Breeding for virus resistance in cereals
Frank Ordon

**Important viruses of Poaceae (Gramineae)**

- **Barley** - *Hordeum*
  - Barley yellow mosaic virus
  - Sheath blight mosaic virus
  - Barley stripe mosaic virus
  - Barley yellow mosaic virus
  - Barley black stem mosaic virus
  - Barley yellow rust mosaic virus

- **Wheat** - *Triticum*
  - Wheat yellow mosaic virus
  - Wheat spindle streak mosaic virus
  - Barley yellow mosaic virus
  - Barley yellow mosaic virus
  - Northern cereal mosaic virus
  - Wheat yellow mosaic virus
  - Wheat black stem mosaic virus

- **Rye** - *Secale*
  - Barley yellow mosaic virus
  - Wheat yellow mosaic virus
  - Soil-borne cereal mosaic virus
  - Wheat spindle streak mosaic virus

- **Triticale** - *Triticosecale*
  - Barley yellow mosaic virus
  - Wheat yellow mosaic virus
  - Soil-borne cereal mosaic virus
  - Wheat spindle streak mosaic virus

- **Corn** - *Zea*
  - Maize dwarf mosaic virus
  - Johnsongrass mosaic virus
  - Sugarcane mosaic virus
  - Maize rough dwarf virus
  - Maize chlorotic mottle virus
  - Maize chlorotic dwarf virus
  - Maize bushy stunt virus
  - Cereal chlorotic mottle virus
  - Barley yellow mosaic virus
  - Sorghum chlorotic spot virus
  - High Plains virus
  - Wheat streak mosaic virus

- **Rice** - *Oryza*
  - Rice tungro virus
  - Rice dwarf virus
  - Rice gall dwarf virus
  - Rice grassy stunt virus
  - Rice hoja blanca virus
  - Rice necrosis mosaic virus
  - Rice ragged stunt virus
  - Rice stripe necrosis virus
  - Rice yellow mottle virus
  - Barley yellow mosaic virus

- **Sorghum / Millet** - *Sorghum* / *Pennisetum*
  - Maize dwarf mosaic virus
  - Sorghum yellow banding virus
  - Sorghum chlorotic spot virus

**Genetic base of BaMMV/BaYMV-resistance**

- **Economic loss caused by BaMMV/BaYMV**
  - Acreage (2010): 1303000 ha
  - Yield: 6.66 t = 8677980 t
  - Barley price: 150 € per t
  - Economic value: 1301697000 €

- **50% of barley acreage potentially infested (Huth 1988): 651500 ha**

- **Moderate yield loss of 25%: 1074975 t**

- **Economic loss: 161246250 €**

- **BaMMV, BAMMV-SIL, BaMMV-Teik, BaYMV, BaYMV-2**

**Barley yellow mosaic virus disease**

- **Table:**
  - Cultivar | BaMMV/BaYMV | Yield relative |
  - ---------------- | ------------- | --------------|
  - Aserbia (6-rowed) | resistant | 5.33 | 100 |
  - Corona (6-rowed) | susceptible | 3.23 | 50 |
  - Romanza (2-rowed) | resistant | 4.20 | 100 |
  - Marinka (4-rowed) | susceptible | 3.00 | |
  - Yuka (6-rowed) | resistant | 7.66 | 100 |
  - Grete (6-rowed) | susceptible | 4.10 | 54 |
  - Duet (2-rowed) | resistant | 6.30 | 100 |
  - Angora (2-rowed) | susceptible | 4.24 | 67 |

- **1=minimum, 9=maximum, List of registered cultivars, Federal Seedboard, different years**
- **48:** rym4 derived from Ragusa
- **4:** rym5 Tokyo (1996): [(Fallon x 13060) x 87-5381 B] x Swift
- **Resistant Ym. No.1 x Igri**
- **(Hemker, pers. Comm.)**

**Genetic base of BaMMV/BaYMV-resistance**

- **Table:**
  - Year | No. Cultivars | Yield resistant | susceptible |
  - ----------------- | --------------- | ---------------|
  - 1986 | 6 | 37 | 43 |
  - 1995 | 24 | 41 | 65 |
  - 2005 | 52** | 23 | 67 |
  - 2011 | 55 | 9 | 69 |

- **1=minimum, 5=maximum, List of registered cultivars, Federal Seedboard, different years**
- **48:** rym4 derived from Ragusa
- **4:** rym5 Tokyo (1996): [(Fallon x 13060) x 87-5381 B] x Swift
- **Resistant Ym. No.1 x Igri**
- **(Hemker, pers. Comm.)**
Screening for resistance and genetic analysis

<table>
<thead>
<tr>
<th>Hordeum vulgare sp. vulgare</th>
<th>BaYMV</th>
<th>BaYMV-2 Mo</th>
<th>None</th>
</tr>
</thead>
<tbody>
<tr>
<td>Cross</td>
<td>F₂</td>
<td>Segregation</td>
<td>Inf. - rate (%)</td>
</tr>
<tr>
<td>Hordeum vulgare sp. vulgare</td>
<td>-</td>
<td>-</td>
<td>201</td>
</tr>
<tr>
<td>Hordeum vulgare sp. spontaneum</td>
<td>-</td>
<td>+</td>
<td>86</td>
</tr>
</tbody>
</table>

- = negative ELISA (resistant), + = positive ELISA (susceptible)

For more details, see Ordon et al. (1992), Habekuss et al. (2000).

Prebreeding

Reliable selection on the single plant level (A₀, F₃) in the lab independently from the incidence of viruses in the field and symptom development in early developmental stages.

- Viruses do not incite each year
- Symptom development is often influenced by environmental factors

Wheat – SBCMV-Resistance

3 alleles identified in about 100 genotypes tested. 154 bp diagnostic for „Cadenza-derived resistance“, 152 bp for „Tremie/Claire-derived resistance“.

Marker assisted backcrossing

Donor (R) x Recurrent Parent (S)

Determination of the genomic portion of the recurrent parent

R S

Marker assisted backcrossing
Pyramiding of BaMMV/BaYMV Resistance Genes

BoYMV  BoYMV-2  BoMMV  BoMMV-SIL  BoMMV-E1K

\[
\begin{align*}
\text{rym4} & : r \quad s \quad r \quad r \quad r \\
\text{rym5} & : r \quad r \quad r \quad s \quad s \\
\text{rym9} & : s \quad s \quad r \quad r \quad r \\
\text{rym11} & : r \quad r \quad r \quad r \quad r
\end{align*}
\]

Barley yellow dwarf virus (BYDV)

Luizenzirus

\[
\text{BYDV-PAV} \quad \text{Rhopalosiphum padi} \quad \text{Microsiphon avenae}
\]

Polarovirus

\[
\text{CYDV-MPV} \quad \text{Rhopalosiphum padi}
\]

Identification von QTL for BYDV-tolerance

Relation between BYDV attack of winter barley in spring and temperature in autumn

BYDV – Pyramiding of QTL in winter barley and spring barley

\[
\begin{align*}
\text{rym4} & : 22,15,3,2,4 \\
\text{rym5} & : 22,15,3,2,4 \\
\text{rym9} & : 22,15,3,2,4 \\
\text{rym11} & : 22,15,3,2,4
\end{align*}
\]

Isolation of resistance genes - allele mining
Summary and future prospects

Molecular markers facilitate already today efficient selection procedures to improve virus resistance in cereals.

The availability of dense marker maps, high throughput genotyping platforms, physical maps and genome sequences of cereals itself and related species will facilitate an enhanced isolation of resistance genes in the future thereby leading to a deeper understanding of virus resistance and the transfer of marker based selection to the allele level.

This together with new selection strategies, e.g. genomic selection procedures, will lead to an enhanced breeding of virus resistant cultivars.

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