OPPORTUNITIES FOR DAIRY SHEEP GENOMICS IN NEW ZEALAND

Suzanne Rowe, John McEwan, Rudiger Brauning, Ken Dodds, Sheryl-Anne Newman & Shannon Clarke

Animal Genomics Team
Animal Productivity
Invermay
NEW Zealand

agresearch

Dear ~~Santa~~/MBIE……
Please send me the perfect dairy sheep.

It needs to be healthy and kind with
milk high in angiotensin and a fatty acid
profile that is just right…..

I promise to be good (ish)

HARNESSING VARIATION

Bedouin goats tolerate a 50 to 55 percent reduction. The Bedouin animals had a 53 percent lower fasting heat production under feed restriction.

the North Ronaldsay, diet consisting mainly of the seaweed *Limnaria* (NCR, 1993). It can cope with a diet very low in copper and very high in sodium

SLIC gene for heat tolerance

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Example project: "Magic cow"

Long term goal to create **genetically modified cattle** resistant to **African trypanosomiasis** by gene-editing approach (baboon gene APOL1 confers resistance)

To-date: platform development (gene-editing, cloning)

Trypanosomiasis infested cow

"Tumaini" – cloned (somatic cell nuclear transfer) Boran bull, with his progeny

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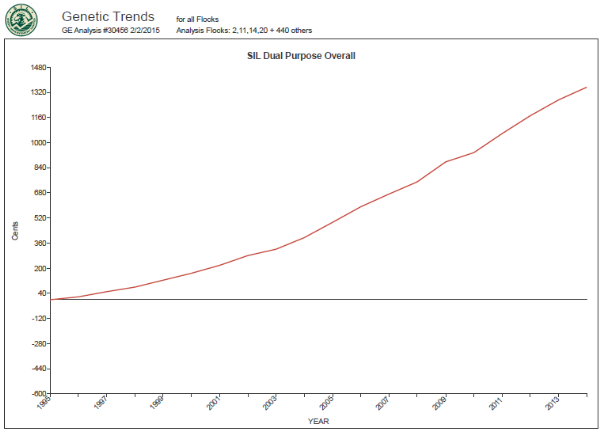
Karen Marshall ILRI, 2015.

GENOMICS & GENETICS



Livestock breeding

- Typically ~50% of efficiency and productivity gains come from genetics
- Dairy cattle 21 litres/yr, NZ Angus – 50kg carcass weight in 30 yrs
- Recording systems, Breeding values and selection indices
- Genomic selection, CVM, BLAD, PrP, DGAT, BOOROOLA
- Permanent, sustainable, and cumulative
- Can be slow, **relies on identifying elite animals accurately**

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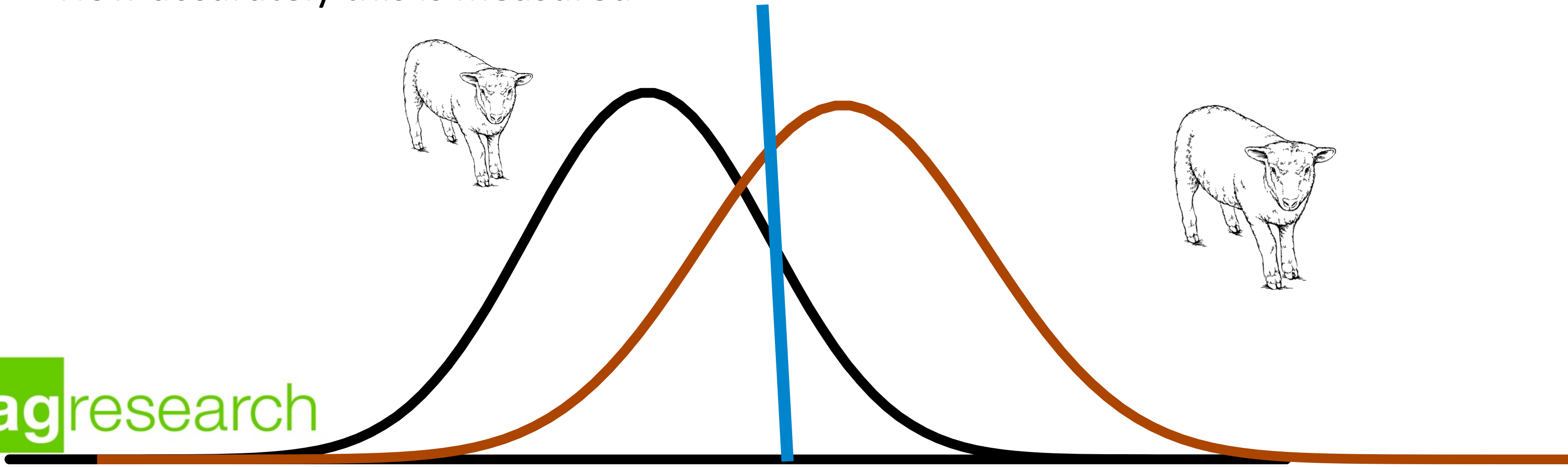
LIVESTOCK BREEDING

$$\Delta G = \frac{h.i.\sigma_a}{L}$$

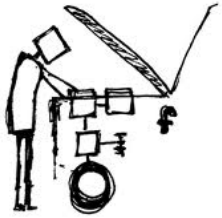
Rate of genetic progress

Depends on a few factors

- Heritability – proportion under genetic control
- Generation interval
- How much better the candidates chosen are from the average
- How accurately this is measured

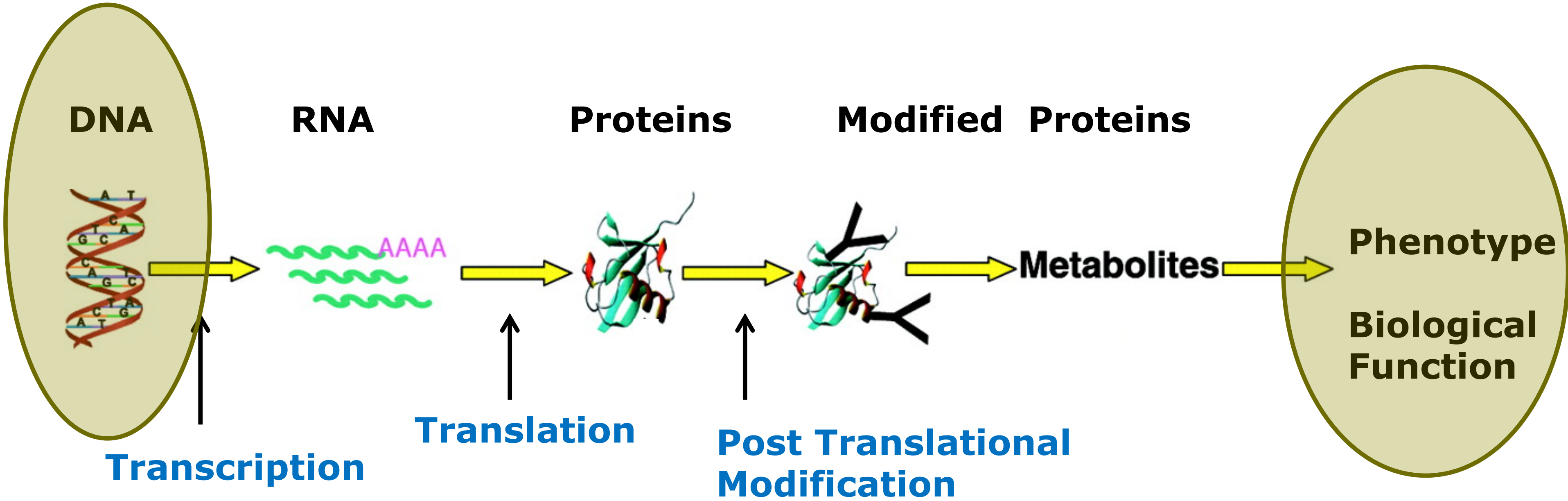


GENOMIC PREDICTION



Genetic Potential

Blind selection can be dangerous, faster progress if we get under the hood and look at the DNA itself



DNA **RNA** **Proteins** **Modified Proteins**

Metabolites

Phenotype

Biological Function

Transcription

Translation

Post Translational Modification

DNA

GWAS
Trait prediction

Phenotype

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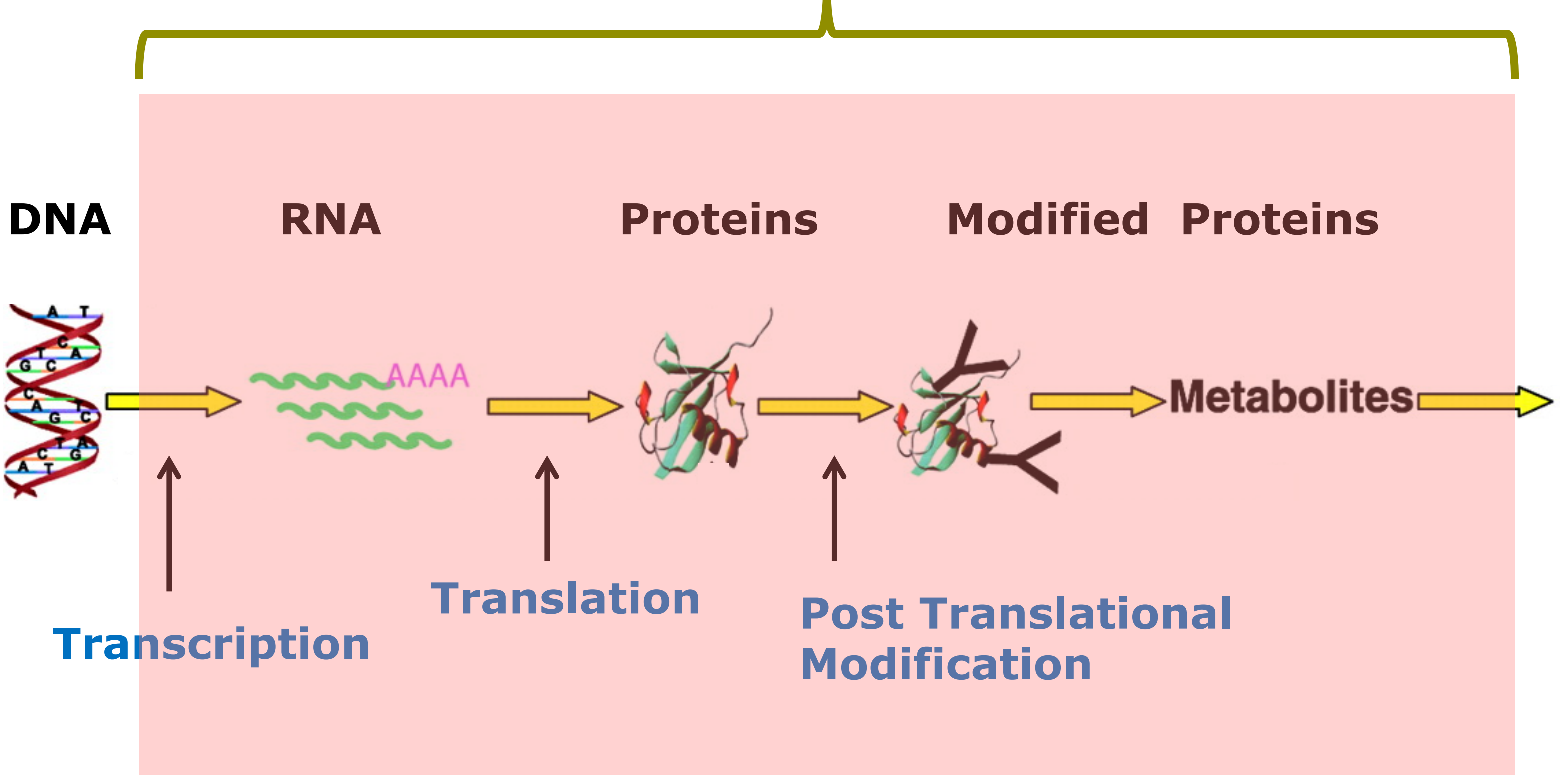
James Kijas ISGC, 2015

Why don't we exploit knowledge about this stuff in th



Answer: We don't know much about it

1. We haven't had decent genome assemblies

2. We haven't have the methodological approaches

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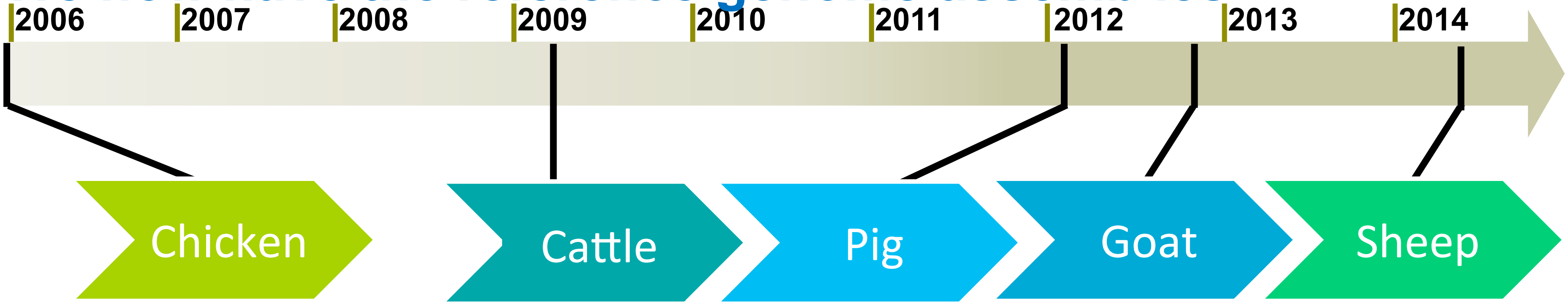
James Kijas ISGC, 2015

We now have the reference genome assemblies



nature

The chicken genome

Cracking the code

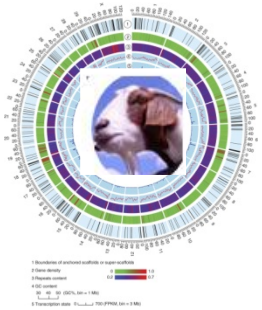
Science

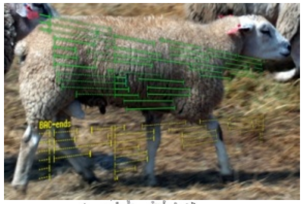
Livestock Decoded

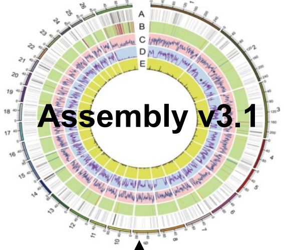
AAAS

nature

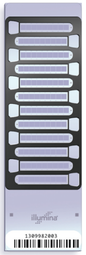
BRINGING HOME THE BACON



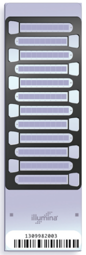




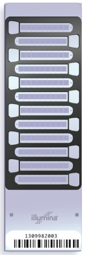
SNP50 cattle



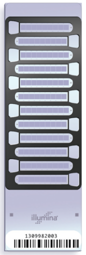
SNP50 sheep



HD SNP cattle



SNP50 goat



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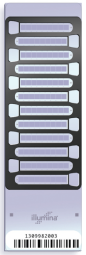

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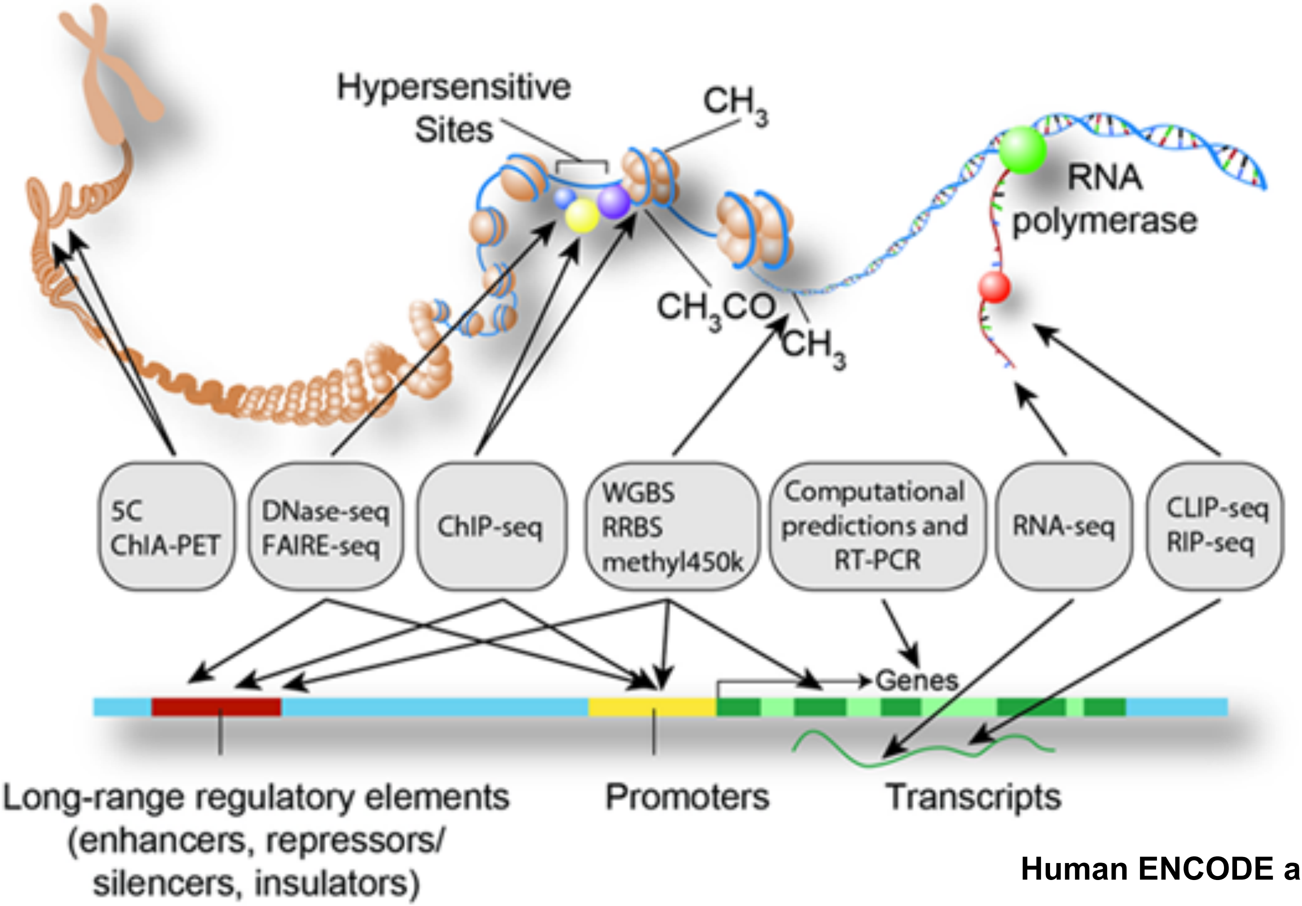
James Kijas ISGC, 2015

We now have the methodological approaches…



Human ENCODE assays

Now at the start line….

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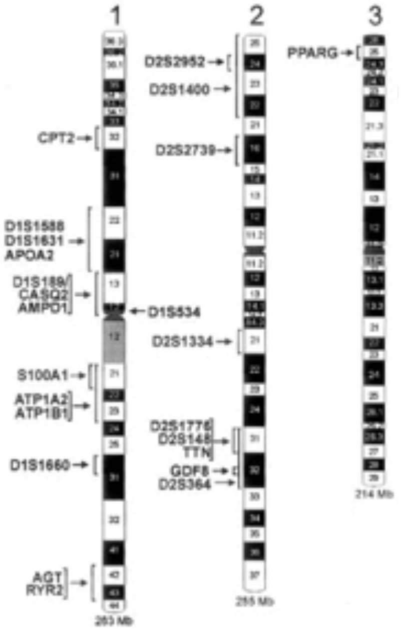
James Kijas ISGC, 2015

What is functional annotation?

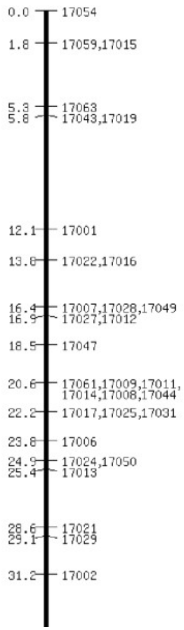
- Identifying the genomic elements controlling
- gene expression and regulation

Gene maps



➡

SNP maps



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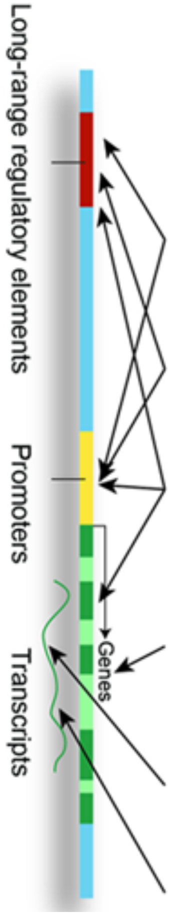


Mapped locations for:

Enhancer elements

Gene Promoters

TF Binding Sites

Transcription Start Sites

Tissue specific transcripts

Transcript iso-forms

Mono-allelic expression

LncRNAs

What can we use functional annotation for?

- ➢ RIGHT NOW: Interpretation of genomic scan results

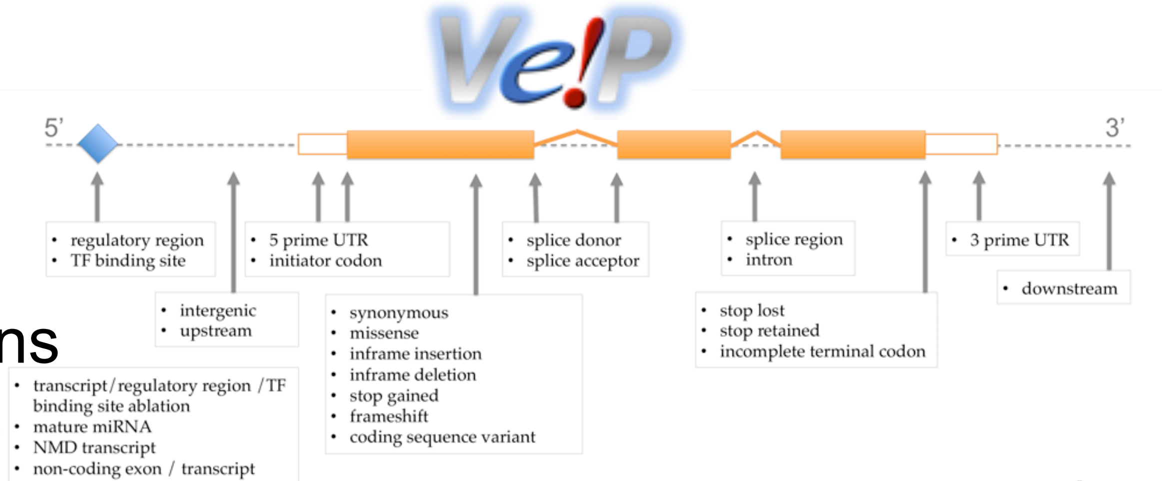
- ➢ MEDIUM TERM: Improve the accuracy of prediction

  - Number of variants available > the number that can be used for prediction

  - Prioritisation: <u>currently:</u> evenly spaced neutral variants

  - Prioritisation: <u>future:</u> trait specific functional and biological information

SNP collections ➡



- regulatory region
- TF binding site

- intergenic
- upstream

- transcript/regulatory region /TF binding site ablation
- mature miRNA
- NMD transcript
- non-coding exon / transcript

- 5 prime UTR
- initiator codon

- synonymous
- missense
- inframe insertion
- inframe deletion
- stop gained
- frameshift
- coding sequence variant

- splice donor
- splice acceptor

- splice region
- intron

- stop lost
- stop retained
- incomplete terminal codon

- 3 prime UTR

- downstream

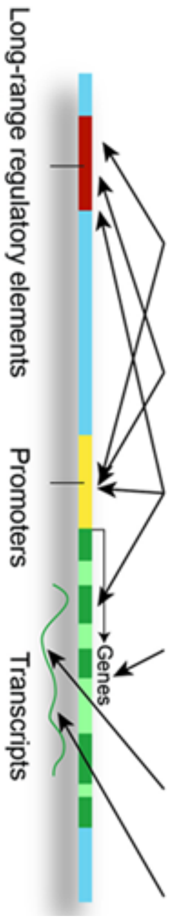
➡ Effect prediction

James Kijas ISGC, 2015

Prioritisation via SNP weightings

Mapped locations for:

- **Enhancer elements**
- **Gene Promoters**
- **TF Binding Sites**
- **Transcription Start Sites**
- **Tissue specific transcripts**
- **Transcript iso-forms**
- **Mono-allelic expression**
- **LncRNAs**



➡

Assign SNP Weightings

Probability to influence any phenotype

Trait specific SNP weightings

⬇

Use Weightings to Prioritise SNP

Improved accuracy of prediction

James Kijas ISGC, 2015

What can we use functional annotation for?

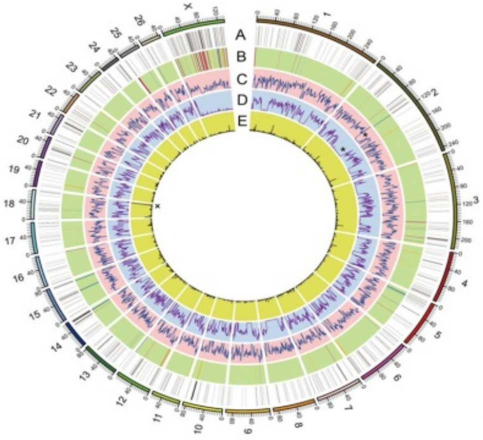
- RIGHT NOW: Interpretation of GWAS results
- MEDIUM TERM: Improve the accuracy of prediction
- **THE DREAM: Interpret whole genome sequence**

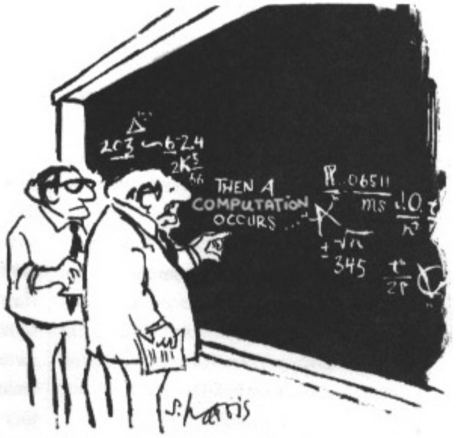
- all regulatory elements identified

- their interactions all mapped and understood

- their tissue and trait specificity elucidated (phew..)

Genome of an animal





“ good call using a computer here in step two.”

Performance predicted

James Kijas ISGC, 2015

FAANG

Functional Annotation of Animal Genomes

A coordinated international action to accelerate genome to phenome

http://www.faang.org
@faangomics
faang@iastate.edu

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Why FAANG is important?

- **Understanding the genotype to phenotype link**
  - Genomic selection
  - Improving fundamental understanding of Biology
- **This needs**
  - High quality reference genome sequence
  - Comprehensive annotation of the functional elements in the genome
  - Common infrastructure providing
    - Biological resources
    - Bioinformatics tools
    - Databases

FAANG
Functional Annotation of Animal Genomes

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Current Projects

- WUR-pigENCODE
  - Wageningen University, Martien Groenen Univ. Illinois (US) and INRA (France): Elisabetta Giuffra, Funding: ERC-grant. Started: 01/01/2014
- USDA – NIFA project
  - UC-DAVIS: Huaijun Zhou, USDA, ARS ADOL; Iowa State University: Michigan State University: USDA ARS, Miles. Funding: USDA, Chicken, Swine, Bovine Species Genome Coordination Funds, National Pork Board, Aviagen. Started: 01/01/2015 (36 months)
- Fr-AgEncode
  - INRA: Elisabetta Giuffra: INRA Funding: metaprogramme on Genomic Selection (SelGen). Started: 01/01/2015 (30 months)
- FAANG UK BBSRC infrastructure
  - Roslin, Alan Archibald TGAC and EMBL-EBI
- NSF: Research Coordination Network (RCN).
  - Provide for meetings that generate new collaborations and proposals that support FAANG objectives. Provide a conduit for new members to join the FAANG initiative.

JS) and INRA
01/01/2014

niversity: Michigan
en, Swine, Bovine
rd, Aviagen. Started:

on Genomic

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FAANG Functional Annotation of Animal Genomes http://www.faang.org @faangomics faang@iastate.edu

FUNCTIONAL ANNOTATION FOR DAIRY SHEEP

NZ FAANG – Dairy sheep

Health and production traits
    yield, composition, scc, disease

Measure in thousands of animals

Find underpinning genes/mechanisms

Develop means of selecting robust high performance stock

Dear Santa/MBIE…….
Please send me the perfect
dairy sheep.

It needs to be healthy and
kind with milk high in
angiotensin and a fatty acid
profile that is just right…..

I promise to be good (ish)

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BACK TO DAIRY SHEEP

Dear Santa/MBIE……
Please send me the perfect
dairy sheep.

It needs to be healthy and
kind with milk high in
angiotensin and a fatty acid
profile that is just right…..

I promise to be good (ish)

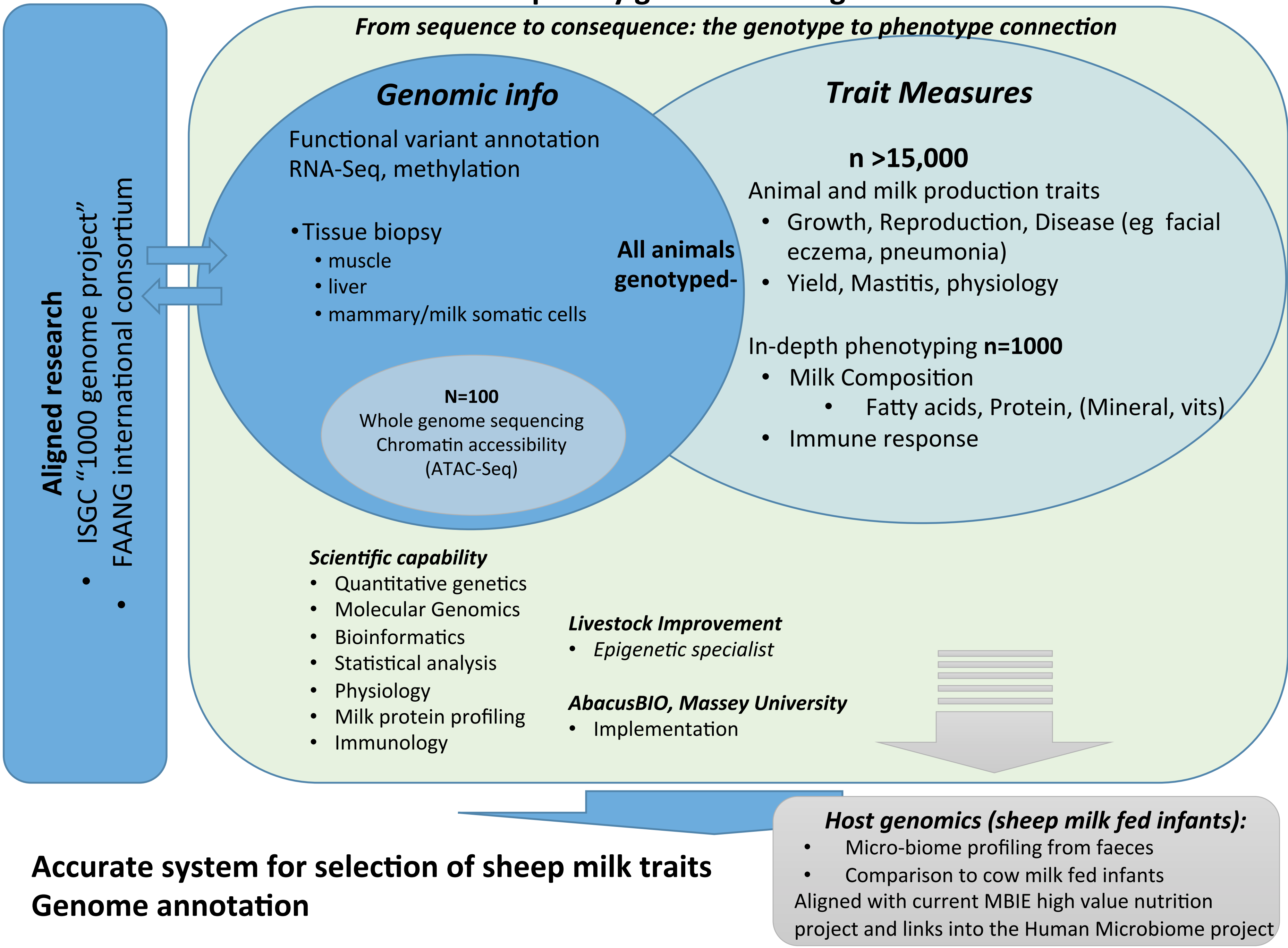
Need for increased production but not any cost

Balance with health and disease resistance

Identify lethal genes/potential zoonoses

We can add considerable value and precision to NZ dairy sheep selection schemes by incorporation of this information.

Sheep dairy genetics for high value milk



From sequence to consequence: the genotype to phenotype connection

Aligned research

- ISGC "1000 genome project"
- FAANG international consortium

Genomic info

Functional variant annotation
RNA-Seq, methylation

- Tissue biopsy
  - muscle
  - liver
  - mammary/milk somatic cells

N=100
Whole genome sequencing
Chromatin accessibility
(ATAC-Seq)

All animals genotyped-

Trait Measures

n >15,000

Animal and milk production traits

- Growth, Reproduction, Disease (eg facial eczema, pneumonia)
- Yield, Mastitis, physiology

In-depth phenotyping **n=1000**

- Milk Composition
  - Fatty acids, Protein, (Mineral, vits)
- Immune response

Scientific capability

- Quantitative genetics
- Molecular Genomics
- Bioinformatics
- Statistical analysis
- Physiology
- Milk protein profiling
- Immunology

Livestock Improvement

- *Epigenetic specialist*

AbacusBIO, Massey University

- Implementation

Host genomics (sheep milk fed infants):

- Micro-biome profiling from faeces
- Comparison to cow milk fed infants

Aligned with current MBIE high value nutrition project and links into the Human Microbiome project

- **Accurate system for selection of sheep milk traits**
- **Genome annotation**

ENGAGEMENT

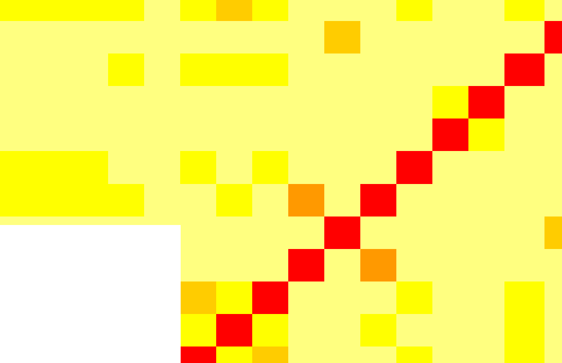
Requires p

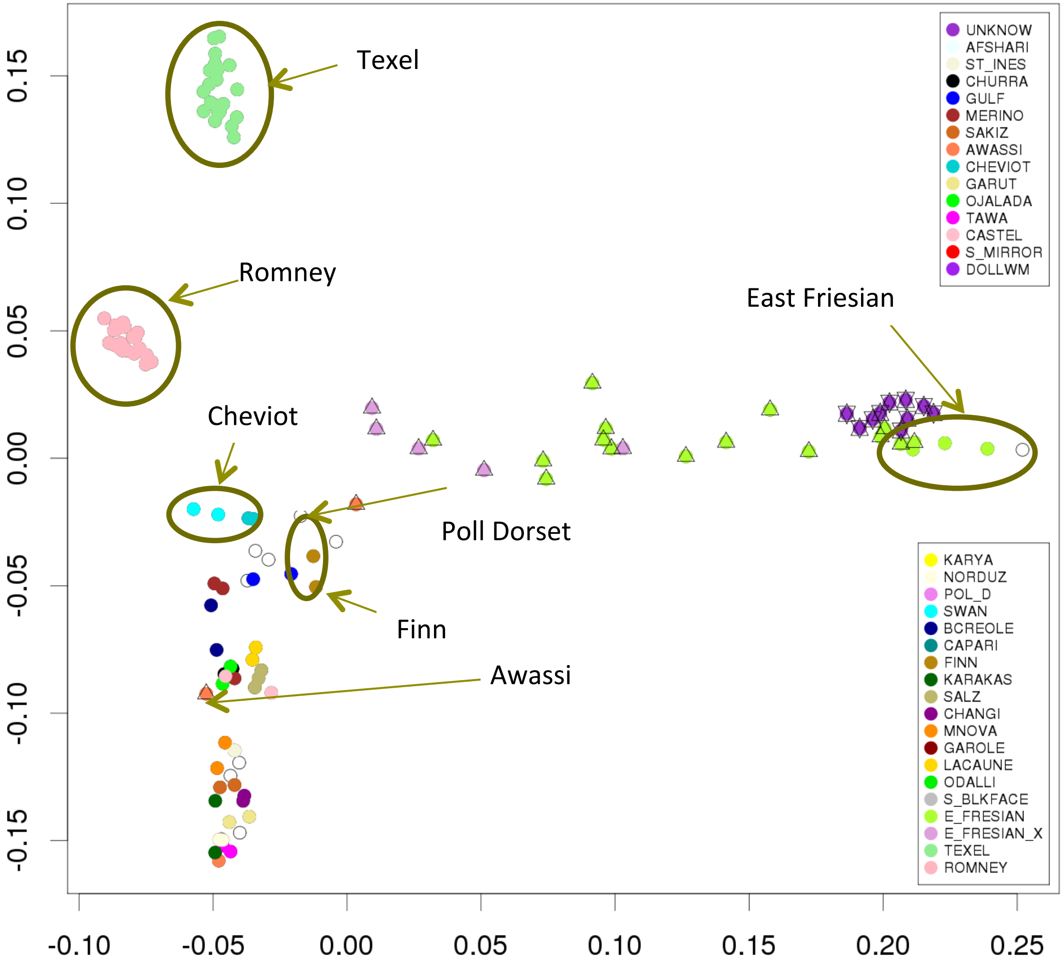
Contributi

Outputs:

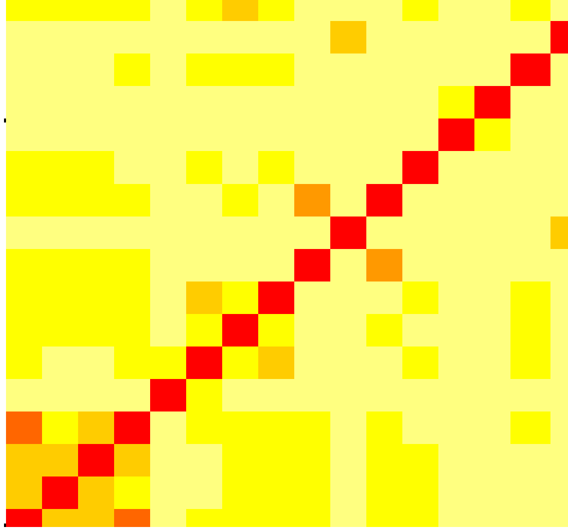
Immediat ed, known

variant





ENGAGEMENT



Requires phenotypes & DNA samples

Contribution $25 per ewe

Outputs:

Immediate – DNA profile, relationships, parentage, breed, BVs

Medium term - genomic breeding values, lethal, desirable variants

Long term - state of the art genomic tools developed specifically accurate selection for robust, high yielding NZ sheep

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OUTPUTS

Genetics for important traits in the NZ dairy sheep industry

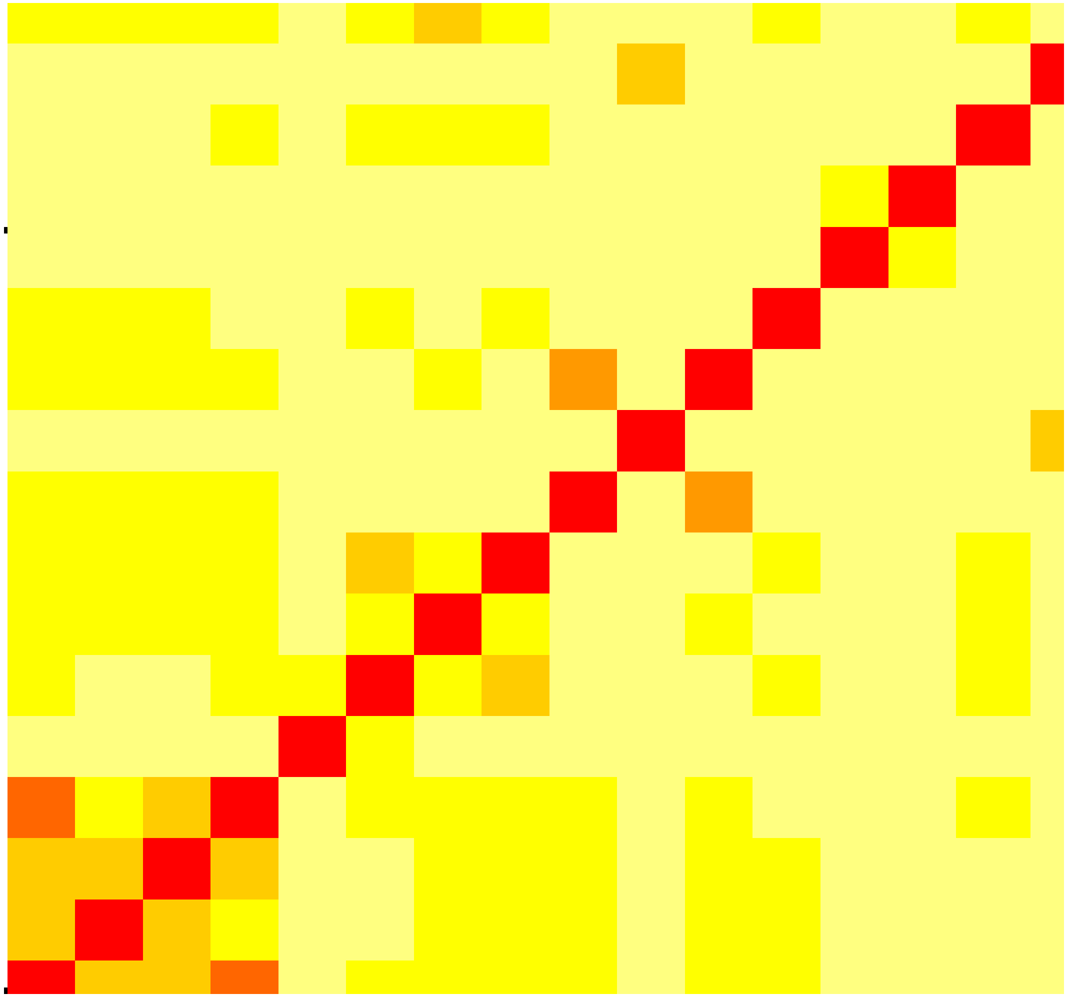
An available training population for genomic prediction

Discovery of variants that can be used;

i) to select for yield and disease traits
ii) to fast track genomic selection
iii) for comparison of NZ dairy sheep to other international dairy sheep breeds
iv Insights into environmental adaptation

Genomic information for immediate use in breeding programs

GENOMIC RELATIONSHIPS



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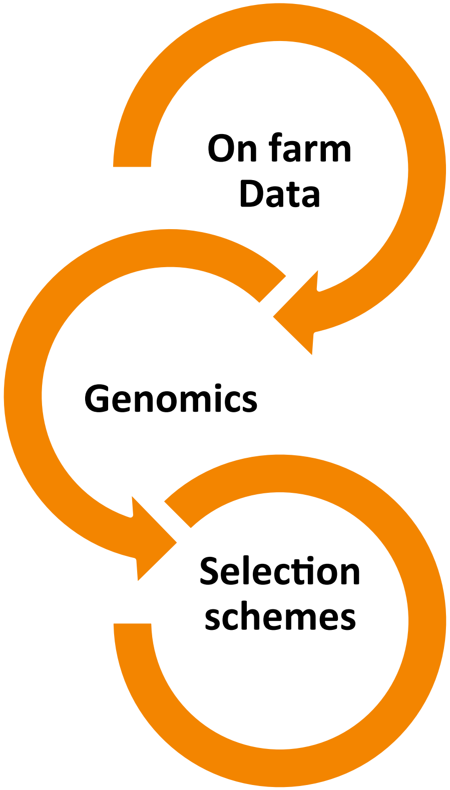
SELECTION STRATEGIES

Data- what, how, frequency,

Genomics – sampling, densities, data handling, interrogation

Selection - combining data, sharing data, models, accuracy, breeding values, dissemination



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SUMMARY – LAST YEAR

The future….

- Get cost of genotyping low equivalent to cost of parentage ~NZ$25 (**adoption**)

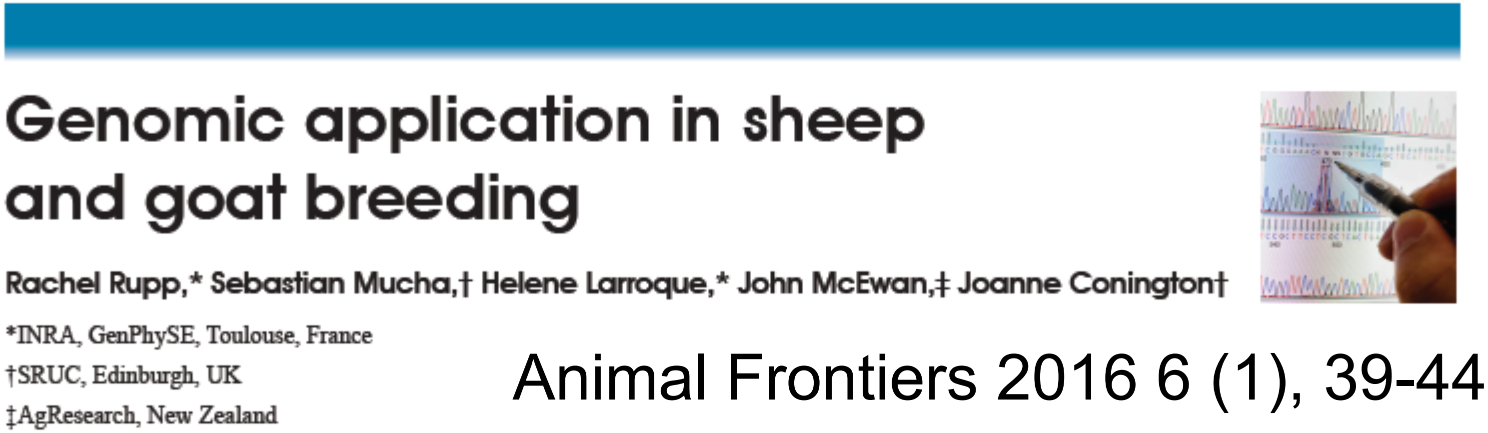
- Review selection indices and BVs (**direction**)
  - New traits
  - Whole supply chain indices
  - Environment challenges

- Alter generation length, industry structure (**ΔG, adoption**)
  - JIVET, multiplier flocks
  - Data capture in plant and on commercial farm (EID, scales)
  - Milk quality, disease, ram contribution

- Future gene editing (**ΔG, accuracy**)….
  - To do successfully we need to understand how genome works much better

RECENT REVIEW

- Genomic selection in sheep



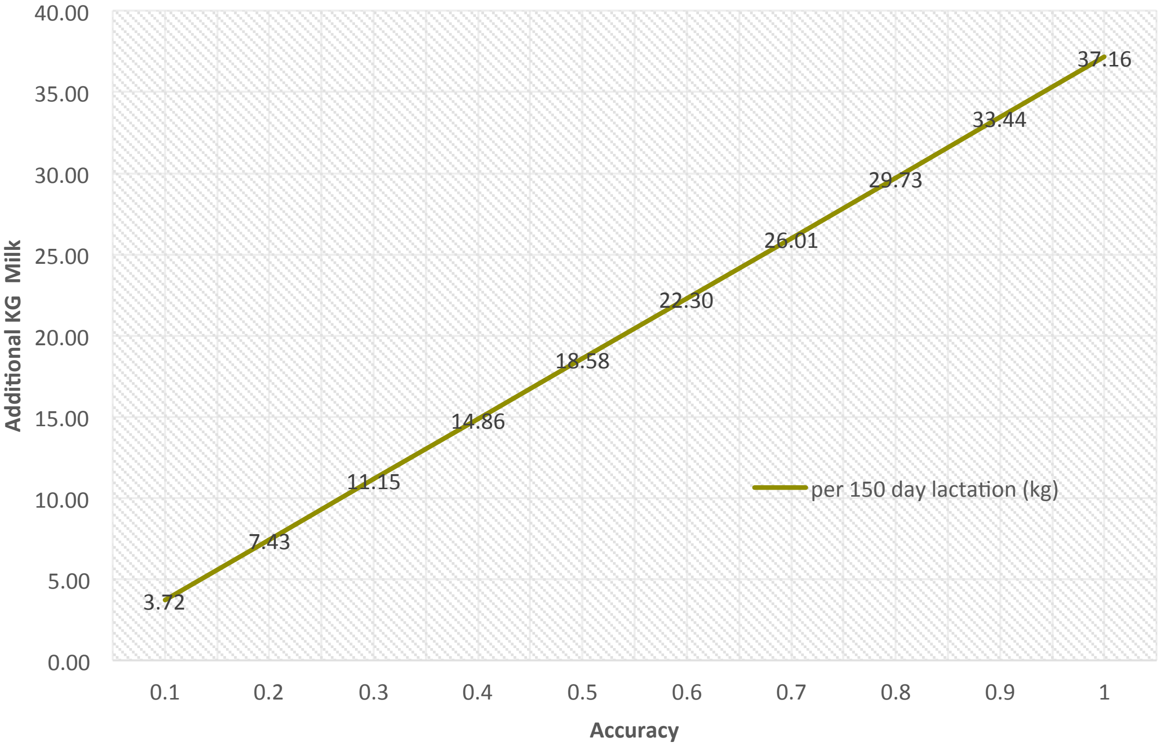
Genomic application in sheep and goat breeding

Rachel Rupp,* Sebastian Mucha,† Helene Larroque,* John McEwan,‡ Joanne Conington†

*INRA, GenPhySE, Toulouse, France
†SRUC, Edinburgh, UK
‡AgResearch, New Zealand

Animal Frontiers 2016 6 (1), 39-44

- Cattle since 2007, sheep 2010 (NZ)
- Dairy Goats: France 2013 and UK 2015
- Often too expensive in minor species
- New wave of genotyping technologies appearing


Additional KG Milk
40.00
35.00
30.00
25.00
20.00
15.00
10.00
5.00
0.00
0.1
0.2
0.3
0.4
0.5
0.6
0.7
0.8
0.9
1
Accuracy
3.72
7.43
11.15
14.86
18.58
22.30
26.01
29.73
33.44
37.16
per 150 day lactation (kg)

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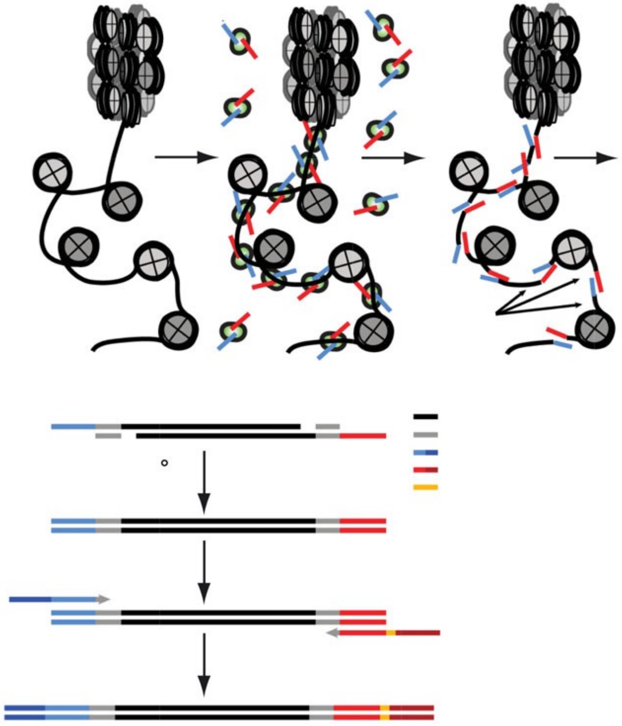
Core Assays

- RNA-Seq
  - Stranded
- Chromatin Accessibility
  - ATAC-Seq
- Histone Modification
  - H3K4me3
  - H3K27me3
  - H3K27ac
  - H3K4me1



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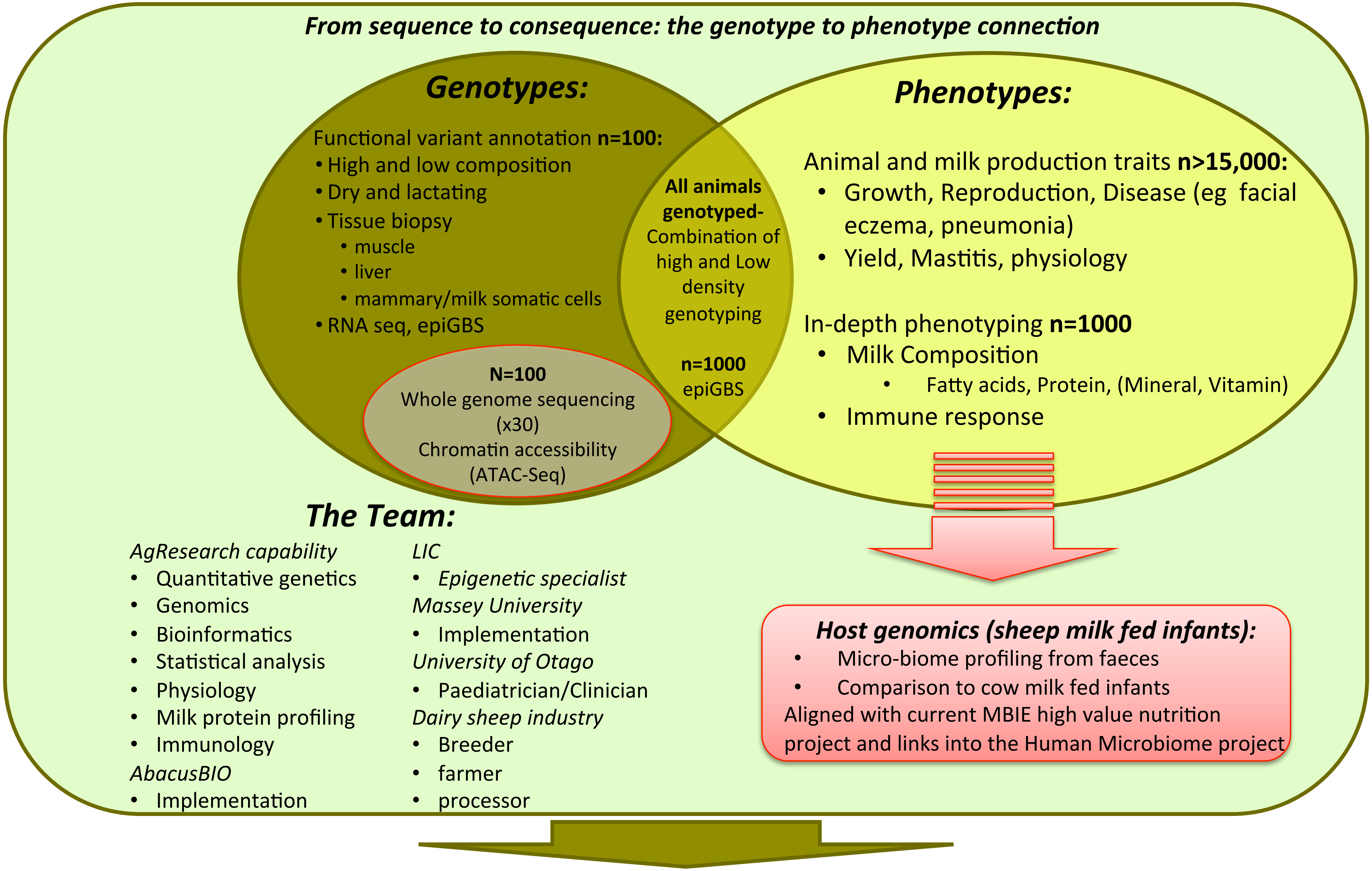

From sequence to consequence: the genotype to phenotype connection

Genotypes:

Functional variant annotation **n=100:**
- High and low composition
- Dry and lactating
- Tissue biopsy
  - muscle
  - liver
  - mammary/milk somatic cells
- RNA seq, epiGBS

N=100
Whole genome sequencing
(x30)
Chromatin accessibility
(ATAC-Seq)

All animals genotyped-
Combination of
high and Low
density
genotyping

n=1000
epiGBS

Phenotypes:

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Aligned with current MBIE high value nutrition project and links into the Human Microbiome project

The Team:

AgResearch capability
- Quantitative genetics
- Genomics
- Bioinformatics
- Statistical analysis
- Physiology
- Milk protein profiling
- Immunology

AbacusBIO
- Implementation

LIC
- *Epigenetic specialist*

Massey University
- Implementation

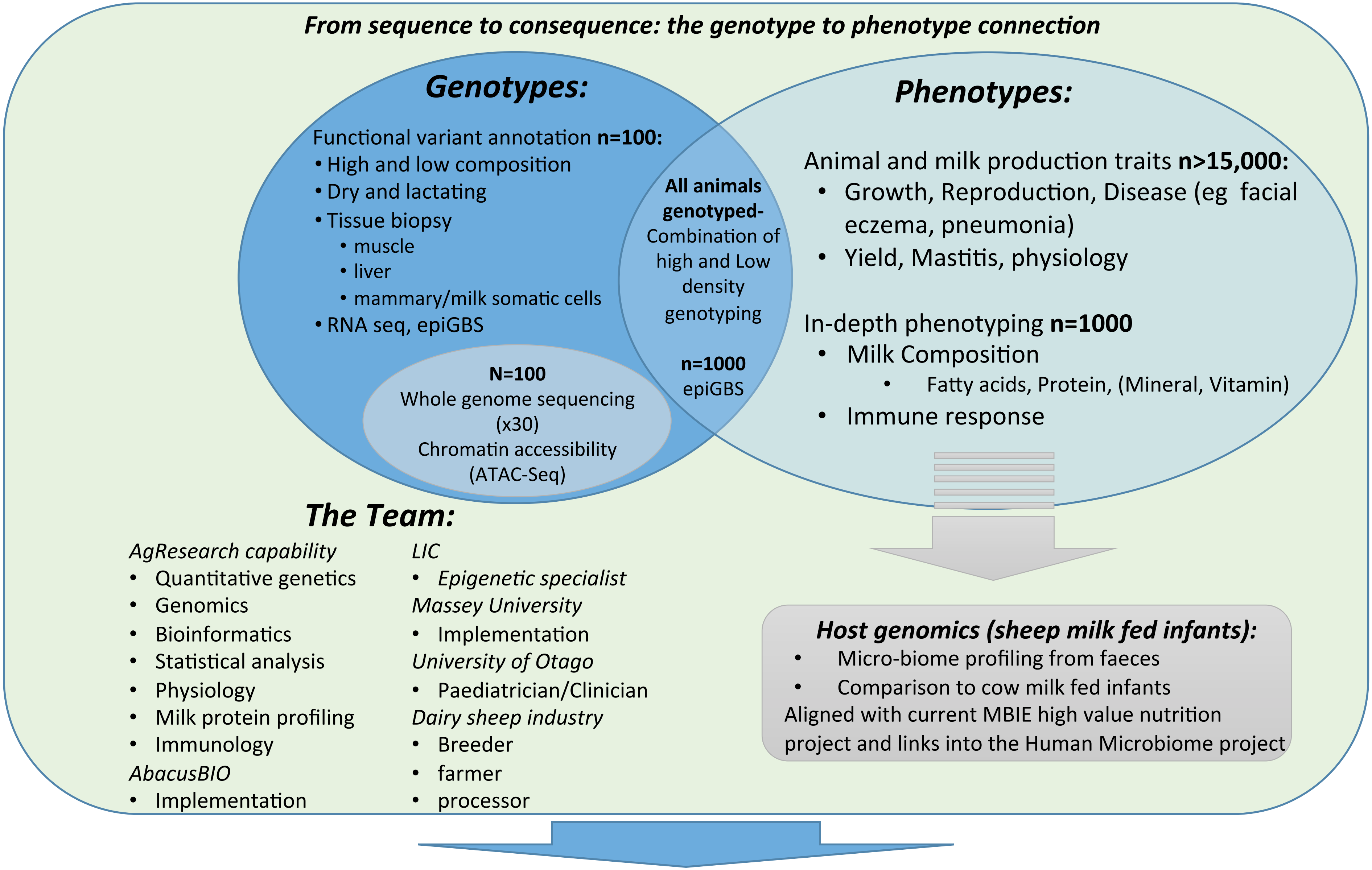
University of Otago
- Paediatrician/Clinician

Dairy sheep industry
- Breeder
- farmer
- processor

- **Accurate system for selection of sheep milk production and health traits**
- **High value sheep milk for infants**

Sheep dairy genetics for high value milk

From sequence to consequence: the genotype to phenotype connection



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Dairy sheep industry

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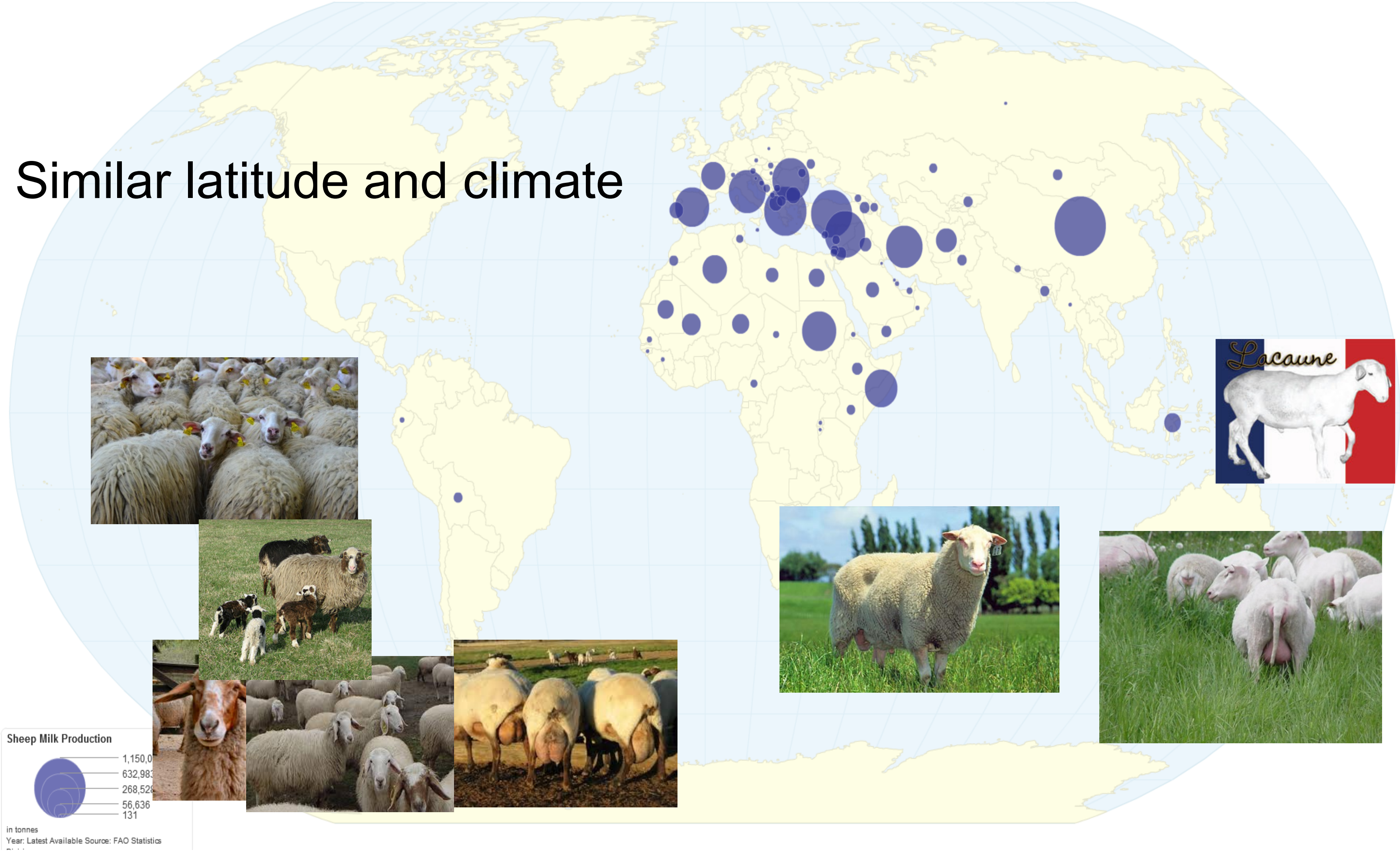
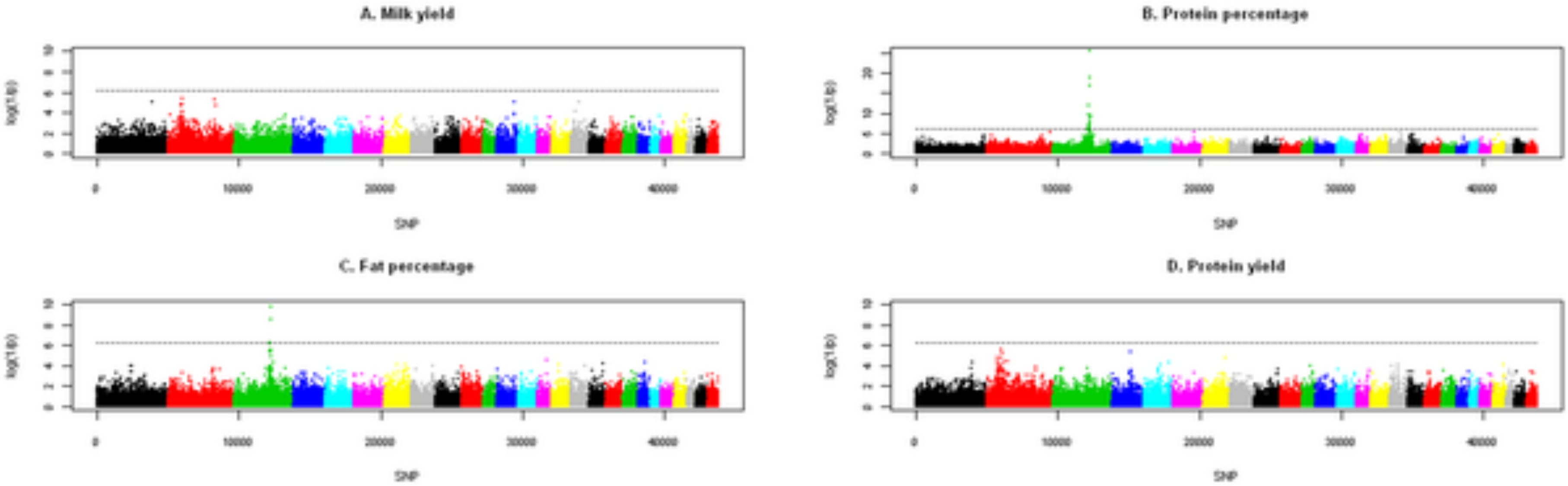
Similar latitude and climate



SPAIN 50K GWAS – ASSAF CHURRA

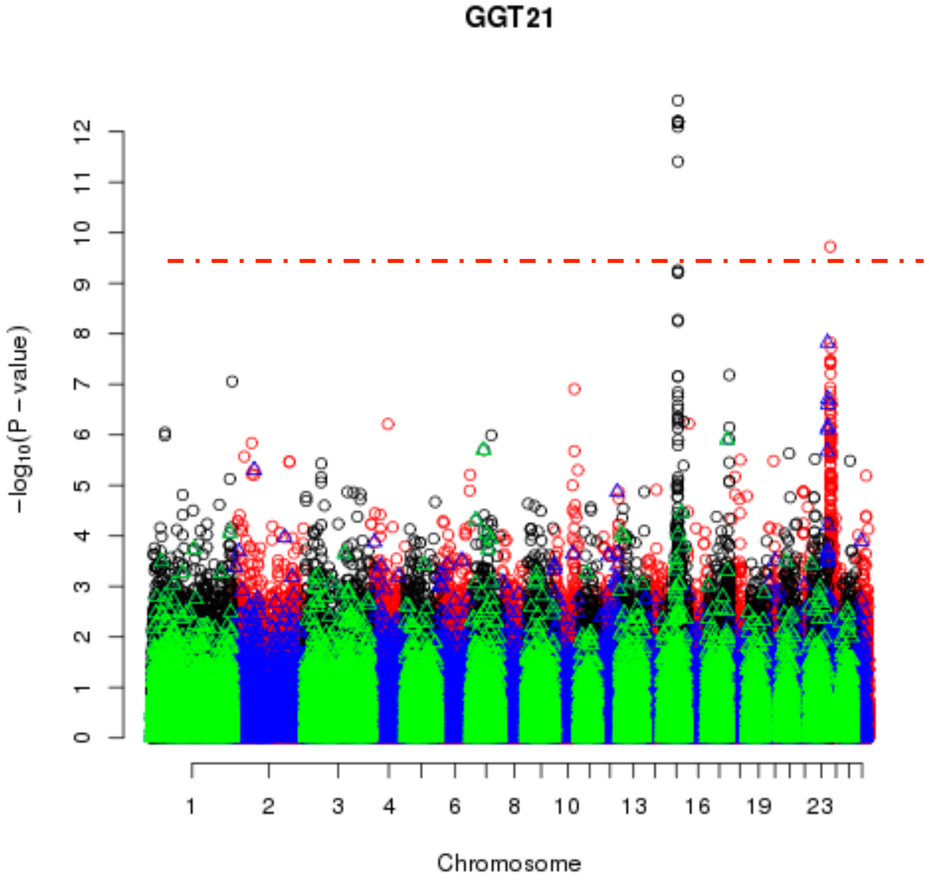


Significance threshold	Chrom	SNP ID	Position(Mbp)	Trait	Allele substitution effecttrait units (SD units)	P-value (Nominal)	P-value (Corrected)*
Experiment-wise significant	3	OAR3_147028849	137.3	PP	0.138±0.013 (0.470)	3.78×10^{-26}	9.24×10^{-23} (2.77×10^{-22})
	3	OAR3_147028849	137.3	FP	0.169±0.026 (0.297)	1.80×10^{-10}	4.39×10^{-7} (1.32×10^{-6})
Chromosome-wise significant	1	OAR1_233634722	216.9	MY	25.824±5.815 (0.210)	9.55×10^{-6}	0.030

García-Gámez E, Gutiérrez-Gil B, Sahana G, Sánchez JP, Bayón Y, et al. (2012) GWA Analysis for Milk Production Traits in Dairy Sheep and Genetic Support for a QTN Influencing Milk Protein Percentage in the LALBA Gene. PLoS ONE 7(10): e47782. doi: 10.1371/journal.pone.0047782
http://127.0.0.1:8081/plosone/article?id=info:doi/10.1371/journal.pone.0047782

PLOS | ONE

FACIAL ECZEMA



Δ Δ Green and blue triangles show significance of the ~41k SNPs from the ovine 50k SNP chip.

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beef+lamb new zealand GENETICS

○ ○ Red and black circles show test statistics for additional

FRANCE GENOMIC SELECTION

Key figures

15 years of scientific genomics research

10 years of genomic application in selection programmes

750 000 animals already genotyped for selection purposes

3 breeds benefitting from genomic evaluations

15 breeds soon able to benefit from genomic evaluations

1 major gene selected for at large-scale in the sheep species

2 large-scale programmes targeting product quality

http://en.france-genetique-elevage.org

SEQUENCE TO CONSEQUENCE

Most phenotypes are complex and quantitative in nature, and a major goal of biological research lies in using genome information to predict such complex outcomes, whether it is the efficacy of a drug, susceptibility to cancer, or the performance of the daughters of an elite dairy bull. Many of the recent advances in biology have been driven by genome sequence information. The capability to sequence and decipher the instructions encoded in complex animal genomes quickly and at modest cost is now well established. The next challenge is to be able to read the subtlety and complexity of these instructions and to predict the resulting phenotypes, that is, to predict the consequences encoded in sequences. While significant progress in functional genome annotation has been made using various human cell types [1], we argue that filling the genotype-to-phenotype gap requires functional genome annotation of species with substantial phenotype information.

The availability of the OvineSNP50 chip from Illumina in 2009 opened the way for the development of genomic selection and its adoption in the Lacaune dairy breed in 2015. Its extension to other breeds is currently challenged by the smaller size of the reference populations, by the relative cost of genotyping, and by the lower gain expected by generation interval. For many sheep breeds, where the impact of AI is low, parentage assignment coupled with genotyping for the known major genes constitutes the preferred path for innovation within the breeding schemes.

1

Lacaune worldwide leader

Genomic selection has been used in **lacaune** dairy since 2015. It is the result of 6 years of Research and Development since the creation of the OvineSNP50 chip by Illumina in 2009. Several programmes contributed to the development of the tools necessary for this major evolution:

- Creation of a reference population of almost 5000 genotyped rams with performance recorded daughters;
- Construction of a process chain for managing the genotypes and genomic evaluation based on Single- Step GBLUP;
- Conception of an original and adapted genomic breeding scheme.

The reduction in the number of rams to be maintained along with the disappearance of progeny testing almost compensates for the costs associated with genotyping: at a similar cost price, the genomic scheme enables increased genetic gain of 10 to 20 % compared to the present scheme, which corresponds to the very impressive figure of almost + 0.25 standard deviation per year.

4

Towards a wider use of genomics

It is important that all sheep populations participate and benefit from the genomic revolution.

For meat breeds, parentage assignment coupled with genotyping of the major known genes, such as PrP, enables increased genetic efficiency of the breeding schemes and facilitates the organisation of these schemes.

In dairy breeds, the cost/benefit ratio of genomic selection should be improved by using the low density chip expected for 2017.

In any case, these gains in genetic efficiency open the way for the introduction of new traits in the selection goals (health, longevity, productive life...).

FRANCE PRODUCTION

3 663 farms under milk recording system

862 000 ewes under milk recording system

481 000 purebred females inseminated

2500 rams with on-station performances evaluation

715 rams with progeny testing

250 rams selected for animal insemination

Annual genetic progress of 5.3 liters (Lacaune breed)

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CONCLUSIONS - GLOBAL

Established Major sheep breeding schemes

Defined measurement protocols

Defined breeding objectives

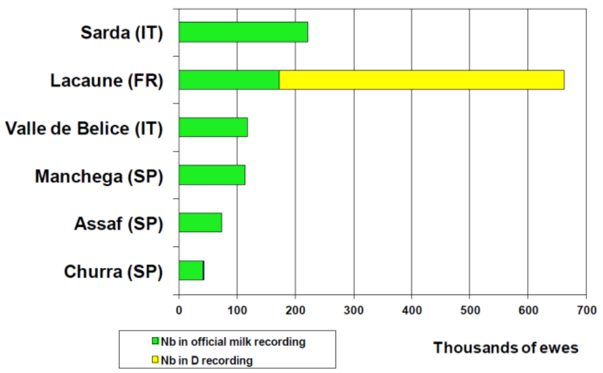
Collaborative elite ram proving schemes

Use genomic selection technologies

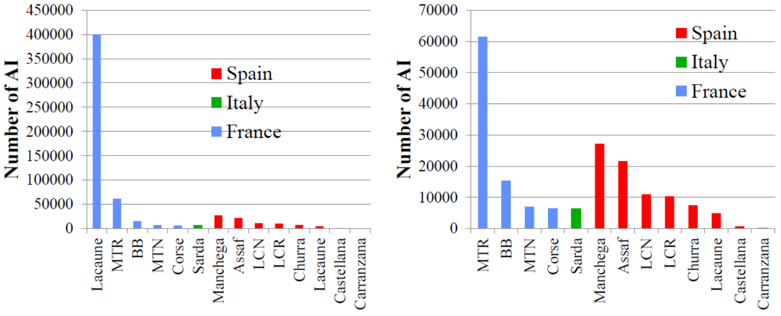
Identified important genes/regions

Increased rate of genetic gain

Sheep milk recording in breeds with more than 400,000 ewes (ICAR Berlin 2014)



Number of AI (ICAR Berlin 2014)



With French Lacaune

Without French Lacaune

579,439 AI on the whole

Figures 2013

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AND THE TOOLS…….

NZ sheep and deer
  improvement system

12 million records

343,000 new animals/year

Linked to genotype database
  800K samples
  100K new samples year

Linked to sequence
  databases

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AND THE RESULTS…….

	1990-91	**2006-07**	
Lambing Percentage (ewe)	101.6	117.9	(122% usual)
Hogget lambs as % all lambs	-	3.5	
Average Lamb Wt (kg)	14.35	16.90	+17%
Lamb sold Kg/Ewe	9.76	16.83	**+72%**
Wool kg/head	5.28	5.60	+6%
Average Steer Wt (kg)	297	320	+8%
Milk solids per cow (kg)	260	325	+25%

Source M&WNZ

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beef+lamb new zealand

OPPORTUNITIES FOR INCREASED GENETIC GAIN

Recording yield and pedigree – breeding values ⬆⬆
Availability of proven rams
Introgression of large effects ⬆⬆
Elite sire proving scheme
Genomic selection ⬆⬆
Access to overseas breeds ⬆⬆⬆

Requires

- Recording systems
- Pedigree/parentage assignment
- Trait definitions
- Breeding objectives
- Collaboration

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WHERE FROM HERE?

See what we have got

- Genomic tools to establish genetic diversity in NZ

Compare with international breeds

- Compare genetic composition of global breeds
- Look for major dairy genes segregating in NZ population

Define breeding objectives for NZ market/economy

Tools & Technology

- BLNZG
- SIL database
- Genomics parentage
- Flock/National breeding values

Planned industry structure

- Ram reference scheme?
- Importation

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QUESTIONS

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IS THERE NZ SUPPORT FOR DAIRY SHEEP?
MBIE SHEEP MILK PROJECT

Research aims

To enable the emerging NZ Dairy Sheep industry to reach $200m in export earnings by 2030.

Creating greater value from sheep milk through

- knowledge of its *composition* and the *functionality* of its components
- improving net *volume* of harvested milk
- establishing criteria to ensure the *environmental sustainability* of sheep dairying in NZ

Contract summary

- $6.6 m (excl. GST, over 6 years; currently in year 2), funded by MBIE
- Collaborators: University of Otago, Callaghan Innovation, Victoria University
- Industry partners: Blue River Dairy, Waituhi Kuratau Trust, Kingsmeade Cheese

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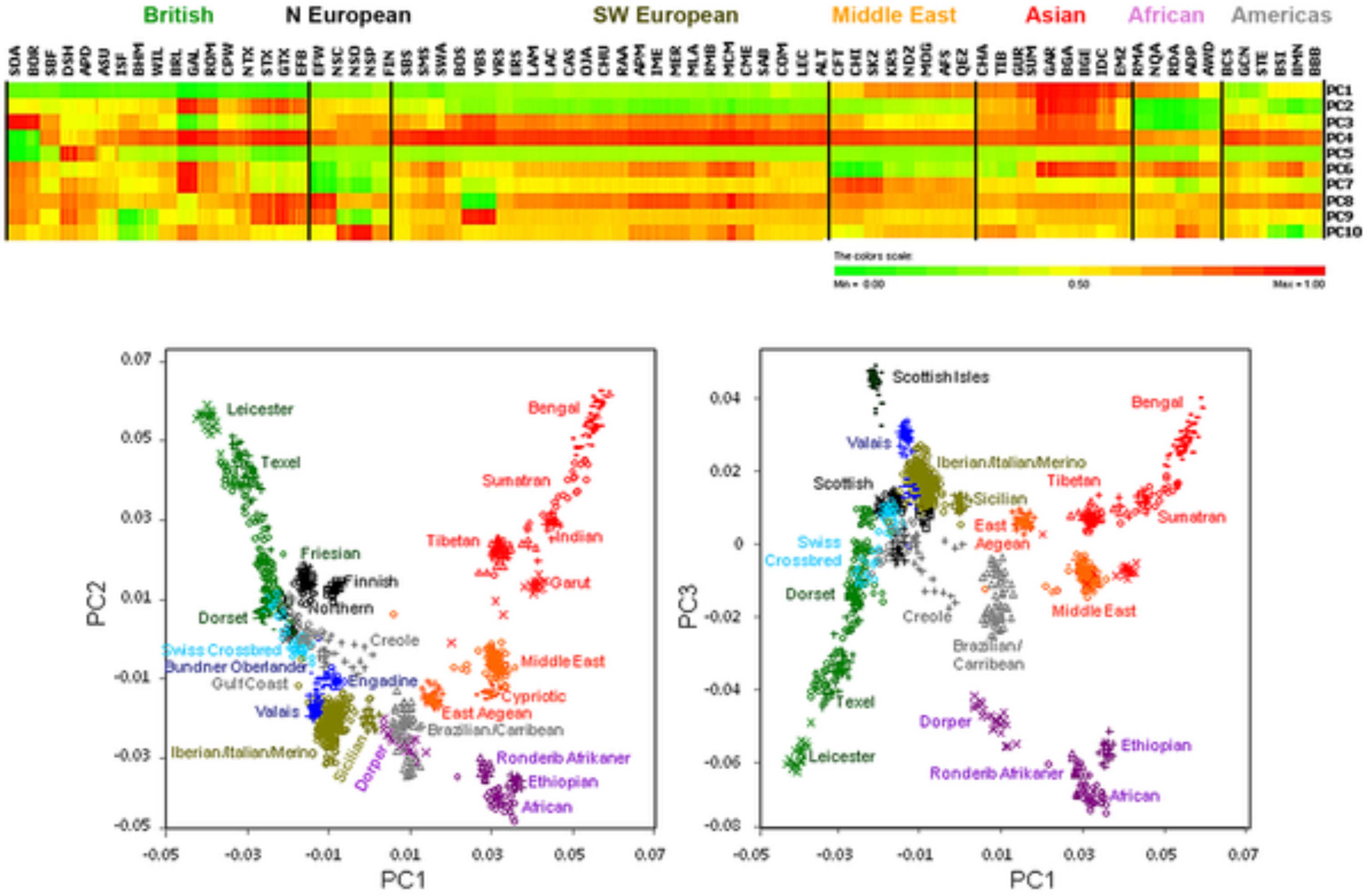
Ministry of Business,
Innovation & Employment

Table 2. Diversity of the main milk sheep regions in the world

	Spain (1)	Spain (1)	Spain (2)	France (3)	France (4)	France (3)	Italy (5)	Greece (6)
	Castile the Mancha	**Castile & Leon**	**Basque**	**Basque**	**Roquefort**	**Corsica**	**Sardinia**	**Greece**
No. of ewes per farm	900-1000	-	360	235	400	225	-	210
Production (l/ewe)	180	-	-	115	150-250	110	180-200	100-140
Dominant breeds	Manchega	Assaf, Churra	Latxa	Manech, Basco béarnaise	Lacaune	Corsican	Sardinian	Chios, Karagouniko
% mechanized milking	100	-	-	50	100	50	-	10
Main cheese	Manchego	Zamorano	Idiazabal	Ossau Iraty	Roquefort	Brocciu	Pecorino	Feta
Price of the milk	1.08-1.20 in PDO, 0.8 non PDO	-	0.96	1	1.13 in PDO 0.73 non PDO	1.15	0.65	-

Sources: in 2010, (1) & (2) Caja *et al.*, (2) Arranz, (3) & (4) Morin, (4) Frégeat, (5) Carta, (6) Vallerand and Arsenos.

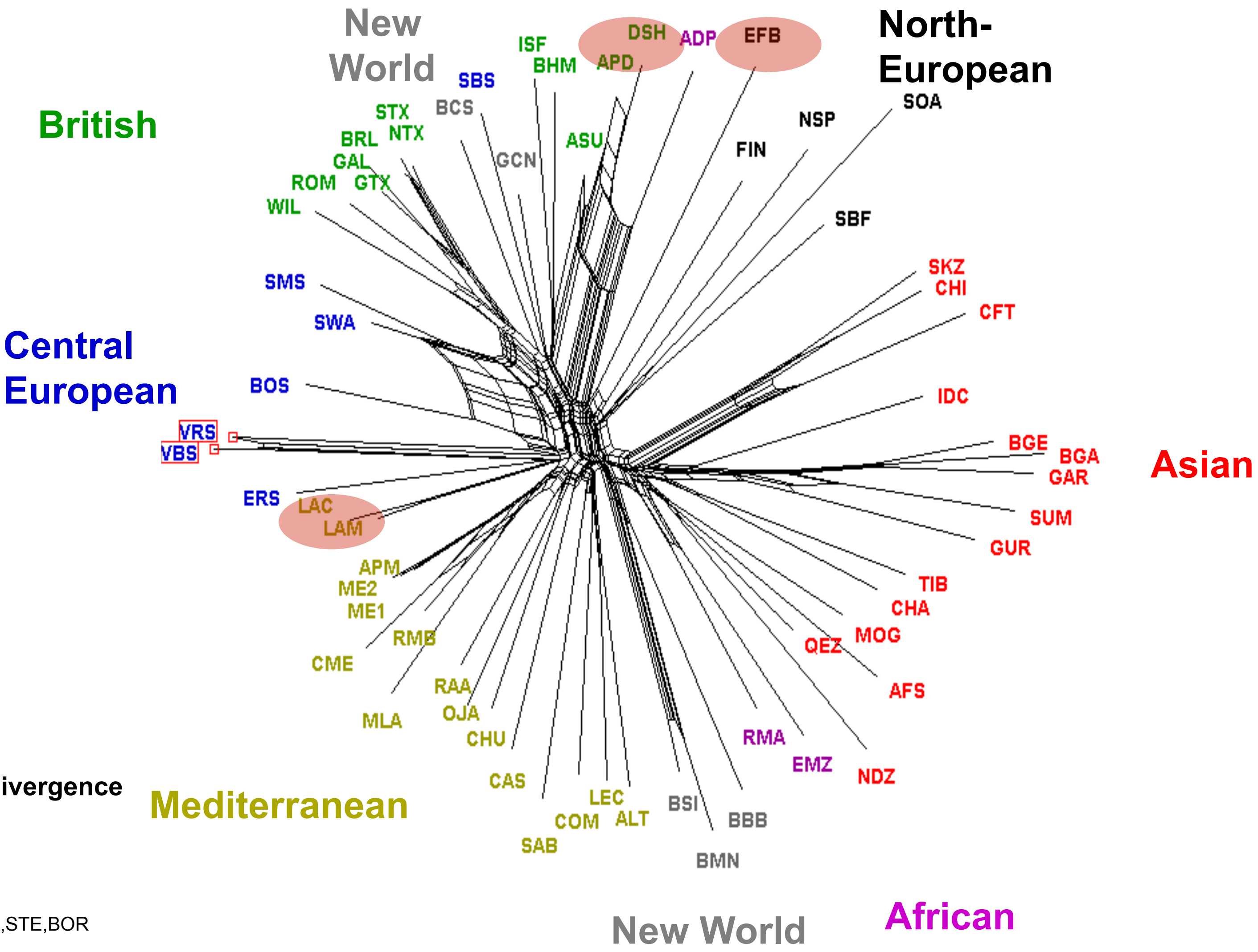
Figure 2. Population structure within the global sheep diversity panel.



Kijas JW, Lenstra JA, Hayes B, Boitard S, Porto Neto LR, et al. (2012) Genome-Wide Analysis of the World's Sheep Breeds Reveals High Levels of Historic Mixture and Strong Recent Selection. PLoS Biol 10(2): e1001258. doi:10.1371/journal.pbio.1001258
http://127.0.0.1:8081/plosbiology/article?id=info:doi/10.1371/journal.pbio.1001258

PLOS | BIOLOGY

IN THE BEGINNING…..



NeighborNet graph of LD-based divergence times, 63 breeds
Color by region
091130
Not (<20)
AWD,CPW,EFW,KRS,MCM,NQA,NSO,NSC,RDA,STE,BOR

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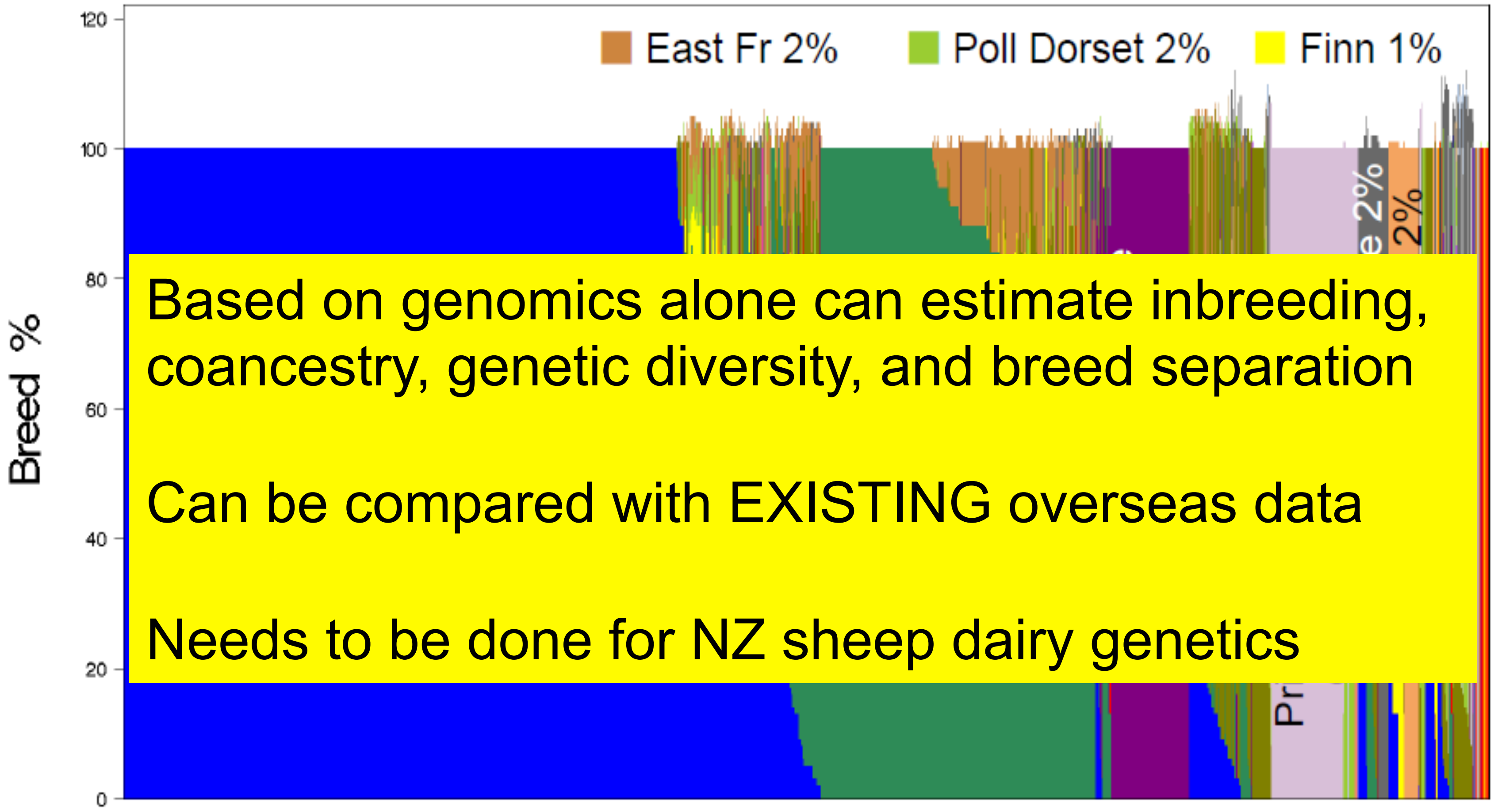
NZ SHEEP - SIL RECORDED BREED COMPOSITION



Based on genomics alone can estimate inbreeding, coancestry, genetic diversity, and breed separation

Can be compared with EXISTING overseas data

Needs to be done for NZ sheep dairy genetics

Figure 1. SIL-recorded breed composition of the 13,468 SIL recorded animals (including SIL animals not in the GWS flocks). SIL rounding off rules can result in totals exceeding 100%.

INTERNATIONAL COMMITTEE FOR ANIMAL RECORDING - ICAR

World-wide organization for the standardization of identification,
performance recording and evaluation of farm animals.

establishes rules and standards and specific guidelines for
- Identification of animals
- Registration of parentage
- Recording performance and evaluation
- Specific for each trait

Dairy Sheep working group

Welcome to the ICAR web site

- International Committee for Animal Recording
- Comité International pour le Contrôle des Performances en Élevage
- Internationales Komitee für Leistungsprüfungen in der Tierproduktion
- 國際畜政聯盟

ICAR
Via Savoia 78, sc. A int. 3
00198 Rome, Italy
E-mail: icar@icar.org

Highlights

- ICAR Newsletter - June 2014
- ICAR Technical Series no. 17. "Challenges and benefits of health data recording in the context of food chain quality, management and breeding" (freely available for downloading)
- ICAR Technical Series no. 16. "International Strategies and New Developments in Milk Analysis" (freely available for downloading)
- Interbeef: Interbeef Code of Practice
- IDF/ICAR Project on Reference System for Somatic Cell Counting in Milk. More info: here

Vacancies at Interbull Centre

Two vacancies at the Interbull Centre (deadline for application: 29 August 2014)

Future Meetings

- ICAR Technical Meeting 2015. Krakow, Poland 10-12 June 2015 (Slides about Krakow presented at the Berlin Session)
- ICAR 40th Biennial Session, 24-28 October 2016, Puerto Varas, Chile.
  Contact the organisers: here

Previous Meetings

- ICAR 39th Biennial Session 2014. Berlin, Germany 19-23 May 2014.
  - Presented files (as PDF)
  - Pictures
- ICAR Technical Workshop 2013 and Health Data Conference Aarhus, Denmark (29-31 May 2013)
  - Presented files (as PDF)
  - Pictures

What's new

- Berlin 2014 - Presentations and pictures
- NEW ICAR Guidelines (v. 2012)
- ICAR approved "Permanent plastic eartags"
- Strategic Plan (2012-2015)
- ICAR in a changing environment for animal production (By ICAR President, Berlin 2014)
- Glossary by "Beef Working Group"

The on-line databases on:
- "The yearly cow

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Milk yield : results for some population (ICAR Berlin 2014)

Countries [2013]	Average MY per recorded ewe in liters (length in days) [a = TMY / b = TMM / c = TSMM / ref = reference length in days]		
	Yearlings	Adults	All ewes
CROATIA	[b]	[b]	[b]
East Friesian	99	137	122
Istrian Pramenka	132	142	145
Paška	79	101	101
CZECH REP.			[?]
East Friesian			218
GERMANY			[a]
East Friesian			245 (ref: 150)
Lacaune			320 (ref: 150)
FRANCE	[b]	[b]	[b]
Lacaune	237 (149)	306 (174)	289 (167)
Manech tête rousse	175 (140)	215 (163)	203 (161)
Basco-Béarnaise	136 (103)	194 (158)	183 (148)
Manech tête noire	104 (105)	155 (146)	151 (143)
Corse	89 (131)	147 (197)	137 (185)

Breeding schemes and selection criteria

(ICAR Berlin 2014)

FRANCE - 2013

	Number of AI progeny-tested rams (2013)	AI (2012) Fresh	Year of starting	Selection criteria
Lacaune	403	399,239	1968	(FY+PY+1/16F%+1/8P%) + 0.5 SCC + 0.5 Udder
Manech tête rousse	150	61,526	1977	FY+PY+F%+P%
Manech tête noire	27	7,010	1977	FY+PY+F%+P%
Basco-Béarnaise	49	15,355	1977	FY+PY+F%+P%
Corse	25	6,483	1992	MY

+ PrP : selection on scrapie resistance

Recording of other traits (ICAR Berlin 2014)

Countries [2013]	TRAITS REPORTED TO BE AT LEAST ON-FARM RECORDED
BELGIUM	none
CROATIA	Reproductive traits, Birth weight
CZECH REP.	Reproductive traits, Weights
FRANCE	Reproductive traits, Udder score (Lacaune only), Causes of culling
GERMANY (2011)	Reproductive traits, Udder score, Wool quality, Appearance, Longevity, Weights
ITALY	Morphological evaluation, Udder score (Sarda)
SPAIN	Udder score (Churra, Lacaune, Latxa, Manchega), reproductive traits

Recorded population - countries (ICAR Berlin 2014)

Countries	Size of population		Recorded population (official milk recording)		% recorded population
	#flocks	# ewes	#flocks	# ewes	
Italy (2013)		[5,484,000 [1]]	2,805	**399,610**	7.3%
Spain (2013)		>1,987,000 [2,850,000 [1]]	593	**359,781**	12.6%
France (2013) [2]	5,055	1,405,000	760	**305,490**	21.7%
Greece (2013)		>681,724 [7,200,000 [1]]	459	**85,345**	1.2%
Portugal (2011)	386	>41,129 [417,000 [1]]	338	**20,926**	4.8%
Slovak Rep (2013)		[162,000 [1]]	92	**10,306**	6.4%

[1] figures 2012 from STATFAO

[2] 536,460 in D recording

Recorded population - countries (ICAR Berlin 2014)

Countries	Size of population		Recorded population		% recorded population
	#flocks	# ewes	#flocks	# ewes	
Croatia (2013)	688	34,871	96	**8,354**	24.0%
Slovenia (2013)	115	5,750	41	**4,507**	78.4%
Czech Rep (2013)		[63,000 [1]]	30	**1,669**	2.6%
Canada (2013)	-	-	8	**1,485**	-
Germany (2013)	137	2,421	29	**666**	27.5 %
Belgium (2013)	14	1,500	-	**-**	-
TOTAL			**5,251**	**1,198,139**	

---

[1] figures from STATFAO

Molecular information (ICAR Berlin 2014)

Countries [2013]	FILIATION TEST	PRP GENOTYPING	OTHER
FRANCE	870 rams progeny-tested	14,649 analysis (use in selection)	SNP genotyping (about 6,800) for experimental genomic selection
ITALY		9,713 analysis (use in selection)	SNP genotyping for experimental genomic selection
SLOVAK REP.		6,577 analysis (use in selection	
SLOVENIA		1,781 analysis (use in selection)	
CZECH REP.		Yes (use in selection)	
SPAIN	33,684 animals	10,265 (use in selection)	

WHAT'S NEEDED FOR AN NZ BREEDING PROGRAM?

Breeding objectives

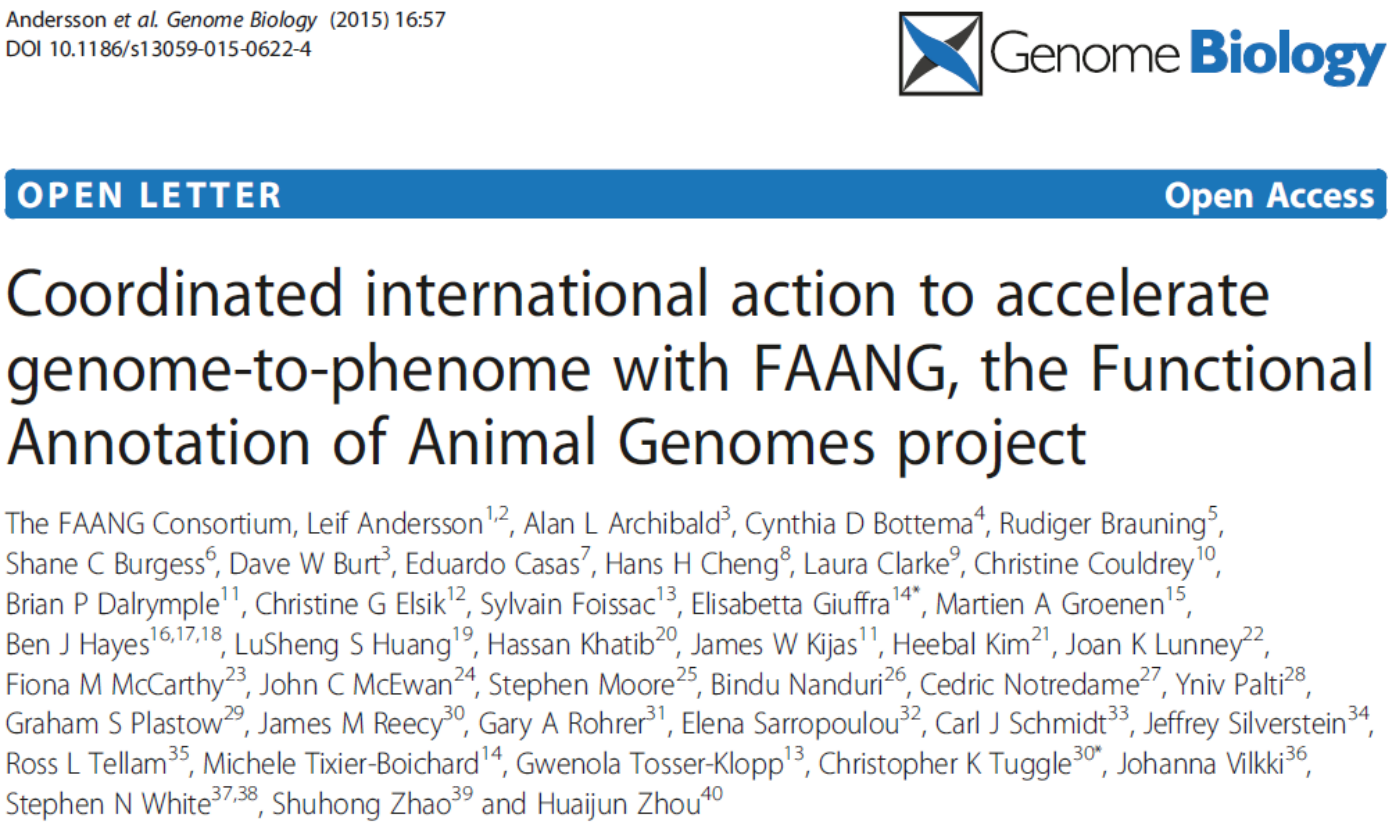
Trait definitions

Recording system
  Parentage
  Individual animal recording
  meta data/ contemporary group

Data storage – training set

Analysis & dissemination of breeding values

The Research Community is mobilizing….



Andersson *et al. Genome Biology* (2015) 16:57
DOI 10.1186/s13059-015-0622-4

Genome **Biology**

OPEN LETTER **Open Access**

Coordinated international action to accelerate genome-to-phenome with FAANG, the Functional Annotation of Animal Genomes project

The FAANG Consortium, Leif Andersson[1,2], Alan L Archibald[3], Cynthia D Bottema[4], Rudiger Brauning[5], Shane C Burgess[6], Dave W Burt[3], Eduardo Casas[7], Hans H Cheng[8], Laura Clarke[9], Christine Couldrey[10], Brian P Dalrymple[11], Christine G Elsik[12], Sylvain Foissac[13], Elisabetta Giuffra[14*], Martien A Groenen[15], Ben J Hayes[16,17,18], LuSheng S Huang[19], Hassan Khatib[20], James W Kijas[11], Heebal Kim[21], Joan K Lunney[22], Fiona M McCarthy[23], John C McEwan[24], Stephen Moore[25], Bindu Nanduri[26], Cedric Notredame[27], Yniv Palti[28], Graham S Plastow[29], James M Reecy[30], Gary A Rohrer[31], Elena Sarropoulou[32], Carl J Schmidt[33], Jeffrey Silverstein[34], Ross L Tellam[35], Michele Tixier-Boichard[14], Gwenola Tosser-Klopp[13], Christopher K Tuggle[30*], Johanna Vilkki[36], Stephen N White[37,38], Shuhong Zhao[39] and Huaijun Zhou[40]

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THANKS

Kijas, Barendse, Bottema, Brauning, Chamberlain, Clarke, Dalrymple, Hayes, McEwan and Moore.

DAIRY SHEEP GENOMICS & GENETICS

What can genetics & genomics add?

- Recording systems
- Breeding values and indices
- Breeding scheme design
- Source dairy sheep genetics in NZ: Dorset & East Friesian ….?????
- Measure NZ genetic variation and inbreeding
- Genomic selection
- Identify sources of international dairy sheep genetics
- Typically ~50% of efficiency and productivity gains come from genetics

Invermay Animal Genomics Team

- Estimation of eBVs and mBVs for sheep and deer via SIL
- Development of genotyping platforms for sheep, cattle, deer, salmon……
- ISGC and other international collaborations
- BLNZG, FarmIQ, PGGRC & Deer genetics research
- Plant and Aquaculture genomics

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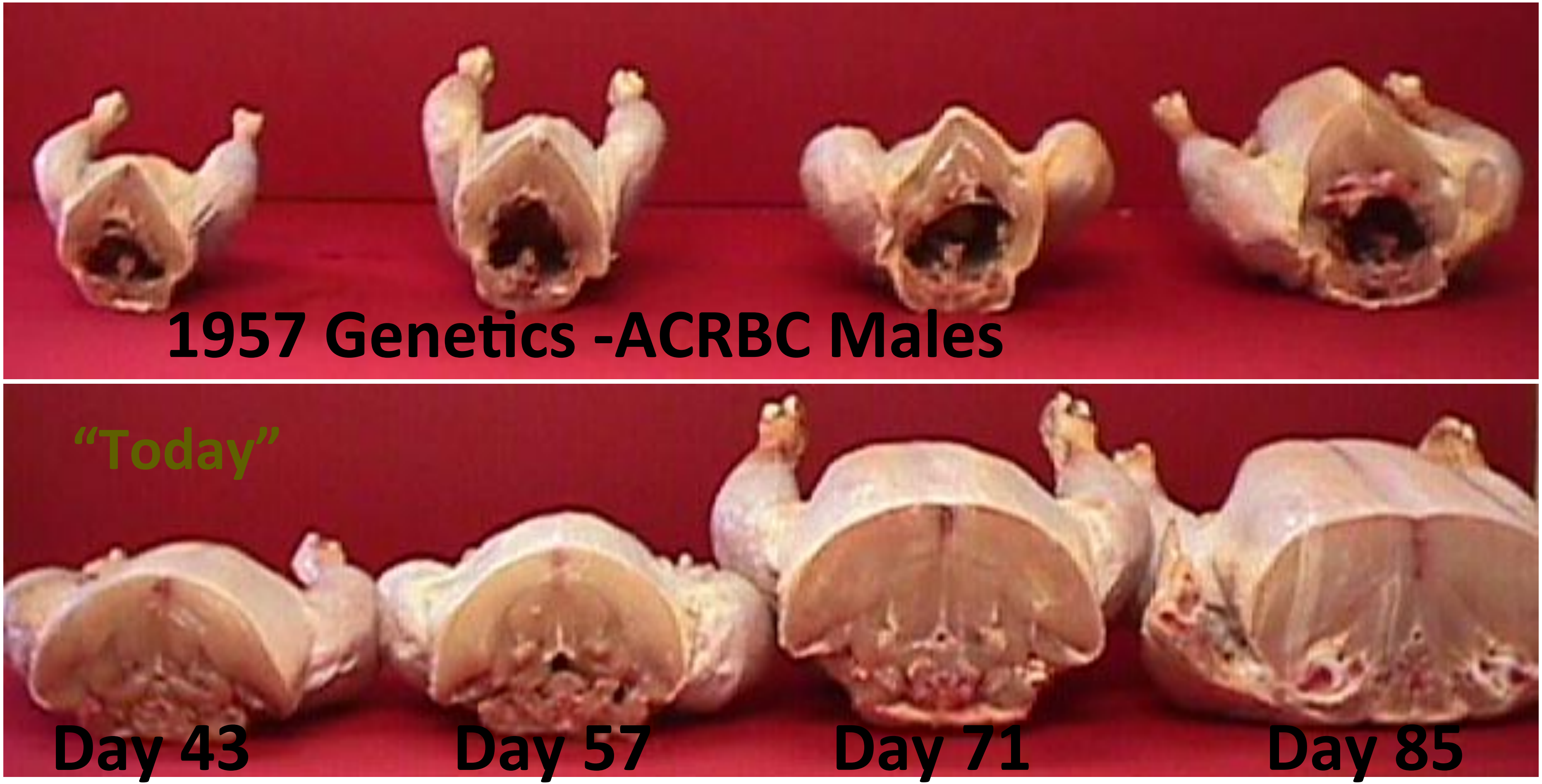
WITHIN BREED SELECTION



(Havenstein *et al*., 2003a)

DAIRY SHEEP

Niche specialised or artisan products

Demanding markets

Consumer health and nutrition traits

Food safety – subclinical mastitis SCC

Complex selection objectives

Expensive phenotypes

Genomics/Phenomics tools well suited

CORE FUNDING PROJECT

Assay genetics in NZ

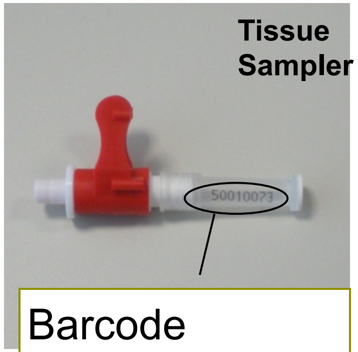
Look at breed composition

Run HD

Partnership for GRM, parentage, breed, breeding values,

NZ ALREADY HAS THE TECHNOLOGY……………

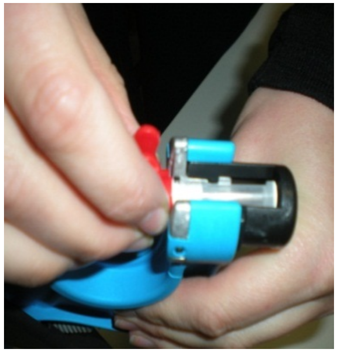
1

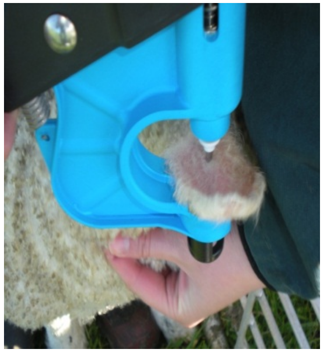


Tissue Sampler

Barcode Number = EID Tag number

Applicator





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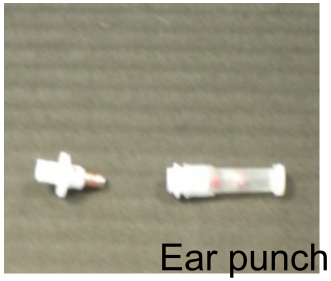
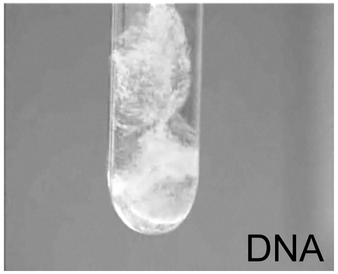
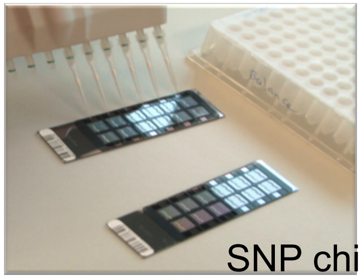


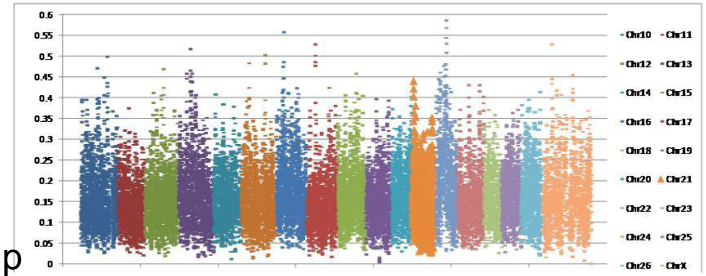
Ear punch



DNA



SNP chip



3

Trait prediction equations → mBV + eBV = gBV → gBV Report sent to breeder for selection decisions

mBV= molecular breeding value; eBV= estimated (phenotypic) breeding value; gBV=genomic breeding value

LATEST CHIP

Name	Annotation
MSTN.1	GDF8
Myostatin_1	GDF8
oar3_OAR2_118150665	GDF8
Booroola_FecB_1	booroola
oar3_OAR6_29382188	booroola
SpiderLamb_FGFR3_1	spiderlamb
RXFP2_insert_L2	horns
RXFP2_insert_L1	horns
RXFP2_insert_R1	horns
RXFP2_insert_R2	horns
15k_OAR13_46225660	scrapie
oar3_OAR13_46225660	scrapie
15k_OAR13_46225714	scrapie
oar3_OAR13_46225714	scrapie
15k_OAR13_46225764	scrapie
15k_OAR13_46225765	scrapie
15k_OAR13_46225766	scrapie
BCO2	BCO2

Name	Annotation
15k_OAR17_4832881_a	TMEM
15k_OAR17_4832881_b	TMEM
15k_OAR17_4832914	TMEM
15k_OAR17_4857244_a	TMEM
15k_OAR17_4857244_b	TMEM
15k_OAR17_4857272	TMEM
15k_OAR17_4857350	TMEM
15k_OAR17_4857385_a	TMEM
15k_OAR17_4857385_b	TMEM
Callipyge_1	callipyge
PITX3	micropthalmia
oar3_OARX_50971224_dup	Inverdale
oar3_OARX_50971224	Inverdale

- Loss of function
- Literature
- Unpublished trait associated

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