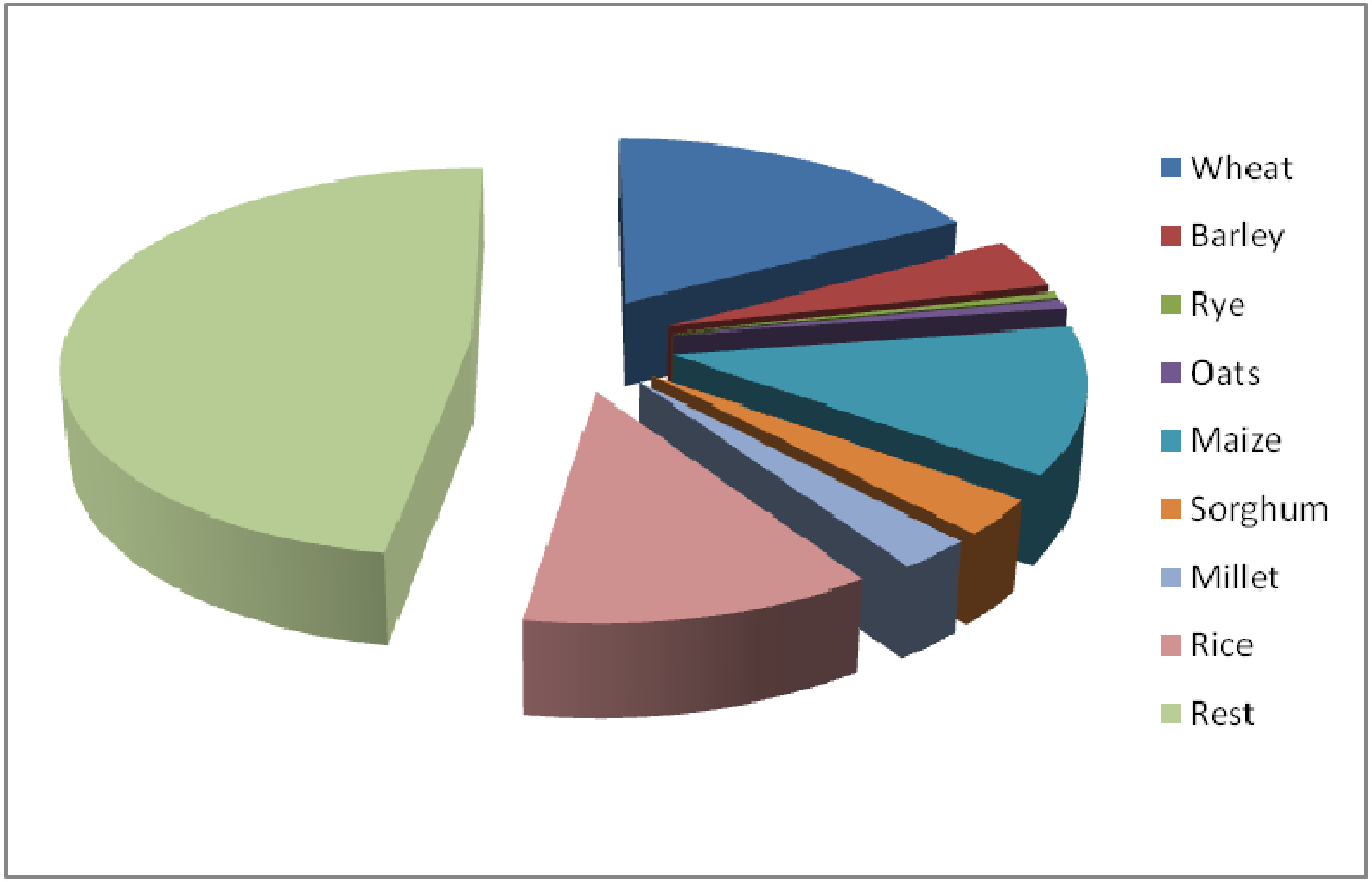
Julius Kühn-Institut
Bundesforschungsinstitut für Kulturpflanzen
Federal Research Centre for Cultivated Plants

# Breeding for virus resistance in cereals

**Frank Ordon**

# Worldwide acreage of cereals 2009




http://faostat.fao.org

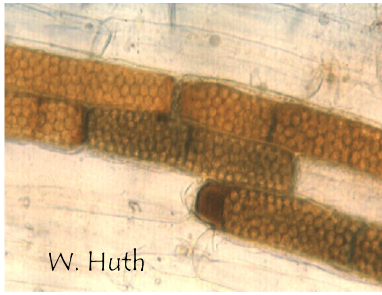
# Important viruses of *Poaceae* (*Gramineae*)

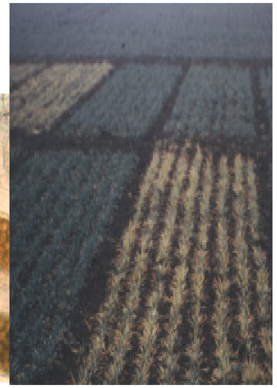
| | |
|---|---|
| **Wheat - *Triticum*** | Barley yellow dwarf virus, Wheat dwarf virus, Soil-borne wheat mosaic virus, Wheat spindle streak mosaic virus, **Soil-borne cereal mosaic virus**, Wheat yellow mosaic virus, Aubian wheat mosaic virus, Barley yellow striate mosaic virus, Indian peanut clump virus, Wheat rosette stunt virus, Wheat American striate virus |
| **Barley - *Hordeum*** | **Barley yellow dwarf virus**, Wheat dwarf virus, **Barley mild mosaic virus**, **Barley yellow mosaic virus**, Barley stripe mosaic virus, Northern cereal mosaic virus, Barley yellow streak mosaic virus, Arabis mosaic virus, Tobacco rattle virus |
| **Rye - *Secale*** | Barley yellow dwarf virus, Wheat dwarf virus, Soil-borne cereal mosaic virus, Wheat spindle streak mosaic |
| **Triticale - *Triticosecale*** | Barley yellow dwarf virus, Wheat dwarf virus, Soil-borne cereal mosaic virus, Wheat spindle streak mosaic virus |
| **Oat - *Avena*** | Barley yellow dwarf virus, Oat sterile dwarf virus, Oat golden stripe virus, Oat chlorotic stunt virus, Oat mosaic virus, Wheat dwarf 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 dwarf virus, Sorghum chlorotic spot virus, High Plains virus, Wheat streak mosaic virus |
| **Rice - *Oryza*** | Rice tungro viruses, 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 dwarf virus |
| **Sorghum / Millet - *Sorghum*/*Pennisetum*** | Maize dwarf mosaic virus, Sorghum yellow banding virus, Sorghum chlorotic spot virus |

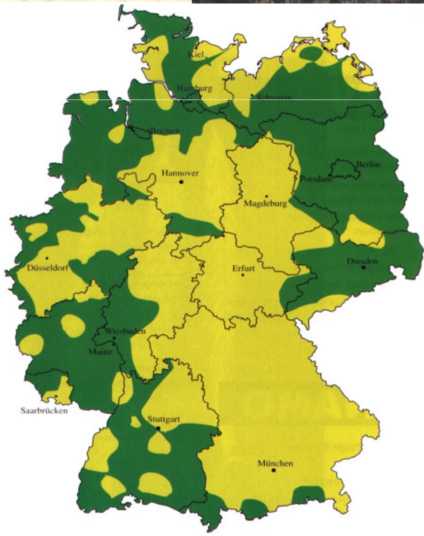
# Barley yellow mosaic virus disease

| Cultivar | BaYMV/BaMMV-Reaction | Yield t/ha | relative |
|---|---|---|---|
| Asorbia (6-rowed) | resistant | 5.33 | 100 |
| Corona (6-rowed) | susceptible | 3.53 | 65 |
| Romanze (2-rowed) | resistant | 4.20 | 100 |
| Marinka (2-rowed) | susceptible | 2.38 | 57 |
| Yuka (6-rowed) | resistant | 7.66 | 100 |
| Grete (6-rowed) | susceptible | 4.10 | 54 |
| Duet (2-rowed) | resistant | 6.30 | 100 |
| Angora (2-rowed) | suceptible | 4.24 | 67 |

10 $m^2$ plots, 3 replications; LSD (5%) = 0.25 t/ha and 0.35 t/ha; yield in ATM





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

# 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 €

# Genetic base of BaMMV/BaYMV-resistance

| | No. Cultivars | | Yield | |
|---|---|---|---|---|
| Year | resistant | susceptible | resistant | susceptible |
| 1986 | 6 | 37 | 4.3* | 5.6 |
| 1995 | 24 | 41 | 6.5 | 6.3 |
| 2005 | 52** | 23 | 6.7 | 6.1 |
| 2011 | 55 | 9 | 6.9 | 6.4 |

***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.)**

# Screening for resistance and genetic analysis

| | BaMMV | BaYMV | BaYMV-2 | No. Genotypes |
|---|---|---|---|---|
| *Hordeum vulgare* ssp. *vulgare* | | | | |
| | - | - | - | 201 |
| | - | - | + | 86 |
| | + | - | - | 53 |
| | - | + | + | 43 |
| *Hordeum vulgare* ssp. *spontaneum* | | | | |
| | - | + | + | 3 |
| | - | - | - | 2 |

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

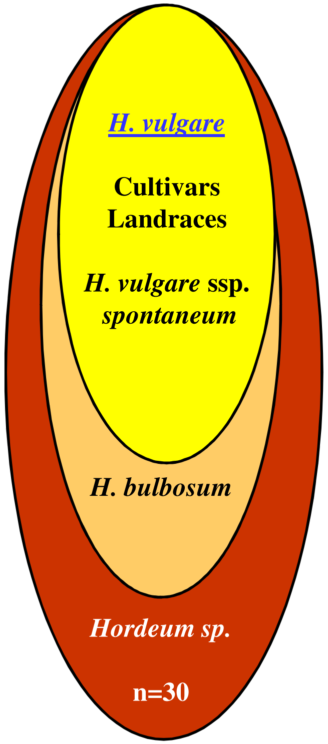
Ordon et al. 1993, Habekuss et al. 2000

| Cross | $F_2$ Segregation r : s | $\chi^{2**}$ 7r:9s | Infect.-rate (%) |
|---|---|---|---|
| *H. vulgare ssp vulgare* | | | |
| Chikurin Ibaraki 1 x Ogra | 49 : 69 | 0.233 | 98 |
| Russia 57 x Diana | 68 : 81 | 0.214 | 95 |
| Bulgarian 347 x Diana | 61 : 89 | 0.574 | 95 |
| Bulgarian 347 x Russia 57 | 42 : 73 | 2.442 | 100 |
| Taihoku A x Chikurin Ibaraki 1 | 50 : 68 | 0.091 | 100 |
| Bulgarian 347 x Chikurin Ibaraki | 53 : 63 | 0.0114 | 100 |

Götz & Friedt 1993, Ordon & Friedt 1993

# Breeding for virus resistance

## Identification of genetic variation




## Backcrossing procedures

P rym15/rym15 (r) x Rym15/rym15 (s)

$F_1$ rym15/Rym15 (s) Sellfing

$F_2$ Rym15/Rym15(s):2Rym15/rym15(s):rym15/rym15(r)

Resistance test

x Rym15/Rym15

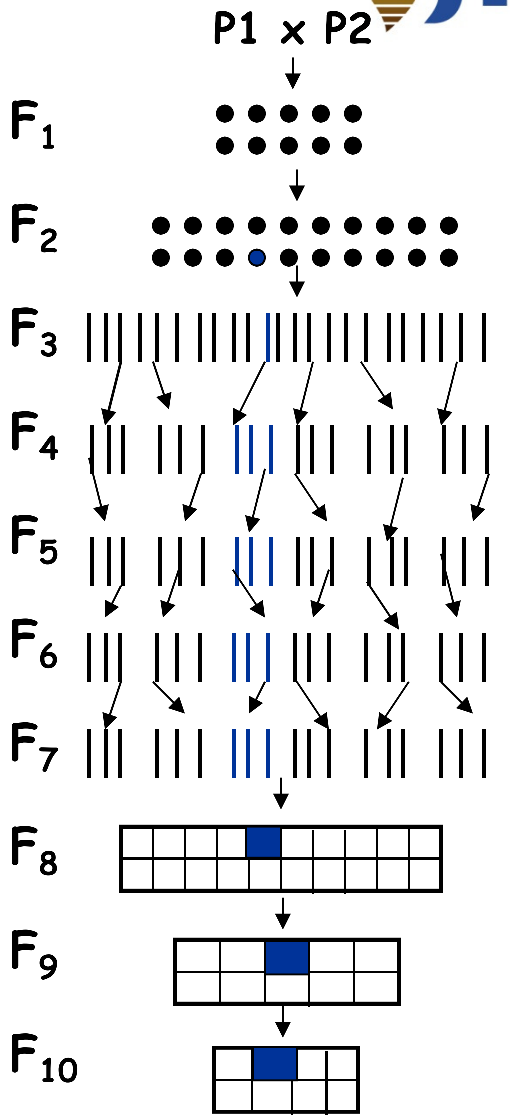
$F'_1$ $BC_1$ rym15/Rym15 (s)

Selbstung

$F'_2$ Rym15/Rym15(s):2Rym15/rym15(s):rym15/rym15(r)

Resistance Test

x Rym15/Rym15




Utilization of genetic variation

Use of genetic variation

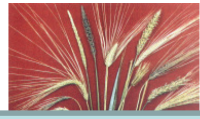
## Pedigree Selection

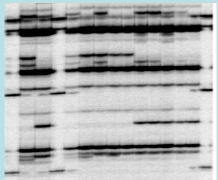
# Breeding for virus resistance

**Success of selection**

$R=h^2xS_D$

**Phenotype**





**Reliable selection on the single plant level ($A_1$, $F_2$) in the lab independently from the incidence of viruses in the field and symptom development in early developmental stages**

**Heritability**

$h^2=V_g/V_p$

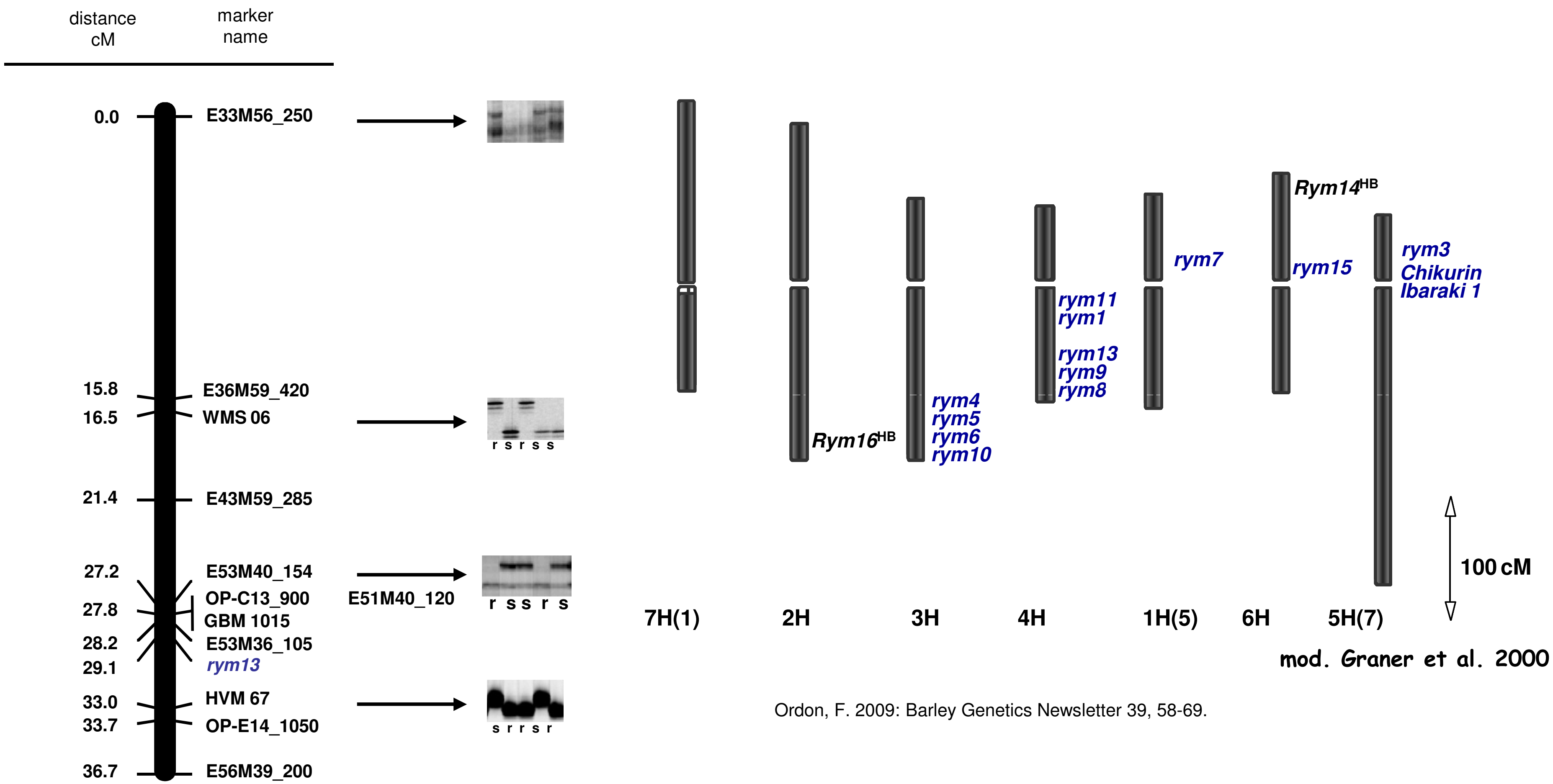
$V_p=V_g+V_E+V_{gE}$

**The better the inference from the phenotype to the genotype the higher the success of selection**

- **No reliable selection on a single plant level ($A_1$, $F_2$)**
- **Viruses do not incide each year**
- **Symptom development is often influenced by environmental factors**

**Reliable selection for resistance on the phenotypic level can not be carried out each year**

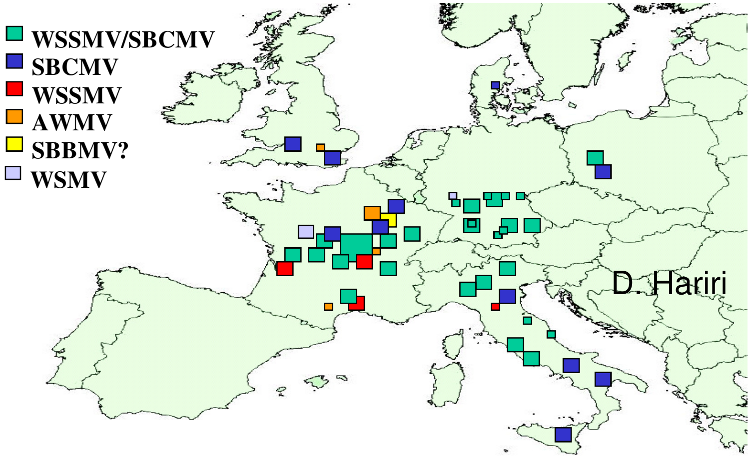
# Mapped resistance genes against BaMMV/BaYMV



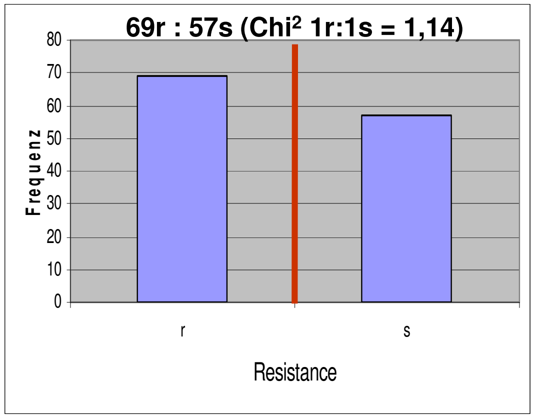

Humbroich, K., H. Jaiser, A. Schiemann, P. Devaux, A. Jacobi, L. Cselenyi, A. Habekuss, W. Friedt, F. Ordon, 2010. Plant Breeding **129**, 346-348.

Ordon, F. 2009: Barley Genetics Newsletter 39, 58-69.

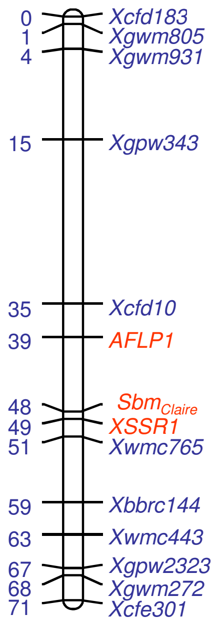
# Wheat – SBCMV-Resistance



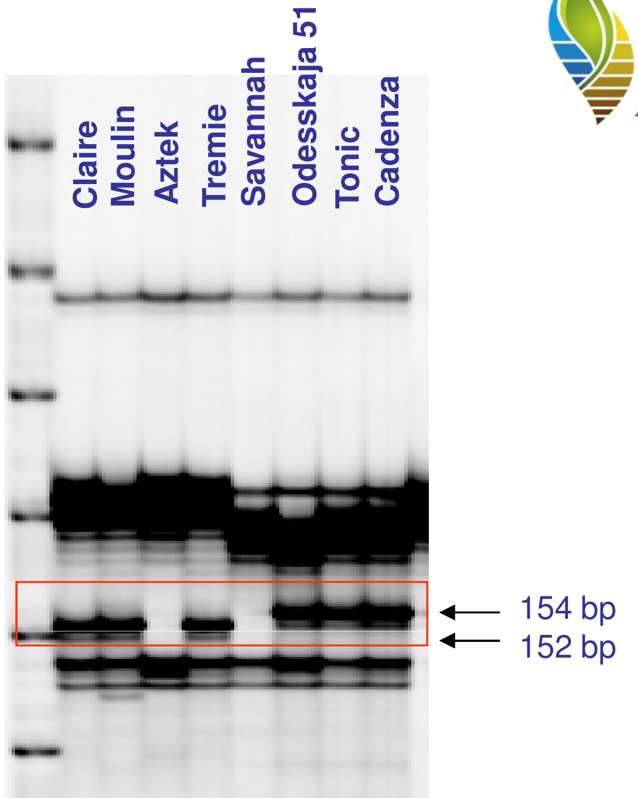

Savanah x Claire




Savannah x Claire




Chromosome 5DL




**3 alleles identified in about 100 genotypes tested.154bp diagnostic for „Cadenza-derived resistance“, 152 bp for „Tremie/Claire-derived resistance“. All suceptible genotypes displayed a null allele.**

Perovic, D., J. Förster, P. Devaux, D. Hariri, M. Guilleroux, K. Kanyuka, R. Lyons, J. Weyen, D. Feuerhelm, U. Kastirr, P. Sourdille, M. Röder, F. Ordon, 2009. Molecular Breeding **23**, 641-653.

# Marker assisted backcrossing

Jahr

## Conventional backcrossing

P rym15/rym15 (r) x Rym15/rym15 (s)

$F_1$ rym15/Rym15 (s) Selfing

$F_2$ Rym15/Rym15(s):2Rym15/rym15(s):rym15/rym15(r)

Resistance test

x Rym15/Rym15

$F'_1$ $BC_1$ rym15/Rym15 (s) Selbfing

$F'_2$ Rym15/Rym15(s):2Rym15/rym15(s):rym15/rym15(r)

Resistance test

x Rym15/Rym15

0

1

2

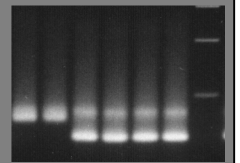
3

4

5

## Marker assisted backcrossing

P rym15/rym15 (r) x Rym15/Rym15 (s)



$F_1$ rym15/Rym15 (s) x Rym15/Rym15

$F'_1$ $BC_1$ Rym15/Rym15 (s) rym15/Rym15 (s)

x Rym15/Rym15

$F''_1$ $BC_2$ Rym15/Rym15 (s) rym15/Rym15 (s)

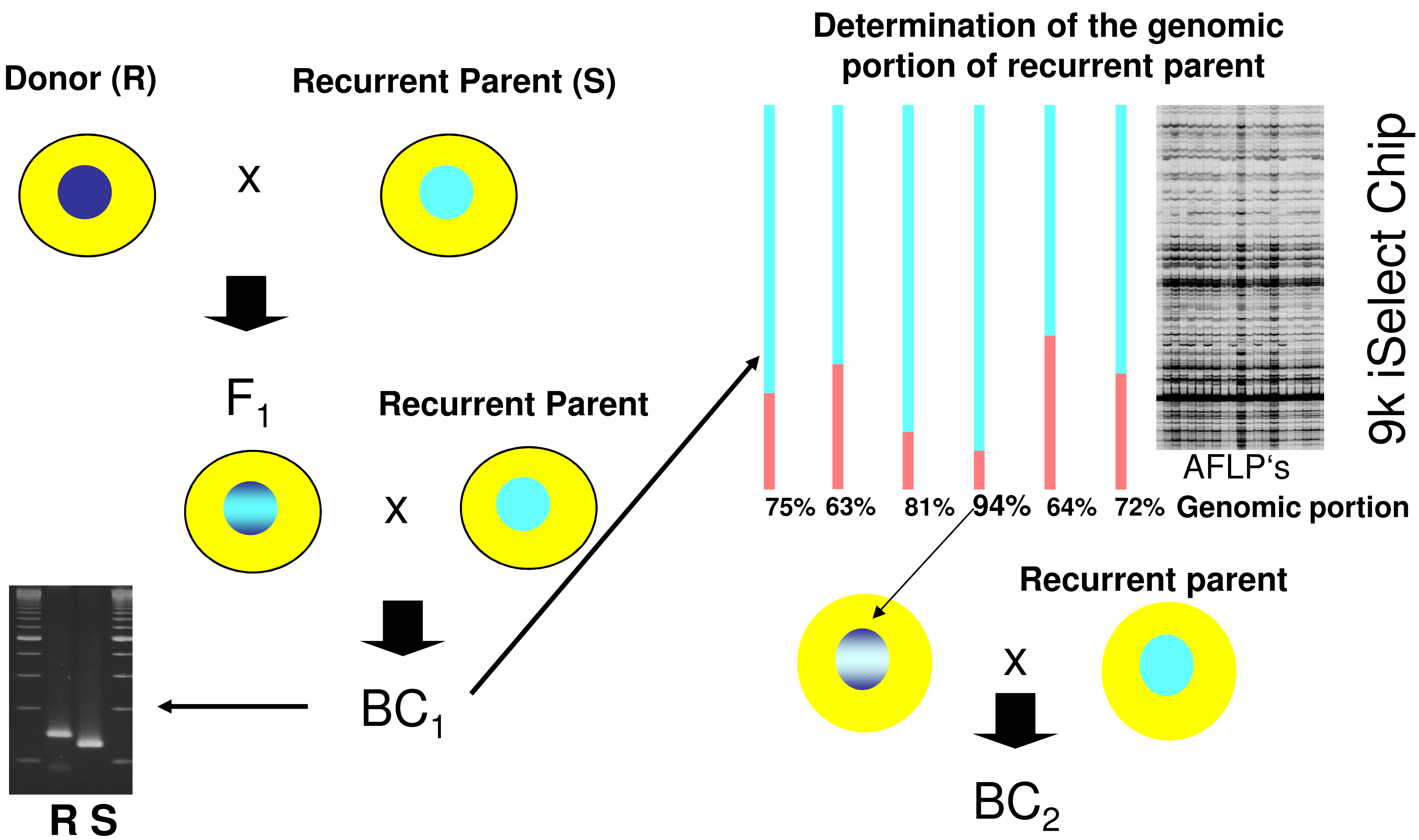
x Rym15/Rym15

$F'''_1$ $BC_3$ Rym15/Rym15 (s) rym15/Rym15 (s)

x Rym15/Rym15

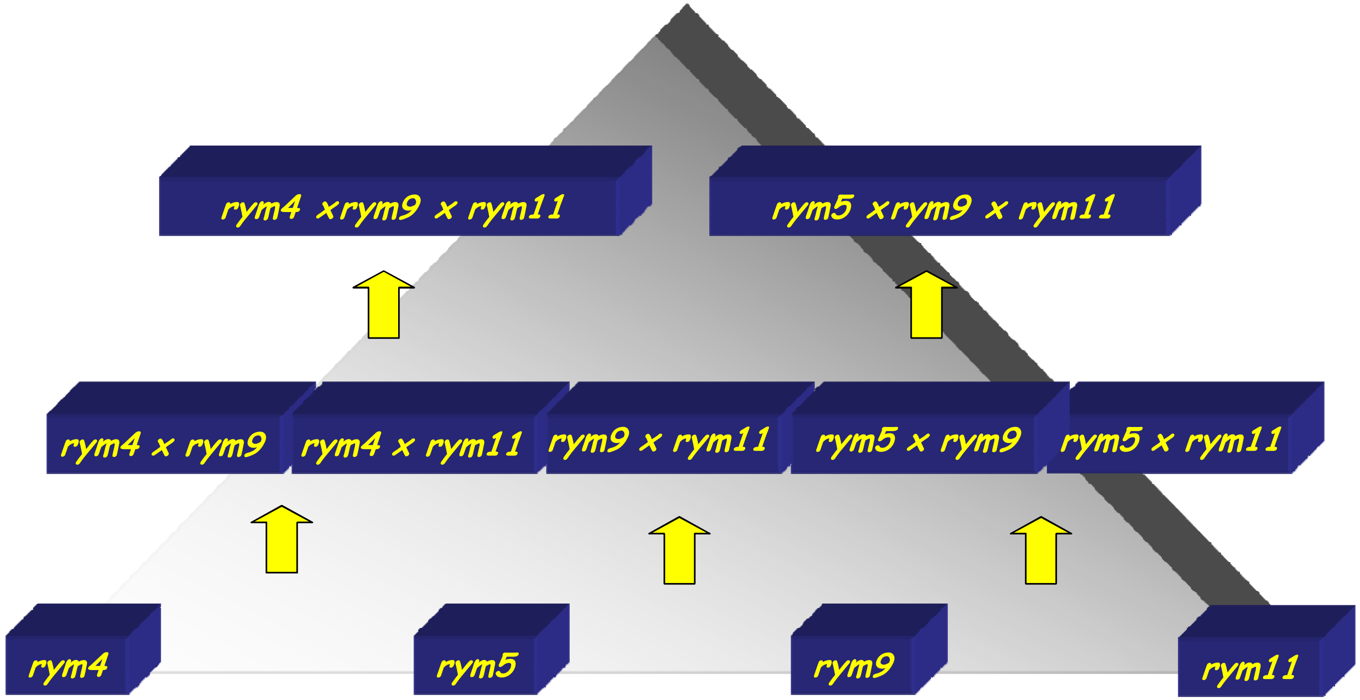
Ordon, F., B. Pellio, K. Werner, A. Schiemann, W. Friedt, A. Graner, 2003. J. Plant Diseases and Protection **110**, 287-295.

# Marker assisted backcrossing

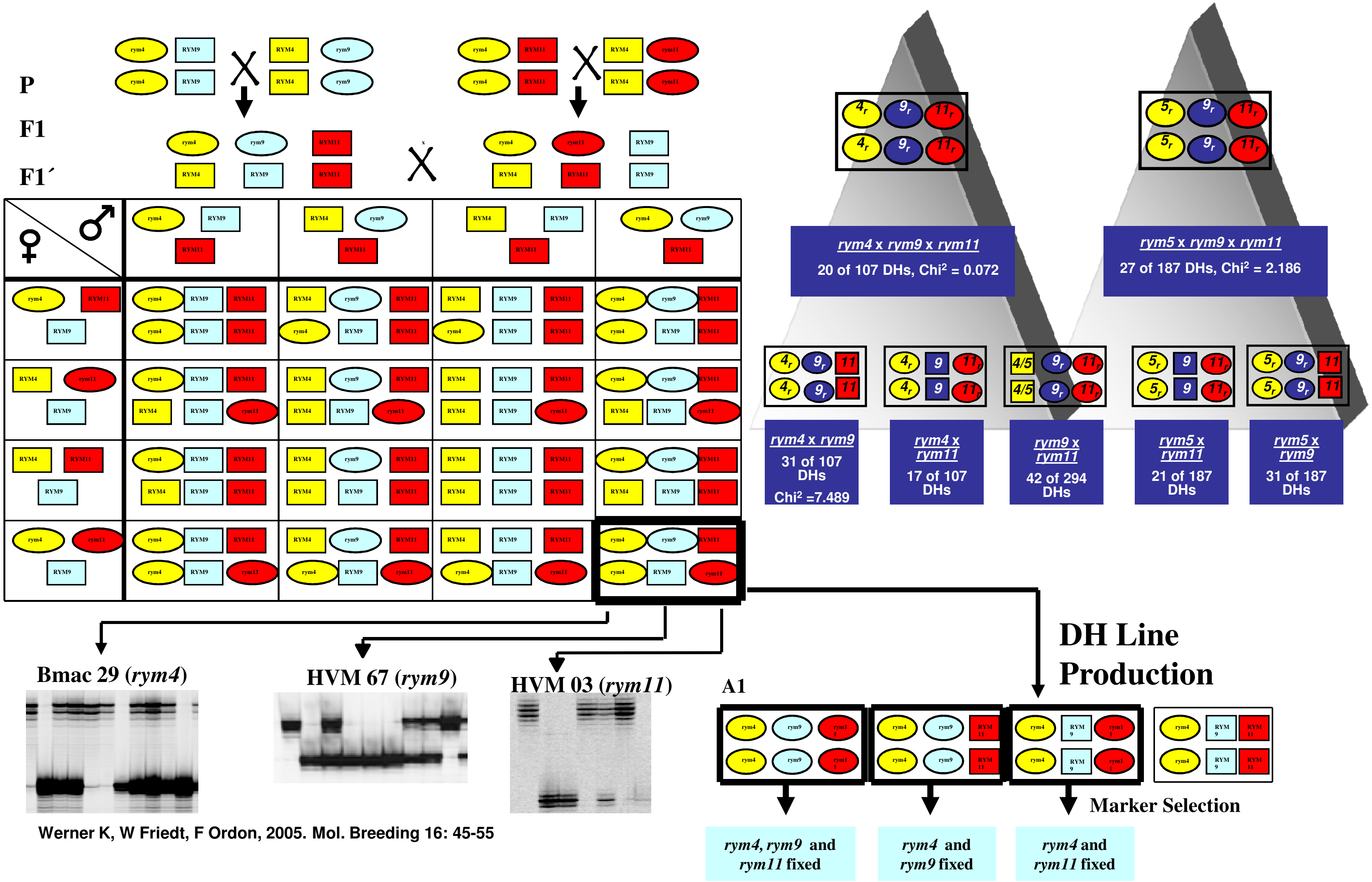


# Pyramiding of BaMMV/BaYMV resistance genes

| | BaYMV | BaYMV-2 | BaMMV | BaMMV-SIL | BaMMV-EIK |
|---|---|---|---|---|---|
| *rym4* | r | s | r | r | r |
| *rym5* | r | r | r | s | s |
| *rym9* | s | s | r | r | r |
| *rym11* | r | r | r | r | r |



# Pyramiding of BaMMV/BaYMV resistance genes




Werner K, W Friedt, F Ordon, 2005. Mol. Breeding 16: 45-55

## *Barley yellow dwarf virus* (BYDV)

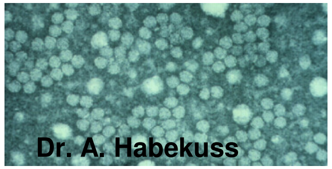
**Luteovirus**

BYDV-PAV → *Rhopalosiphum padi & Macrosiphum avenae*

BYDV-MAV → *Macrosiphum avenae*

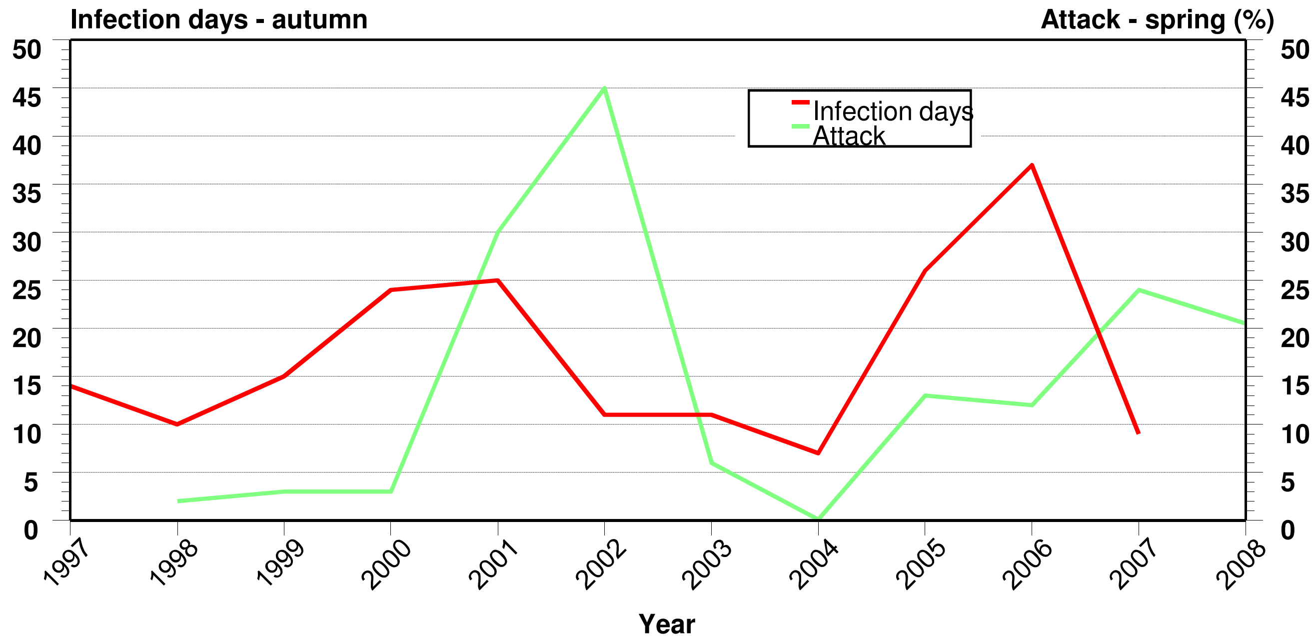
**Polerovirus**

CYDV-RPV → *Rhopalosiphum padi*




+ssRNA-Virus, isometric particles (25-30 nm), phloem limited
yield losses 20-40%

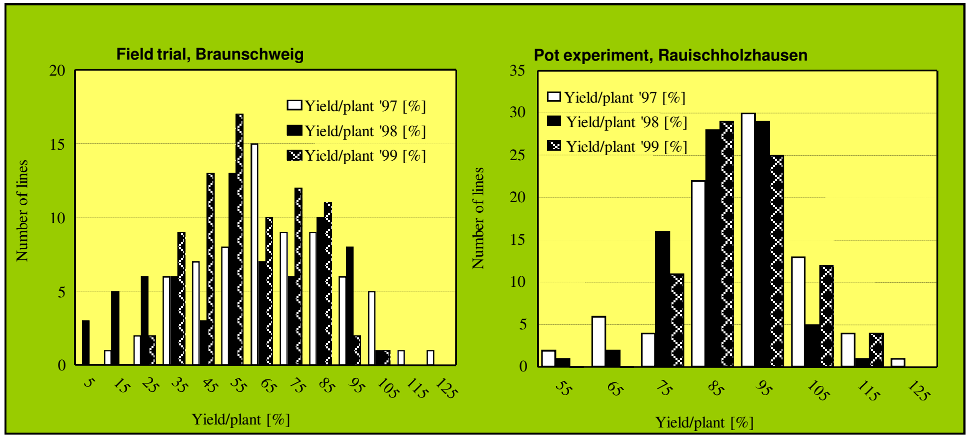
**Relation between BYDV-attack of winter barley in spring and temperature in autumn**



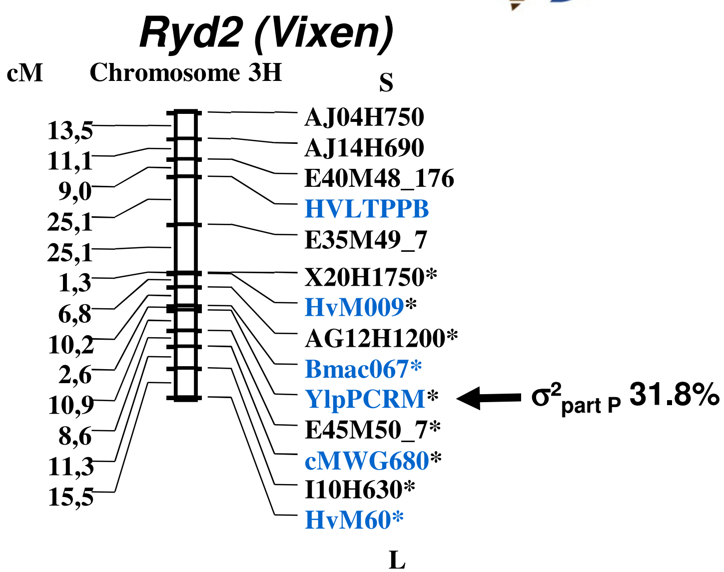

Infection days = Number of days with a diurnal mean temperature >= 10°C between 1st of October and 31st of December

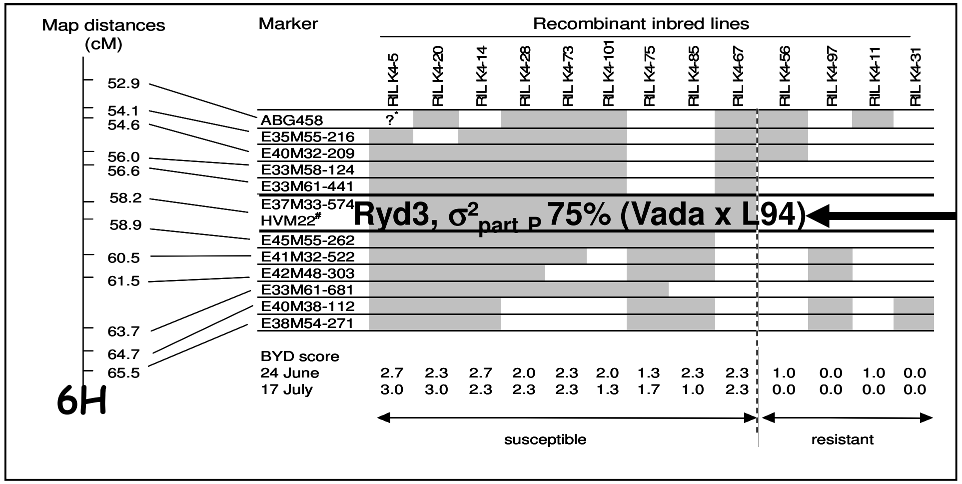
Habekuß, A., C. Riedel, E. Schliephake, F. Ordon, 2009. J. of Cultivated plants **61**, 87-91.

# Identification von QTL for BYDV-tolerance

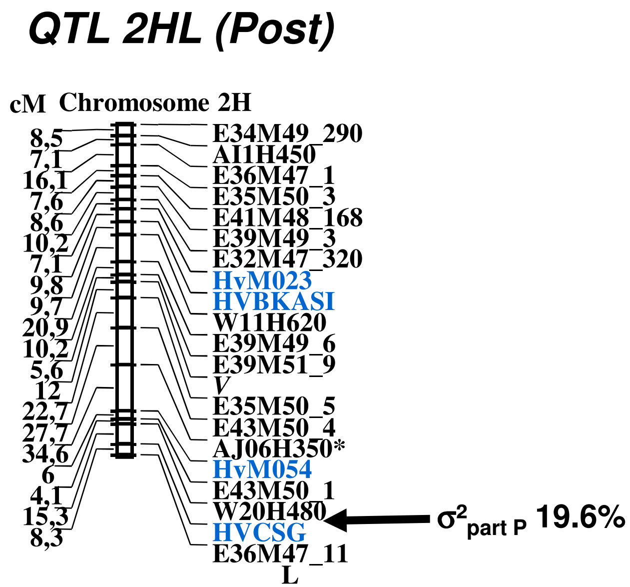



Scheurer, K., W. Huth, R. Waugh, W. Friedt, F. Ordon, 2001. Theor. Appl. Genet. 103:1074-1083



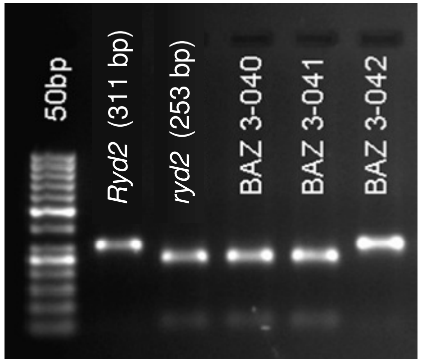

Niks, R.E., A. Habekuß, B. Bekele, F. Ordon, 2004. Theor. Appl. Genet. Theor. Appl. Genet. **109**, 1536-1543




Scheurer, K., W. Huth, R. Waugh, W. Friedt, F. Ordon, 2001. Theor. Appl. Genet. 103:1074-1083

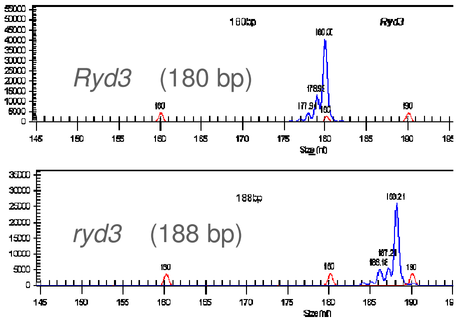
# Pyramiding of BYDV-QTL

´RIL K4-56´ (*Ryd3*) x ´DH21-136´ (*Ryd2* + QTL Post)



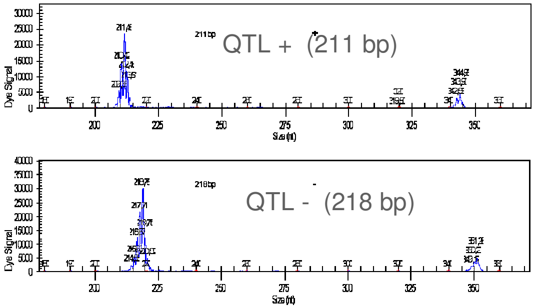

*Ryd2*

(YLP + HSP92 II)



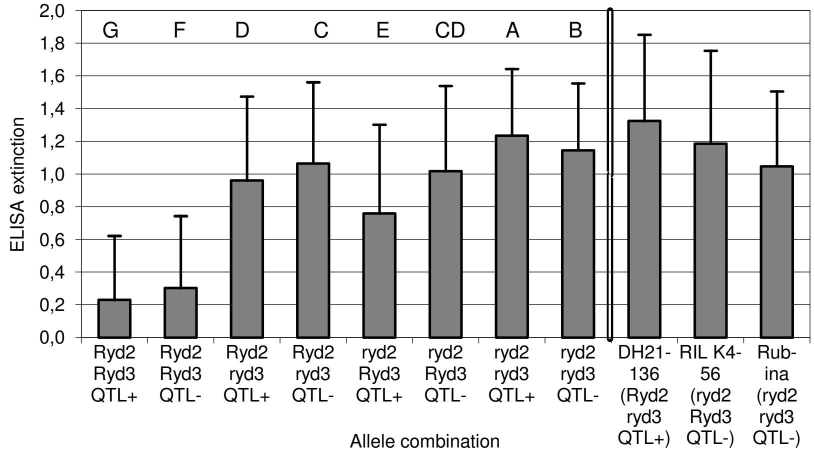

*Ryd3*

(HVM74)




QTL Post 2H

(HVCSG)




Segregation *Ryd2/ Ryd3/ Post-QTL*

| | rrr | rrs | rsr | srr | ssr | srs | rss | sss |
|---|---|---|---|---|---|---|---|---|
| No. DH-lines | 89 | 49 | 45 | 99 | 49 | 77 | 38 | 29 |

(*ryd2, ryd3*, QTL-) (*Ryd2, Ryd3*, QTL+)
winter barley, Quedlinburg, April 2008

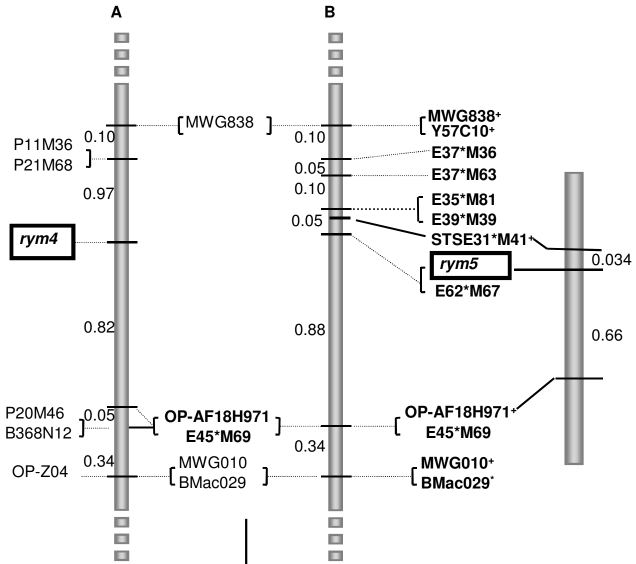
Institute for Resistance Research and Stress Tolerance

Riedel, C., A. Habekuss, E. Schliephake, R. Niks, I. Broer, F. Ordon, 2011 Theor. Appl. Genet. **123**, 69-76.

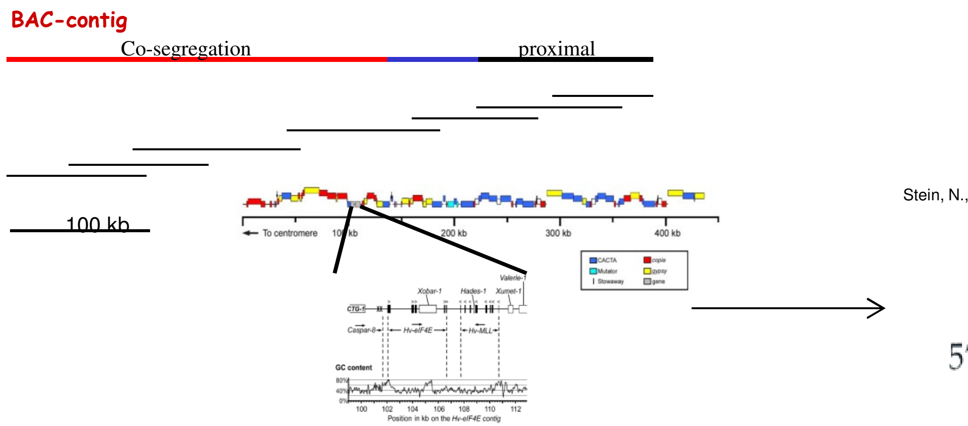
# Isolation of resistance genes - allele mining

***Rym4/Rym5***

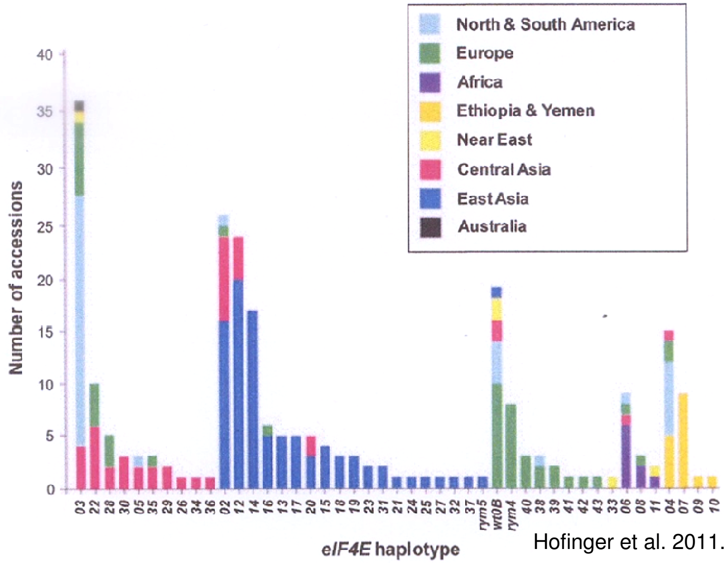
## High resolution mapping



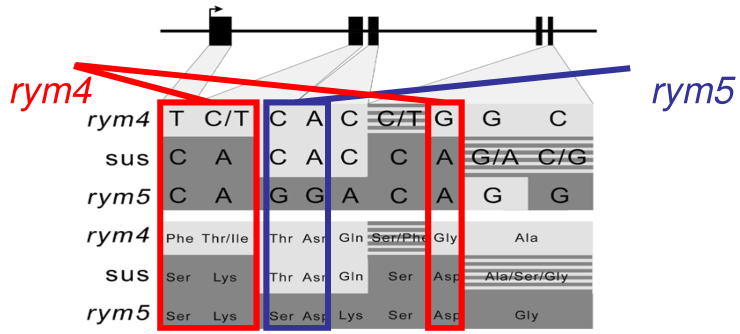
Pellio, B., S. Streng, E. Bauer, N. Stein, D. Perovic, A. Schiemann, W. Friedt, F. Ordon, A. Graner 2005. Appl. Genet. **110**, 283-293.



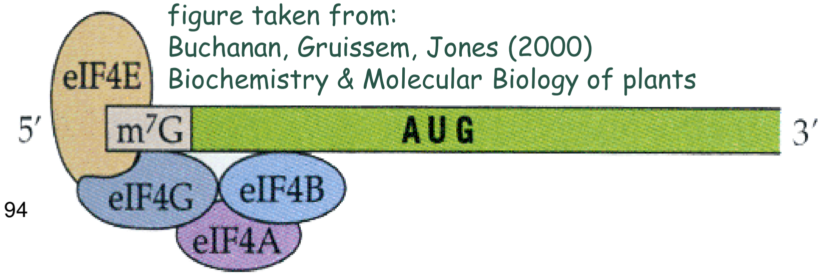

Wicker et al. 2005. The Plant Journal, 41, 184-194




Hofinger et al. 2011. Molecular Ecology 20, 3653-3668

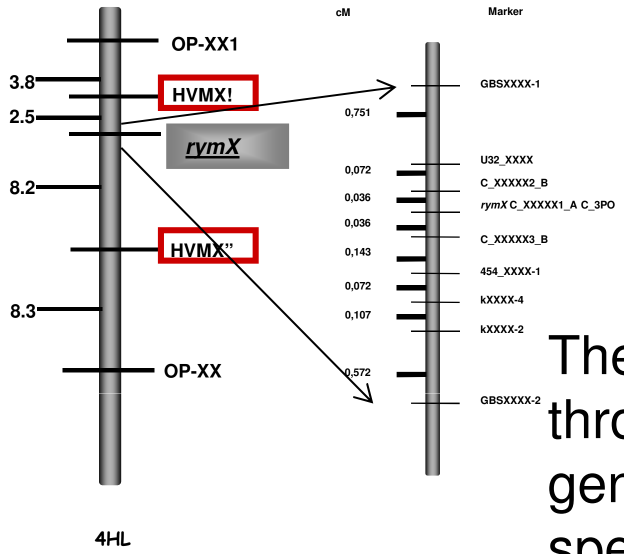


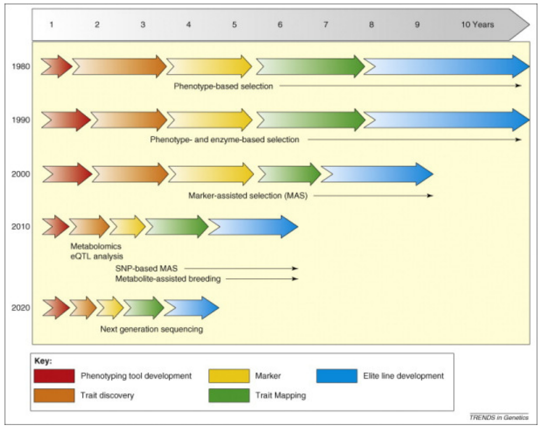

Stein, N., D. Perovic, J. Kumlehn, B. Pellio, S. Stracke, S. Streng, F. Ordon, A. Graner, 2005. The Plant Journal **42**, 912-922



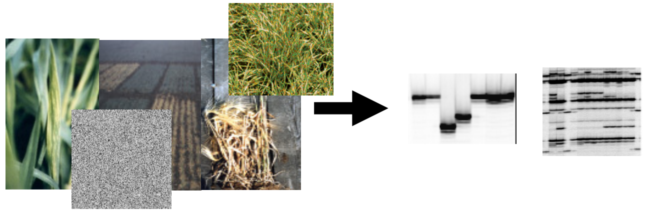
# Summary and future prospects

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




Fernie, A.R., N. Schauer, 2008: Trends in Genetics 25, 39-48



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 virus 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.

# Thanks

## BaMMV/BaYMV
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Prof. Dr. Andreas Graner
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