Practical applications of genomics in livestock

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The challenge for Livestock Production

<u>2050:</u> Feeding 9 billion people within the carrying capacity



of planet earth

2 times more with 2 times le**ss**





Challenges for Livestock (Production)

Measuring and predicting (new) phenotypes for:

On-farm management

- Fine-tune nutrition, etc.
- <u>Predict</u> status: disease, pregnancy
- Breeding purposes
 - Measuring (new) traits
 - <u>Predict</u> breeding value (for genomic selection)

=> Genomics: measure and predict an animals' phenotype



Genomics applications for breeding purposes

Marker assisted selection & Genomic selection





Marker-assisted selection

 Selection (partly) based on few genetic DNAmarkers linked with QTL

Limited uptake:

- A small part of genetic variance captured
- QTL discovery costs are high

Availability of genome-wide dense markers enabled <u>'Genomic Selection'</u>



Genomic Selection

Genome of animal X (SNPs A, B, ..., J):



Breeding value animal X = A1 + A2 + B2 + B2 + ... + J1 + J2



200 alleles per line.dat - WordPad

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GGGGCCTGCCCGC

AAGGCTTGCATTGC

GAGGCCTGCCCTGC

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GGGGACCGCACCGC

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GAGGCCCGCACCGT

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AGGGACT

GGGGACO

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GAGGCCT

GAAGATI

GAGGCTC

AAGGACT

GGGGACI

AAGGACT



SNP chips:

Pigs: 64k

Poultry: 57k

GTCCAACTCCGGCTGCACGCTCGGCC LATCTAATTTCAGC-ATACGCTCAGCC LCGCCAATTTCGGC-GTACGCGCGGCC LATCTAATTTAAGTTGCACGCTTAGCC JAGCTAATTCCAGCTGCACGCGCGGCC LATTCAATTTCGGCCGTACGTTCAACC LATCCAATTTCGGCCGCACGCGCAGCC **JATTCAATTTCAACTGTACGCTTGATC** FATCCGGTCTCAGCCGCACGCGCGATC **JATTTAATTTAGGTTATATGCGCAAT** CTCCGATTCCGGCCGCACGCGCGAC1 LATTTAATTTC-ATTACACGCGCGGTT SATTCAACTTC-GTTGCACGCGCGGTC LATTTAATTTCAGTTGCACGCGCGGCC FATCCAATTTCGGTTGCACGCGCGGCC LATCTAACTTCAGTCATACGTTCAATC **JATCCAACTTCAGTCATACGCGCGGCC JATCTAATTTAGGTTGTACGTGCAGTC** CTCCAACCCCGGCTGCACGCGCGGTC LATCCAATTTA-GTTGTACGCTCGGT1 FATCCGGTTTC-GCTGCACGCGCGGCC LATCCAATTTCAGCTGTATGCTCGATT LAGCCAGCTTCGGCTGCACGCTCGGCC LATCTAATTTA-GTTGTACGCTTGGT1 LAGCCAACTTC-GTTGCACGCGCGGCC

Cattle: 6k, 54k, 640k & 777k SNP

Whole genome sequence:

Cattle: 3,500,000,000 base pairs

<u>>10,000,000 SNP ???</u>

12 2

Adobe

200 allele.

CTCAGCTGCACGCTCGGCC TTCGGTTACACGCTTAGTC CTCGGCTGCACGCTCAGCC TTCAGTTGCACGTTCAAT1 TCCGGCTGCACGCGCGGCC **TTCGGTTATACGCTTAGTC** TTCGGCCGCACGCGCGGTC TTAGGT-ATACGCTTAGTC TTCGGC-ACACGCGCGGCC TTCAATTATACGCGCAACC TTCGGCTGCACGCGCAGCC **TTAAGCTGTATGCTTGGT**(TTCAGCTGCACGCGCGGCC TCAGGTTGCACGCTCAGT1 TCCGGCCGCACGCGCGGCC TTCAGCTATACGCGCAAT1

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Reference data

Key for accurate prediction

Size reference dataUp to 16,000 animals

=> Increasing reference data <u>improves accuracy GS</u> for all traits



			Genomic selection in Irish dairy cattle breeding scheme.			
	Genomic selection	on	Nofima			
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	Arnhem, 16 oktober 2006		Genomic Selection will be possible in VikingGene	tics in August. The breeding		
	Ministry of Agriculture & Forestry Print	🛅 Email 🖂 RSS 🔊	plan will be far more effective and we will be abl progress by 50% or more. At the moment we wo researchers from Aarhus University in introducin	e to improve the breeding rk closely together with g Genomic Selection.		
H te	LIC salutes breeding revoluti	on 7	h _p -lanuosc.2008 a new cot of markers became available. This	sot bas 60.000 markers		
g	4:00AM Thursday Oct 09, 2008 By Owen Hembry	- 1	Genomic Selection traits of an animal markers to test for			
G S G G By V	New DNA breeding technology is being launched o Kiwi farmers outstrips expectation, says listed ani co-operative LIC. Speaking at the annual meeting yesterday, chairma	Genomic Selection	ion-A Practical Explanation			
it	introduced in the 1950s.	A	ugust 21, 2008			
Ge	"The cumulative effect to the dairy industry will be dollars in years to come."	ince December, 2007 roughly 15,000 sing a technology called the Illumin eveloped in a partnership between ervice, the National Association of A	0 North American dairy bulls have been genotyped a BovineSNP50 BeadChip. This technology was Illumina Inc., the USDA Agricultural Research Animal Breeders, Merial, and researchers at several			
thi pri LI(ge thi	LIC's (Livestock Improvement) genomic selection part their DNA, compared with a conventional method to several cows and then production-testing the daugnters of milk.	ther universities and institutes. The rate ability to carry out 54,000 DNA main \$250 per animal. These single when they come into	major breakthrough delivered by this technology is arker tests simultaneously, for a modest cost of less nucleotide polymorphism (SNP) markers, which News Dairy Beef Products Technology Technology - Genomics	Repro Company Contact		
sa	Current selection systems could return an increase of 1.3	per cent in milk	The Genomics Revolution Is Upon Us	Accelerated Genetics		
	production from a cow in a year but LIC expected the new improve that result by at least half.	DNA process to	Genetic progress just got faster with the release of <u>Genomic</u> Evaluations during the recent Dairy Sire Summary. A quick bit of history - prior to 1935 there was no national program for evaluating dairy cattle breeding and no real genetic progress was made. Over the past 74 years various programs and/or traits have been introduced, each increasing the rate of genetic progress in differing amounts and improving the dairy cow. The recent employment of genomic evaluations is projected to have one of the SEARCH			
	Chief executive Mark Dewdney said the initial estimate fo genetic sales in the first year was about 300,000 insemin holding orders for about 700,000 straws.	r DNA-proven ations <mark>but LIC</mark> was				

Genomic selection for new traits

For traits that are hard or expensive to measure

Allows for: ⇒ 'deep-phenotyping' difficult to measure traits (e.g. progesterone, methane emission, etc.)

⇒ Re-focussing breeding goal

Reference data is required!











Building unique reference data

- Unique data available from experiments & research herds
- RobustMilk (EU-project) combines cow data 4 countries:
 - Feed intake
 - Progesterone measurements
 - Database of 1,000 2,000 animals

Interest to increase this database
 Contact <u>roel.veerkamp@wur.nl</u>





GS - Future perspectives

Selection for "new" traits
 More balanced selection

Complete populations are genotyped
 Better identification best breeding animals

Extensions towards whole genome sequence selection
 Closer to causal loci



Whole genome sequence data

Meanwhile the Price of Large-Scale Genetic Analysis to Discover and Utilize SNPs Dropped Precipitously...







Genomics: more than DNA





Genomics applications for on-farm management









Requirements for on-farm management

- Measuring for monitoring:
 - Cheap
 - Accurate
 - Fast
- Different levels
 - Individual
 - Herd





Depending on purpose, find a balance between accuracy and costs



Pilot predicting pregnancy in dairy cows

Protein profiles on day 21 after insemination

- Using 18 pregnant & 14 non-pregnant cows & 1 protein
- 93% pregnant animals correct classified (sensitivity)
- 67% of non-pregnant animals (specificity)
- Pregnancy status can be predicted using milk samples
- Results are not reliable enough yet to develop practical test







Serum protein profiles to predict infectious disease status in pigs

Pilot infection experiment
 Control + 2 experimental groups



 Classification
 Use protein profiles for classification of animals (PLS regression)

Leave-one-out cross-validation
 Predict every record using the rest of the data



True and predicted disease status

		Day 5				Day 19		
	-	True status				True status		
		PPV	Control	PRRSV	PPV	Control	PRRSV	
predicted status	PPV	2	2	1	5	3	4	
	Control	4	7	0	1	4	0	
	PRRSV	1	0	8	2	0	3	

Using 50 preselected proteins on combined data of day 5 and 19

Serum protein profiles have potential for detection of (viral) infection in pigs in early phase of the disease

Classification accuracy was moderate - good



Perspectives on-farm genomics applications

Potential is huge

• Bridging gap between DNA and phenotype

Few practical applications so far

Large data sets needed to allow accurate prediction





Unravelling black box (approaches)

Presented approaches driven by statistical associations, not causality

Opening black box' may improve performance
 Improved understanding underlying mechanisms

Practical applications generate large data
 This helps to increase understanding



Conclusions

Predicting & measuring phenotypes using genomics:

- Requires <u>sufficiently large data</u> for deriving prediction equations
- Requires <u>appropriate statistical methodology</u>:
 y = b₁X₁ + b₂X₂ + ... + b_nX_n



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