# Comparison of Domestic and Foreign Genotypes by Country and Continent

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# Introduction

- The Council on Dairy Cattle Breeding (CDCB) genomic database:
  - Over 1 million genotyped animals
  - From 47 countries
  - 18 different chip types
  - And counting . . .

# Methods

- Genomic information from April 2015 examined by country code and continental region
  - Central and South America grouped into Latin America
  - Western and eastern Europe examined separately

# Genotype contributors

| | | | | | | | | |
|---|---|---|---|---|---|---|---|---|
| **N. America** | CAN | USA | | | | | | |
| **W. Europe** | AUT | BEL | CHE | DEU | DNK | ESP | FIN | FRA |
| | GBR | IRL | ITA | LUX | NLD | NOR | SWE | |
| **E. Europe** | BLR | CZE | HUN | POL | ROU | RUS | SRB | SVK |
| | SVN | | | | | | | |
| **Oceania** | AUS | NZL | | | | | | |
| **L. America** | ARG | BRA | CHL | COL | CRI | ECU | GTM | MEX |
| | PER | URY | | | | | | |
| **Asia** | CHN | IND | IRN | JPN | KAZ | SAU | THA | TWN |
| **Africa** | ZAF | | | | | | | |



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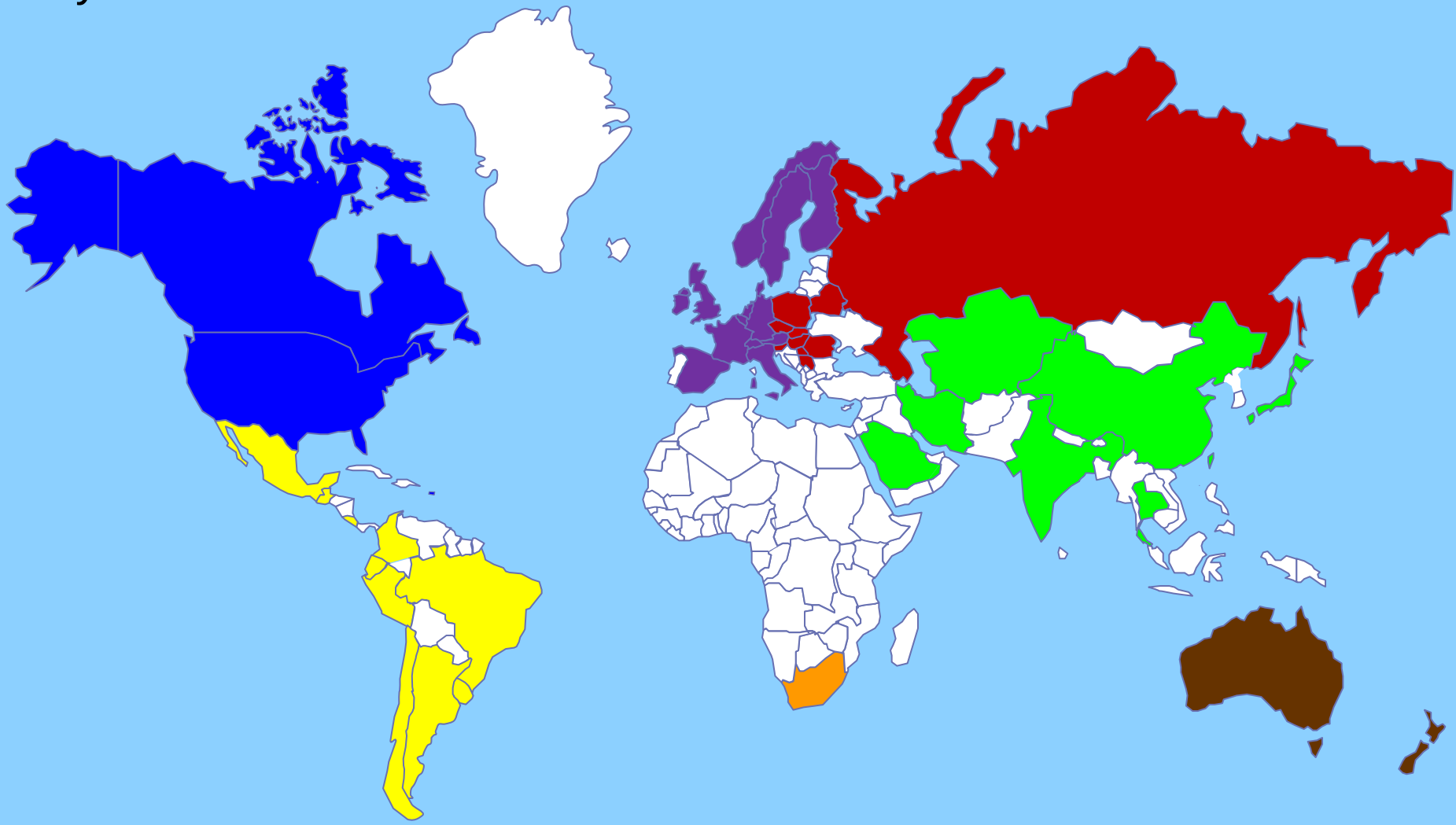
# Genotype Contributors

by continent



# Benefits of exchanging genotypes

- Smaller countries or those countries without advanced data collection:
  - Obtain predictions from larger databases
  - Use a larger reference population
  - More traits, more efficient service
  - Genomic reliabilities increase

# Exchanging genotypes (cont.)

- United States exchanges genotypes
  - HOL: Canada, Great Britain, and Italy
  - BSW: Intergenomics (Interbull)
  - JER: Denmark
- North America – HOL and JER sires
- Foreign - BSW and RDC sires

# Genotyped population April 2015

| Breed | Reference population | | | Total genotypes |
|---|---|---|---|---|
| | U.S. bulls | Foreign bulls | U.S. cows | |
| HOL | 15,288 | 11,941 | 124,666 | 764,029 |
| JER | 3,005 | 1,529 | 31,233 | 99,212 |
| BSW | 970 | 5,155 | 1,367 | 18,805 |
| RDC | 188 | 523 | 95 | 4,228 |

# Pedigree completeness

- 100% when all paths trace back to an ancestor born before 1970
- 100% if the animal itself is born before 1970
- 50% if one parent is unknown and the other has a complete pedigree
- 0% when both parents are unknown

# Pedigree analysis by continent

| Continent | Pedigree Completeness (%) | % Sires from CAN | % Sires from USA |
|---|---|---|---|
| N. America | 86.1 | 10 | 84 |
| W. Europe | 97.6 | 13 | 49 |
| E. Europe | 88.0 | 7 | 61 |
| Oceania | 93.6 | 17 | 44 |
| L. America | 67.7 | 14 | 61 |
| Asia | 71.9 | 7 | 74 |
| Africa | 87.4 | 15 | 67 |

# Inbreeding

- Expected future inbreeding (EFI) =
  - Half the average pedigree relationship of an animal to recent U.S. cows
- Genomic future inbreeding (GFI) =
  - Half the average genomic relationship to recent reference bulls
  - Realized, instead of expected

# Relationships (N. America and Foreign)

| Continent | Future Inbreeding (%) | |
|---|---|---|
| | Pedigree | Genomic |
| N. America | 6.4 | 6.9 |
| W. Europe | 6.1 | 6.7 |
| E. Europe | 5.8 | 6.2 |
| Oceania | 5.8 | 6.2 |
| L. America | 6.0 | 6.0 |
| Asia | 6.0 | 6.3 |
| Africa | 6.6 | 7.3 |

# When a genotype is submitted

- Initial status of the sire:
  - Confirmed
  - Conflict
  - Missing
  - Reported, not genotyped
- Corrections due to genomics are tracked through a secondary code

# Initial sire status (confirmed or conflict)

| Continent | Confirmed | Conflict | |
|---|---|---|---|
| | | Corrected | Not corrected |
| N. America | 84.5 | 7.0 | 0.5 |
| W. Europe | 89.1 | 1.6 | 0.4 |
| E. Europe | 88.9 | 1.6 | 0.1 |
| Oceania | 71.2 | 1.6 | 0.9 |
| L. America | 61.5 | 8.0 | 2.9 |
| Asia | 62.0 | 9.0 | 2.7 |
| Africa | 87.7 | 6.6 | 0.3 |

# Initial sire status (missing or not genotyped)

| Continent | Missing | | Reported, not genotyped | |
|---|---|---|---|---|
| | Discovered | Not discovered | Discovered | Not discovered |
| N. America | 4.1 | 2.5 | 0.2 | 1.3 |
| W. Europe | 1.0 | 1.0 | 0.2 | 6.7 |
| E. Europe | 0.0 | 2.0 | 0.2 | 7.2 |
| Oceania | 0.0 | 2.9 | 0.4 | 23.1 |
| L. America | 2.9 | 9.9 | 5.4 | 9.4 |
| Asia | 0.1 | 14.8 | 0.3 | 11.2 |
| Africa | 0.0 | 0.0 | 1.3 | 4.0 |

# Sires of genotyped animals by continent

| Africa | | E. Europe | |
|---|---|---|---|
| Shottle | 20 | Shottle | 60 |
| Goldwyn | 16 | Massey | 50 |
| Gold Chip | 16 | Altaross | 39 |
| Tbone | 14 | Altaiota | 38 |

| Oceania | | W. Europe | |
|---|---|---|---|
| Man-O-Man | 183 | Shottle | 1,473 |
| Supersire | 162 | Goldwyn | 1,340 |
| Goldwyn | 152 | Man-O-Man | 1,312 |
| Snowman | 141 | NumeroUno | 1,162 |

# Sires of genotyped animals by continent

| L. America | | N. America | |
|---|---|---|---|
| *unknown* | 685 | *unknown* | 15,790 |
| Bogart | 172 | Mogul | 6,927 |
| Elias | 159 | Planet | 6,900 |
| Dover | 155 | Shamrock | 6,166 |

| Asia | |
|---|---|
| Otto | 46 |
| Sudan | 43 |
| *unknown* | 40 |
| Altanato | 24 |

# Average genomic Net Merit (NM$)

| Continent | Genomic NM$ | | |
|---|---|---|---|
| | Animal | Parent Average | Difference |
| N. America | 191 | 171 | 20 |
| W. Europe | 146 | 130 | 16 |
| E. Europe | 111 | 72 | 39 |
| Oceania | 44 | 20 | 24 |
| L. America | 9 | -22 | 31 |
| Asia | 64 | 51 | 13 |
| Africa | 48 | 11 | 37 |
| Average | 184 | 165 | 19 |

# Published Net Merit reliability

| Continent | Genomic NM reliability (%) | | |
|---|---|---|---|
| | Animal | Parent Average | Increase |
| N. America | 71 | 34 | 37 |
| W. Europe | 73 | 37 | 36 |
| E. Europe | 71 | 33 | 38 |
| Oceania | 69 | 33 | 36 |
| L. America | 69 | 25 | 44 |
| Asia | 70 | 28 | 42 |
| Africa | 68 | 34 | 34 |
| Average | 71 | 34 | 37 |

# Denmark Jersey genotype exchange

- U.S. and Denmark contributed genotypes from 1,157 Jersey bulls
  - Danish bulls - same reliability
  - Lower PA reliability
  - 10% larger gain vs. U.S. only
  - US bulls reliability gained 2% over U.S. only

**Wiggans et al., J. Dairy Sci. 2014, 98:3508–3513**

# Holstein genomic validation reliabilities

| | Observed Genomic Reliability (%) | | | | | |
|---|---|---|---|---|---|---|
| | Reliability | | | | Gain over PA | |
| Trait | USA | PA | Foreign | PA | USA | Foreign |
| Milk yield | 73.8 | 40.0 | 74.5 | 37.3 | 33.8 | 37.2 |
| Fat yield | 73.1 | 40.0 | 77.1 | 37.3 | 33.1 | 39.8 |
| Protein yield | 65.3 | 40.0 | 68.0 | 37.3 | 25.3 | 30.7 |
| Productive life | 75.9 | 34.0 | 78.7 | 31.8 | 41.9 | 51.9 |
| Somatic Cell Score | 71.1 | 36.5 | 74.9 | 34.7 | 34.5 | 46.8 |
| Daughter Pregnancy Rate | 57.8 | 33.5 | 64.7 | 32.3 | 24.3 | 41.5 |
| Udder depth | 86.5 | 41.6 | 83.9 | 34.3 | 45.0 | 49.6 |

# Conclusions

- Breeders in many countries are choosing to genotype their animals in the U.S.
- Genotyped animals have a high relationship to the North American reference population
- Evaluations should be nearly as accurate as for U.S. animals
- 7% of sires are misidentified; 90% of those are found and corrected

# Conclusions

- PowerPoint is available: http://aipl.arsusda.gov/publish/present.htm
- Current country counts: https://www.cdcb.us/Genotype/cur_ctry.html

# Acknowledgments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