Overview of the Mendelian Sampling Variance Test Pilot Study

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Behind the Scenes of the Pilot Study
Data Call & Requirements
Data Received
General Results
General Comments
Acknowledgments
✓ **2012**: Test software developed for Interbull service users
   (Tyrisevä et al, 2012)

✓ **2013**: During the IB meeting in Nantes got the ok to proceed for a pilot study

✓ **April 2014**: Data call and data reception

✓ **May 2014**: Results of the pilot study are discussed during the current ITC meetings
   ✓ ITC will decide if include the Mendelian Sampling Variance Test as part of the Interbull validation procedures.
Data Call & Requirements

- **Mandatory**: Protein, Somatic Cells Score, Stature
  - Traits with moderate-high $h^2$ ok to test on bulls and cows

- **Optional**: two traits with $h^2 < 0.1$
  - Low heritable traits to test on BULLS only
  - Software’s requirement of a minimum MS reliability of 0.1

- National Genetic Evaluation based on “Animal Models”
Data Received: Information per Breed

BSW | GUE | HOL | JER | RDC | SIM
---|---|---|---|---|---

120 | 20 | 100 | 40 | 20 | 10
Data Received: Traits

Graph showing the received traits with vertical bars for each trait, such as cc1, cc2, crc, dio, fan, fat, hco, hde, int, mas, mil, msb, msp, pro, rlr, scs, and sta.
## General Results for the Trend

<table>
<thead>
<tr>
<th>Trend outcome</th>
<th>Frequency</th>
<th>Percent (%)</th>
</tr>
</thead>
<tbody>
<tr>
<td>Trend did not deviated significantly from 0</td>
<td>82</td>
<td>42</td>
</tr>
<tr>
<td>trend deviated significantly from 0 but within +2%</td>
<td>63</td>
<td>32</td>
</tr>
<tr>
<td>trend deviated significantly from 0 and higher than +/-2%</td>
<td>50</td>
<td>26</td>
</tr>
<tr>
<td><strong>Tot PASSED</strong></td>
<td><strong>145</strong></td>
<td><strong>74</strong></td>
</tr>
<tr>
<td><strong>Tot FAILED</strong></td>
<td><strong>50</strong></td>
<td><strong>26</strong></td>
</tr>
<tr>
<td><strong>Grand Total</strong></td>
<td><strong>195</strong></td>
<td><strong>100</strong></td>
</tr>
</tbody>
</table>
## Protein – Trend Results for M&F-HOL

<table>
<thead>
<tr>
<th>PROTEIN</th>
<th>Frequency</th>
<th>Percent (%)</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>Males</td>
<td>Female</td>
</tr>
<tr>
<td>Trend did not deviated significantly from 0</td>
<td>7</td>
<td>0</td>
</tr>
<tr>
<td>trend deviated significantly from 0 but within +/2%</td>
<td>3</td>
<td>11</td>
</tr>
<tr>
<td>trend deviated significantly from 0 and higher than +/2%</td>
<td>7</td>
<td>5</td>
</tr>
<tr>
<td>Tot. PASSED</td>
<td><strong>10</strong></td>
<td><strong>11</strong></td>
</tr>
<tr>
<td>Tot. FAILED</td>
<td>7</td>
<td>5</td>
</tr>
<tr>
<td>Grand Total</td>
<td><strong>17</strong></td>
<td><strong>16</strong></td>
</tr>
<tr>
<td>Somatic Cells Score</td>
<td>Frequency</td>
<td>Percent (%)</td>
</tr>
<tr>
<td>---------------------------------------------------------</td>
<td>-----------</td>
<td>-------------</td>
</tr>
<tr>
<td></td>
<td>Males</td>
<td>Female</td>
</tr>
<tr>
<td>Trend did not deviated significantly from 0</td>
<td>11</td>
<td>0</td>
</tr>
<tr>
<td>Trend deviated significantly from 0 but within +-2%</td>
<td>4</td>
<td>11</td>
</tr>
<tr>
<td>Trend deviated significantly from 0 and higher than +-2%</td>
<td>0</td>
<td>0</td>
</tr>
<tr>
<td><strong>Tot. PASSED</strong></td>
<td><strong>15</strong></td>
<td><strong>11</strong></td>
</tr>
<tr>
<td>Tot. FAILED</td>
<td>0</td>
<td>0</td>
</tr>
<tr>
<td>Grand Total</td>
<td>15</td>
<td>11</td>
</tr>
</tbody>
</table>
## Stature– Trend Results for M&F- HOL

<table>
<thead>
<tr>
<th>Stature</th>
<th>Frequency</th>
<th>Percent (%)</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>Males</td>
<td>Female</td>
</tr>
<tr>
<td>Trend did not deviated significantly from 0</td>
<td>11</td>
<td>1</td>
</tr>
<tr>
<td>Trend deviated significantly from 0 but within +/-2%</td>
<td>3</td>
<td>8</td>
</tr>
<tr>
<td>Trend deviated significantly from 0 and higher than +/-2%</td>
<td>0</td>
<td>4</td>
</tr>
<tr>
<td><strong>Tot. PASSED</strong></td>
<td>14</td>
<td>9</td>
</tr>
<tr>
<td><strong>Tot. FAILED</strong></td>
<td>0</td>
<td>4</td>
</tr>
<tr>
<td><strong>Grand Total</strong></td>
<td>14</td>
<td>13</td>
</tr>
</tbody>
</table>
### Longevity – Trend Results for HOL Males

<table>
<thead>
<tr>
<th>Direct Longevity</th>
<th>Frequency</th>
<th>Percent (%)</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>Males</td>
<td>Males</td>
</tr>
<tr>
<td>Trend did not deviated significantly from 0</td>
<td>2</td>
<td>0.2</td>
</tr>
<tr>
<td>Trend deviated significantly from 0 but within +2%</td>
<td>1</td>
<td>17</td>
</tr>
<tr>
<td>Trend deviated significantly from 0 and higher than +2%</td>
<td>3</td>
<td>50</td>
</tr>
<tr>
<td><strong>Tot. PASSED</strong></td>
<td>3</td>
<td>50</td>
</tr>
<tr>
<td>Tot. FAILED</td>
<td>3</td>
<td>50</td>
</tr>
<tr>
<td><strong>Grand Total</strong></td>
<td>6</td>
<td>100</td>
</tr>
</tbody>
</table>
## CC2 – Trend Results for HOL Males

Lactating cow’s ability to conceive | Frequency | Percent (%) |
-----------------------------------|-----------|-------------|
                                  | Males     | Males       |
Trend did not deviated significantly from 0 | 1         | 20          |
trend deviated significantly from 0 but within +2% | 1         | 20          |
trend deviated significantly from 0 and higher than +2% | 3         | 60          |
*Tot. PASSED* | 2         | 40          |
Tot. FAILED | 3         | 60          |
Grand Total | 5         | 100         |
Software tested by 21 countries, no major difficulties encountered by the users

The majority of data has passed validation, only 26 % has failed it (50 out of 195 available data).

Inbreeding correction rarely applied (4 countries out of 21)

Adjustment for heterogeneous variance applied by the majority of the countries participating to the pilot study.

Female reliabilities mostly calculated by: Approximate reliability source method, K. Meyer and Misztal & Wiggans
Acknowledgments

MTT, WG & Participating countries