How to select foreign young bulls when no domestic information is available?

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INRA GABI G2B
20/05/14
The genomic era: new contrasts

North-American consortium
EuroGenomics consortium
Other countries implementing GS

Surplus
Balance
Deficit
« GenoSouth » project

• Increased genetic progress in countries with GS
• Gap between North and South is becoming bigger and bigger

⇒ How to take advantage of genomic tools?

• Collaboration between INRA and large emerging countries:
  • Opportunities on the long-term?
  • Opportunities on the short-term?
### Information available for a breeding scheme

#### 4 country cases:

<table>
<thead>
<tr>
<th>Cases</th>
<th>Domestic scale</th>
<th>Foreign scale</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>Domestic sires</td>
<td>Foreign sires</td>
</tr>
<tr>
<td>1</td>
<td>EBV + GEBV</td>
<td>MACE + GMACE</td>
</tr>
<tr>
<td>2</td>
<td>EBV</td>
<td>MACE</td>
</tr>
<tr>
<td>3</td>
<td>EBV</td>
<td>none</td>
</tr>
<tr>
<td>4</td>
<td>none</td>
<td>none</td>
</tr>
</tbody>
</table>

#### Interbull members:
1. with GS
2. without GS

#### Outside Interbull:
3. Genetic evaluations
4. No genetic evaluations
Aim of the study

• Measuring the consequences on genetic progress regarding contrasted levels of information:

  Interbull members:
  1. with GS
  2. without GS

  Outside Interbull:
  3. Genetic evaluations
  4. No genetic evaluations

⇒4 scenarios to mimic selection choices
How to mimic selection choices

• Based on all breeding values available on the French scale:
  – National evaluations (EBV, GEBV)
  – International evaluations (MACE, GMACE)
  – Data transmitted to France/available in France on Foreign scales

• Then, cut off data according to country case

• Focus on:
  – Candidate bulls born between 2003 and June 2012
  – The 30 best animals on:
    • Production => INEL
      INEL = 0.98*(0.2*Fat yield + Protein yield + 0.5* Fat content + Protein content)

• Average of the genetic level, composition of the population
Holstein bulls with breeding values

On the FRA scale: with value at least for Milk production and $R^2 > 50$

<table>
<thead>
<tr>
<th>Cases</th>
<th>Production (INEL)</th>
<th>Fertility</th>
<th>Udder health</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>51,617</td>
<td>31,077</td>
<td>32,238</td>
</tr>
<tr>
<td>2</td>
<td>40,472</td>
<td>21,899</td>
<td>27,049</td>
</tr>
<tr>
<td>3</td>
<td>4,551</td>
<td>4,099</td>
<td>3,727</td>
</tr>
<tr>
<td>FS1</td>
<td>46,233</td>
<td>31,010</td>
<td>30,903</td>
</tr>
<tr>
<td>FS2</td>
<td>28,452</td>
<td>-</td>
<td>-</td>
</tr>
<tr>
<td>FS3</td>
<td>13,721</td>
<td>-</td>
<td>-</td>
</tr>
</tbody>
</table>

FS = foreign scale

Domestic + Foreign bulls: with & without progeny

Domestic + Foreign bulls: with progeny only

Only Domestic bulls: with progeny only

Only Foreign bulls: with & without progeny

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The best 30 bulls on Production

- Average genetic level of the top 30 bulls and range (min, max):
The best 30 bulls on functional traits

Fertility: despite the availability of young bulls GEBV on FS1, the average genetic level on the national scale significantly dropped relative to case1.

<table>
<thead>
<tr>
<th>Case 1</th>
<th>Case 2</th>
<th>Case 3</th>
<th>FS1</th>
</tr>
</thead>
<tbody>
<tr>
<td>2.38</td>
<td>2.03</td>
<td>1.71</td>
<td>1.12</td>
</tr>
<tr>
<td>3.2</td>
<td>2.96</td>
<td>2.44</td>
<td>2.97</td>
</tr>
<tr>
<td>Fertility</td>
<td>Udder health</td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

Average genetic level (in genetic standard deviation)

\[ \rho(\text{FRA}, \text{FS1}) < 0.80 \]

\[ \rho(\text{FRA}, \text{FS1}) \sim 0.90 \]
Conclusion (1)

• The highest genetic gain can be expected:
  – With the largest pool of candidates: foreign + domestic
  – With the youngest pool of candidates: including genomically selected bulls
⇒ In spite of domestic GE, there is a big gap between countries member of Interbull and the others

• Long procedures:
  – To implement GE
  – To be part of Interbull : 1/ selection choice + 2/ access to a large RP
  – To implement GS

• On the short-term:
  – Very tempting to look at foreign scales
⇒ Avoid broadening the gap, allow genetic improvement (genetic level, genetic diversity)
• Looking at foreign scales:
  – Can be hazardous for traits with low genetic correlations at the international level
  – Gathering, interpreting and comparing (G)EBV from different foreign scales requires expertise
  – No information on the local genetics and way to improve it

⇒ Not a solution on the long-term!
⇒ Looking at foreign scale should not prevent from investing efforts in genomic evaluations on the most relevant scale, i.e., the domestic scale
⇒ A need for support from the countries with GS
Thank you for your attention