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Enhancement of Bovine LD BeadChip and Bovine SNP50 for consolidation of genotype information and improved utility in different cattle breeds

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Outline

- Evolution of cattle genomics
- Development of genomic tools
- New tool development
  - Current
  - Future
- Some conclusions

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Evolution of Cattle Genomics

Osteopetrosis

Idiopathic Epilepsy

Pulmonary Hypoplasia with Anasarca

Tibial Hemimelia

Neuropathic Hydrocephalus

AM, Curly Calf

Fawn Calf, Contractural Arachnodactyly

K- Casein

BLAD

Coat Colour

DUMPS

DGAT1

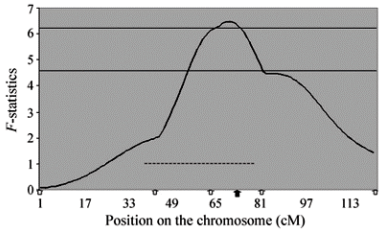
A2

CVM

Brachyspina

1990 1995 2000 2005 2010 2015

Microsatellite markers:
parentage and QTL scans



Single genes, QTLs, Candidate genes, recessives
Marker assisted selection

Genome sequencing, large scale SNP discovery, whole genome scans
GWAS, GBLUP

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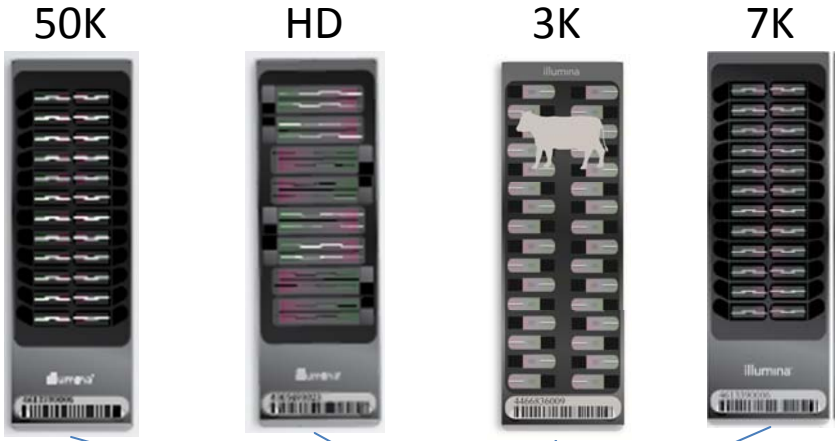
Evolution of Genomic Tools



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New Tools for increased flexibility?

The Problem

- Our customer base
  - Breed Associations
  - Genetic evaluation providers
  - Commercial breeding organisations and AI companies
  - Research community
- The tests and applications required:
  - Parentage, recessives, HD, 50K, 7K for research and GEBVs
- Multiple sample submissions and/or multiple tests on multiple platforms

The Solution

- Combining multiple tests and applications on one platform
- Increase efficiency, reduce cost
- One Sample, One Stop: Turning 'Off-The-Shelf' SNP Chips into Informational Powerhouses

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The Opportunity

Chip for

tion

6:00

MN -
low

to

custom high-density arrays and provides a significant benefit to customers who want to add newly discovered content after the initial design period is completed."

extending the application of genomic information to more animals than ever before. The BovineLD BeadChip complements the

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What did we do?

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- 7k LD SNPs
- Additional imputation SNPs
- SNPs for SNP to microsatellite imputation
- Public recessives and trait SNPs
- Royalty bearing SNPs

Imputation SNPs

	No. SNPs
Bovine LD	6909
3K	518
50K	702
HD	479
new markers	45
Total	8653

SNPs chosen by USDA

Objective:

- Filling in gaps and taking into account MAF
- Ease transition from 3K to 7K
- Increase imputation accuracy?
- Increase utility in other breeds?

Imputation SNPs

Genomic Evaluations – USDA

	Bovine3K*	BovineLD*	GGP**
No. SNP used	2,900	6,909	8,031
Call Rate	-	99.4%	>99%
Imputation Accuracy Holstein	95.9%	98.9%	99.2%
Jersey	94.6%	98.3%	98.9%
Brown Swiss	93.9%	97.9%	-
Reliabilities		+5% more than 3K	+0.3% more than 7K

*Figures courtesy of USDA, Based on 19,515 animals since Nov 2011
** Since March 2012

Parentage

- 121 USDA parentage SNPs
  - These are also within the original 7K
- As part of the masking and reporting developed for the chip we are able to pull out the SNPs and provide parentage assignments if required
- SNP to Microsatellite imputation

SNP to Microsatellite Imputation

- Dr Matthew McClure, USDA Beltsville
- Imputation of microsatellite alleles from SNP haplotype data
- Inexpensive and efficient way to transition from microsatellite- to SNP-based parentage verification without having to genotype a generation with both marker sets

SNP to Microsatellite Imputation

- 420 SNPs included to enable the imputation
- Impute microsatellite alleles for the ISAG recommended bovine parentage panel with >98% accuracy in 4 breeds
- Majority of cases a haplotype is only associated with one microsatellite allele, even across breeds
- ~5% of haplotypes associate with a different allele across breeds
  - But some patterns emerging and further work underway to explain some of the remaining anomalies and single marker non-inheritance

Dr Matthew McClure, personal communication

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Recessives

Public

Osteopetrosis (Marble Bone Disease)
Alpha Mannosidosis
Citrullinemia
DUMPS
BLAD
Factor XI
Hypotrichosis_PMel17
Idiopathic Epilepsy
Beta Lactoglobulin
Holstein Haplotypes1 USDA
Holstein Haplotypes2 USDA
Holstein Haplotypes3 USDA
Jersey Haplotypes1
Dun Colour
Coat Colour (346, 358, 373) & Dilutor
Chondrodysplasia
Beta Casein A/B
Kappa Casein I
Kappa Casein II
Y chromosome infertility
Calpain 316
Calpain 4751
Calpain 530

Royalties

Tibial Hemimelia
Pulmonary Hypoplasia with Anasarca
Neuropathic Hydrocephalus
Hypotrichosis_KRT71
Arthrogryposis (Curly Calf, AM)
Fawn Calf Syndrome or Contractural Arachnodactylyl
Beta Casein A2
Brachyspina
CVM

Summary

- One sample, multiple testing options
  - 6909k LD SNPs
  - 1744 additional imputation SNPs
  - 420 SNPs for SNP to microsatellite imputation
  - 23 Public recessives and trait SNPs
  - 9 Royalty bearing SNPs

- Reach back option
  - Retrieve additional information retrospectively

Future Add-on Content and Customised Chips

GGP Version 2

- Further add-on content for beef
- Many additional recessives

Higher Density Chips

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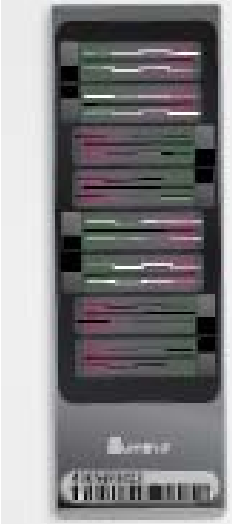

BovineHD

~777K SNPs

BovineSNP50

~50K SNPs

BovineLD

~7K SNPs

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Objectives

- More informative for beef
- More Bos Indicus friendly
- Ability to get recessives and traits all on the same chip

Conclusions

- Cattle genomics has evolved rapidly and is being widely implemented in commercial breeding and research
  - Genomic evaluation
  - Parentage and Identity
  - Recessive defects
- Add on capability to DNA chips has enabled development of new a tool to satisfy multiple testing requirements from one sample submission
- Further developments underway to enhance higher density DNA chips

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Thank you for your attention

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