Analyses of different brown cattle breeds and their crosses in Switzerland
Anet Spengler Neff¹, Dominique Mahrer¹,²,³, Jürg Moll³, Alexander Burren², Christine Flury²

¹FiBL (Research Institute of Organic Agriculture), Ackerstrasse 21, 5070 Frick, Switzerland; ²Bern University of applied Sciences, Länggasse 85, 3052 Zollikofen, Switzerland; ³Qualitas AG, Chamerstrasse 56, 6300 Zug, Switzerland

Anet Spengler (anet.spengler@fibl.org), EAAP Meeting, Bratislava, Aug. 29th 2012

Introduction

› In Swiss mountain regions it has become common to inseminate dairy cows of the Swiss Brown Cattle breed (BV) with bulls of the Swiss Original Brown Cattle breed (OB).
› BV originates from crosses of OB-cows with US-Brown Swiss (BS)-sires starting back in the sixties of the last century. BV-cows usually have a high percentage of BS-blood (>75%).
› The goals of crossing BV x OB - which is especially practiced on organic farms in mountain regions - are to improve robustness and animal health and to turn the character of the breed to a dual purpose breed.
Aims of this study

› To search for effects of cross breeding BV x OB on different phenotypic characteristics (i.e. heterosis)
› To examine differences between F1-crosses and F1 x OB-crosses as well as F1 x BV-crosses, compared to “pure” breeds (OB and BV).
› To derive practical consequences for breeders and advisors
Methods I

› The sample consisted of 1st-lactation-data from 163'734 cows, born between 2000 and 2010.

› Animals were grouped into 6 breed categories:
  I: OB  7'819 cows
  II: BV  147'679 cows*
  III: OB x BV (F1)  4'880 cows
  IV: F1 x BV (F2)  2'695 cows
  V: F1 x OB (F2):  961 cows
  VI: F1 x F1 (classic F2)  45 cows (omitted)

*Random sample of animals living in valley regions was eliminated, to get the same ratio of animals from mountain regions and from valley regions as in the OB-category.

Methods II

› General linear models (GLM) were calculated using LSQ-means:

› Dependent variables:
  - milk-production traits (kg, %) and persistency
  - somatic cell score (SCS)
  - fertility traits
  - life production and lactation number (n= 83'495)

› Fixed effects: breed category, production area, age at first calving, calving month, and days open (the latter only in models with SCS, persistency, and milk production parameters as dependent variables).

› Interactions between breed category and production area were integrated in separate models.
Results I: Development of number of animals in different breed categories

A trend to replacement crossings with OB can be observed

Not all animals had calved, yet

Results II: Effect of breed category was significant in all models.
Here: Milk production

GLM, Tukey-Kramer (p<0.05)
Results II: protein content

GLM, Tukey-Kramer (p<0.05)

Results II: persistency

Interaction: breed x region

GLM, Tukey-Kramer (p<0.05)
Results II: somatic cell score (SCS)

Interaction: breed x region

GLM, Tukey-Kramer (p<0.05)

Results II: days open

GLM, Tukey-Kramer (p<0.05)
Results II: number of lactations

GLM, Tukey-Kramer (p<0.05)

<table>
<thead>
<tr>
<th>Breed Category</th>
<th>LSQ-Means</th>
</tr>
</thead>
<tbody>
<tr>
<td>100% OB</td>
<td>3.2</td>
</tr>
<tr>
<td>100% BV</td>
<td>3.4</td>
</tr>
<tr>
<td>F1: 50% OB, 50% BV</td>
<td>3.5</td>
</tr>
<tr>
<td>F2: 25% OB, 75% BV</td>
<td>3.6</td>
</tr>
<tr>
<td>F2: 75% OB, 25% BV</td>
<td>3.8</td>
</tr>
</tbody>
</table>

Results III: heterosis

<table>
<thead>
<tr>
<th>Crosses</th>
<th>Milk kg ECM</th>
<th>Fat %</th>
<th>Protein %</th>
<th>Persistency</th>
<th>SCS</th>
<th>Days Open</th>
<th># Inseminations</th>
<th>Interval 1st to Last Insem. (days)</th>
<th>Interval Calving to 1st Insem. (days)</th>
</tr>
</thead>
<tbody>
<tr>
<td>F1 (50% OB)</td>
<td>-508.74</td>
<td>-0.04</td>
<td>-0.09</td>
<td>-1.20</td>
<td>0.01</td>
<td>-1.12</td>
<td>-0.11</td>
<td>-4.00</td>
<td>2.88</td>
</tr>
<tr>
<td>F2 (25% OB)</td>
<td>-44.67</td>
<td>-0.005</td>
<td>-0.01</td>
<td>-0.23</td>
<td>-0.04</td>
<td>2.52</td>
<td>0.03</td>
<td>1.63</td>
<td>0.89</td>
</tr>
<tr>
<td>F2 (75% OB)</td>
<td>-359.22</td>
<td>-0.02</td>
<td>-0.09</td>
<td>-0.60</td>
<td>0.01</td>
<td>0.16</td>
<td>-0.03</td>
<td>-2.08</td>
<td>2.24</td>
</tr>
</tbody>
</table>

= positive heterosis effect
= negative heterosis effect
= no heterosis effect
Comparison of crosses and parental breeds (LSQ-means: phenotypes)

<table>
<thead>
<tr>
<th>Crosses compared to</th>
<th>milk kg ECM</th>
<th>fat %</th>
<th>protein %</th>
<th>persis-tency</th>
<th>SCS</th>
<th>days open</th>
<th># insemi-nations</th>
<th># lactations</th>
</tr>
</thead>
<tbody>
<tr>
<td>F1 (50%OB) OB</td>
<td>↑</td>
<td>↓</td>
<td>↓</td>
<td>↑</td>
<td>↑</td>
<td>↓</td>
<td>↑</td>
<td>↓</td>
</tr>
<tr>
<td>F2 (25%OB) OB</td>
<td>↑</td>
<td>↑</td>
<td>↓</td>
<td>↑</td>
<td>↑</td>
<td>↓</td>
<td>↑</td>
<td>↓</td>
</tr>
<tr>
<td>F2 (75%OB) OB</td>
<td>↓</td>
<td>↑</td>
<td>↓</td>
<td>↑</td>
<td>↑</td>
<td>↓</td>
<td>↑</td>
<td>↓</td>
</tr>
<tr>
<td>F1 (50%OB) BV</td>
<td>↓</td>
<td>↓</td>
<td>↑</td>
<td>→</td>
<td>↓</td>
<td>↓</td>
<td>→</td>
<td>↓</td>
</tr>
<tr>
<td>F2 (25%OB) BV</td>
<td>↓</td>
<td>↓</td>
<td>↓</td>
<td>→</td>
<td>↓</td>
<td>↓</td>
<td>→</td>
<td>↓</td>
</tr>
<tr>
<td>F2 (75%OB) BV</td>
<td>↓</td>
<td>↓</td>
<td>↓</td>
<td>↑</td>
<td>↓</td>
<td>↓</td>
<td>→</td>
<td>↓</td>
</tr>
</tbody>
</table>

- = crosses better than pure bred animals
- = crosses worse than pure bred animals
- = crosses similar to pure bred animals

Results III: heterosis

- Heterosis effects (= difference between crosses and average of parents) were found for several traits:
- F1 (OB x BV)-crossings were better than average of OB and BV in: days open, number of inseminations, and interval from first to last insemination. In all other traits F1-crossings were worse than average of BV and OB.
- F2 (25% OB = BV x F1)-crossings were better than average of parents in SCS. In all other traits they were worse.
- F2 (75% OB = OB x F1)-crossings were better than average of parents in number of inseminations and interval from first to last insemination. In all other traits they were worse.
Discussion

› All crosses are worse than pure bred BV in all production traits, but **better than** or equal as BV in functional traits.
› Crosses are similar in production traits as pure bred OB, but they are **worse than** or equal as OB in all functional traits.
› In high mountain regions SCS, persistency, and days open of pure OB are better than or equal as crosses and BV. So, OB is functionally the best brown breed for mountain areas.
› Replacement crossings with OB take a long time (more than two generations) until animals show constantly good functional and production traits.
› Crosses show not many positive heterosis effects. The reason for that is that OB are better than crosses or equal as crosses in most traits.

Conclusions

› Crossbreeding with OB is recommended to ameliorate functional traits in BV herds, especially in mountain regions
› Changing to pure OB individuals is expected to lead to a faster and probably more solid success regarding health and robustness
› Since good functional traits are especially important on organic farms the use of OB is warmly recommended to them
› It would be interesting to analyse the effect of crossbreeding in other breeds with similar backgrounds (as for example Holsteins (HO) and Deutsches Schwarzbuntes Niederungsrand (DSN) and their crossings) to know more about characteristics of crossings, which are often used on organic farms
Thanks to:
Bio Suisse for financial support

Thank you for your attention