Genetic evaluation for carcass traits in French dairy cattle

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- Background
- Traits for veal calves (VC)
  - Material and Methods
  - Results
- Traits for young bulls (YB)
  - Material and Methods
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- Comparison of YB traits with other traits
- Conclusion
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- **Comparison of YB traits with other traits**
- **Conclusion**
Background

Veal Calves (VC) in dairy herds
- 86% of veal calves slaughtered in France
- 30% are crossbred between dairy dam and beef sire
- Main dam breeds: Holstein, Montbéliarde, Normande
- Main sire breeds: Holstein, Montbéliarde, Normande, Charolaise (CHA), Limousine (LIM), Blonde d’Aquitaine (BLA), Belgian Blue (BB), INRA95

Young Bulls (YB) in dairy herds
- 25% of young bulls slaughtered in France are pure dairy breed
- Main breeds: Montbéliarde, Normande, Simmental
Background

NORMABEV database
- Created since mid 2000’s
- Commercial carcass data (weight, conformation, fatness, meat color)
- Routinely recorded
- In all French slaughterhouses
- On every animal (males, females, purebred, crossbred, …)

2010: Convention NORMABEV - Idele
⇒ NORMABEV database can be used by Idele and INRA for genetic and genomic evaluations
Background

- French Dual-purpose breeds (Montbéliarde, Normande, Simmental) mainly selected on dairy traits
  \[\Rightarrow \text{add carcass traits in their breeding goals}\]

First Steps

- Develop a **genetic evaluation for carcass traits of crossbred and purebred veal calves**
  born from dairy dams of breeds Montbéliarde and Normande (dual-purpose breeds) and Holstein

- Develop a **genetic evaluation for carcass traits of purebred young bulls** of breeds Montbéliarde, Normande, Simmental
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Veal Calves: Material and Methods

3 populations analyzed separately

- **MON** population: only phenotypes of calves born from a Montbéliarde dam
- **NOR** population: only phenotypes of calves born from a Normande dam
- **HOL** population: only phenotypes of calves born from a Holstein dam

Data Selection in each population

- **Purebred or crossbred calves** (only **CHA**, **LIM**, **BLA**, **BB** or **INRA95** sire breeds)
- Calves born since 2007,
- Age at slaughter between 70 days and 250 days
- Carcass weight between 50 kg and 250 kg
Veal Calves: Material and Methods

- **3 populations analyzed separately**
- **Data Selection in each population**
  - Purebred or crossbred calves (only **CHA**, **LIM**, **BLA**, **BB** or **INRA95** sire breeds)
  - Calves born since 2007,
  - Age at slaughter between 70 days and 250 days
  - Carcass weight between 50 kg and 250 kg

<table>
<thead>
<tr>
<th>Dam Breed</th>
<th>HOL</th>
<th>MON</th>
<th>NOR</th>
</tr>
</thead>
<tbody>
<tr>
<td>Purebred calves</td>
<td>3 270 660</td>
<td>693 463</td>
<td>284 600</td>
</tr>
<tr>
<td>Crossbred Calves: Sire breeds</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>BB</td>
<td>238 028</td>
<td>51 297</td>
<td>15 872</td>
</tr>
<tr>
<td>LIM</td>
<td>144 822</td>
<td>55 930</td>
<td>16 036</td>
</tr>
<tr>
<td>CHA</td>
<td>129 284</td>
<td>223 304</td>
<td>17 254</td>
</tr>
<tr>
<td>BLA</td>
<td>21 993</td>
<td>5 690</td>
<td>3 644</td>
</tr>
<tr>
<td>INRA95</td>
<td>75 425</td>
<td>14 315</td>
<td>4 918</td>
</tr>
</tbody>
</table>
Veal Calves: Material and Methods

Evaluating traits

- Carcass Weight (CW, in kg)
- Age at Slaughter (AGE, in days)
- Carcass Conformation score (CC, EUROP grades, each divided into 3 subclasses: -, =, +)
- Meat Color score (COLOR, 4-point scale)

<table>
<thead>
<tr>
<th>Trait</th>
<th>HOL</th>
<th>MON</th>
<th>NOR</th>
</tr>
</thead>
<tbody>
<tr>
<td>CW (kg)</td>
<td>133 ± 19</td>
<td>136 ± 24</td>
<td>131 ± 21</td>
</tr>
<tr>
<td>CC * (cl)</td>
<td>0 ± 2 subcl</td>
<td>R ± 2 subcl</td>
<td>R- ± 2 subcl</td>
</tr>
<tr>
<td>COLOR* (cl)</td>
<td>2 ± ½ cl</td>
<td>2 ± ½ cl</td>
<td>2 ± ½ cl</td>
</tr>
<tr>
<td>AGE (days)</td>
<td>175 ± 16</td>
<td>166 ± 22</td>
<td>167 ± 22</td>
</tr>
</tbody>
</table>

Phenotypic statistics
Veal Calves: Material and Methods

**Statistical model**

Animal multitrait mixed model: AGE, CW, CC and COLOR

\[ y_{ijklmn} = \mu + C_i + b_j + p_k + s_l + W_m + a_n + \varepsilon_{ijklmn} \]

- **\( y_{ijkl} \)**: performance
- **\( \mu \)**: mean
- **\( C_i \)**: fixed effect of contemporary group (fattening herd*birth year*slaughter season)
- **\( b_j \)**: fixed effect of sire breed
- **\( p_k \)**: fixed effect of age at calving of dam
- **\( s_l \)**: fixed effect of sex of calves
- **\( W_m \)**: maternal permanent environment effect for AGE in MON and NOR population only
- **\( a_n \)**: animal genetic effect
- **\( \varepsilon_{ijklmn} \)**: residual error

For AGE in MON and NOR population only
### Veal Calves: Results

<table>
<thead>
<tr>
<th>Population</th>
<th>NOR</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>CW</td>
</tr>
<tr>
<td>CW</td>
<td>0.24 (0.01)</td>
</tr>
<tr>
<td>AGE</td>
<td>0.09 (0.02)</td>
</tr>
<tr>
<td>FLESH</td>
<td>0.66 (0.01)</td>
</tr>
<tr>
<td>COLOR</td>
<td>-0.03 (0.02)</td>
</tr>
</tbody>
</table>

Heritabilities on diagonal, genetic correlations above, *phenotypic correlations* below

- $h^2$ moderate for CW and CC for all breeds
- $h^2$ low for COLOR for all breeds
- High genetic correlations between CW and CC for all breeds

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**Genetic evaluation for carcass traits in dairy cattle – Interbull 2016, Chile**
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Young Bulls: Material and Methods

- **3 populations analyzed separately**
  - **MON** population: only phenotypes of purebred Montbéliarde young bulls
  - **NOR** population: only phenotypes of purebred Normande young bulls
  - **SIM** population: only phenotypes of purebred Simmental young bulls

- **Data Selection in each population**
  - Young bulls born since 2006
  - Age at slaughter between 12 months and 24 months
  - Carcass weight between 170 kg and 600 kg
Young Bulls: Material and Methods

3 populations analyzed separately

- **MON** population: only phenotypes of purebred Montbéliarde calves
- **NOR** population: only phenotypes of purebred Normande calves
- **SIM** population: only phenotypes of purebred Simmental calves

Data Selection in each population

<table>
<thead>
<tr>
<th>Breed</th>
<th>Nb of young bulls</th>
<th>Nb of sires</th>
</tr>
</thead>
<tbody>
<tr>
<td>Montbéliarde</td>
<td>156,226</td>
<td>4,282</td>
</tr>
<tr>
<td>Normande</td>
<td>160,361</td>
<td>2,061</td>
</tr>
<tr>
<td>Simmental</td>
<td>8,691</td>
<td>368</td>
</tr>
</tbody>
</table>
Young Bulls: Material and Methods

**Evaluated traits**

- Carcass Weight (CW, in kg)
- Age at Slaughter (AGE, in days)
- Carcass Conformation score (CC, EUROP grades, each divided in 3 subgrades: -, =, +)

<table>
<thead>
<tr>
<th>Trait</th>
<th>MON</th>
<th>NOR</th>
<th>SIM</th>
</tr>
</thead>
<tbody>
<tr>
<td>CW (kg)</td>
<td>382.9 ± 51.4</td>
<td>381.9 ± 49.9</td>
<td>387.7 ± 54.2</td>
</tr>
<tr>
<td>CC * (cl)</td>
<td>R- ± 1 subcl</td>
<td>O+ ± 1 subcl</td>
<td>R- ± 1 subcl</td>
</tr>
<tr>
<td>AGE* (cl)</td>
<td>621.9 ± 67.5</td>
<td>633.5 ± 63.1</td>
<td>615.2 ± 78.8</td>
</tr>
</tbody>
</table>

Phenotypic statistics
Young Bulls: Material and Methods

Statistical model

Animal multitrait mixed model: AGE, CW and CC

\[ y_{ijkl} = \mu + C_i + p_j + s_k + a_l + \varepsilon_{ijkl} \]

\( y_{ijkl} \): performance
\( \mu \): mean
\( C_i \): fixed effect of contemporary group (finishing herd*season of slaughter*year of slaughter)
\( p_j \): fixed effect of parity*age at calving of dam
\( s_k \): fixed effect of season of birth
\( a_l \): animal genetic effect
\( \varepsilon_{ijkl} \): residual error
Young Bulls: Results

Breeds | SIM | CW | AGE | CC
---|---|---|---|---
CW | 0.17 (0.04) | -0.71 (0.15) | 0.30 (0.13) |
AGE | 0.31 (0.03) | 0.08 (0.03) | 0.11 (0.18) |
FLESH | 0.53 (0.02) | 0.07 (0.03) | 0.21 (0.04) |

Breeds | NOR | CW | AGE | CC
---|---|---|---|---
CW | 0.12 (0.01) | -0.49 (0.06) | 0.47 (0.04) |
AGE | 0.27 (0.01) | 0.17 (0.01) | -0.02 (0.05) |
FLESH | 0.60 (0.01) | 0.04 (0.01) | 0.26 (0.02) |

Breeds | MON | CW | AGE | CC
---|---|---|---|---
CW | 0.19 (0.01) | -0.58 (0.05) | 0.52 (0.03) |
AGE | 0.27 (0.01) | 0.09 (0.01) | -0.25 (0.06) |
FLESH | 0.55 (0.01) | 0.08 (0.01) | 0.23 (0.01) |

**heritabilities** on diagonal, genetic correlations above, *phenotypic correlations* below

- $h^2$ moderate for CW and CC for all breeds
- High genetic correlations between CW and CC for all breeds
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Correlations of YB traits with other traits: Materials and Methods

- Population = young bulls + paternal half-sibs
  - Milk production trait: half-sisters evaluated for milk production
  - Veal calf production traits: half-brothers with carcass phenotypes

Young bull phenotypes

- Young bull traits evaluation model
- Correction for environmental effects

Young bull preadjusted phenotypes

Other production phenotypes

- Evaluation model
- Correction for environmental effects

Preadjusted phenotypes

A simple model:

$$y_{ijk} = \mu_t + year_j + a_k + \varepsilon_{ijk}$$
Correlations of YB traits with other traits: Results

Correlations young bulls and veal calves carcass traits

<table>
<thead>
<tr>
<th></th>
<th>CW</th>
<th>AGE</th>
<th>CC</th>
</tr>
</thead>
<tbody>
<tr>
<td>MON</td>
<td>0.43 (0.05)</td>
<td>0.40 (0.08)</td>
<td>0.54 (0.04)</td>
</tr>
<tr>
<td>NOR</td>
<td>0.44 (0.06)</td>
<td>0.32 (0.09)</td>
<td>0.70 (0.03)</td>
</tr>
</tbody>
</table>

Correlations between young bulls and milk production trait

<table>
<thead>
<tr>
<th></th>
<th>CW</th>
<th>AGE</th>
<th>CC</th>
</tr>
</thead>
<tbody>
<tr>
<td>MON</td>
<td>0.18 (0.04)</td>
<td>-0.21 (0.06)</td>
<td>-0.02 (0.04)</td>
</tr>
<tr>
<td>NOR</td>
<td>0.08 (0.05)</td>
<td>-0.21 (0.05)</td>
<td>-0.13 (0.04)</td>
</tr>
<tr>
<td>SIM</td>
<td>0.26 (0.09)</td>
<td>-0.36 (0.14)</td>
<td>-0.01 (0.09)</td>
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Conclusion

Genetic parameters of VC and YB carcass traits
- Consistent for VC and YB
- Consistent in all breeds

Carcass Weight and Carcass Conformation
- Moderate heritabilities for both VC and YB
- High correlations for both VC and YB
  ⇒ *can be improved by selection*

Favorable correlations between YB and VC carcass traits
No unfavorable correlations between YB carcass traits and milk production trait
Conclusion

- National genetic evaluation for VC carcass traits officially implemented in April 2015
- National genetic evaluation for YB carcass traits will be officially implemented in 2017

Next steps:
- Implementation of a national genomic evaluation for VC and YB underway
- Update breeding goals for dual-purpose breeds
The authors acknowledge the financial support for this project provided by transnational funding bodies, being partners of the FP7 ERA-net project, CORE Organic Plus, and the cofound from the European Commission.