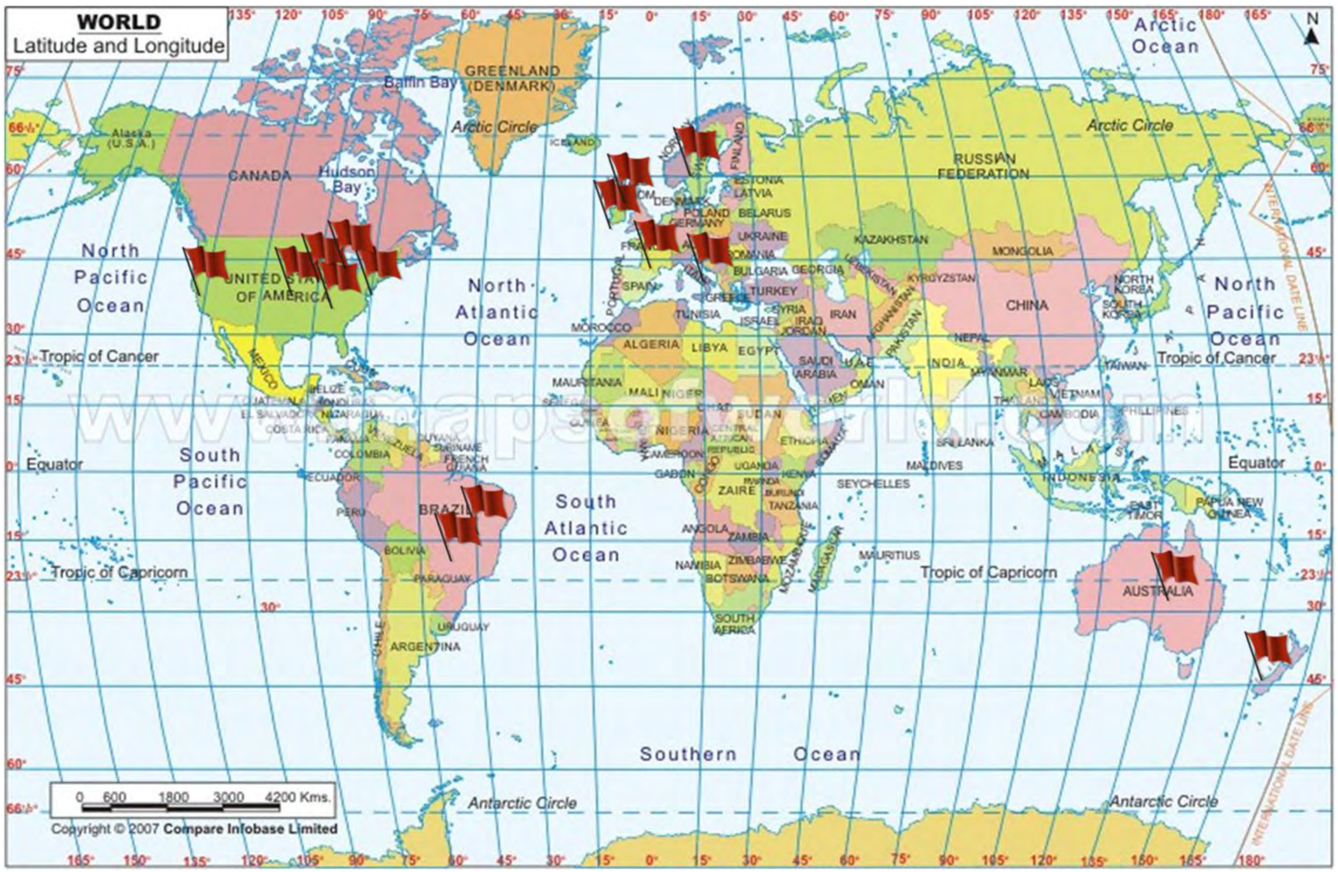
>86% Concordance

MS Imputation from SNP

Round 2

Matthew McClure, Tad S. Sonstegard, George R. Wiggans, Alison Van Eenennaam, Kristina Weber, M. Cecilia Penedo, Donagh P. Berry, John Flynn, Jose Fernando Garcia, Adriana Santana do Carmo, Luciana C.A. Regitano, Milla Albuquerque, Marcos V. Silva, Mike Coffey, Kristy Moore, Marie-Yvonne Boscher, Lucie Genestout, Raffaele Mazza, Jeremy Taylor, Robert Schnabel, Marcos Antonio Machado, **Barry Simpson, John C. McEwan, Andrew Cromie**, Luiz Lehmann Coutinho, Larry A. Kuehn, John W. Keele, Emily Kate Piper, Jim Cook, Elisa Marques

Microsatellite Imputation 2nd Study



Breed	SNP	SNP+MS
Abondance	172	165
Angus	623	235
Aubrac	239	234
Ayshire	523	86
Bazadaise	80	53
Beefmaster	36	36
Belmont Red	40	
Belgian Blue	210	12
Blonde D'Aquitain	225	201
Brahman	410	364
Brangus	13	13
Braunvieh	17	17
Bretonne Pie Noire	27	16
Brown Swiss	91	64
Brune Des Alpes	109	109
Charolais	1449	1109
Chiangus	19	0
Crossbred	506	3
Devon	16	16
Dexter	15	15
Fresian	163	35
Gasconne	142	142
Gelbvieh	44	0
Gir	209	101
Guernsey	110	18
Hereford	853	243
Holstein	2596	678
Jersey	87	131
Kerry	1	0
Limousin	2171	1572
Longhorn	13	13
Maine Anjou	38	16
Montbeliarde	257	251
Murray Grey	22	
N'Dama	24	0
Nelore	2659	135
Normande	256	242
Parthenaise	291	218
Pie Rouge Des Plaines	160	116
Piedmontese	24	17
Red Angus	61	47
Red Pie (italial)	2	0
Romagnola	23	23
Rouge Flamande	41	41
Salers	258	234
Santa Gertrudis	99	0
Sheko	18	0
Shorthorn	188	0
Simmental	907	324
Swedish Red	12	9
Tarentaise	167	155
Tropical Composite		336
Vosgienne	53	49
Watusi	15	15
TOTAL	**17138**	**8259**

Initial Results:

60-80 SNP/MS needed

Count	642	456	312	233	220	341	838	572	431
% allele max	1.00	1.00	1.00	0.99	0.99	0.97	0.99	0.96	0.93
	BBAAABA	AABBBAB/	AABBBAB/	AABAABB.	AABBBAB/	AABBBAB/	AABBBAB/	BBAAABA	AABAABB.
178	641	454			1		3	3	1
180		2	312		2		1	2	1
182	1			231	217	332	3	13	
184						8			
186								5	25
188				2		1	830	547	402
190							1	2	1
192									1

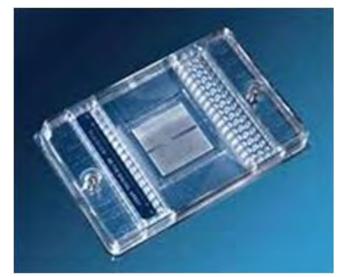
Initial Results

		642	456	312	233	220	341	838	572	431
breed	BM1824	BBAAABA	AABBBAB	AABBBAB	AABAABB	AABBBAB	AABBBAB	AABBBAB	BBAAABA	AABAABB
Angus	184						1			
Ayshire	184						6			
Abondance	186									22
Gelbvieh	186									2
Montbeliarde	186									1
TropicalComposit	186								5	
Abondance	188							2		70
Angus	188							42	2	47
Aubrac	188							10		1
Ayshire	188								4	
Bazadaise	188									
Beefmaster	188									
BelgianBlue	188							69	10	
BlondeDAquitain	188							18		31
Brahman	188							1	2	
Brangus	188									1
Braunvieh	188							2	2	
BretonnePieNoir	188							2	2	3
BrownSwiss	188							7		12
BruneDesAlpes	188							28		28
Charolais	188				2			23	40	8
cross	188							2		3
Freisan	188									
Gasconne	188							17		10
Gelbvieh	188							1		6
Guernsey	188							2		
Hereford	188							19	7	18
Holstein	188							11		
Jersey	188							4		
Limousin	188							213	397	41
Montbeliarde	188							147	1	11
Normande	188							3	2	14
Parthenaise	188							28	15	3
Piedmontese	188							2	1	3
PieRougeDesPlai	188						1		2	
RedAngus	188									18
RougeFlamande	188									6
Salers	188									
Shorthorn	188								1	
Simmental	188							79	32	7
Tarentaise	188							82		48
TropicalComposit	188							10	27	8
Unknown	188							2		1
Vosgienne	188							4		4

Producer Application

- Semi-custom SNP chips
  - MS imputation
  - Parentage verification
  - Genetic Improvement
    - Selection
    - Genetic Diseases

Utilize Microsatellite and SNP data



Acknowledgements

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  - Curt Van Tassell
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  - Derek Bickhart
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  - Euisoo Kim
  - Lakshmi Matukumalli

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  - Paul VanRaden
  - Dan Null
  - John Cole
  - George Wiggans
  - Tabatha Cooper

- Microsatellite
  - Bovine HapMap
  - Breed Associations
  - Sue Denise
  - Alison Van Eneenaam
  - Cecilila Penedo
  - John Keele
  - Mike Coffey
  - Marie-Yvonne Boshcher
  - Donagh Berry
  - Andrew Cromie
  - Fernando Garcia
  - Milla Albuquerqu
  - Luciana Regitano

Funding

USDA-ARS CRIS 1265-31000-098-00D

USDA-NIFA 1265-31000-098-42R

Developing a custom SNP chip for dairy and beef cattle in Ireland

Working group:

Mike Mullen[1], Donagh Berry[2], Sinead Waters[3], Paul Flynn[4], John Flynn[4], Rebecca Weld[4], Francis Kearney[5] and Andrew Cromie[5]

[1] *Teagasc, Athenry,* [2] *Moorepark,* [3] *Grange*
[4] *Weatherbys,* [5] *ICBF*

michael.mullen@teagasc.ie

Genomics – a new era for cattle breeding. Portlaoise, November 2012

Motivation

Parentage verification

BLAD
CVM
DUMPS…

Genomic selection

A1/A2
MSTN
DGAT1

It is now possible to develop an inexpensive technology to include all the above !!

Objectives

- Develop an inexpensive SNP chip for maximum exploitation of parentage verification and genomic selection in dairy and beef cattle
- Incorporate testing for known major genes / lethal recessives / congenital disorders
- Update annually

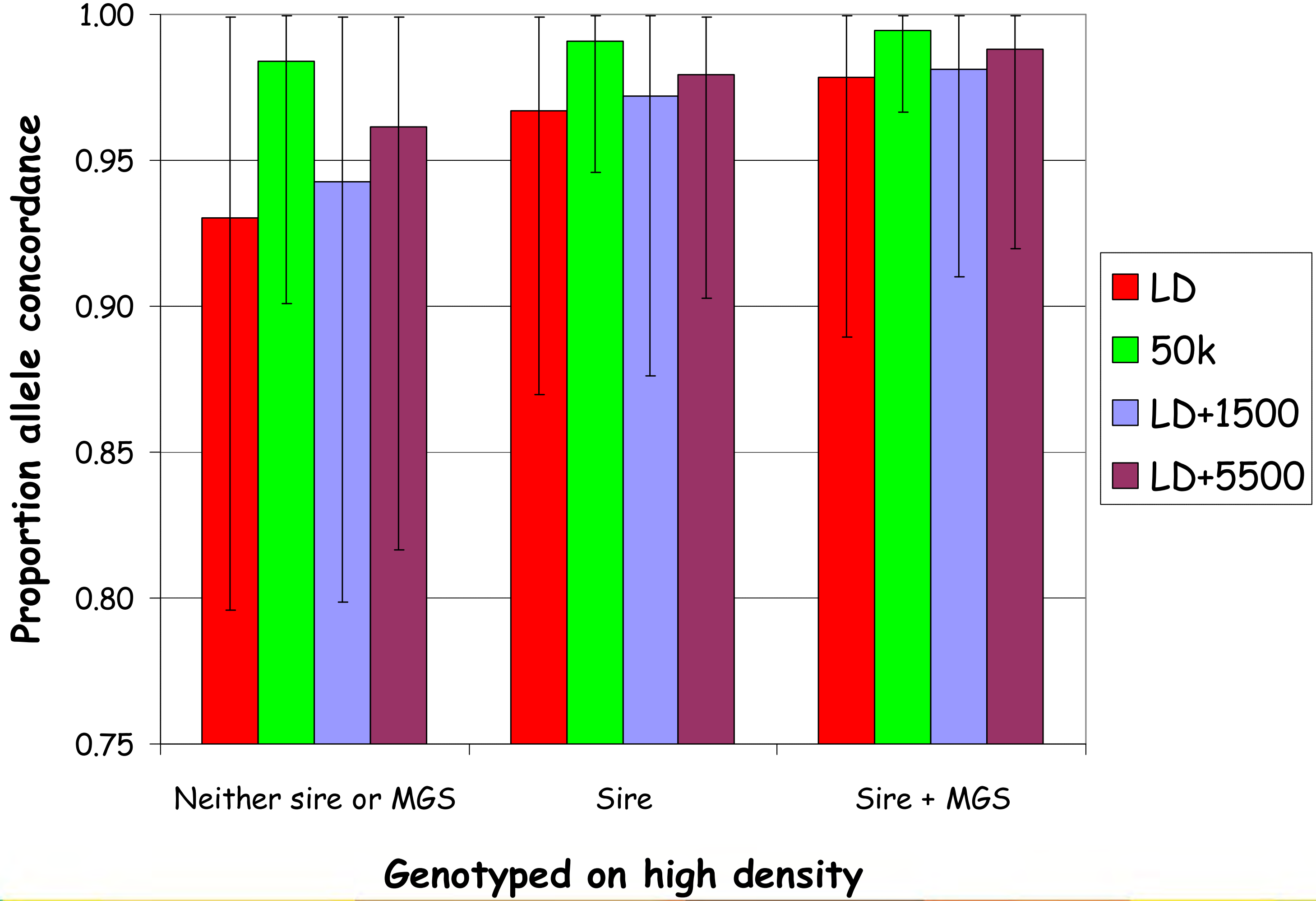
LD+ content (V1-19K)

- Genomic selection - imputation to HD ~12,500 SNPs
  - Standard ~7,000 Illumina LD 'base' panel
  - Additional ~5,500 for imputation
- Parentage ~2,500 SNPs
  - ~200 SNPs per microsatellite (n=12)
- Lethal recessives (n=4)
- Congenital disorders (n=35)
- Major genes (n=17)
- Research component <2,000 SNPs

Imputation to high density

- ~ 5,500 SNPs in addition to the base 7,000
- High frequency within our 3,124 HD genotyped beef and dairy animals
- Increased coverage at chromosomal ends
- SNPs as independent as possible

Imputation to HD



Parentage verification

- Imputation to microsatellites

ACAGCTATTGTACAGAGAGAGAGAGCTGCCTAGTAC

TCACCTATTCTACAGAGAGAG CTGCGTATTAG

"Tag" the microsatelites with SNPs in the vicinity

Lethal Recessives

- CVM
- BLAD
- DUMPS
- Brachyspina

Congenital defects

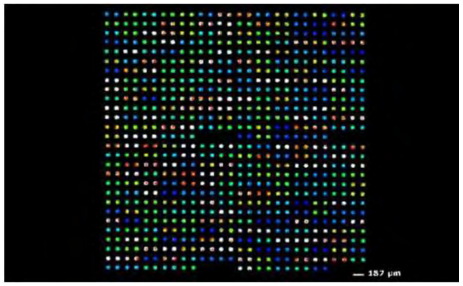
- 35 covered inc.:
  - Curly calf
  - Fawn calf
  - Spiderleg
  - Tibial Hemimelia
  - Hairlessness (Hypotrichosis)
  - Scurs
  - Mulefoot
  - Black/Red coat colour/Red factor
  - Red recessive coat colour

Major genes

- 14 major genes including:
  - MSTN
  - DGAT1
  - A1/A2 beta casein
  - Kappa casein
  - Fertility haplotypes
    - (HH1, HH2, HH3, JH1)

Research

- Goal – to identify novel functional SNPs and feed into genomic selection
- <2000 selected
  - Ongoing research in Teagasc on both dairy and beef cattle
    - novel mutations
  - Validation of previous mutations associated with performance



From just 1 hair sample!

Calf ID	CVM	BLAD	DUMPS	Brachyspina	A1/A2	DGAT1	Parentage	Suggested sire	GEBI
IE123 456	-	-	-	-	+/-	-	✓	n/a	€220
IE135 7911	-	-	-	-	-	+/-	X	BJY	€230

Time line and release

- First discussions – 10th September
- V1 – <u>January 2013</u>
- Updated annually with V2 – January 2014
  - V2 possibly 50K Affymetrix chip, could include more species…
    - Cattle
    - Sheep
    - Horses

Conclusions

- Custom chip - value for money
- Eliminating need for standalone testing
  - Lethal recessives/congenital disorders
  - Major genes and Fertility haplotypes
  - Parentage
  - Genomic selection
    - Improve existing LD chip imputation to HD
    - Research
- One-stop-shop for both dairy and beef cattle genotyping in Ireland

Acknowledgements

- **Chip design:**
  - Breed Societies and AI stations
  - Matt McClure, USDA
  - Paul VanRaden, USDA
  - Jon Beever, Illinois university
- **Bioinformatics support**
  - Chris Creevey, Teagasc Grange
- **Funding:**
  - Research Stimulus Fund (RSF-06-353; 11/S/112)
  - SFI (08/SRC/B1156)
  - Breed Societies and AI stations
  - ICBF & Teagasc

WEATHERBYS IRELAND
LIMITED

Implementation of Genomic Services

John M Flynn

ICBF & Teagasc Genomics Conference 14th November 2012

Basic function of the laboratory

- Genotyping and Parentage Analysis (Registration).
- Animal Identification/Forensic Cases.
- Species – Cattle, Horses, Sheep, Dogs, Pigs.
- Sample Source – Blood, Hair, Semen, Tissue, Ear Tags and Swabs.

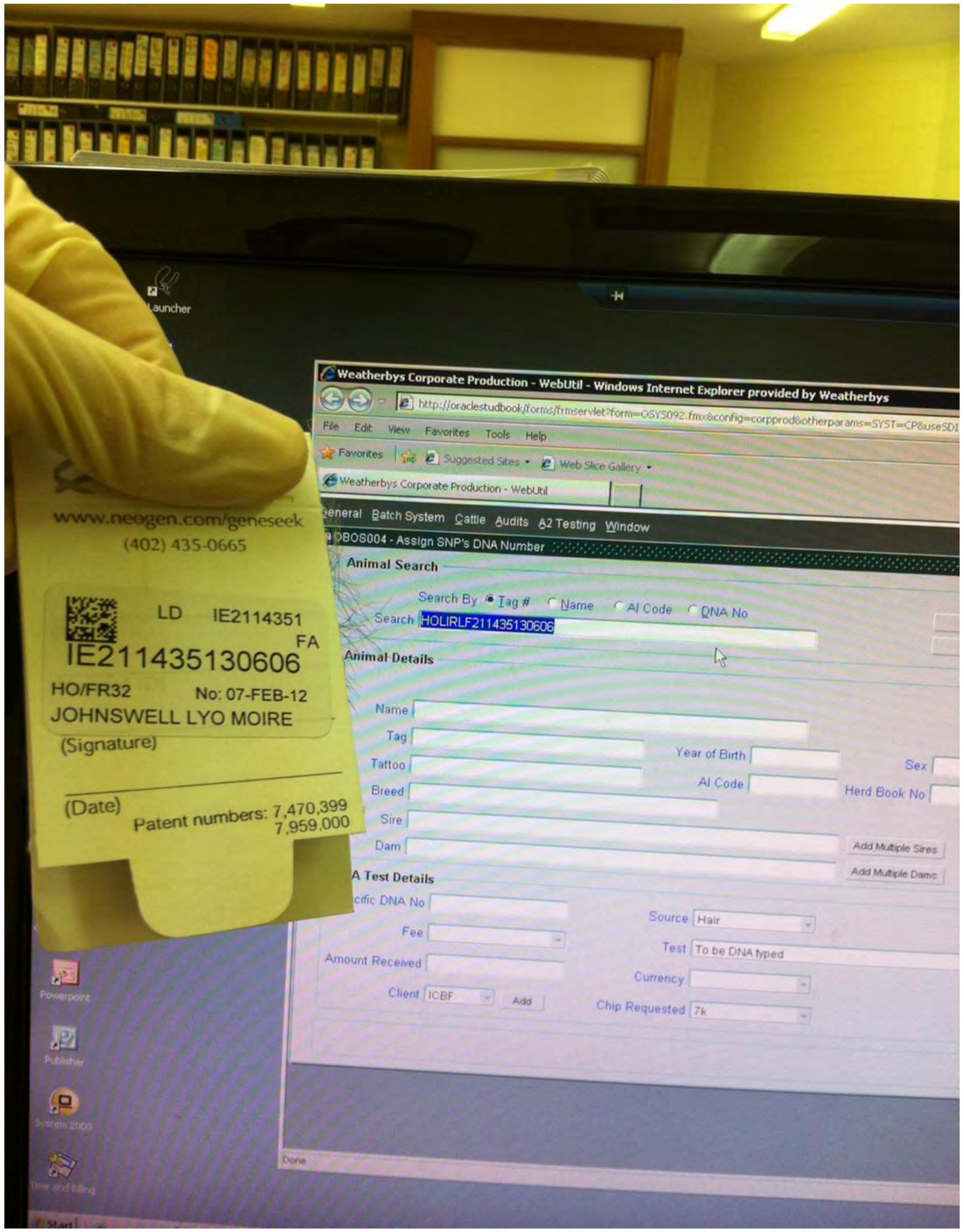
What is Genotyping?

- Identifying genetic markers inherited from Sire and Dam using DNA fragment analysis.
- Advent of PCR revolutionised molecular DNA technologies.
- Common markers used – microsatellites and single nucleotide polymorphisms (SNPs)
- SNPs are suitable for microarray chip technology, where in excess of 1 million SNPs can be genotyped.

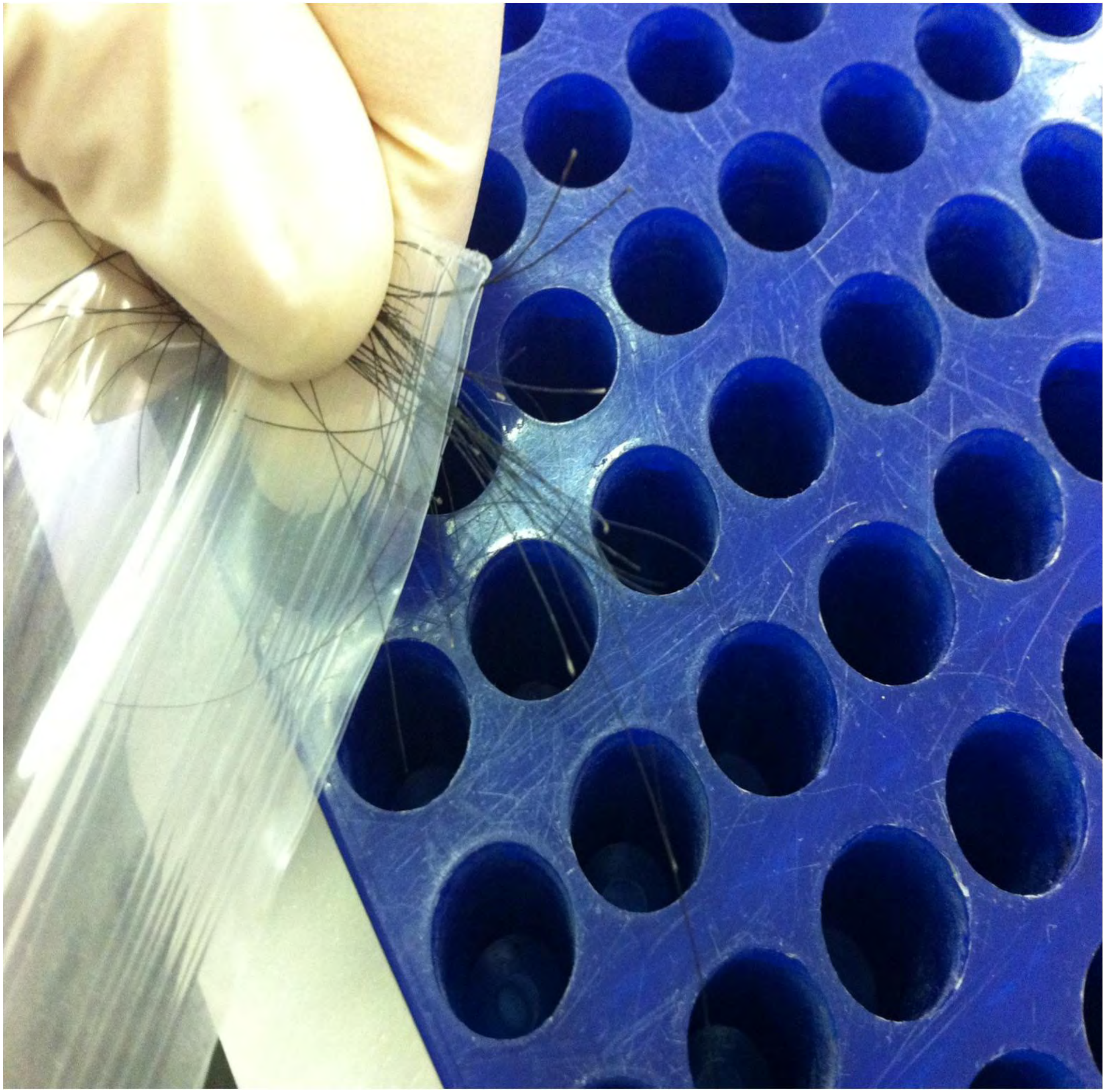
Benefit of SNPs

- As SNPs can be tested in such great numbers this provides the opportunity to detect particular patterns or genetic signatures throughout the genome that are associated with particular traits.
- This forms the basis for genomic studies.
- Going forward SNPs are the marker of choice for the overall benefit of the livestock industry.

Typical example of processing a Bovine Low Density (LD) SNP chip using Illumina Infinium® based Chemistry with hair samples.



Animal ID (ITT code) scanned from data matrix code & laboratory number assigned.



Good quality follicles
are essential.

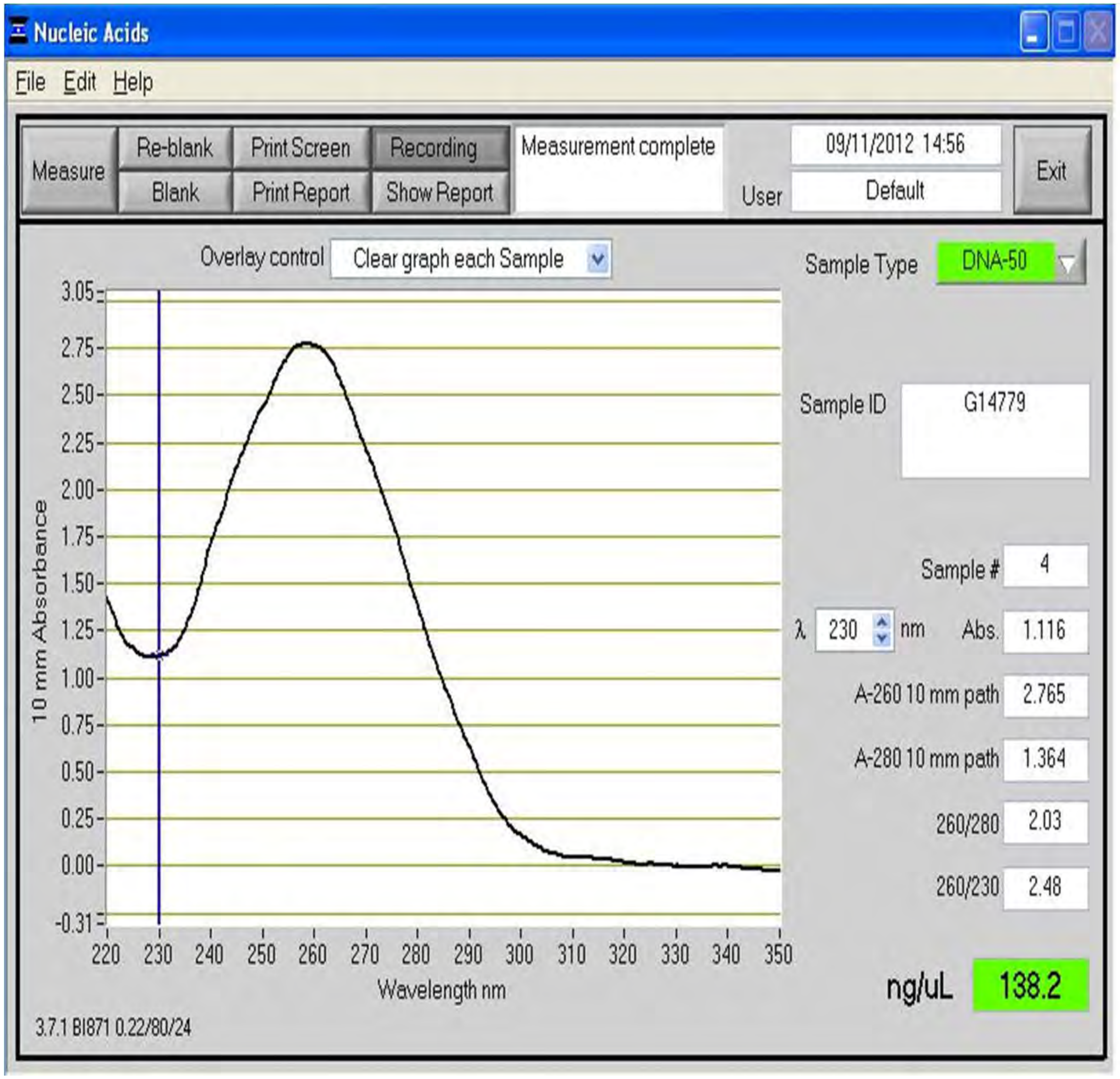
Clump of clean, dry good quality hair follicles .

Lysis solution added & incubated over night.

Transfer to 96 well extraction plate.

DNA Extraction using a commercial kit in a 96 well plate format.

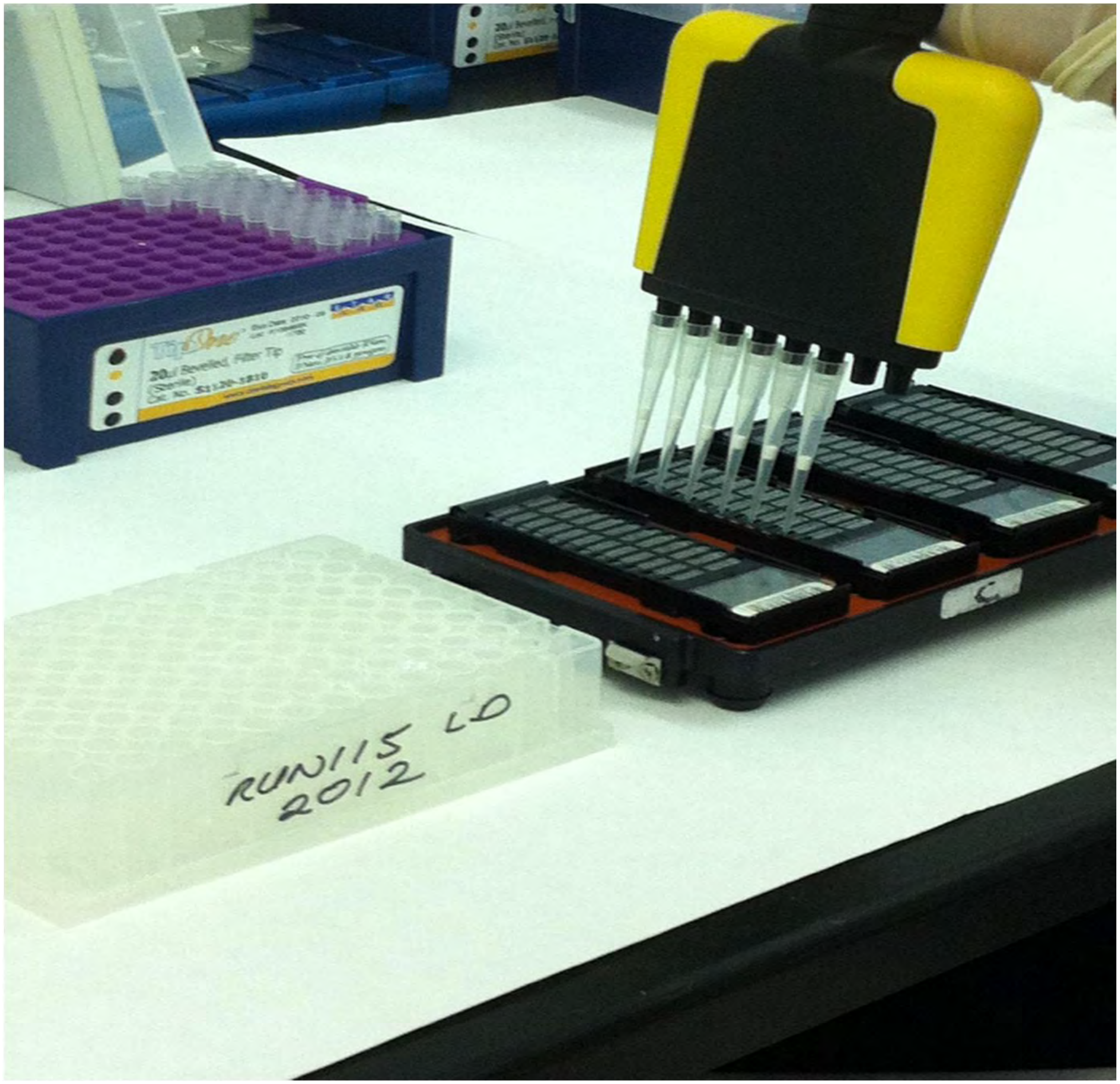
Extensive in-house optimisation to ensure good quality DNA.



<u>DNA QC</u>

Quantitation
>50ng/µl

Qualitation/Purity
260/280 ratio range 1.8-2.1



Whole genome amplification (approx 1000 fold) /over night.

DNA Fragmentation, precipitation & re-suspension.

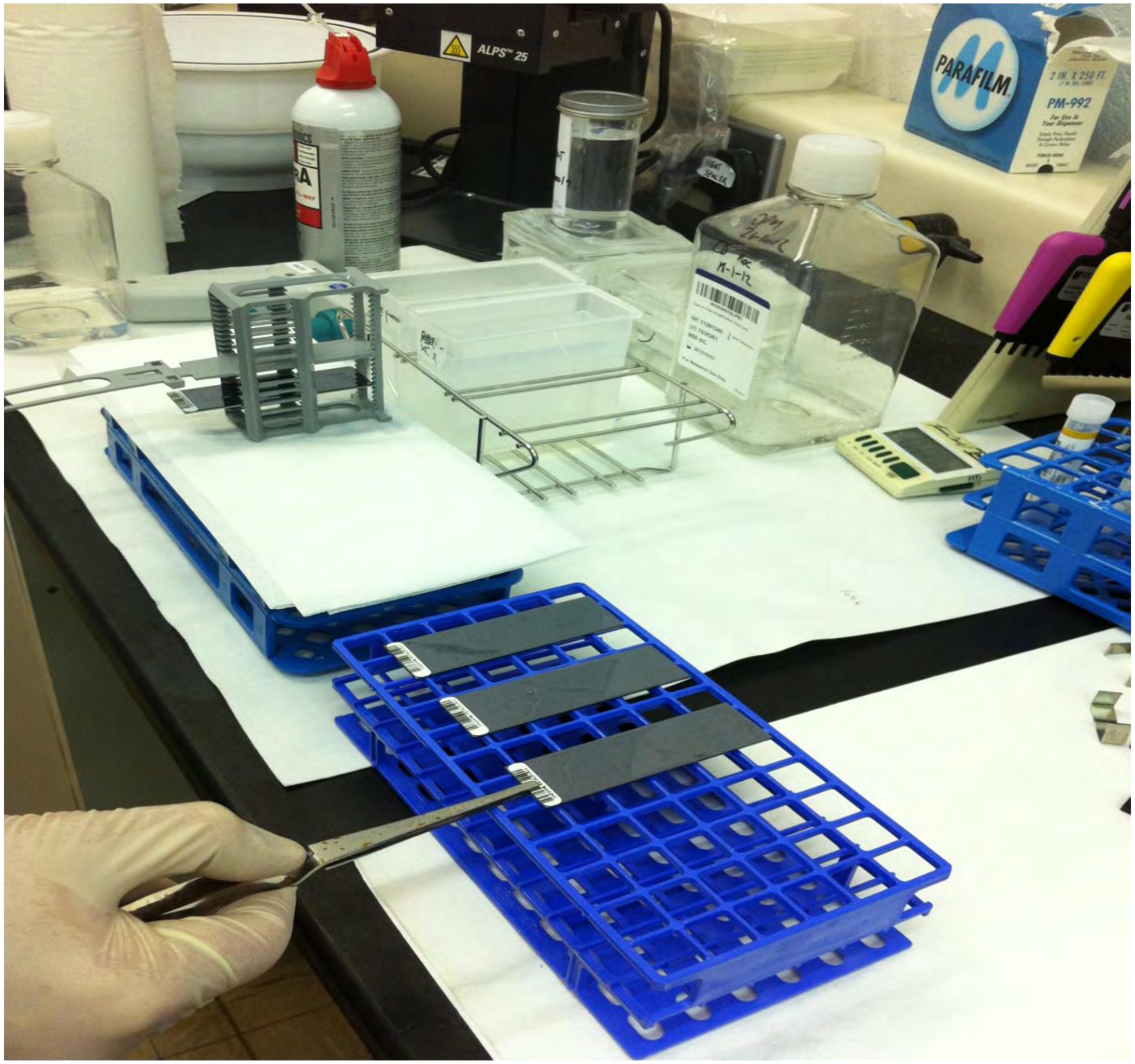
DNA added to chips.

DNA hybridisation to SNP beads over night.

One LD chip = 24 samples.

4 chips = 96 samples.

Staining of DNA products with Fluorophores.
Red/Green.
Approx 3.5 hours.



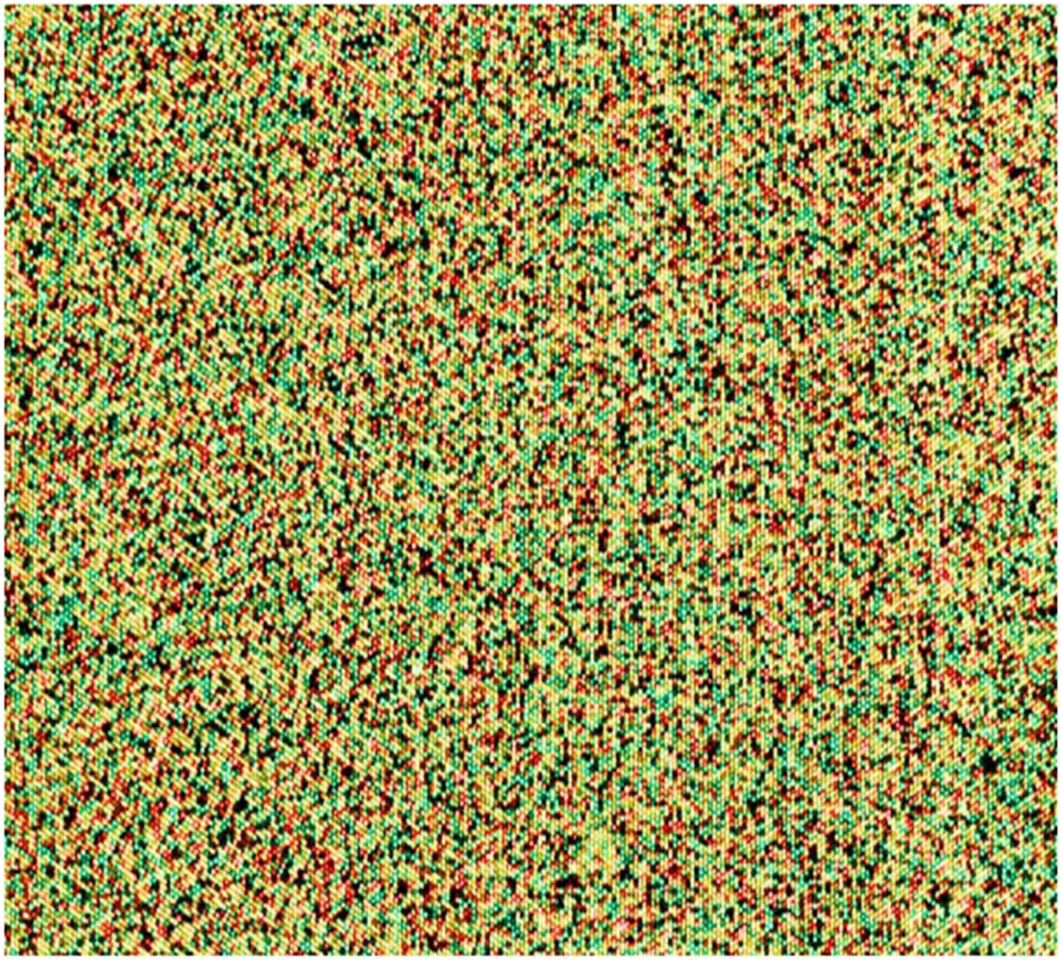
Chips washed and coated to preserve.

Chips dried in vacuum - 1 hour.

Load cassette for scanning .

Load iScan for imaging of chips.

Raw Intensity data for Bead Scan Image



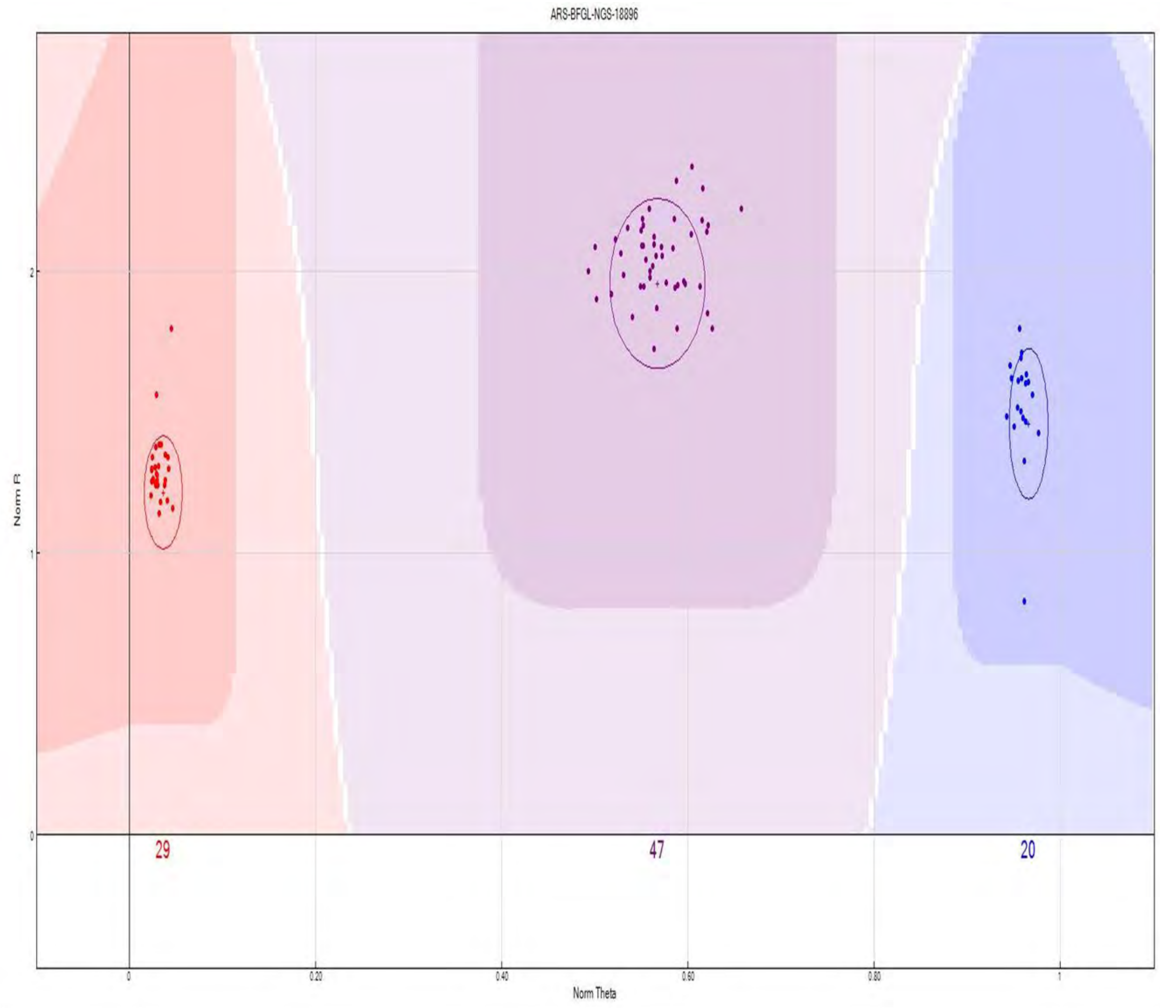
Bead scan image of the 7K SNPs for 1 animal (approx 30 bead replicates per SNP)

2 possible inherited alleles per SNP A or B

Red – (A/A)

Green – (B/B)

Yellow – (A/B)



Cluster analysis on the basis of the Intensity versus Dye colour.

Cluster plot for 1 SNP generated from bead image intensity data for 96 animals.

Genotype calls made for all 7000 SNPs using specific clustering regions ensuring high confidence in genotype calls.

- Report generation is carried out using GenomeStudio software.

- Report files uploaded to client via a secure FTP site.

- Normal throughput capacity per week (7 working days) = 864 animals.

- Can potentially be increased to 1728.

Work Flow Summary

- Sample assignment
- Hair cutting
- DNA extraction
- DNA QC
- Whole Genome amplification
- Fragmentation, precipitation & re-suspension.
- Hybridisation
- Staining
- Drying
- Imaging
- Data analysis
- Reporting
- Throughput

Future Strategy

- To design a low cost customised chip to cater for parentage, genomic evaluations and recessive trait screening.
- The logical approach is to pursue a SNP testing package that is affordable and informative for the industry.
- Cost is very much determined by demand.
- Commitment from the industry will help to aspire to this objective.

IRISH CATTLE BREEDING FEDERATION

Genomic Service Implementation

Mary McCarthy, Karl O’Connell & Francis Kearney

ICBF

mmccarthy@icbf.com

Wednesday 14th November 2012

National Development Plan

Transforming Ireland

Genomic Service History

- The ICBF Genomic Service provides parentage verification & genomic breeding values.
- DNA extracted from hair or other sample types.
- Analysed on a SNP chip.
- Launched in February 2011 using the Illumina Bovine 3K chip for male dairy animals mainly.
- December 2011 we advanced to the Bovine LD chip at no extra cost.
- Spring 2012 service provided for genotyping females.
- **Opportunity to genotype beef animals in 2013**

Genotyping Chips

- Illumina Bovine3K (2,900 SNPs) *Replaced*
  - €50 (all inclusive) Holstein Friesians
- Illumina BovineLD (6,900 SNPs) *Current*
  - €50 Holstein Friesian/Pure Friesian
  - Special offer on female genomics €30 (Full cohorts)
  - New Chip LD+ (19,000 SNPs) *Future*
- Illumina Bovine SNP50 (~54,000 SNPs) *Current*
  - €94 Pure Friesians where sire not already genotyped.
- Illumina BovineHD (777,000 SNPs) *Research*
  - *Beef animals-reference population.*

Current criteria

- Animals must be Holstein or Friesian and not more than 6.25% of a third breed or unknown.
- *HO (75%)- FR (21.88%)- UN (3.13%)* √
- *HO (75%)- FR (15.75%)- MO (9.25%)* ✗
  - The reference population consists only of these breeds.

- Pure Friesians (>75% Fr) can be genotyped on the 7k chip if the sire has already been done on the 50k chip. *Animal must be genotyped on the 50k chip otherwise.*
- **Changing soon to include beef animals.**

Sire and maternal grandsire must be recorded in the ICBF database.

User friendly, fully integrated, traceable process

1.
Animals are selected for genotyping and request submitted by web or phone

2.
Hair sampling kits generated and posted

3.
Samples collected, returned for QA, tracking & dispatched to lab regularly.

4.
Laboratory extracts DNA and its analysed on the SNP-chip

5
Genotypes received into the database

6.
Files loaded to the database. Animals validated, sires checked and tracking updated

7.
Animal groups are extracted for evaluation

8.
Genomic breeding values are computed.

9.
Genomic EBI's are published and reports generated

ICBF DATABASE

Users

- Artificial Insemination Companies.
  - A file of recently registered male calves is sent from ICBF each week.
  - Animals are selected for genotyping with a view to purchase for entry into an AI station.

- Herd-owners signed up to HerdPlus®
  - This is ICBF’s breeding information service.

- Breed Societies.

AI Company/Breed Society Order Screen

Enter animal number to validate tag-choose chip type and sample type and submit order.

This generates a request for a sample kit to be issued from ICBF.

BACK

Request Animal to be Genotyped

Enter Animal Number: IE151013781535

Animal Eligible for Genotyping

Name	Breed	Sire	Owner Name	Herd No.
	HO (84.38%), FR (15.63%)	SFW	KEVIN DOWNING	IE1510137

Chip Type: LD

Sample Type: HAIR

Submit

By Clicking Submit you are requesting a sample kit to be issued from ICBF

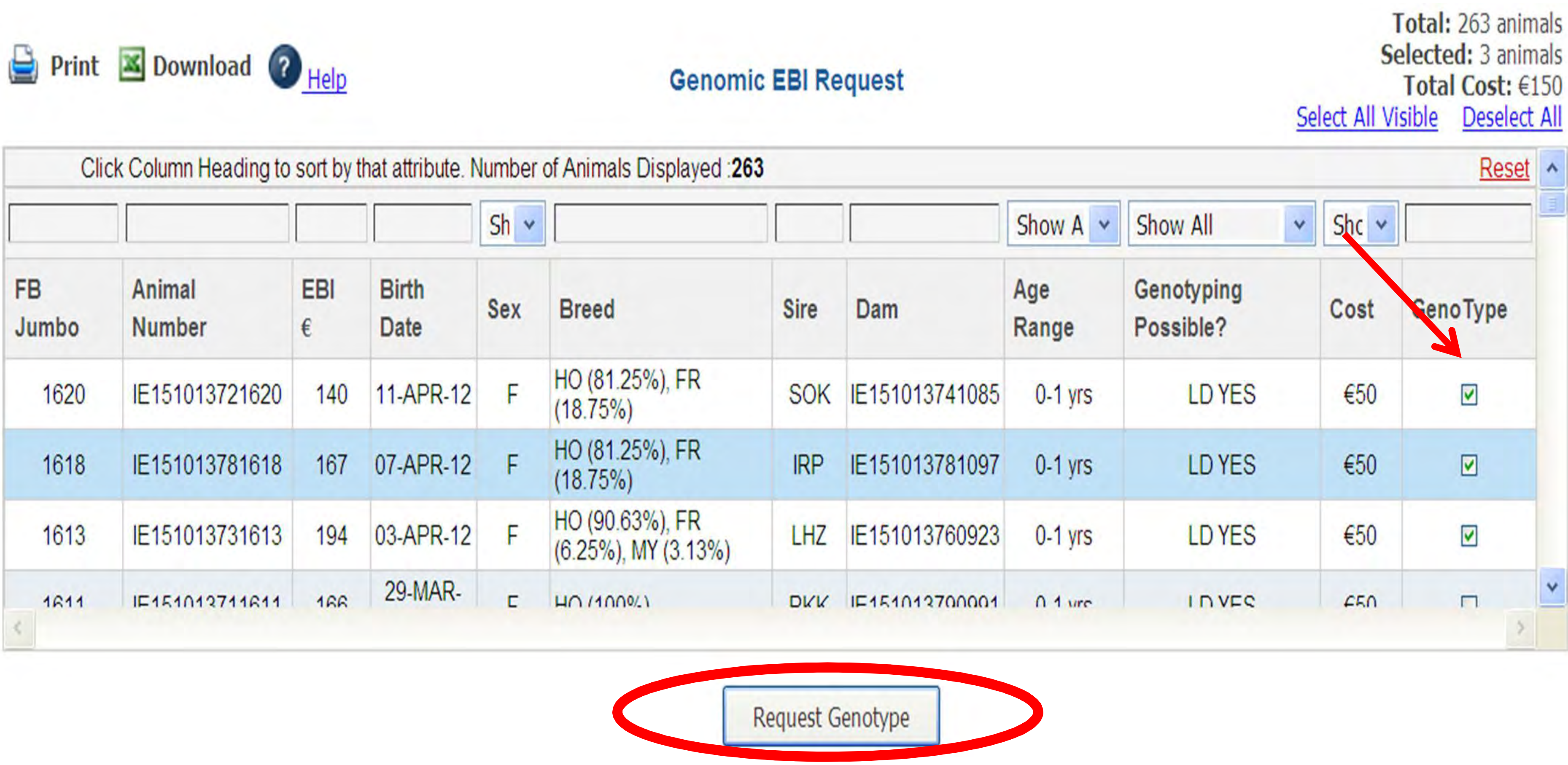
ICBF.com

HerdPlus® User screen

Select Genomics Link and Place Order

HerdPlus® User genotype request screen.

-Tick the required eligible animal from this online profile.



ICBF.com

Genotype Orders

- After the orders are received, hair kits are mailed directly to the herd-owner.
- Pack contains:
  - Hair sampling cards, 1 per animal, barcoded with the full International number.
  - Hair collection instructions
  - Cover letter.
  - Return using prepaid envelopes.

Hair collection instructions

1. Check that the animal identification on the label collection card perfectly matches the ID of the animal (see Figure 1).

Figure 1

2. Hair samples should be pulled from the end of the tail.

3. The hair must be clean and dry with <u>the roots</u> attached.

4. Extreme care must be taken to avoid contamination of hair roots from one animal to another.

5. Make sure that the hair samples have follicles as it is the <u>root</u> follicles that contain the DNA and not the hair itself. 40 to 60 root follicles are required for each sample.

Sample Receipt

- Hair samples and contracts are returned by the herd-owner.
- The samples and contracts are scanned into the database. Samples are posted to the lab weekly.

Record Received Hair Samples

Box Number: 132-2012 FIND

Total: 20 samples

Tag	Details
HOLIRLM30101717121	n/a
HOLIRLM30101716121	n/a
HOLIRLM28156542082	n/a

AI Company Contracts

- AI companies request an animal genotype.
- In the case of multiple companies requesting the same animal:
  - one hair card
  - An AI Company letter and contract for each company
- The owner returns one contract per animal.
- The contract indicates the organisation that is to receive the genotype.

NCBC Ireland Genetics

The National Cattle Breeding Centre (NCBC)
Bull Calf Contract 2012

12

I (Name, Address ....

and Herd Number ....)

1. Agree to allow NCBC genotype the BULL Calf tag number

I	E											

Born on .... (and who's Dam is tag number

IE.................................. and sire is A.I.Code............)

2. I agree to retain the calf in good health until it's Genomic breeding value is known.
3. If selected I agree to sell the calf to NCBC for a fee based on the calf's EBI.
4. If selected and subject to meeting health requirements, NCBC agrees to purchase the bull calf.
5. If not selected into the breeding programme, NCBC will pay the breeder €100 and release the breeder of all NCBC claims to the calf.

Dovea GENETICS

November 14th 2012

National ID: IE1234567

JOHN FARMER
HIGHFIELD HOUSE
BANDON
CO. CORK

GENOTYPING SERVICE

Dear Herd-owner,

Many thanks for agreeing to genotype your bull calf with Dovea Genetics.

Please find enclosed:

- 1 Hair sampling card per animal, labelled with the animal details.

GENESEEK
a Neogen Company
www.neogen.com/geneseek
(402) 435-0665

(Name)

LD IR171395
EU
IE351257572047
HOLSTEIN No: 31102012

(Date)
Patent number: 7,470,399

EUROGENE AiSERVICES (IRELAND) LTD
CARRIGEEN INDUSTRIAL ESTATE,
CAHIR, CO TIPPERARY
IRELAND
TEL: + 353 (0) 52 74 42940
FAX: + 353 (0) 52 74 45731
E-mail: tom@eurogeneaiservices.com

eurogene aiservices IRELAND Ltd

Re: Letter of Offer for a High Genomic Bull Calf

Dear Sir,

I am pleased to inform you that your calf meets Eurogene Ai Services Irl. Ltd.'s required selection criteria to be eligible for entry to our Irish Breeding Programme.

GENESEEK
a Neogen Company
www.neogen.com/geneseek
(402) 435-0665

(Name)

(Animal ID)

(Signature)

(Date)
Patent number: 7,470,399

Results/Evaluations

- The labs automatically transmit the results to the ICBF database.
- Results are loaded, animals validated, sires checked and tracking updated.
- Results with low call rates <90% are discarded and retest kits issued.
- Valid animals with valid genotypes are evaluated and GEBI's are generated.
- Results are published and reports generated.

Genomic Evaluation Report

Clients receive a report for each animal via the web or post

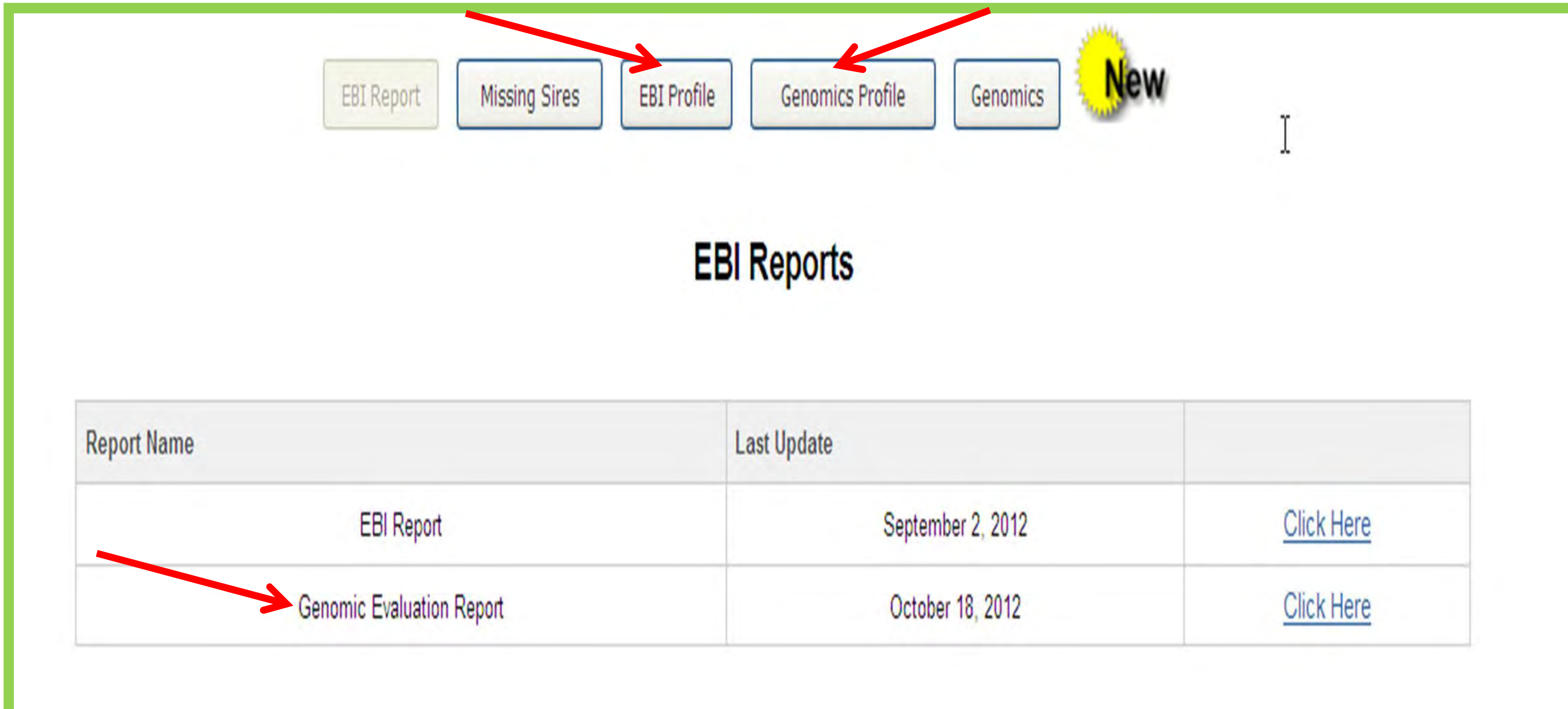
Genomic Evaluation Report

Jumbo	1563	**Lact. No**	
Tag	IE151013731563	**Sex**	M
Name		**Sire**	LHZ (€ 248)
DOB	13-Feb-2012 0y 2m	**Dam**	IE151013721067 (€ 141)
Breed	HO (91%), FR (9%), MY (3%)	**Dam's Sire**	HFL (€ 170)
Date of Evaluation	11-Apr-2012		

Index	**Official Genomic Evaluation**	**Reliability**	**Weighting on Genomics**	**DNA Value**	**Parent Average Evaluation**	**Reliability**	**Diff.from Parent Avg**	**Increase In Reliability**
EBI €	**255**	**46%**	31%	235	191	26%	+64	20%
Milk Sub Index €	**90**	**54%**	39%	82	80	31%	+10	23%
Fertility Sub Index €	**151**	**38%**	26%	140	93	19%	+58	19%
Calving Sub Index €	**26**	**52%**	24%	22	27	36%	-1	16%
Beef Sub Index €	**-20**	**37%**	24%	-17	-15	21%	-5	16%
Maintenance Sub Index €	**16**	**39%**	26%	15	11	22%	+5	17%
Health Sub Index €	**-7**	**49%**	40%	-6	-6	24%	-1	25%
Milk Sub Index								
Milk (Kg)	**156**	**54%**	39%	113	257	31%	-101	23%
Fat (Kg)	**12.7**	**54%**	39%	11.2	14.1	31%	-1.4	23%
Protein (Kg)	**14.5**	**54%**	39%	12.9	14.3	31%	+0.2	23%
Fat (%)	**0.12**	**54%**	39%	0.13	0.09	31%	+0.03	23%
Protein (%)	**0.18**	**54%**	39%	0.17	0.12	31%	+0.06	23%
Fertility Sub Index								
Calv Int (Days)	**-9.16**	**40%**	28%	-8.6	-5.52	21%	-3.64	19%

VIEW YOUR RESULTS

Genomic Evaluation Reports/ EBI & Genomics profiles/Bull Search



EBI Reports

Report Name	Last Update	
EBI Report	September 2, 2012	Click Here
Genomic Evaluation Report	October 18, 2012	Click Here

Track your order

All the different stages from date requested to genotype published can be tracked by the user who placed the order.

Click on animal link to view status of result.

BACK

Genotype Request Tracking

Search for samples by herd number, animal number or batch number: Go

OR

Search for samples requested between two dates. Start Date: 16-Dec-2011 End Date: 16-Dec-2011 Go

Print Download Help

Click Column Heading to sort by that attribute. Number of Batches Displayed :43 Reset

Date Requested	Herd	Owner	Animal Number	Sex	Breed	Sample	Org	Sent to Farm	ICBF Received	Sent to Lab	Chip	Genotype Received	Genotype Published
16-DEC-11	IE1510137	Kevin Downing	IE151013771393	F	HO	HAIR	FA	16-DEC-11	30-JAN-12	30-JAN-12	LD	20-FEB-12	01-MAR-12
16-DEC-11	IE1510137	Kevin Downing	IE151013751400	F	HO	HAIR	FA	16-DEC-11	30-JAN-12	30-JAN-12	LD	20-FEB-12	01-MAR-12
16-DEC-11	IE1510137	Kevin Downing	IE151013711405	F	HO	HAIR	FA	16-DEC-11	30-JAN-12	30-JAN-12	LD	16-FEB-12	24-FEB-12
16-DEC-11	IE1510137	Kevin Downing	IE151013781411	F	HO	HAIR	FA	16-DEC-11	30-JAN-12	30-JAN-12	LD	20-FEB-12	01-MAR-12

Turnaround Times

- 23 days for AI requested animals
  - Date hair sample received to results

- Farmers returning samples is longest step in the process (average = 12 days)

Incorrect Sires

- Animals that have incorrect sires are identified.
  - Currently 7.5% error rate on sire.
- These are checked against sires in the database.
- Reduces error rate down to 1.5%.
- Changes are made and farmers and Breed Societies notified. Unassigned sires are likely to be un genotyped stock bulls.

	% WRONG SIRE	% SIRE ASSIGNED	% SIRE REMOVED
MALES	7	76	24
FEMALES	8	73	27

Number of animals genotyped

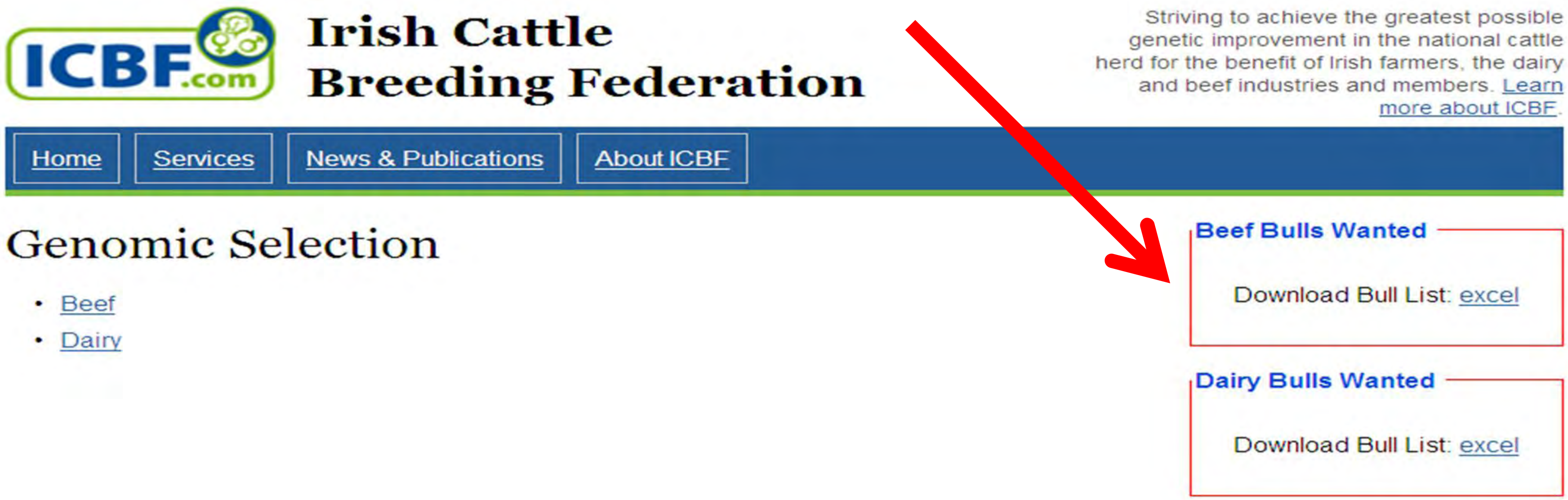
Chip Type	AI Companies 2011	AI Companies 2012	Farmers 2011	Farmers 2012	Others 2011	Others 2012	Totals
3k	1,768	35	351	10	297	0	2,461
7k-LD	6	3,301	0	6,587	20	496	10,410
54k	117	240	46	2	54	27	486
800K-HD	0	0	0	0	1,999	781	2,780
Totals	1,891	3,576	397	6,599	2,370	1,304	
Overall animals genotyped =16,137							

BEEF BULLS WANTED

Large reference population needed for each breed to estimate the genetic marker (SNP) effects.

LIST OF BEEF BULLS WANTED

Contact ICBF on 1850 600 900 if you have any of these straws



ANALYSIS OF MAIN BEEF BREEDS IN MASTERFILE ABOVE			
BREED	HD GENOTYPES	HAVE DNA	WANT
AA	364	63	268
CH	866	192	403
HE	284	44	426
LM	951	163	203
SI	343	40	176

Future

- Sample type will continue to be hair in 2013

- Ear tags may be used in 2014
  - Either a voluntary double DNA tag or a BVD sample tag

- Research on providing genomic breeding values for other dairy breeds is underway.

- **Spring 2013, service will be available for beef animals.**

Thank you

IRISH CATTLE BREEDING FEDERATION

Role of Genomics in Irish Dairy and Beef Breeding Programs. Part I. Parentage Verification.

Andrew Cromie, ICBF.

12th November 2012.

National Development Plan

Transforming Ireland

Genomics & Breeding Programs

- Genetic improvement (€);
  - Quality & quantity of data (***ID, ancestry*** & performance).
  - Profit based genetic indexes (EBI & €uro-Stars),
  - ***Selecting the best*** to breed the next generation.
- Focus on two areas; ***(i) parentage verification*** and (ii) genetic gain.

Pedigree beef registrations (2011).

Herbook Association	Births	Males	DNA	DNA/males
Belgian Blue Cattle Breeding Sc	855	424	316	75%
Irish Aberdeen Angus Associati	1,283	678	102	15%
Irish Angus Cattle Society				
Irish Aubrac Cattle Society	488	149	70	47%
Irish Blonde d'Aquitaine Breed C	433	195	48	25%
Irish Charolais Cattle Society	9,263	4,798	743	15%
Irish Hereford Breed Society	3,124	1,649	318	19%
Irish Limousin Cattle Society Ltd	8,483	4,246	906	21%
Irish Parthenaise Cattle Society	285	136	23	17%
Irish Piemontese Cattle Society	197	85	55	65%
Irish Simmental Cattle Society L	2,142	1,047	196	19%
Irish Speckle Park Cattle Societ	43	23	32	139%
Irish Shorthorn Cattle Society	1,104	290	54	19%
Saler Cattle Society	736	322	82	25%
Total	**28,436**	**14,042**	**2,945**	**21%**

- ~3k pedigree animals were DNA'd in 2011 with micro-sattelites.
- Combination of; (i) random, (ii) ET's, and (iii) sire now has pedigree progeny.
- Linked to males.

Pedigree dairy registrations (2011)

Herbook Association	Births	Males	DNA	DNA/males
Jersey Cattle Society of Ireland	440	35	25	71%
Irish Holstein Friesian Associati	79,896	5,476	7,907	144%
Irish Normande Cattle Society				
Kerry Cattle Society of Ireland				
Meuse Rhine Issel Cattle Socie	85	30		0%
Montbeliard Cattle Society	380	16	29	181%
Norwegian Red Cattle Society	254	64	16	25%
Total	**81,055**	**5,621**	**7,977**	142%

- ~8k pedigree animals were DNA'd in 2011 with micro-sattelites.
- IHFA insist on all pedigree males being DNA'd (part of cost of registration).

Pedigree registration & parentage verification.

- Part of "quality assurance" aspect of herdbook (~20% calves).
  - Still high level of errors (~5-10%).
- Seen as a "cost" rather than a benefit.
  - ~€120k in beef herds & ~€200k in dairy herds.
- What are the additional costs of moving to SNP's?
  - Initial focus on beef. Dairy is much simpler!

Moving Beef to SNP's for parentage verification.

Breed	Ped Males	Sire with SNP's	Sire with Microsat	Sire with SNP's and/or microsat	% total
AA	2,235	621	1,564	1,744	78.0%
AU	149	16		16	10.7%
BA	195	15	114	125	64.1%
BB	424	77	48	105	24.8%
CH	4,798	2,816	3,044	4,214	87.8%
HE	1,649	576	1,207	1,461	88.6%
LM	4,246	1,962	2,193	3,368	79.3%
PI	85	2		2	2.4%
PT	136	32	55	73	53.7%
SA	322	77	190	229	71.1%
SH	290	40	136	173	59.7%
SI	1,047	665	754	942	90.0%
SP	23				
Total	15,599	6,899	9,305	12,452	79.8%

- Of the 15.5k pedigree beef males born in 2011, 45% already have their sire genotyped.
- 80% have their sire genotyped or we can "predict" parentage SNP's from micr0-sattelites.
- Compelling case to move to SNP's.

Moving industry to SNP's (process).

1. Pedigree registration through Animal Events.
2. Database generates DNA kit to farmer.
3. Farmer returns DNA kit to HB/ICBF, with payment.
4. HB/ICBF forward hair samples to Weatherby's.
5. Weatherby's extract DNA. Generate genotype. Parentage verification off ICBF database. Database confirms parentage, suggests alternative or generates error. HB/ICBF communicate with farmer.
6. Valid registration, load to ICBF database & generate genomic index. Invalid registration, follow up by HB/ICBF.
7. HB generates pedigree cert & completes charge for service.
8. ICBF & HB generate genomic report. Posted on websites

Moving beef industry to SNP's for males (costs)

- Proposition to move all pedigree beef males to "new" genomic service.
- 15k pedigree males in 2013.
- "Full cost" of service = €40/animal (chip, extraction, post, pack, administration, gen EBI & initial 20% errors) = €600k.
- Beef farmers currently paying €120k (for MS based services). How do we "close the gap"?
- Establish a 5 year plan, including relevant funding models.

Moving IHFA to SNP's for males.

- Of the 5.5k pedigree males born/annum, 10% are genotyped, 56% sires are genotyped & 97% sires have a genotype or micro-satellite.
- IHFA already undertaking parentage verification on 100% males.
  - No "long-term" impact on male registrations.
  - Part of overall registration fee.
- Opportunity for "seamless" move to SNP's. More benefits for members.
  - Suggested sires with SNP's, MGS validation.
- Other dairy breeds – follow beef model.

Quantifying the Benefits. A quick summary.

- Parentage verification on all breeding males.
- Major genes & recessives.
  - Screening out & new genes.
  - Genomic mating's.
- Genomic indexes (in time).
  - Selecting the best.
- Further quantification of benefits, including examples in part II.

Summary. Role of genomics in Irish breeding programs – Parentage Verification (i)

- Case is compelling. Infra-structure is in place; (i) customised chip (under constant improvement), (ii) database, (iii) service providers (Weatherby's, HB, & ICBF), & (iv) appetite amongst breeders.
- Need to establish operational & funding models.
  - Present to HB councils (mandatory, voluntary….?).
- Shared approach (HB , ICBF, Teagasc & Weatherby's) = better service for farmers.
- Opportunity to become world leaders in implementation of genomic technologies.