Introduction to Animal Breeding & Genomics

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Overview

- Changes to traditional animal breeding
- Using DNA in animal breeding
- What is a SNP?!
- De-mystify genomic selection!!
Traditional Animal Breeding

• Calf has weaning weight of 250 kg
• Bull reliability 25%
Bull completes his progeny test

- Bull has 100 calves on the ground
- More of his DNA expressed in the population
- Bull reliability increases to ~80%
At birth we know about parts of the calf DNA
Calf BV reliability increases to ~ 58%
Equivalent to 54 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?
What is a SNP?

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

• Single **Nucleotide Polymorphism** Change

... `ACGTACGTCAATGACTTTTTTACGTAT...`

... `ACGTACGTA CAATGACTTTTTTACGTAT...`
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

<table>
<thead>
<tr>
<th>SNP</th>
<th>Var</th>
<th>Carcass Fat</th>
<th>Wean Wt</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>A</td>
<td>+5</td>
<td>-0.6</td>
</tr>
<tr>
<td>1</td>
<td>G</td>
<td>+20</td>
<td>-0.4</td>
</tr>
<tr>
<td>2</td>
<td>A</td>
<td>12.3</td>
<td>-0.6</td>
</tr>
<tr>
<td>2</td>
<td>T</td>
<td>-14.46</td>
<td>+20.2</td>
</tr>
<tr>
<td>n</td>
<td>A</td>
<td>+25</td>
<td>+5.2</td>
</tr>
</tbody>
</table>
Genomic selection

- Increase accuracy of selection at a younger age

- Traditionally used parental information
  - Progeny = \( \frac{1}{2} \) mother + \( \frac{1}{2} \) 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

(G)EBV

Full sib family

The Irish Agriculture and Food Development Authority
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

Applied Biosciences (2004)  $15,000,000

Illumina (2011)  $15,000
Different SNP platforms (levels of DNA information) available

54,609 SNPs

50k chip

IMPUTE

15,000 SNPs

IBD

777,962 SNPs

High Density chip
Imputation

Sire

.....TCACCGCTGAG.....
.....CAGATAGGATT.....

Offspring

.....??G??????A??.....
.....??T??????T??.....

Offspring
Imputation

Sire

......TCACCGCTGAG......

......CAGATAGGGATT......

Offspring

......CAGATAGGGATT......

......??T????????T??......
Accuracy in dairy populations

Sire is known – 99%

No sire or MGS – 98%
Parentage

Sire

..TCACCGCTGAG...
..CAGATAGGATT..

Offspring

..??G???????A??....
..??T???????T??.....
Parentage

Sire 1 ........TCGGGCTGTG........
Sire 2 ........CAGATAGGATT........
Sire 3 ........TCACCGCTGAG........
Sire 4 ........CAAATAGGGCTTT........

Database

Sire

Offspring

........TCACCGCTGAG........
........CAGATAGGATT........
........??T??????T??........

Sire

............
........TCACCGCTGAG........
........CAGATAGGATT........

......??A??????C??....
......??T????????T??.....

X

Offspring
80% of parentage errors corrected using this method
Additional advantage of the IDB

• Screening of
  • Deleterious recessive disorders
  • Congenital disorders
  • Major genes
Deleterious recessive genetic disorders

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

Has CVM

Carries CVM

No CVM
Screen for CVM through genotyping

- 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
- Customised chip developed for Ireland for beef & dairy animals
- SNP information can also be used to predict parentage accurately & identify disorders
Thank you for your attention