Optimum breeding schemes for hybrid wheat

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Target criterion = maximum selection gain

\[ \Delta G_a = \frac{ih\sigma_{gca}}{y} \]

• \( i \) = selection intensity,
• \( h \) = square root of the heritability,
• \( \sigma_{gca} \) = squareroot of GCA variance
• \( y \) = number of years required to finish 1 breeding cycle

→ The number of lines, locations and testers is optimized
→ Software: R package 'selectiongain'
Breeding schemes

| Year 1 | P1 x P2, ... |
| Year 2 | DH-Production |
| Year 3 | $N_1$ DH lines - multiplication |
| Year 4 | Hybrid seed prod. $N_2 \times T_2$ |
| Year 5 | Field test $N_2 \times T_2 \times L_2$ |
| Year 6 | Hybrid seed prod. $N_3 \times T_3$ |
| Year 7 | Field test $N_3 \times T_3 \times L_3$ |

Year 8, 9,...  Pre-registration trials

Source: Longin et al. 2015
# Breeding schemes

<table>
<thead>
<tr>
<th>Year 1</th>
<th>PS&lt;sub&gt;standard&lt;/sub&gt;</th>
<th>P1 x P2, …</th>
<th>GS&lt;sub&gt;standard&lt;/sub&gt;</th>
<th>P1 x P2, …</th>
</tr>
</thead>
<tbody>
<tr>
<td>Year 2</td>
<td>DH-Production</td>
<td>DH-Production</td>
<td></td>
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</tr>
<tr>
<td>Year 3</td>
<td>N&lt;sub&gt;1&lt;/sub&gt; DH lines - multiplication</td>
<td>N&lt;sub&gt;1&lt;/sub&gt; DH lines - multiplication</td>
<td>Genomic selection</td>
<td>N&lt;sub&gt;1&lt;/sub&gt;,</td>
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<td></td>
<td></td>
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<tr>
<td>Year 4</td>
<td>Hybrid seed prod. N&lt;sub&gt;2&lt;/sub&gt; * T&lt;sub&gt;2&lt;/sub&gt;</td>
<td>Hybrid seed prod. N&lt;sub&gt;2&lt;/sub&gt; * T&lt;sub&gt;2&lt;/sub&gt;</td>
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<tr>
<td>Year 5</td>
<td>Field test N&lt;sub&gt;2&lt;/sub&gt; * T&lt;sub&gt;2&lt;/sub&gt; * L&lt;sub&gt;2&lt;/sub&gt;</td>
<td>Field test N&lt;sub&gt;2&lt;/sub&gt; * T&lt;sub&gt;2&lt;/sub&gt; * L&lt;sub&gt;2&lt;/sub&gt;</td>
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<tr>
<td>Year 6</td>
<td>Hybrid seed prod. N&lt;sub&gt;3&lt;/sub&gt; * T&lt;sub&gt;3&lt;/sub&gt;</td>
<td>Hybrid seed prod. N&lt;sub&gt;3&lt;/sub&gt; * T&lt;sub&gt;3&lt;/sub&gt;</td>
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<tr>
<td>Year 7</td>
<td>Field test N&lt;sub&gt;3&lt;/sub&gt; * T&lt;sub&gt;3&lt;/sub&gt; * L&lt;sub&gt;3&lt;/sub&gt;</td>
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</tbody>
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Source: Longin et al. 2015
Increase in selection gain with GS

The higher the prediction accuracy the larger is the advantage of GS schemes

Source: Longin et al. 2015
Reduce cycle length with GS

<table>
<thead>
<tr>
<th>Year</th>
<th>PS&lt;sub&gt;standard&lt;/sub&gt;</th>
<th>GS&lt;sub&gt;standard&lt;/sub&gt;</th>
<th>GS&lt;sub&gt;rapid&lt;/sub&gt;</th>
<th>GS&lt;sub&gt;only&lt;/sub&gt;</th>
</tr>
</thead>
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<tr>
<td>Year 1</td>
<td>P1 x P2, …</td>
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<td>DH-Production</td>
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<td>N₁ DH lines - multiplication</td>
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<tr>
<td></td>
<td>Genomic selection N₁</td>
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<tr>
<td>Year 4</td>
<td>Hybrid seed prod. N₂ * T₂</td>
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<td>Field test N₂ * T₂ * L₂</td>
<td>Field test N₂ * T₂ * L₂</td>
<td>Field test N₂ * T₂ * L₂</td>
<td>Field test N₂ * T₂ * L₂</td>
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<tr>
<td>Year 6</td>
<td>Hybrid seed prod. N₃ * T₃</td>
<td>Hybrid seed prod. N₃ * T₃</td>
<td>Hybrid seed prod. N₃ * T₃</td>
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<td>Year 7</td>
<td>Field test N₃ * T₃ * L₃</td>
<td>Field test N₃ * T₃ * L₃</td>
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Up to 4 years faster breeding schemes feasible with GS

Source: Longin et al. 2015
Genomic selection is promising for grain yield especially when **used to shorten breeding cycle length**

Source: Longin et al. 2015
GS for yield is interesting

With recent GS accuracy breeding scheme $\text{GS}_{\text{rapid}}$ seems most promising: +35% in annual selection gain

Source: Longin et al. 2015
Allocation of resources

**Table:** Numbers of DH lines \((N_x)\), locations \((L_x)\) and testers \((T_x)\) maximizing annual selection gain \((\Delta G_a)\) and its standard deviation (SD)

<table>
<thead>
<tr>
<th>Scheme</th>
<th>Acc</th>
<th>(N_1)</th>
<th>(N_2)</th>
<th>(N_3)</th>
<th>(L_2)</th>
<th>(L_3)</th>
<th>(T_2)</th>
<th>(T_3)</th>
<th>(\Delta G_a)</th>
<th>SD</th>
</tr>
</thead>
<tbody>
<tr>
<td>(PS_{standard})</td>
<td>NA</td>
<td>0</td>
<td>680</td>
<td>40</td>
<td>5</td>
<td>10</td>
<td>1</td>
<td>6</td>
<td>0.82</td>
<td>0.65</td>
</tr>
<tr>
<td>(GS_{rapid})</td>
<td>0.3</td>
<td>1519</td>
<td>130</td>
<td>NA</td>
<td>10</td>
<td>NA</td>
<td>3</td>
<td>NA</td>
<td>1.11</td>
<td>0.75</td>
</tr>
</tbody>
</table>

With **\(GS_{rapid}\)** a much higher initial number of DH lines is tested but with less intensive phenotyping.
Extension to pre-breeding programs

- Hybrids seem promising also in wheat

- **Genomic selection** is able to **increase selection gain**

→ Could these methods also be used to boost other breeding scenarios? Especially complicated long-term issues like **long-term pre-breeding for grain yield??**
How to use genetic resources for yield?

**Usefulness** = \( \mu + \Delta G = \mu + i h \sigma \)

*Source: Longin and Reif 2014*
How to use genetic resources for yield?

Source: Longin and Reif 2014
How to use genetic resources for yield?

- Select resources with high breeding value and maximize speed of introgression, but how?

Source: Longin and Reif 2014
Genotyping of gene banks seems to be possible now; but all nice GS predictions are only possible, when we have reliable phenotypic data of genetic resources

Major bottle neck: High throughput phenotyping
- Possible on a large scale for diseases and some qualities
- For grain yield ??

Source: Reif
Uncovering breeding values of resources

- Breeding value of resources $\rightarrow$ line breeding
- GCA value of resources $\rightarrow$ hybrid breeding

Source: Longin and Reif 2014
Realization requires field power!

In Germany, IPK and LSA makes each year with wheat genetic resources from the gene bank Gatersleben:

- **2000 observation rows**
  - 2 locations
  - Diseases: rusts, mildew, septoria
  - Heading, plant height, (frost)
  - Anther extrusion, flowering time

- **Hybrid seed production**
  - ≥ 300 genetic resources with few elite testers
  - Gametozid based sterilization

- **Hybrid yield tests**
  - > 300 hybrids with genetic resources
  - ≥ 5 locations yield trials
  - ≥ 3 locations observation trials
How to introgress best resources?

AIM: Use resource as crossing partner in elite breeding program

- Probability low that resources are found, which can directly be used in elite breeding
  → we need pre-breeding programs
How to introgress best resources?

**AIM: Use resource as crossing partner in elite breeding program**

- Probability low that resources are found, which can directly be used in elite breeding
  → **we need pre-breeding programs**

- **Breeding scheme: main pillars**
  - Mating design
  - Population size
  - Speed → **rapid recycling based on genomic selection**
Conclusions

- The implementation of genomic selection maximizes selection gain in wheat breeding and especially for hybrid wheat.

- We propose a breeding scheme based on 1 stage GS followed by 1 stage phenotypic selection before entering pre-registration trials.

- Testing the breeding value of wheat genetic resources gets feasible with hybrid method.

- Genomic selection is of utmost importance for pre-breeding programs targeting wheat grain yield.
Thanks
Input variables

- **Annual budget** = 10,000 yield plots ~ 300,000€ for producing DH lines + markers + hybrid seed production + field tests

- **Costs** for
  - Producing 1 DH line = 1 plot
  - Genotyping 1 DH line = 2 plots
  - Producing hybrid seed of 1 DH line = 4 plots

- **Variance components** from trials: $\sigma^2_{GCA} = 5.7$, $\sigma^2_{GCA \cdot L} = 5.19$, $\sigma^2_{SCA} = 1.88$, $\sigma^2_{SCA \cdot L} = 2.94$, $\sigma^2_{error} = 24.37$

- **Maximum number of test locations**: Max(1st yield trial) = 5, Max(2nd yield trial) = 10