CDCB tools for the improvement of the Jersey breed

21st International Conference of the World Jersey Cattle Bureau
150th Anniversary of the American Jersey Cattle Association
Canton, OH - June 30, 2018
João Dürr & Duane Norman
Outline

• CDCB Overview
• The genomics era
• Dealing with the reality of crossbreds
• Opportunities
• Take home
21st International Conference of the World Jersey Cattle Bureau
150th Anniversary of the American Jersey Cattle Association

CDCB OVERVIEW
The Council on Dairy Cattle Breeding (CDCB) is an industry collaboration that benefits the dairy community by promoting dairy cattle improvement and establishing the gold standard of dairy genetics.
Organization

- 12 voting members (3 from each sector)
US Genetic Evaluation Process

Data
- DRP
- DRPC
- PDCA
- NAAB

R&D
- AGIL/USDA

Implementation
- AGIL/USDA
- CDCB

Services
- CDCB

U.S. Genetic & Genomic Evaluations
Genomic data flow

DNA laboratory

Genotypes

Quality reports

DNA samples

Genotypes

Nominator Certification

Council on Dairy Cattle Breeding (CDCB)

Dairy Record Provider

(farmer or controller)

DNA samples

Genomic evaluations

Nominations, pedigrees

Genomic Nominator

Lab Certification
CDCB Genomic Data Certification Process

- Application submission
- Proficiency test
- Certification status notification
- Monthly report cards
- Annual review
The CDCB is the result of the U.S. dairy industry working together for the common good, empowering dairy farmers to fulfill their essential role of feeding the world.
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THE GENOMICS ERA
## Cows on DHIA per breed

<table>
<thead>
<tr>
<th>Year</th>
<th>Jersey</th>
<th>%</th>
<th>Holstein</th>
<th>Ayrshire</th>
<th>Brown Swiss</th>
<th>Guernsey</th>
</tr>
</thead>
<tbody>
<tr>
<td>1990</td>
<td>163,085</td>
<td>3.5</td>
<td>4,358,298</td>
<td>16,818</td>
<td>26,431</td>
<td>40,432</td>
</tr>
<tr>
<td>2000</td>
<td>157,845</td>
<td>3.8</td>
<td>3,968,052</td>
<td>8,235</td>
<td>16,384</td>
<td>12,846</td>
</tr>
<tr>
<td>2005</td>
<td>169,624</td>
<td>4.5</td>
<td>3,594,321</td>
<td>6,643</td>
<td>14,042</td>
<td>8,758</td>
</tr>
<tr>
<td>2010</td>
<td>220,419</td>
<td>5.5</td>
<td>3,729,507</td>
<td>4,865</td>
<td>12,086</td>
<td>5,904</td>
</tr>
<tr>
<td>2014</td>
<td>273,645</td>
<td>7.0</td>
<td>3,594,321</td>
<td>4,132</td>
<td>11,179</td>
<td>4,340</td>
</tr>
<tr>
<td>2015</td>
<td>307,622</td>
<td>7.7</td>
<td>3,668,546</td>
<td>3,891</td>
<td>10,585</td>
<td>3,989</td>
</tr>
<tr>
<td>2016</td>
<td>320,400</td>
<td>8.1</td>
<td>3,615,132</td>
<td>3,436</td>
<td>10,291</td>
<td>4,330</td>
</tr>
<tr>
<td>2017</td>
<td>321,706</td>
<td>8.2</td>
<td>3,594,876</td>
<td>3,205</td>
<td>10,079</td>
<td>3,948</td>
</tr>
<tr>
<td>2018</td>
<td>338,697</td>
<td>8.7</td>
<td>3,545,514</td>
<td>2,600</td>
<td>10,198</td>
<td>3,613</td>
</tr>
</tbody>
</table>

**Trend**

| ↑↑ | ↓ | ↓↓ | ↓ | ↓↓ |

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13
## U.S. domestic semen sales per breed

<table>
<thead>
<tr>
<th>Year</th>
<th>Jersey</th>
<th>%</th>
<th>Holstein</th>
<th>Ayrshire</th>
<th>Brown Swiss</th>
<th>Guernsey</th>
</tr>
</thead>
<tbody>
<tr>
<td>1980</td>
<td>532,746</td>
<td>4.0</td>
<td>12,089,797</td>
<td>75,866</td>
<td>139,104</td>
<td>326,105</td>
</tr>
<tr>
<td>1990</td>
<td>610,154</td>
<td>4.6</td>
<td>12,276,057</td>
<td>51,866</td>
<td>251,834</td>
<td>176,525</td>
</tr>
<tr>
<td>2000</td>
<td>771,160</td>
<td>5.8</td>
<td>12,271,730</td>
<td>33,955</td>
<td>118,954</td>
<td>55,662</td>
</tr>
<tr>
<td>2005</td>
<td>1,362,705</td>
<td>7.5</td>
<td>16,257,394</td>
<td>41,044</td>
<td>165,495</td>
<td>44,101</td>
</tr>
<tr>
<td>2010</td>
<td>1,985,997</td>
<td>9.1</td>
<td>19,306,931</td>
<td>54,229</td>
<td>125,162</td>
<td>33,870</td>
</tr>
<tr>
<td>2015</td>
<td>3,053,900</td>
<td>12.9</td>
<td>20,230,156</td>
<td>41,257</td>
<td>103,232</td>
<td>30,093</td>
</tr>
<tr>
<td>2016</td>
<td>2,947,587</td>
<td>13.1</td>
<td>19,299,126</td>
<td>39,569</td>
<td>109,660</td>
<td>29,326</td>
</tr>
<tr>
<td>2017</td>
<td>3,435,468</td>
<td>14.8</td>
<td>19,540,530</td>
<td>32,639</td>
<td>109,562</td>
<td>27,134</td>
</tr>
</tbody>
</table>

**Trend**

↑↑↑↑  ▲  ↓  ↓  ↓  ↓↓↓↓
### Gain in Standardized Fat + Protein (lbs.)

<table>
<thead>
<tr>
<th>Difference with Base Year</th>
<th>Jersey</th>
<th>Holstein</th>
<th>Ayrshire</th>
<th>Brown Swiss</th>
<th>Guernsey</th>
</tr>
</thead>
<tbody>
<tr>
<td>2011 vs. 2010</td>
<td>42</td>
<td>24</td>
<td>0</td>
<td>17</td>
<td>-1</td>
</tr>
<tr>
<td>2012 vs. 2010</td>
<td>79</td>
<td>58</td>
<td>14</td>
<td>46</td>
<td>17</td>
</tr>
<tr>
<td>2013 vs. 2010</td>
<td>123</td>
<td>87</td>
<td>24</td>
<td>51</td>
<td>20</td>
</tr>
<tr>
<td>2014 vs. 2010</td>
<td>175</td>
<td>111</td>
<td>60</td>
<td>67</td>
<td>43</td>
</tr>
<tr>
<td>2015 vs. 2010</td>
<td>191</td>
<td>129</td>
<td>72</td>
<td>86</td>
<td>62</td>
</tr>
<tr>
<td>2016 vs. 2010</td>
<td>231</td>
<td>160</td>
<td>82</td>
<td>89</td>
<td>60</td>
</tr>
</tbody>
</table>
## Genotypes in CDCB-Cooperators’ Database (7/18)

<table>
<thead>
<tr>
<th>Breed</th>
<th>Reference</th>
<th></th>
<th>Young</th>
<th></th>
<th>Total</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>Male</td>
<td>Female</td>
<td>Male</td>
<td>Female</td>
<td></td>
</tr>
<tr>
<td>Holstein</td>
<td>40,813</td>
<td>480,454</td>
<td>213,658</td>
<td>1,360,433</td>
<td>2,095,358</td>
</tr>
<tr>
<td>Jersey</td>
<td>5,937</td>
<td>89,287</td>
<td>23,265</td>
<td>155,872</td>
<td>274,361</td>
</tr>
<tr>
<td>Brown Swiss</td>
<td>7,037</td>
<td>2,514</td>
<td>22,071</td>
<td>5,471</td>
<td>37,093</td>
</tr>
<tr>
<td>Ayrshire</td>
<td>843</td>
<td>370</td>
<td>1,211</td>
<td>6,193</td>
<td>8,617</td>
</tr>
<tr>
<td>Guernsey</td>
<td>490</td>
<td>984</td>
<td>380</td>
<td>2,191</td>
<td>4,045</td>
</tr>
<tr>
<td>Total</td>
<td>55,120</td>
<td>573,609</td>
<td>260,585</td>
<td>1,530,160</td>
<td>2,419,474</td>
</tr>
</tbody>
</table>
## Percentage of Milk Recorded Cows in Herd by Breed

<table>
<thead>
<tr>
<th>Year</th>
<th>Ayrshire</th>
<th>Brown Swiss</th>
<th>Guernsey</th>
<th>Holstein</th>
<th>Jersey</th>
<th>Milking Shorthorn</th>
<th>Multiple-Breed Herds</th>
</tr>
</thead>
<tbody>
<tr>
<td>1998</td>
<td>0.2</td>
<td>0.4</td>
<td>0.3</td>
<td>93.4</td>
<td>3.3</td>
<td>0.1</td>
<td>2.4</td>
</tr>
<tr>
<td>2008</td>
<td>0.1</td>
<td>0.3</td>
<td>0.2</td>
<td>90.5</td>
<td>4.3</td>
<td>0.1</td>
<td>4.5</td>
</tr>
<tr>
<td>2018</td>
<td>0.1</td>
<td>0.2</td>
<td>0.1</td>
<td>80.9</td>
<td>7.7</td>
<td>&lt;0.1</td>
<td>10.9</td>
</tr>
</tbody>
</table>

↓↓  ↓↓  ↓↓↓  ↓↓  ↑↑↑  ↓  ↑↑↑↑
Breed of Cows Calving (2017) in Multiple-Breed Herds

<table>
<thead>
<tr>
<th>Animal</th>
<th>AYR</th>
<th>BSW</th>
<th>GUE</th>
<th>HOL</th>
<th>JER</th>
<th>Milking Shorthorn</th>
<th>Other breeds</th>
<th>Cross-breds</th>
</tr>
</thead>
<tbody>
<tr>
<td>Cows</td>
<td>0.9</td>
<td>2.2</td>
<td>0.7</td>
<td>42.3</td>
<td>20.8</td>
<td>0.6</td>
<td>1.1</td>
<td>31.5</td>
</tr>
<tr>
<td>Sires</td>
<td>1.2</td>
<td>3.3</td>
<td>0.9</td>
<td>52.7</td>
<td>34.8</td>
<td>0.8</td>
<td>6.3</td>
<td>0.1</td>
</tr>
<tr>
<td>Dams</td>
<td>0.9</td>
<td>2.4</td>
<td>0.8</td>
<td>51.3</td>
<td>19.9</td>
<td>0.6</td>
<td>1.2</td>
<td>22.7</td>
</tr>
</tbody>
</table>
Changes in breed composition in the U.S.

• Increases in cheese consumption along with changes in milk pricing that pays for the true value of milk have led to growth of the Jersey breed in the U.S.

• A number of herds have used Jersey bulls on cattle of other breeds because of a shortage of Jersey replacements to fill their demands

• The number of crossbreds in US herds have increased by 400% in the last decade
Changes in breed composition in the U.S.

- Production for Jerseys has been increasing at an impressive rate
- Genomics has substantially increased genetic gains and produced new competitive opportunities within the dairy industry
- Breeds can only compete in the genomic era if they have a large reference base
Reality check

• Dairy industry business environment is changing rapidly.
  • Are our business models still relevant in the new environment?
  • How are we securing innovation?
  • Is the future leadership part of the conversation?
  • New players: can we afford NOT to work with (for) them?
DEALING WITH THE REALITY OF CROSSBREDS
Handling crossbred genotypes within a purebred framework

- Over 20,000 genotyped animals received no genomic predictions because they don’t meet the minimum genomic standards for purebreds.
- Genomic predictions in the U.S. rely on separate reference populations for each breed.
- Worldwide attempts of calculating genomic predictions for crossbreds using mixed reference populations have delivered inconsistent results so far.
The route to estimate genomic PTAs for crossbreds

- Research
- BBR
- All-breeds genomic evaluations
- Test evaluations for crossbreds
- Implement evaluations for crossbreds
Two-step Crossbred Genomic Evaluations
(Olson et al., 2012; VanRaden & Cooper, 2015)

- Crossbred phenotypes are extracted and EBV calculated using SNP effects, frequency and inbreeding for each of the 5 genomic breeds
- Marker effects for each breed are blended by BBR to compute evaluations for crossbreds
Main research conclusions (Tooker et al., 2017)

• Accurate GPTAs computed for crossbreds as weighted average of purebred marker effects
• Genomic evaluations of purebreds change little when computed on all-breed scale
• Gains small from multi-trait, multi-breed
Breed Base Representation (BBR)
Breed Discovery through Genotyping

• As DNA can determine who the parents and grandparents are, it can also indicate the breeds of those ancestors
• DNA markers from different dairy breeds can be detected, regardless of whether or not pedigree information is limited or missing
Breed Base Representation (BBR) Defined

• The BBR procedure estimates the similarity of alleles present in 5 purebred reference groups to those of each individual genotyped

• If breeds other than AYR, BSW, GUE, HOL and JER are part of the animal’s ancestry then BBR will not be accurate
BBR Interpretation

• BBRs for the primary breed can be lower than 100% because the animal is an outcross to the primary population or because it has one or more other breeds somewhere in the pedigree.

• Even animals whose ancestors have been true purebreds for many generations often obtain a BBR percentage for their primary breed less than 100%.

• Cases where the principal breed is 90 to 97% can reveal the presence of outcross bloodlines, but if lower usually indicates evidence of crossbreeding.
U. of Minnesota Holstein Selection Project

• The BBRs for an outcross animals will be shown in the next slide. It shows a control bull having “1960s Holstein” genetics from the University of Minnesota’s selection project. This bull has a relatively low relationship to today’s Holstein population because the alleles in the breed have changed over the last half-century.
BBR Outcross Example

- Case: control bull having “1960s Holstein” genetics from the University of Minnesota’s selection project
- This bull has a relatively low relationship to today’s Holstein population because the alleles in the breed have changed over the last half-century
- This bull was tested and had a BBR of 93% Holstein. Other percentages were Ayrshire 3%, Brown Swiss 1%, Guernsey 1%, and Jersey 2%
- Other bulls from the same study were as low as 87%
BBR Presentation

- Reference groups are updated regularly
- BBRs is calculated only once, unless genotyped with a higher density chip
- CDCB Decision: animals that have a BBR derived of greater than or equal to 94 for a breed are considered to have one-breed background and will be expressed as 100% for that breed, and other breeds’ percentages will be set to zero
BBR Distribution

• Breed associations receive a file of BBRs for animals if their breed code has the highest percentage
• Nominators receive the BBRs for the animals that they nominated
• Official BBRs are a prerogative of each breed association, so publication should adhere to the official breed policy
• CDCB does not make BBRs public
## Average BBR Percentage of the Primary Breed (Cows)

<table>
<thead>
<tr>
<th>Year</th>
<th>Ayrshire</th>
<th>Brown Swiss</th>
<th>Guernsey</th>
<th>Holstein</th>
<th>Jersey</th>
<th>Crossbreds</th>
</tr>
</thead>
<tbody>
<tr>
<td>1997</td>
<td>-</td>
<td>97.9</td>
<td>100.0</td>
<td>98.4</td>
<td>99.1</td>
<td>-</td>
</tr>
<tr>
<td>2007</td>
<td>97.6</td>
<td>98.8</td>
<td>97.0</td>
<td>99.0</td>
<td>98.1</td>
<td>66.6 HO</td>
</tr>
<tr>
<td>2017</td>
<td>95.9</td>
<td>98.2</td>
<td>97.2</td>
<td>99.0</td>
<td>95.0</td>
<td>78.9 HO</td>
</tr>
</tbody>
</table>
Average BBR Percentage of the Primary Breed (Bulls)

<table>
<thead>
<tr>
<th>Year</th>
<th>Ayrshire</th>
<th>Brown Swiss</th>
<th>Guernsey</th>
<th>Holstein</th>
<th>Jersey</th>
<th>Crossbreds</th>
</tr>
</thead>
<tbody>
<tr>
<td>1997</td>
<td>99.9</td>
<td>99.8</td>
<td>99.8</td>
<td>99.6</td>
<td>99.5</td>
<td>-</td>
</tr>
<tr>
<td>2007</td>
<td>98.0</td>
<td>99.7</td>
<td>99.7</td>
<td>99.6</td>
<td>99.3</td>
<td>-</td>
</tr>
<tr>
<td>2017</td>
<td>97.8</td>
<td>99.0</td>
<td>98.3</td>
<td>99.2</td>
<td>97.4</td>
<td>50 HOL/JER</td>
</tr>
</tbody>
</table>
All-Breed Genomic Evaluations
All-breed system extended to genomic evaluations

• 2007
  • Conventional evaluations combining data for animals of all breeds are calculated on an all-breed genetic base and then converted back to within breed bases before official release

• April 2018
  • All-breed system also applied to genomic evaluations
    • Separate marker effects for each breed still computed
    • Parent averages (PA) calculated using the entire pedigree across breeds
    • More accurate evaluations for animals with other breeds in pedigree
Impact of all-breed genomic evaluations

• Most affected:
  • PTAs for those animals with a second breed in their pedigree
  • Jersey and Ayrshire breeds - higher proportion of animals with some percentage of other-breed genetics in their current population

• All animals affected to a certain degree
  • Improved accuracy of the prediction will bring more stability to the evaluations
The route to estimate genomic PTAs for crossbreds
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OPPORTUNITIES
Traits recently added to the CDCB portfolio

- Cow livability
- Gestation length
- Health traits (Holstein)
  - Milk fever, displaced abomasum, ketosis, clinical mastitis, metritis, retained placenta
New data

Cooperator Database

AMS

Phenotype farms

Herd profiling

Novel milk analyses

Existing databases / networks

On farm software

Existing databases / networks
Expected enhancements to CDCB evaluations

• Include crossbred animals in genomic evaluations
• Develop residual feed intake evaluations
• Update Predictive SNPs (77K)
• Revisit fertility and calving traits evaluations
Research and Development

• CDCB is engaged with the Dairy Innovation Center in developing a sustainable innovation framework for the U.S. dairy industry
Acknowledgments:
• All dairy producers and industry support people who provided data to CDCB’s national database
• Paul VanRaden, Katie Olson, Melvin Tooker and Tabatha Cooper who developed BBR
• CDCB staff
Thank you!

www.uscdcb.com