RightMate: Precision Breeding by Genomic Mating

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Breeding Decisions: Customer Needs and priorities

- Balanced Trait Mating?
- Terminal Mating?
- Heifer Mating?
- Multiply Priorities?
- Genetic Improvement, Genetic Diversity & Uniformity?
Complexity of Animal Breeding:

ORIGINAL ARTICLE

Complexity of animal breeding choice making

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Abstract

The last decades of developments in animal breeding, genetics, genomics and data recording technologies have allowed the evaluation of larger numbers of animal and animal traits than ever before. This should help make animal breeding choices more informed, but it also makes them far more complex. This complexity may be overwhelming farmers, thus compromising realization of potential genetic gain in livestock industries. However, the effect of complexity of animal breeding choices on farmers’ selection of animals has received very little theoretical consideration to date. This paper reviews the theoretical principles of complex decisions, contextualizes the findings to the field of animal breeding, and analyses how farmers and the animal breeding industry are currently dealing with complexity. According to the findings of the analyses of complex decisions in other fields, the complexity of animal breeding choices is likely to lead to farmers using conscious or unconscious simplifying strategies (heuristics) to handle such complexity. When these heuristics are ineffective, poor selection decisions and a potential loss of genetic progress can be expected. Further, studies using survey experiments to understand farmer behaviour and selection preferences may be compromised by the complexity of the survey's
Complexity of Animal Breeding:

**FIGURE 1** Description of how complexity might be affecting animal breeding choices made by individual farmers according to the theoretical principles of complex decisions. Key sources of complexity, potential heuristics used by farmers to simplify the decisions, and types of suboptimal decisions which may occur due to that complexity.
So...What is RightMate?

• Genomic based Precision Breeding Tool.
• Primarily Designed for Seedstock Providers.
• Generations of Improvement per Mating Cycle.
• More Uniform Calf Crops.
• Optimized genetic diversity/Improvement with customized breeding objectives by integrating into MateSel software.
• Uses both EPDs and the Power of High Impact Genes.
Prediction of expected genetic variation within groups of offspring for innovative mating schemes

Dierck Segelke1,2*, Friedrich Reinhardt1, Zenting Liu1 and Georg Thaller2

Abstract

Background: Experience from progeny-testing indicates that the mating of popular bull sires that have high estimated breeding values with excellent dams does not guarantee the production of offspring with superior breeding values. This is explained partly by differences in the standard deviation of gamete breeding values (SDGBV) between animals at the haplotype level. The SDGBV depends on the variance of the true effects of single nucleotide polymorphisms (SNPs) and the degree of heterozygosity. Haplotypes of 58,035 Holstein animals were used to predict and investigate expected SDGBV for fat yield, protein yield, somatic cell score and the direct genetic effect for stillbirth.

Results: Differences in SDGBV between animals were detected, which means that the groups of offspring of parents with low SDGBV will be more homogeneous than those of parents with high SDGBV, although the expected mean breeding values of the progeny will be the same. SDGBV was negatively correlated with genomic and pedigree inbreeding coefficients and a small loss of SDGBV over time was observed. Sires that had relatively low mean gamete breeding values but high SDGBV had a higher probability of producing extremely positive offspring than sires that had a high mean gamete breeding value and low SDGBV.

Conclusions: An animal's SDGBV can be estimated based on genomic information and used to design specific genomic mating plans. Estimated SDGBV are an additional tool for mating programs, which allows breeders to identify and match mating partners using specific haplotype information.
Table 3 Correlations (r) between SDGBV with real progeny variations for different traits per minimum number of offspring per sire

<table>
<thead>
<tr>
<th>Minimum number of offspring per sire</th>
<th>Number of sires</th>
<th>r_{FY}</th>
<th>r_{PY}</th>
<th>r_{SCS}</th>
<th>r_{SBd}</th>
</tr>
</thead>
<tbody>
<tr>
<td>10</td>
<td>409</td>
<td>0.65</td>
<td>0.56</td>
<td>0.60</td>
<td>0.50</td>
</tr>
<tr>
<td>50</td>
<td>146</td>
<td>0.90</td>
<td>0.78</td>
<td>0.80</td>
<td>0.72</td>
</tr>
<tr>
<td>100</td>
<td>84</td>
<td>0.93</td>
<td>0.83</td>
<td>0.88</td>
<td>0.69</td>
</tr>
<tr>
<td>150</td>
<td>48</td>
<td>0.93</td>
<td>0.90</td>
<td>0.90</td>
<td>0.78</td>
</tr>
<tr>
<td>200</td>
<td>32</td>
<td>0.93</td>
<td>0.91</td>
<td>0.87</td>
<td>0.85</td>
</tr>
<tr>
<td>300</td>
<td>20</td>
<td>0.96</td>
<td>0.93</td>
<td>0.94</td>
<td>0.82</td>
</tr>
<tr>
<td>500</td>
<td>7</td>
<td>0.98</td>
<td>0.88</td>
<td>0.90</td>
<td>0.90</td>
</tr>
</tbody>
</table>

PY = protein yield; FY = fat yield; SCS = somatic cell score; SBd = the direct genetic effect for stillbirth.
Figure 5 Distribution of the breeding values of offspring for protein yield. Two bulls (with MGBV equal to 1.81 $\sigma_h$ and 1.68 $\sigma_h$ and SDGBV equal to 0.29 $\sigma_h$ and 0.52 $\sigma_h$ respectively) are mated with an average female of the population (MGBV equal to 0.55 $\sigma_h$, SDGBV equal to 0.39 $\sigma_h$).
Figure 6 Distribution of SDGBV for fat yield with and without the DGAT1 haplotype.
Large-effect pleiotropic or closely linked QTL segregate within and across ten US cattle breeds

Mahdi Saatchi1, Robert D Schnabel2, Jeremy F Taylor3 and Dorian J Garrick1,2

_**RESEARCH ARTICLE** Open Access_

_** Trait**_  
Breed  
SIM  
RDP  
RAN  
LIM  
HER  
GVH  
CHA  
BSH  
BRG  
AAN  

_** Trait**_  
BWT  
CED  
CEM  
CWT  
FAT  
MRB  
MWT  
REA  
WWD  
WWM  
YGR  
YWT  

- BTA28:6–7  
- BTA4:61  
- BTA5:48–50  
- BTA5:106  
- BTA6:37–42  
- BTA7:93  
- BTA14:23–26  
- BTA15:38–39  
- BTA20:4–5  
- BTA29:30  
- Other QTLs  
- Unexplained
Could functional variants be more effective?

<table>
<thead>
<tr>
<th>Genetic correlations between birth weight and GPE-trained birth weight MBV</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>Marker set</strong></td>
</tr>
<tr>
<td></td>
</tr>
<tr>
<td>F250 shared with SOK</td>
</tr>
<tr>
<td>Significant GPE effects</td>
</tr>
<tr>
<td>LD reduced</td>
</tr>
<tr>
<td>NCAPG</td>
</tr>
</tbody>
</table>

- Small sets of functional variants can explain meaningful phenotypic variation within and across populations
  - depends on number and size of effects • difficult to identify variants causing small effects, especially for traits influenced by many variants with small effects

Which bull do you choose as a heifer bull?
Which bull do you mate to a low growing cow?

That is a Precision Breeding!
Faster Genetic Improvement:
RightMate Validation: API

**Quantiles**
- RightMate=No
  - 100.0% maximum: 186.7
  - 99.5%: 181.19
  - 97.5%: 173.55
  - 90.0%: 166.2
  - 75.0% quartile: 160.4
  - 50.0% median: 153.3
  - 25.0% quartile: 145.7
  - 10.0%: 137.6
  - 2.5%: 117.8
  - 0.5%: 105.99
  - 0.0% minimum: 96.8

- RightMate=Yes
  - 100.0% maximum: 183.1
  - 99.5%: 183.1
  - 97.5%: 182.715
  - 90.0%: 176.06
  - 75.0% quartile: 166.275
  - 50.0% median: 160.4
  - 25.0% quartile: 156.925
  - 10.0%: 153.21
  - 2.5%: 149.1125
  - 0.5%: 147.5
  - 0.0% minimum: 147.5

**Summary Statistics**
- RightMate=No
  - Mean: 152.05846
  - Std Dev: 12.843435

- RightMate=Yes
  - Mean: 162.43125
  - Std Dev: 8.2339133
RightMate Validation: Actual Birth Weight

**Quantiles**
- RightMate=No
  - 100.0% maximum: 108
  - 99.5%: 104
  - 97.5%: 98
  - 90.0%: 87
  - 75.0% quartile: 81
  - 50.0% median: 76
  - 25.0% quartile: 70
  - 10.0%: 65
  - 2.5%: 59.55
  - 0.5%: 55
  - 0.0% minimum: 50

**Summary Statistics**
- Mean: 75.905633
- Std Dev: 9.0881113

**Quantiles**
- RightMate=Yes
  - 100.0% maximum: 100
  - 99.5%: 100
  - 97.5%: 94.575
  - 90.0%: 86.3
  - 75.0% quartile: 80
  - 50.0% median: 75
  - 25.0% quartile: 68
  - 10.0%: 65
  - 2.5%: 59.7
  - 0.5%: 55
  - 0.0% minimum: 55

**Summary Statistics**
- Mean: 75.083333
- Std Dev: 8.4811452
Herd A - Genetic Improvement:

Before RM: +2.09/year
After RM: +3.60/year
Herd A - Uniformity:

![Uniformity - Birth Weight](image)

**Herd A**

**Uniformity - Birth Weight**

<table>
<thead>
<tr>
<th>Year</th>
<th>Mean</th>
<th>Std Dev</th>
</tr>
</thead>
<tbody>
<tr>
<td>2013</td>
<td>81.1</td>
<td></td>
</tr>
<tr>
<td>2014</td>
<td>81.4</td>
<td></td>
</tr>
<tr>
<td>2015</td>
<td>82.0</td>
<td></td>
</tr>
<tr>
<td>2016</td>
<td>81.3</td>
<td></td>
</tr>
<tr>
<td>2017</td>
<td>81.4</td>
<td></td>
</tr>
<tr>
<td>2018</td>
<td>81.9</td>
<td></td>
</tr>
<tr>
<td>2019</td>
<td>77.8</td>
<td></td>
</tr>
<tr>
<td>2020</td>
<td>76.9</td>
<td></td>
</tr>
<tr>
<td>2021</td>
<td>75.3</td>
<td></td>
</tr>
<tr>
<td>2022</td>
<td>74.8</td>
<td></td>
</tr>
</tbody>
</table>
Herd B - Genetic Improvement:

Before RM: +2.55/year
After RM: +11.2/year
Herd C - Genetic Improvement:

Before RM: +2.99/year
After RM: +6.67/year
Herd D - Genetic Improvement:

Before RM: +2.05/year
After RM: +5.91/year
# RightMate Results: 2021 Born Calves

<table>
<thead>
<tr>
<th>Mate</th>
<th>N Calves</th>
<th>$API</th>
</tr>
</thead>
<tbody>
<tr>
<td>Non-RightMate</td>
<td>1274</td>
<td>152.8</td>
</tr>
<tr>
<td>RightMate</td>
<td>1242</td>
<td>158.2</td>
</tr>
</tbody>
</table>

![Graph comparing $API for RightMate vs Non-RightMate Calves]
RightMate Results: 2021 Born Calves

<table>
<thead>
<tr>
<th>Mate</th>
<th>N Calves</th>
<th>$TI</th>
</tr>
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<tbody>
<tr>
<td>Non-RightMate</td>
<td>1274</td>
<td>87.4</td>
</tr>
<tr>
<td>RightMate</td>
<td>1242</td>
<td>90.2</td>
</tr>
</tbody>
</table>

$TI - RightMate vs Non-RightMate Calves
## RightMate Results: 2021 Born Calves

<table>
<thead>
<tr>
<th>Traits</th>
<th>Non-RightMate</th>
<th>RightMate</th>
<th>Diff.</th>
</tr>
</thead>
<tbody>
<tr>
<td>CE</td>
<td>13.6</td>
<td>14.2</td>
<td>+0.8</td>
</tr>
<tr>
<td>BW</td>
<td>-0.3</td>
<td>-0.6</td>
<td>-0.3</td>
</tr>
<tr>
<td>WW</td>
<td>80.2</td>
<td>81.7</td>
<td>+1.5</td>
</tr>
<tr>
<td>YW</td>
<td>125.6</td>
<td>128.3</td>
<td>+2.7</td>
</tr>
<tr>
<td>ADG</td>
<td>0.28</td>
<td>0.29</td>
<td>+0.01</td>
</tr>
<tr>
<td>MCE</td>
<td>7.8</td>
<td>8.1</td>
<td>+0.3</td>
</tr>
<tr>
<td>MILK</td>
<td>26.2</td>
<td>25.7</td>
<td>-0.5</td>
</tr>
<tr>
<td>MWW</td>
<td>66.3</td>
<td>66.5</td>
<td>+0.2</td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>Traits</th>
<th>Non-RightMate</th>
<th>RightMate</th>
<th>Diff.</th>
</tr>
</thead>
<tbody>
<tr>
<td>STAY</td>
<td>17.7</td>
<td>18.1</td>
<td>+0.4</td>
</tr>
<tr>
<td>CW</td>
<td>36.4</td>
<td>37.3</td>
<td>+0.9</td>
</tr>
<tr>
<td>YG</td>
<td>-0.26</td>
<td>-0.26</td>
<td>0</td>
</tr>
<tr>
<td>MRB</td>
<td>0.46</td>
<td>0.51</td>
<td>+0.05</td>
</tr>
<tr>
<td>BF</td>
<td>-0.05</td>
<td>-0.04</td>
<td>+0.01</td>
</tr>
<tr>
<td>REA</td>
<td>0.80</td>
<td>0.83</td>
<td>+0.03</td>
</tr>
<tr>
<td>SHR</td>
<td>-0.35</td>
<td>-0.37</td>
<td>-0.02</td>
</tr>
</tbody>
</table>
Simplify the decision making and reduce the risk

The 3 Accreditation Logos are designed to simplify bull selection and improve buyer confidence and reducing risk.
Mean (Birth Wt)

- ATM: 79.5 Lb
- No-ATM: 77.9 Lb
- Difference: +1.6 Lb

Mean (Wean Wt)

- ATM: 605 Lb
- No-ATM: 563 Lb
- Difference: +42 Lb
RightMate Benefits:

- Precision Breeding using Genomics
- Avoid Wasted Mating to offer more Marketable Bulls and Heifers
- Reduce Variation and More Uniformity
- Genetic Improvement at a Higher Speed
- Managing Inbreeding, Genetic Diversity and Customized Breeding using MateSel
2023 RightMate Statistics (So far):

✓ >11,681 Cows RightMated from >75 Herds

✓ > 4,400 Bulls/Cows RightChoice evaluated from >62 Herds
RightMate Added-Value for Beef Industry:

✓ >10,000 Cows RightMated
✓ >5,000 RightMate Calves
✓ >2,000 RightMate Bull Calves goes to Commercial Herds
✓ ~100 calves per commercial herd bull.
✓ >$5 extra genetic improvement ($API)
✓ > $1,000,000/year RightMate added-value in commercial beef sector.
✓ Much more $ added value for replacement heifers, Seed-stock and AI bulls!
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Genomics wins!

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