ACCURACIES OF MALES AND FEMALES WITH GENOMIC INFORMATION ON MALES, FEMALES, OR BOTH: A BROILER CHICKEN EXAMPLE

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QUESTIONS

- Is genotyping females useful for genetic evaluation?
- Why realized accuracies are lower than theoretical ones and vary by trait?
- Can accuracies be boosted by SNP selection/weighting in chicken?
- Is genomic evaluation maturing?

Reliabilities for young bulls with different training populations

- Holsteins, ~ >500k genotypes
- BLUP: 36.4
- GEN
  • 25k bulls: 67.9
  • 25k bulls+30k cows: 68.3

DATA STRUCTURE

- ~200k broiler chickens with phenotypes
- 4 traits
- ~16k genotyped animals
- 16 Micro-generations

PHENOTYPES FOR REFERENCE POPULATION

<table>
<thead>
<tr>
<th>Trait</th>
<th>$h^2$</th>
<th>Animals</th>
<th></th>
<th></th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td></td>
<td>All</td>
<td>Males</td>
<td>Females</td>
</tr>
<tr>
<td>1</td>
<td>0.28</td>
<td>12748</td>
<td>4648</td>
<td>8100</td>
</tr>
<tr>
<td>2</td>
<td>0.25</td>
<td>9567</td>
<td>2010</td>
<td>7557</td>
</tr>
<tr>
<td>3</td>
<td>0.49</td>
<td>2213</td>
<td>2213</td>
<td>0</td>
</tr>
<tr>
<td>4</td>
<td>0.22</td>
<td>9624</td>
<td>2017</td>
<td>7607</td>
</tr>
</tbody>
</table>

METHODS

- Single-step GBLUP (Aguilar et al., 2009)
- 13k reference population, 3k validation
- Realized accuracy: $\text{corr}(y, \text{GEBV})/h$
Realized accuracies with male, female or both genotypes - Trait 1

Realized accuracies with male, female or both genotypes – Trait 2

Realized accuracies with male, female or both genotypes – Trait 4

DOUBLE COUNTING

\[ \text{phenotype } y = +Zu + e \]
\[ \text{Deregressed proof } DP = +Zu + e \]
\[ \text{DP} = \text{DP}(y_{\text{male}}, y_{\text{fem}}, ...) \]
\[ y_{\text{fem}} = +Zu + e \]

Reduction of accuracy for bulls and cows added (Wigans et al., 2011)
Corrections ad hoc
No double counting with single-step

Sources of information

Decomposition of GEBV in Single-step

\[ \begin{bmatrix} Z' Z + A_1 + \begin{bmatrix} 0 & 0 \\ 0 & G \end{bmatrix} A_2 \end{bmatrix} \tilde{u} = Z'My \]

\[ \text{GEBV} = w_1 CD + w_2 PA + w_3 PC + w_4 DGV + w_5 PI \]
**GEBV for young animals**

\[ GEBV = w_2 PA + w_4 DGV + w_5 PI \]

If no genotype: \( GEBV = PA \), little improvement with genomics if animal not genotyped.

**Realized accuracy under selection**

![Chart showing realized accuracies](image)

- Muir (2007)
- Bijma (2012)

**Why realized accuracies differ by sex?**

Bigger selection pressure on females.

Selection graph for GEBV; possibly more differential selection EBV from BLUP.

**Why realized accuracies differ by traits for similar \( h^2 \)**

![Graphs showing differences](image)

**Increasing accuracy of GEBV by SNP weighting**

- \( G = ZZ' \) unweighted genomic relationships
- \( G = ZDZ' \) weighted G

- Accuracy with weights better if based on SNP regions
- 30 SNP regions best in dairy; 1500 regions (Su et al., 2014)
- Effect of small effective population size? (Goddard, 2008; Daetwyler, 2009)
- Small or no improvement in commercial evaluations when many genotypes
ssGBLUP with large number of genotypes

- **Full inverse of G**
  - Cost cubic
  - Limit ~ 150k genotyped animals

- **APY inverse of G**
  - Cost linear for most animals
  - Cost for 500k genotyped animals as for 60k animals with full inverse

\[ \text{Corr}(\text{GEBV}, \text{GEBV}_{\text{APY}}) > 0.99 \]

**CONCLUSIONS**

- Benefits of genotyping mainly for genotyped animals
- One sex benefits from genotypes of other sex with phenotypes
- Realized accuracy depressed by selection
- Limited number of LD blocks in commercial populations
- Genomic selection mature by end of 2015 (??)

**Acknowledgements**

- **Cobb-Vantress**
- **Collaborators**

  - Shogo Tsuruta
  - Daniela Laurenza
  - Yutaka Masuda
  - Breno Fragomeni
  - Luna Zhang
  - Andres Legarra

  - Studies + papers + social
  - APY + pigs
  - Sound theories + papers
  - Programming + advice
  - Children + WAS

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