Council on Dairy Cattle Breeding

CDCB Services: Continuous Improvement

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Roadmap

- Disease resistance – continuous progress
- New bovine assembly (& co.)
- Genomic evaluations for crossbred animals
- Publication query
- Age at first calving
- Constructed dams
- Genomic Parent Average
- New formats
- Genomic nominators and genotyping labs QC
Disease resistance – continuous progress

- 6 health traits published officially in April 2018 (+ December 2017 test run)
- Official publication is starting point, not final result.
  - Enhancement on models
  - Breeds involved
  - Further developments

Disease resistance – Research on modeling

- Variance pre-adjustments
  - Account for difference in variance among lactations
  - Categorical traits are pre-adjusted using year-groups, lactation number, heritability
    - Livability (LIV) currently uses this pre-adjustment
  - Changes should be small if implemented
    - Most health traits have PTA correlations ~95% or higher among bulls with REL ≥ 50% in testing
Disease resistance – Breeds involved

- Jersey health records
- Sept. 2018 - 117,000 usable health records from 71,000 Jersey animals in 202 herds

<table>
<thead>
<tr>
<th>Health event</th>
<th>Number of records</th>
<th>Number of cows</th>
<th>Number of herds</th>
<th>Incidence</th>
</tr>
</thead>
<tbody>
<tr>
<td>Milk fever</td>
<td>53,807</td>
<td>35,986</td>
<td>78</td>
<td>1.2%</td>
</tr>
<tr>
<td>Displaced abomasum</td>
<td>50,490</td>
<td>33,916</td>
<td>70</td>
<td>1.0%</td>
</tr>
<tr>
<td>Ketosis</td>
<td>34,767</td>
<td>20,527</td>
<td>70</td>
<td>2.8%</td>
</tr>
<tr>
<td>Mastitis</td>
<td>85,826</td>
<td>55,093</td>
<td>160</td>
<td>11.9%</td>
</tr>
<tr>
<td>Metritis</td>
<td>60,453</td>
<td>40,782</td>
<td>74</td>
<td>5.7%</td>
</tr>
<tr>
<td>Retained placenta</td>
<td>49,687</td>
<td>32,920</td>
<td>73</td>
<td>2.3%</td>
</tr>
</tbody>
</table>

Disease resistance – Breeds involved

- Growth in the amount of Jersey health records received
  - Many traits have more than doubled the number of health records in the past 6 months
  - Depending on the trait, Jersey -3 to 6% of the amount of records compared to Holstein.
    - Jersey population is -14% the size of Holstein (based on yield data used for genetic evaluation)
  - Number of records needed for Jersey health evaluations will depend on the reliability deemed acceptable for these low heritable traits
Further developments

• Clinical mastitis PTAs submitted to Interbull for international validation
  • Not many countries submitting direct trait (CAN, FRA, BEL, NLD and ITA)
  • Genetic correlations U.S. SCS with foreign clinical mastitis is \(0.88\) \textit{(SCS has been a good proxy!)}

• Multiple-trait models
  • SCS and clinical mastitis
  • Health traits with other functional traits such as productive life or livability
  • Similar health traits (e.g., reproductive disorders, metabolic disorders)

New bovine assembly (& co.)

• New assembly changes SNP positions, which will likely impact haplotype creation and are expected to have slight impact on imputation result
• Smaller scale: changing of SNP position might affect haplotype calling
• Review of SNPs used for haplotype calling (inclusion of many causative mutations now available)
• CDCB new prediction SNP list 60k \(\rightarrow\) 80k
• Implementation: aim is December 2018
Crossbred evaluations

• How:
  • Predictions are based on purebred reference populations (i.e. SNP effects are breed-specific)
  • Crossbreds: combine single breed SNP effects based on BBR proportions

• Why:
  • CDCB is not promoting crossbreeding, nor the use of one breed or the other.
  • Committed to provide the best possible service to all farmers.
    • 35,000 animals not receiving a genomic evaluation
    • > $1,000,000 spent in genotyping (only) but no genomic evaluation results.

Crossbred evaluations (II)

• When:
  • Research conducted and presented by AGIL (2017)
  • Implementation plan developed by CDCB
  • Business rules under revision
  • Testing and review by industry
  • Expected 2019
Publication (reason) query

- Large # requests for clarification
- Why animals (don’t) receive an evaluation result?
  - Many rules apply and dynamic database (changes may apply after cutoff).
  - Editing and publication criteria may change over time.
  - Publication rules to be applied at cutoff and available immediately.
- Solution:
  - Tool to inform, at the beginning of the evaluation, the reasons why an animal is being published or not.
  - Will allow displaying evaluation history

Age at First Calving

- See Paul’s presentation
- Current status: under research (AGIL)
- Implementation plan to be defined as soon as research is completed at AGIL
- Expected delivery: 2019
Constructed dams

- See Paul’s presentation
- CDCB is communicating with ICAR (International Committee for Animal Recording)
  - Global standard for livestock animal recording
  - Genomics and its role in pedigree identification.
- International standard for constructed dam ID
- Definitions on how to distribute this information

Genomic Parent Average (gPA)

- Industry cooperators’ request
  - Distribute gPA instead of traditional P(T)As in genomic evaluation files
- Implementation in progress (AGIL released software)
  - Probably November 2018.
- Included in **new format** for genomic evaluation files only.
New format for genomic evaluations

- So-called "CSV" and "XML" files, containing genomic evaluations only.
- More than 6 months of discussions with different groups (Nominators, Breed associations, NAAB committees, DRPC).
- Objective: Total flexibility to future changes, standardization of fields and formats.
- Initial test files released (there will be some modifications)
- Implementation:
  - Expected November 2018.
  - Long transition phase
  - XMLs will be discontinued.
- Revision of all other input/output formats will follow.

Quality control of data providers

- Continuous evaluation of the industry providers performance in terms of data quality, their interaction with CDCB systems and their reactivity and accuracy in correcting records.
- Early detection of potential issues
- Open communication channels with providers for problem solving

Objective:
Maintain the highest standard of data quality
Quality control of data providers

- **Genomic nominators**
  - Yearly workshop (2017 / 2018)
    - Including metrics for routine (monthly) evaluation of performance
  - 2017 – Collection of SOP and first formal nominator audit
  - 2018 – Monthly request for feedback on potential issues related to data submission
  - Reports, web stats and graphs of performance (and trajectory) available.

<table>
<thead>
<tr>
<th>Condition</th>
<th>September 2017</th>
<th>October 2017</th>
<th>November 2017</th>
<th>December 2017</th>
<th>January 2018</th>
</tr>
</thead>
<tbody>
<tr>
<td>No nomination when loading</td>
<td>1%</td>
<td>1%</td>
<td>1%</td>
<td>1%</td>
<td>1%</td>
</tr>
<tr>
<td>Unknown animal ID</td>
<td>1%</td>
<td>1%</td>
<td>1%</td>
<td>1%</td>
<td>1%</td>
</tr>
<tr>
<td>Sire pedigree missing</td>
<td>1%</td>
<td>1%</td>
<td>1%</td>
<td>1%</td>
<td>1%</td>
</tr>
<tr>
<td>Dam pedigree missing</td>
<td>1%</td>
<td>1%</td>
<td>1%</td>
<td>1%</td>
<td>1%</td>
</tr>
<tr>
<td>CDCB blanked dams due to conflict</td>
<td>1%</td>
<td>1%</td>
<td>1%</td>
<td>1%</td>
<td>1%</td>
</tr>
<tr>
<td>IDs with 573/574</td>
<td>1%</td>
<td>1%</td>
<td>1%</td>
<td>1%</td>
<td>1%</td>
</tr>
<tr>
<td>Mismatch in fee code 1 or 2</td>
<td>1%</td>
<td>1%</td>
<td>1%</td>
<td>1%</td>
<td>1%</td>
</tr>
<tr>
<td>Herd code discrepancy</td>
<td>1%</td>
<td>1%</td>
<td>1%</td>
<td>1%</td>
<td>1%</td>
</tr>
<tr>
<td>Usability code = N</td>
<td>1%</td>
<td>1%</td>
<td>1%</td>
<td>1%</td>
<td>1%</td>
</tr>
<tr>
<td>Fee code = N</td>
<td>1%</td>
<td>1%</td>
<td>1%</td>
<td>1%</td>
<td>1%</td>
</tr>
<tr>
<td>Genotype withdrawn</td>
<td>1%</td>
<td>1%</td>
<td>1%</td>
<td>1%</td>
<td>1%</td>
</tr>
<tr>
<td>Genotype reassigned</td>
<td>1%</td>
<td>1%</td>
<td>1%</td>
<td>1%</td>
<td>1%</td>
</tr>
<tr>
<td>Changes in pedigree</td>
<td>1%</td>
<td>1%</td>
<td>1%</td>
<td>1%</td>
<td>1%</td>
</tr>
</tbody>
</table>

Total genotypes for Zoetis for 1809
PASS: No nomination when loading
PASS: Unknown animal ID
PASS: Sire pedigree missing
FAIL: Dam pedigree missing
PASS: CDCB blanked dams due to conflict
PASS: IDs with 573/574
PASS: Mismatch in fee code 1 or 2
FAIL: Herd code discrepancy
PASS: Usability code = N
PASS: Fee code = N
PASS: Genotype withdrawn
PASS: Genotype reassigned
FAIL: Changes in pedigree

Quality control of data providers

- **Genotyping laboratories**
  - Yearly workshop (first in 2018)
  - QC guidelines defined in 2017 (GENLAB working group)
    - Definition of genotyping laboratories roles and responsibilities
    - Including metrics for routine (monthly) evaluation of performance
  - Formal need for monthly QC
  - End of 2018 – Collection of SOP and first formal nominator audit
  - 2019 – Monthly request for feedback on potential issues related to data submission
  - Reports, web stats and graphs of performance (and trajectory) available as for genomic nominators
Conclusion

• Projects in this presentation are the ones with direct impact on industry. Many more “behind the scenes” not reported here.
• Most projects close to conclusion (most expected in 2019).
• Communication
• All projects, irrespectively of impact, have the same objective: “providing premier dairy genetic information services and industry collaboration” (rif. CDCB core value)

THANK YOU FOR YOUR ATTENTION