GCIRC technical meeting 2013

ACW Changins, Switzerland
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Biodieselanlage

# Advances in Biotec- and Marker-Assisted Breeding of Oilseed Rape (*Brassica napus*)

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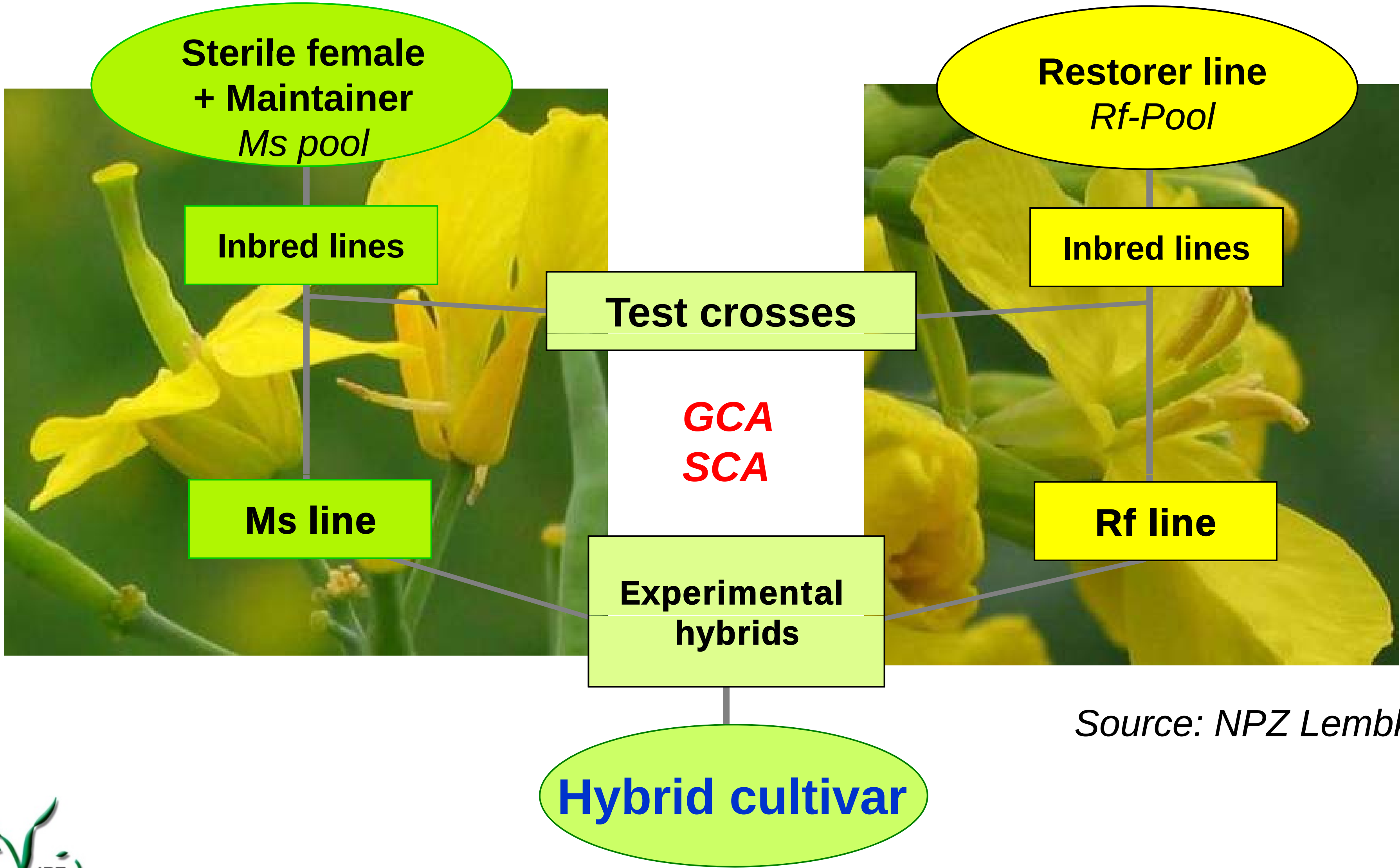
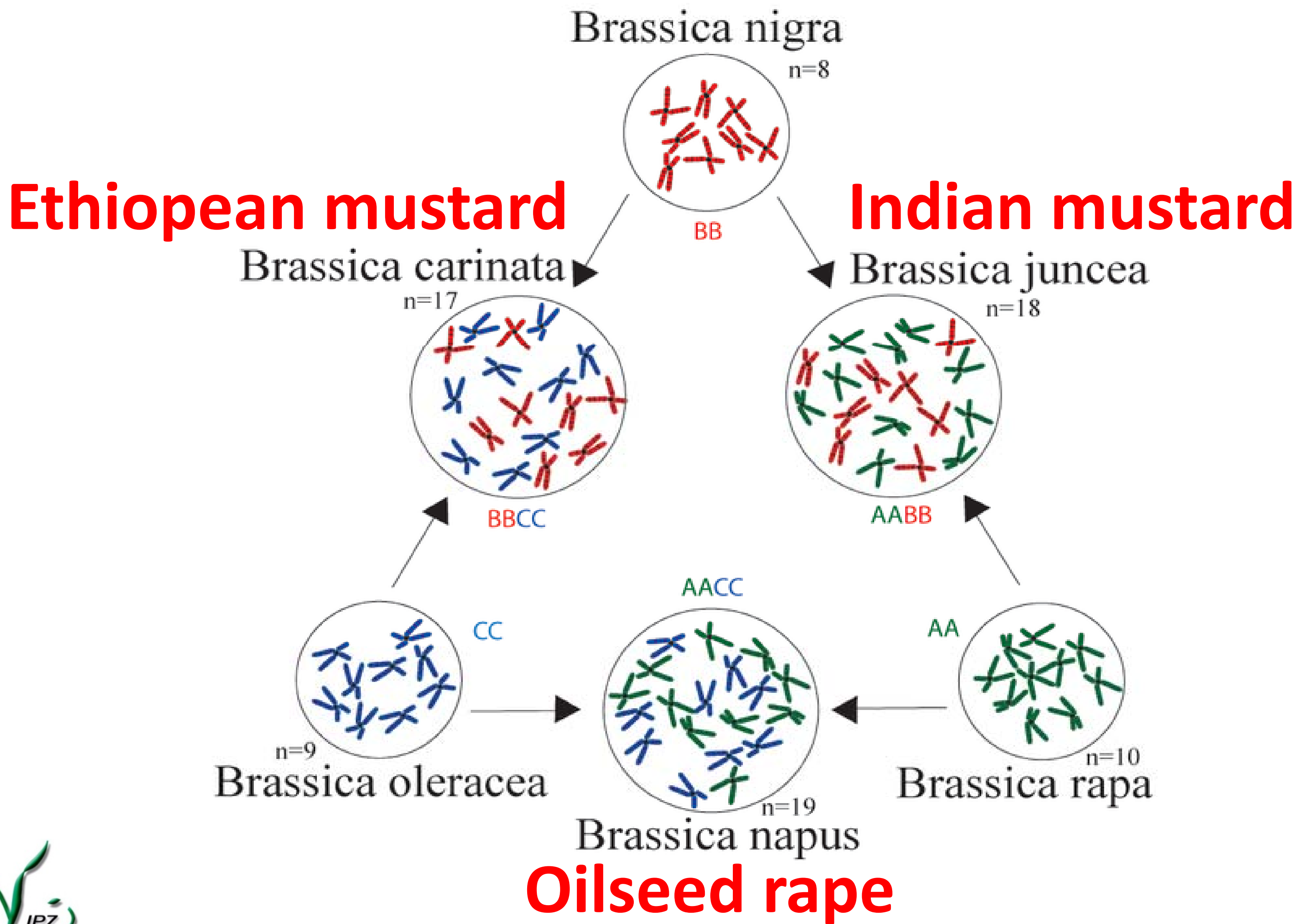
# Hybrid breeding scheme for rapeseed




Source: NPZ Lembke

# Creating diversity: Natural allopolyploids by hybridization and speciation in Brassicaceae




**Woo Jang-Choon**
1898 -1959

# Doubled haploids of novel trigenomic Brassica derived from various interspecific crosses

**X. X. Geng et al. (2013) Plant Cell Tiss Organ Culture**

unique interspecific crosses:

- *Brassica rapa* (genome AA) x *B. carinata* (BBCC)
- *B. nigra* (BB) x *B. napus* (AACC),
- complex cross between *B. juncea* (AABB), *B. napus* and *B. carinata*, relatively stable chromosome number (2n=54)

# Ploidy level in microspore-derived plants

by flow cytometry based on DNA content of controls with known DNA content. Plants were classified as hexaploid (6x), triploid (3x) mixed, or unknown, and doubling frequency (%) is the proportion of hexaploids in the total (Geng X.X. et al. 2013)

| Hybrid code | Hexa-ploid | Triploid | Mixed | Un-known | Total | Doubling frequency (%) |
|---|---|---|---|---|---|---|
| H08-1 | 23 | 16 | 4 | 11 | 54 | 42.6 |
| H11-2 | 370 | 298 | 6 | 19 | 693 | 53.4 |
| H16-1 | 241 | 185 | 3 | 7 | 436 | 55.3 |
| H24-1 | 21 | 19 | 2 | 14 | 56 | 37.5 |

# Broadening genetic variation via „Resynthesis“ of rapeseed

https://www.google.de/search?q=cabbage

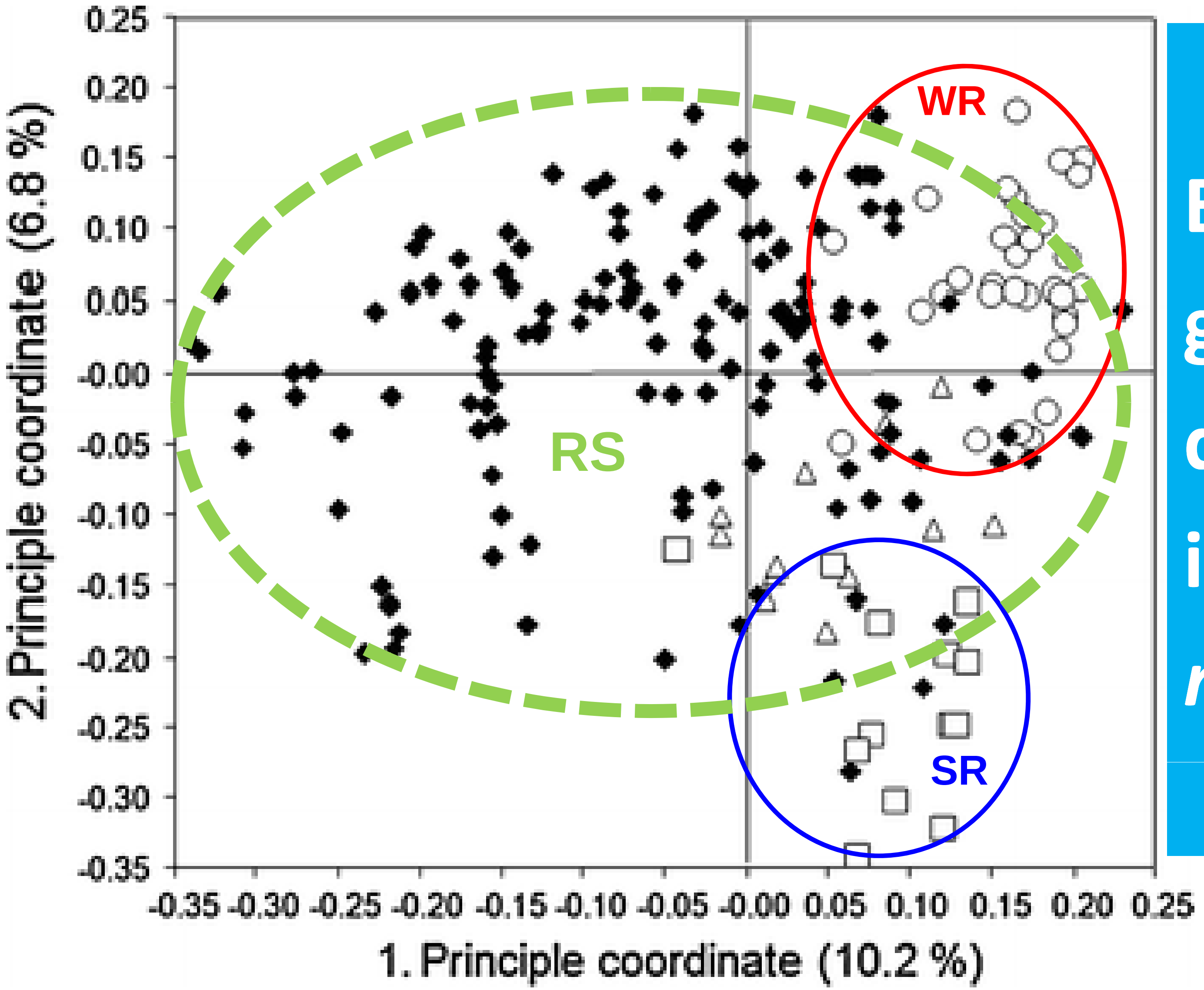
X

http://international.
stockfood.com

*B. oleracea*
*2n=2x=18*

*B. rapa*
*2n=2x=20*

***Brassica napus***
*2n=4x=38*



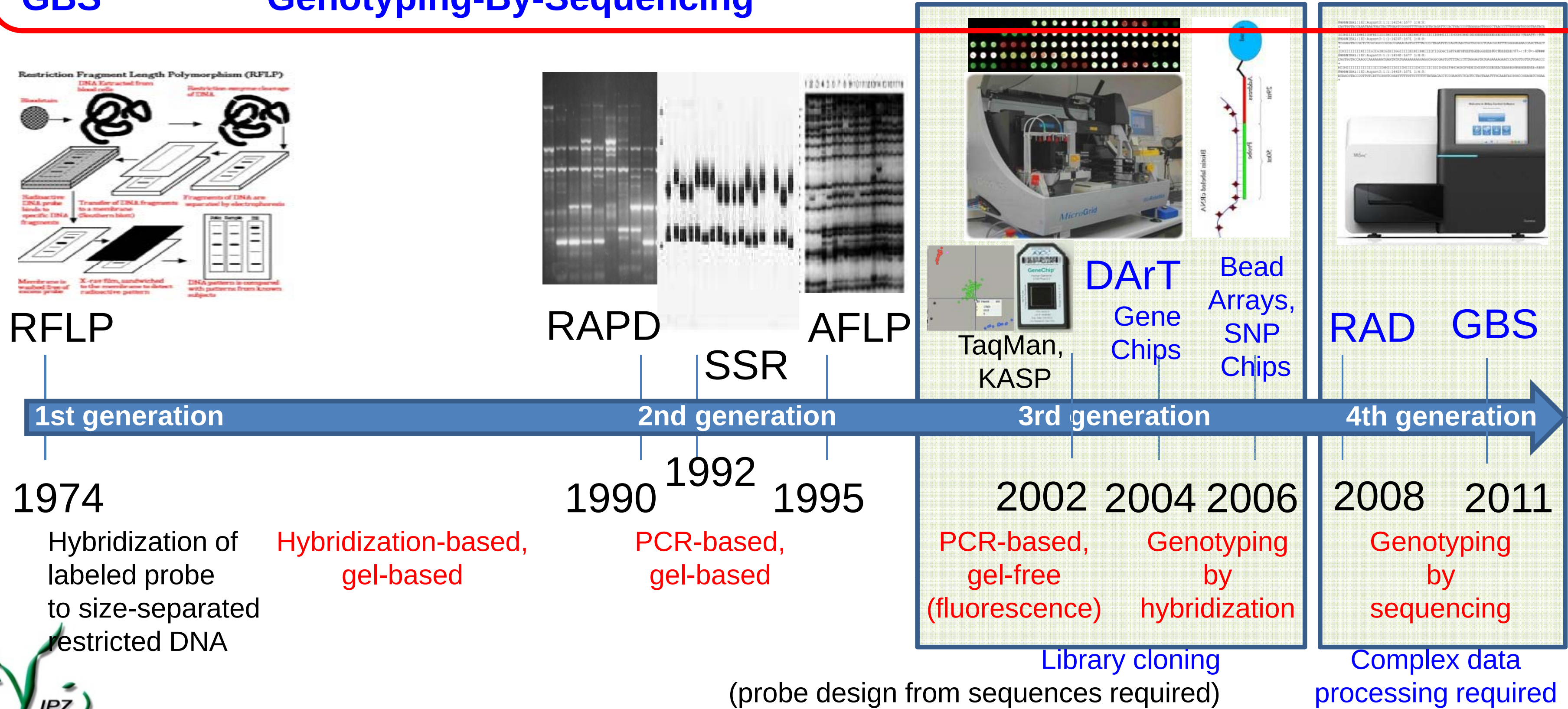

# Extending genetic diversity in *Brassica napus*

**Principle coordinate analysis of 142 resynthesized lines and 57 *B. napus*** L. genotypes of European and Asian origin. Symbols are for winter (circle), for spring-type (square), for Asian *B. napus* (triangle) and for resynthesized lines (filled diamond); Girke et al., GRACE (2012)

# New marker types for high-throughput MAS

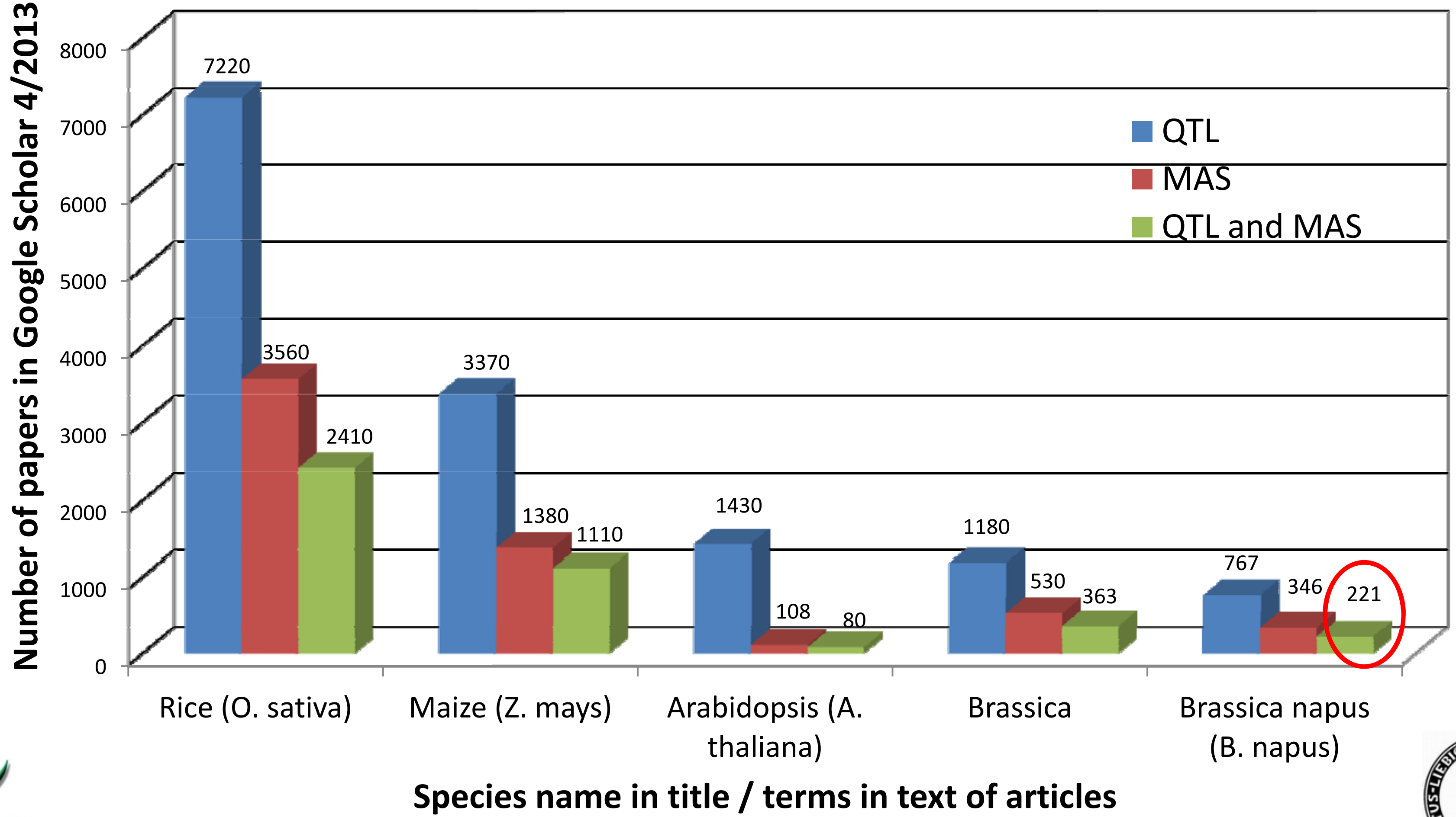
| | |
|---|---|
| RFLP | Restriction fragment length polymorphism |
| RAPD | Random amplification of polymorphic DNA |
| SSR | Simple sequence repeats (microsatellite markers) |
| AFLP | Amplified fragment length polymorphism |
| DArT | Diversity arrays technology |
| SNP Chips | e.g. Infinium Bead Chips, Affymetrix GeneChips |
| RAD | Restriction-site associated DNA |
| **GBS** | **Genotyping-By-Sequencing** |

DArT, SNP Chips, RAD, GBS: **Single nucleotide polymorphism (SNP) markers**

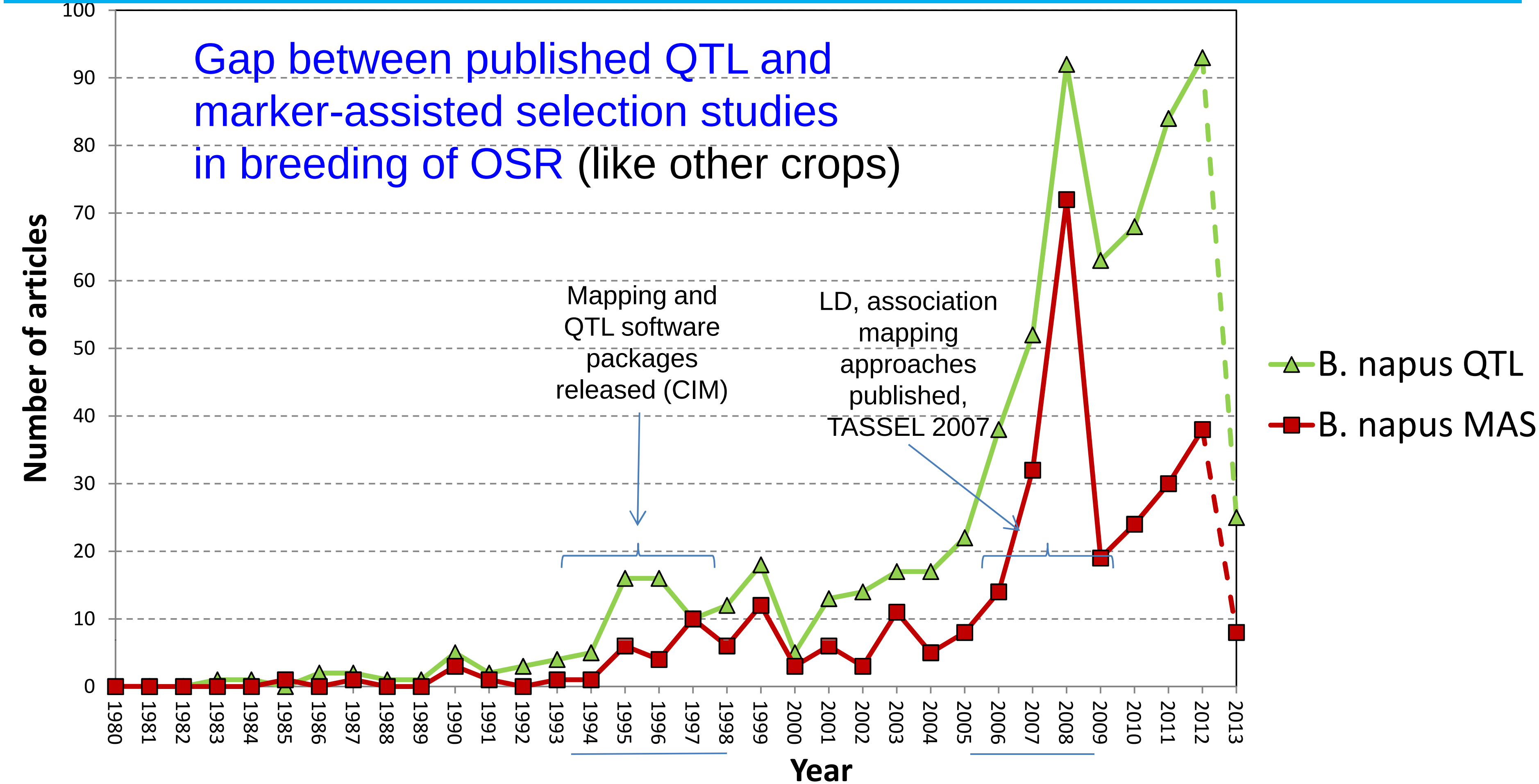


# From QTL mapping to marker-assisted selection (MAS) in OSR breeding

**Papers listed in Google Scholar: 10 April 2013. Note:** Google Scholar indexes papers, not journals. It includes journal and conference papers, theses and dissertations, academic books, pre-prints, abstracts, technical reports and other scholarly literature from all broad areas of research and thus includes doubles and overestimates the relevant literature.

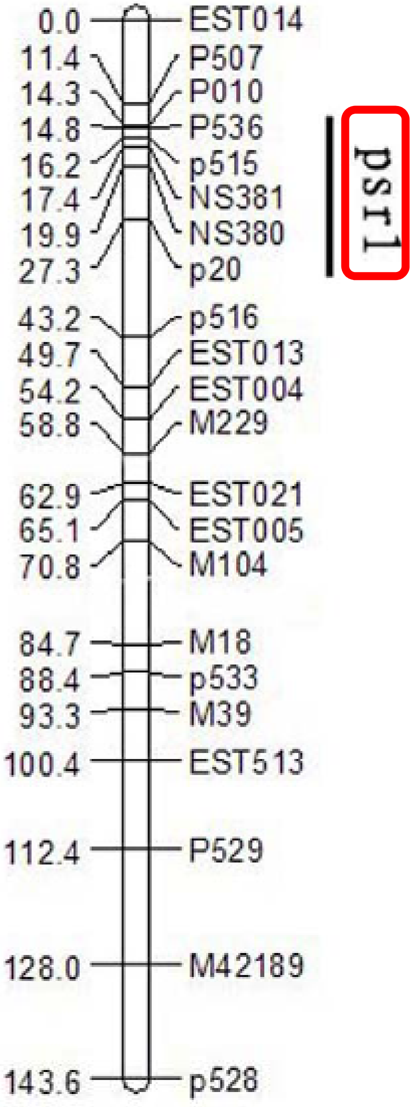


# From QTL mapping to marker-assisted selection (MAS) in OSR breeding




Numbers of articles with the terms "*Brassica napus*" in title and "quantitative trait locus" or "quantitative trait loci" (QTL) and "marker-assisted selection" (MAS) or similar **somewhere within the document** (excluding citations) by years (1980–2013) from Google Scholar (9 April 2013).

# SNP Discovery in Rapeseed: Pod Shatter-Resistant Associated SNPs




**Genetic linkage map of chromosome A09 from rapeseed.**

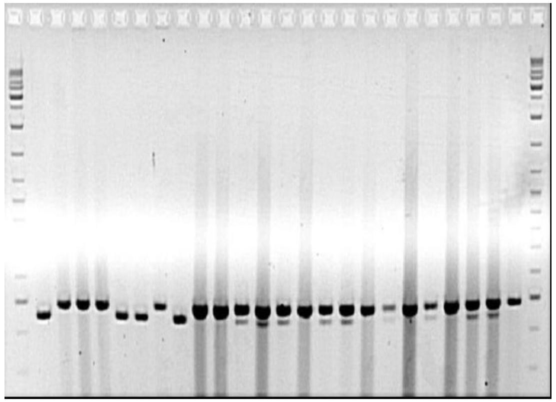
The numerals in left column indicate the genetic distance [cM]. SNP or SSR marker names are indicated in the right column. **Psr1** indicates the QTL region of pod shatter-resistance.*)

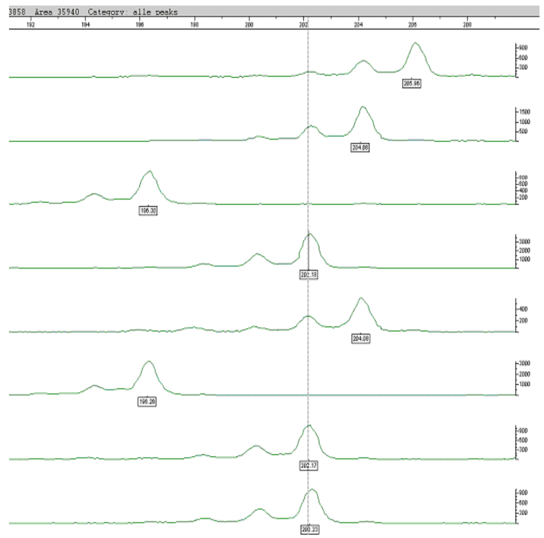
*) genetic contribution rate 47%.

Hu Z et al. (2012) PLoS ONE 7(4): e34253.

# Major OSR traits for which molecular markers are currently used by (German) Breeders

| Trait of interest | Type of marker |
|---|---|
| Genetic distance | SSR, SNP, DArT |
| Clearfield® HT | SNP |
| MSL hybrid system | InDel, SNP, SSR |
| Ogu-Rf hybrid system | SNP, InDel, SSR |
| Dwarf growth type | SNP |
| High oleic/Low linolenic | SNP |
| Phoma resistance | SSR, InDel |
| Clubroot resistance | SSR |





➔Markers for quantitative traits to be used for MAS

# QTL mapping of resistance to fungal diseases

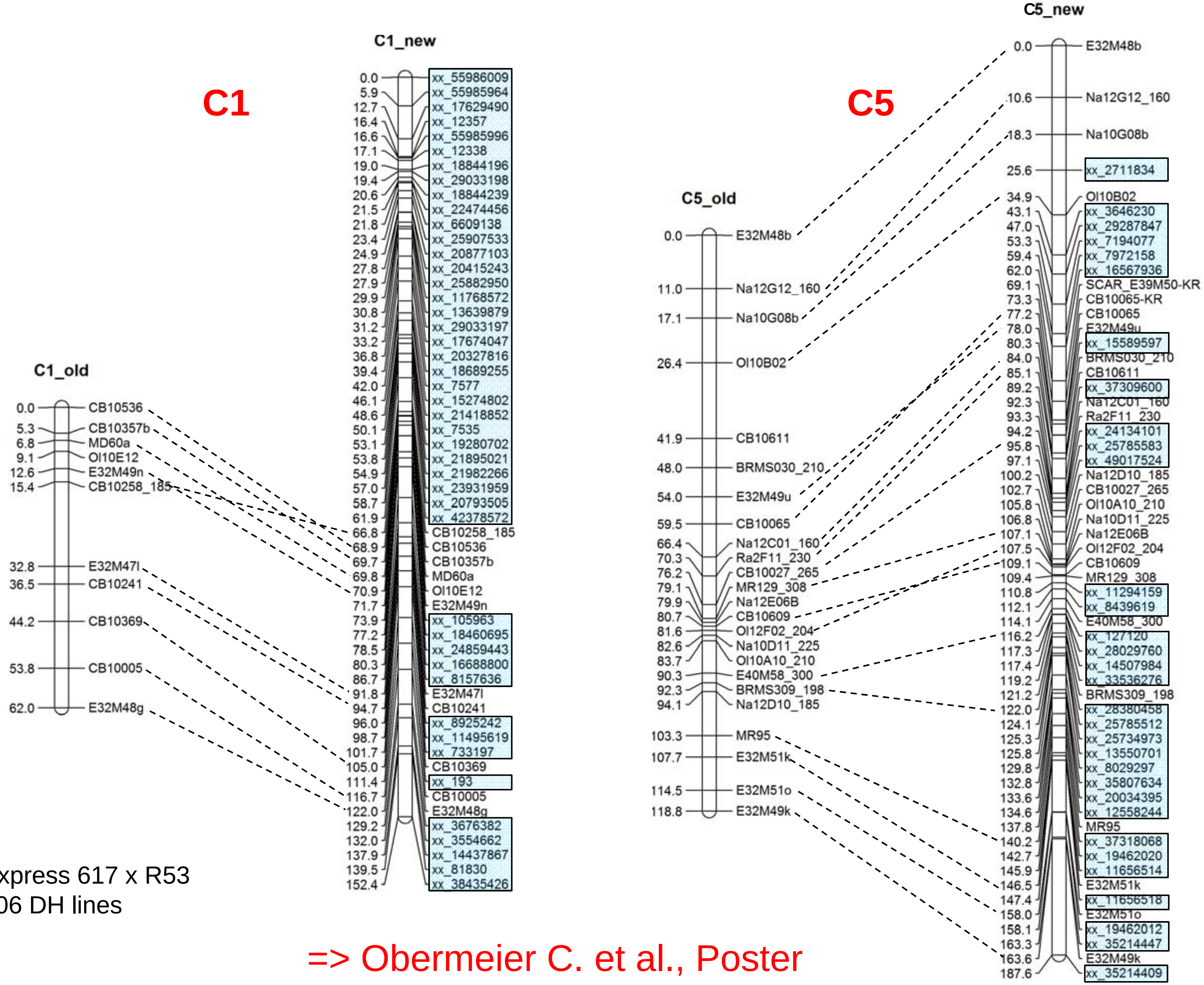
| **Pathogen** | **Brassica species** | **Consensus QTL**<br>(number of populations) |
|---|---|---|
| *Leptosphaeria maculans*<br>(Phoma stem canker, blackleg) | ***B. napus***<br>***B. napus***<br>***B. napus***<br>***B. napus*** | A7, A2, A10 (race-specific)<br>A4 (race non-specific)<br>A1 (4 of 5), A10 (3 of 5), C1 (2 of 4)<br>A10 |
| *Plasmodiophora brassicae*<br>(clubroot) | *B. rapa*<br>*B. rapa*<br>***B. napus***<br>*B. oleracea* | A1, A6, A8<br>A2, A3<br>A2, A3, A8, C3, C5,<br>C3,C5 |
| *Albugo candida*<br>(white rust) | ***B. napus***<br>*B. rapa* | A2 (2 of 2)<br>A4 (race non-specific), A2 (race-sp.) |
| *Sclerotinia sclerotiorum*<br>(Sclerotinia rot) | ***B. napus***<br>***B. napus***<br>***B. napus*** | A3 (2 of 3)<br>C7 (3 of 3)<br>C12 (2 of 3) |
| ***Verticillium longisporum***<br>**(Verticillium disease)** | ***B. napus*** | C5, C4 (major QTL)<br>A6, C8, C1 (minor QTL) |

# Breeding for resistance to *Verticillium longi-sporum* and marker development


1. **Screening** in *B. rapa* and *B. oleracea* for *Verticillium* resistance
2. Creation of **resynthesized *B. napus* (RS)**
3. Production of **DH mapping populations** (elite lines x RS lines)
4. **Genetic mapping** and analysis of resistance
5. **Comparative QTL analysis:** identification of common QTL
6. Development of new **QTL-linked markers**
7. **Oil quality** analysis of DH lines

**=> Obermeier C. et al., Poster**

# A high-density map applying GBS markers

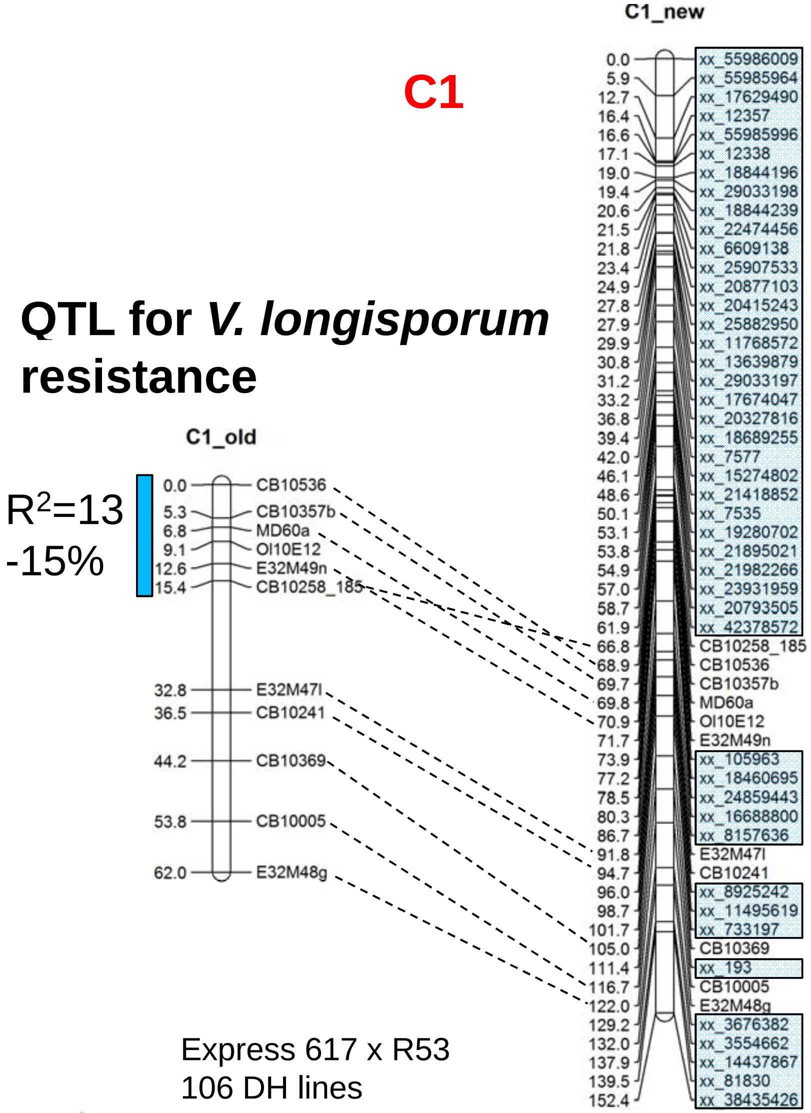


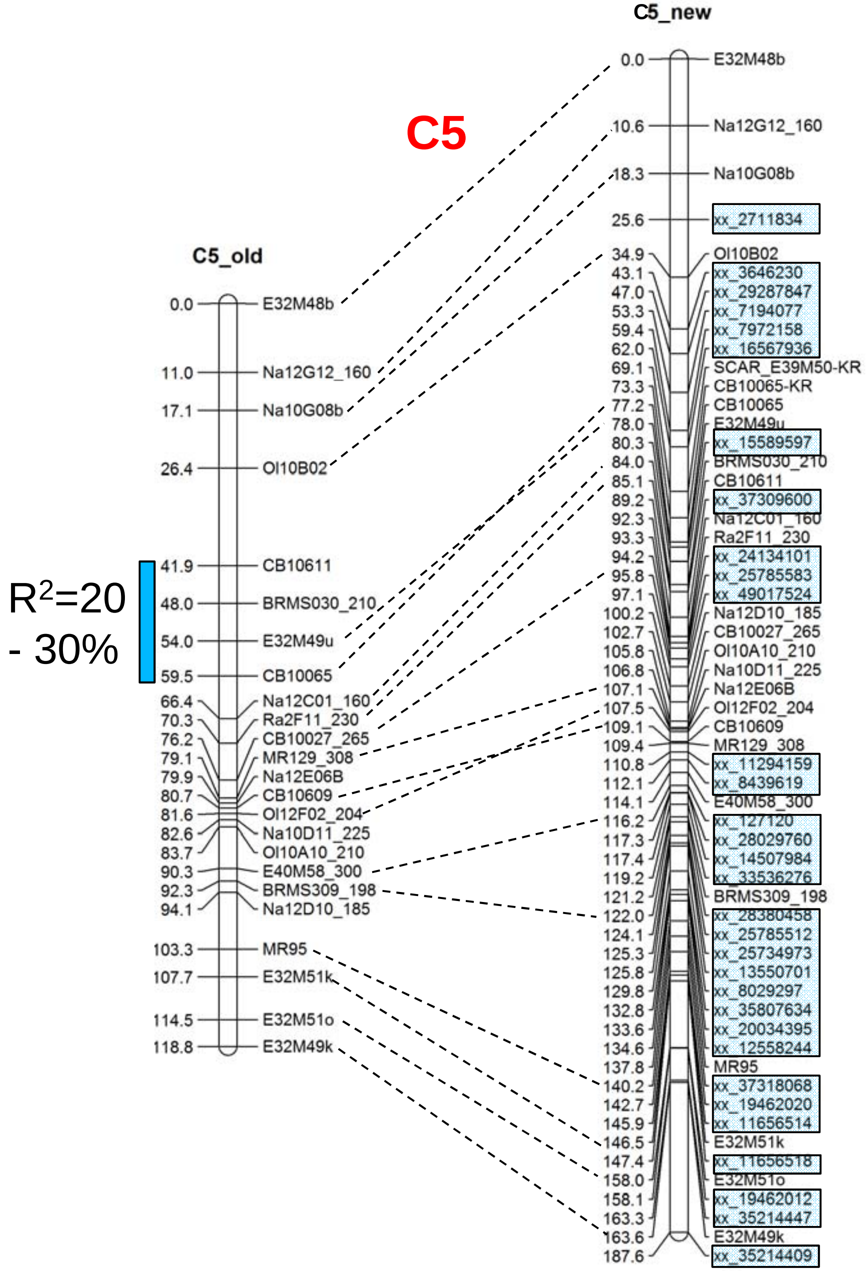

Express 617 x R53
106 DH lines

=> Obermeier C. et al., Poster

# QTL mapping of *V. longisporum* resistance

## QTL for *V. longisporum* resistance



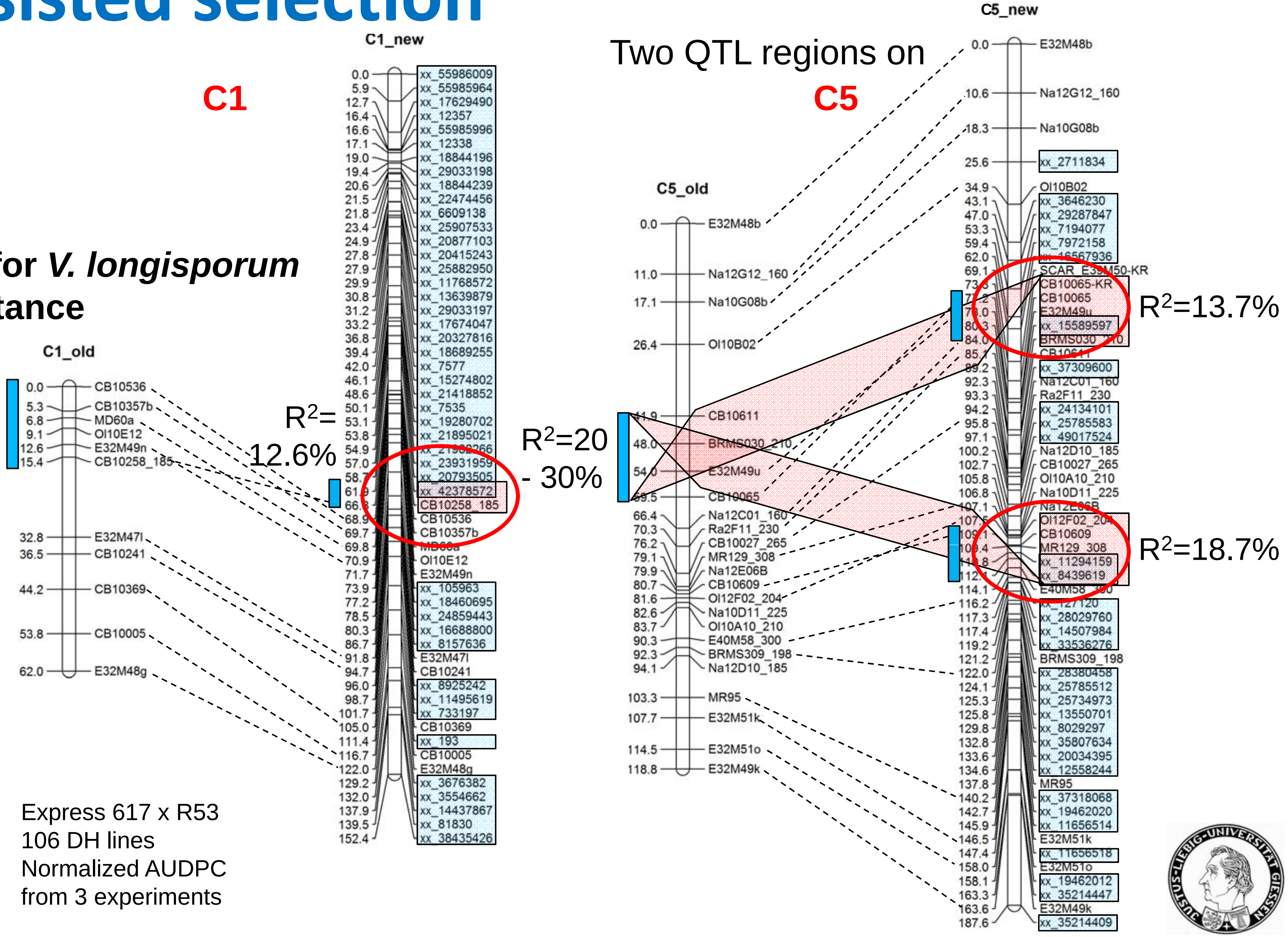




Express 617 x R53
106 DH lines
Normalized AUDPC
from 3 experiments

# Development of new markers for marker-assisted selection

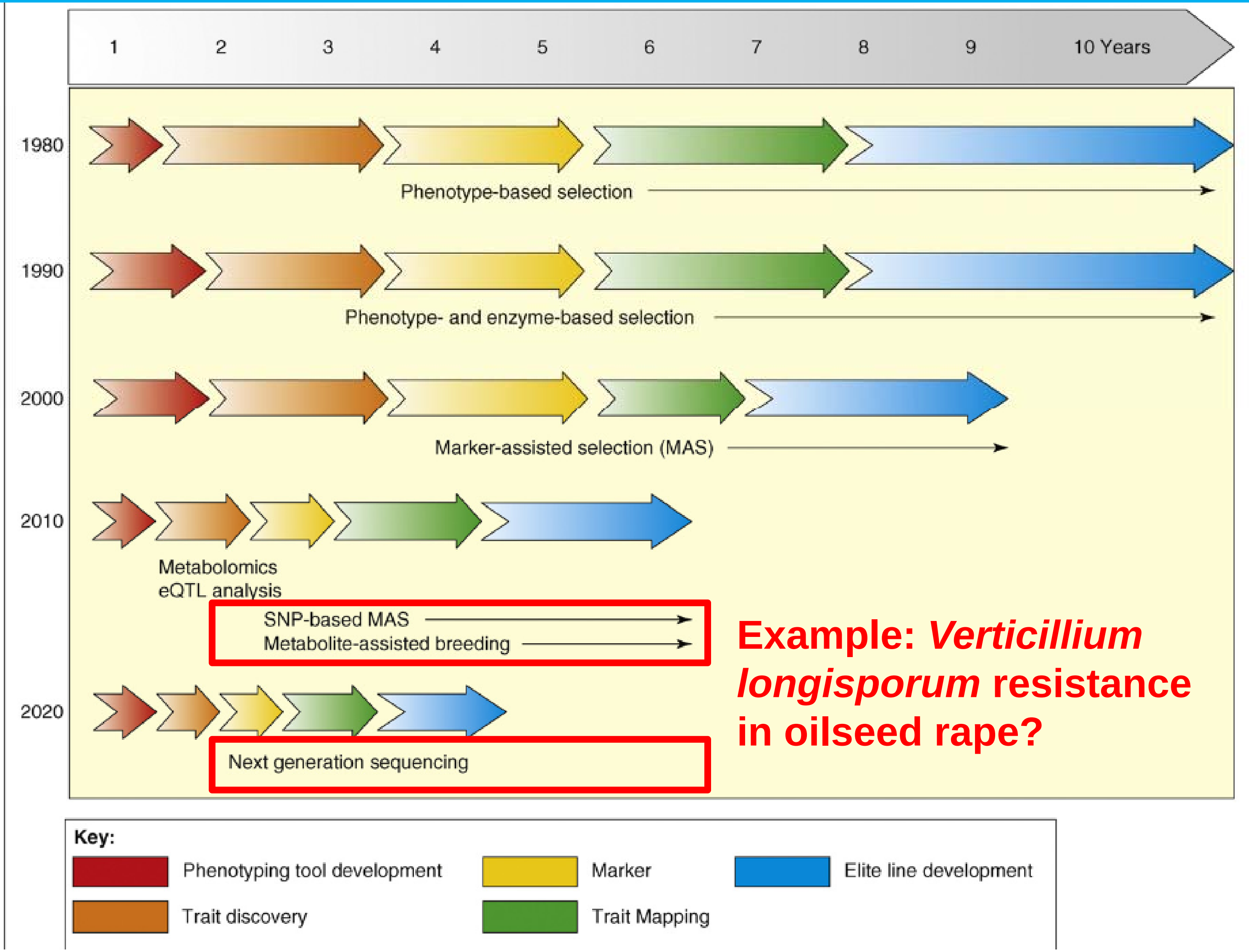
**QTL for *V. longisporum* resistance**

R²=13 -15%




Express 617 x R53
106 DH lines
Normalized AUDPC
from 3 experiments

# Breeding technology pipeline from past to present to future

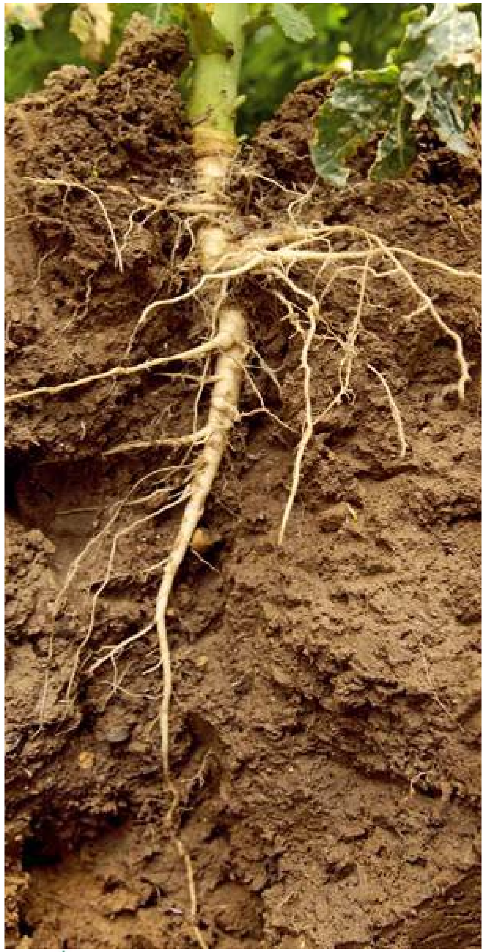



**Example: *Verticillium longisporum* resistance in oilseed rape?**

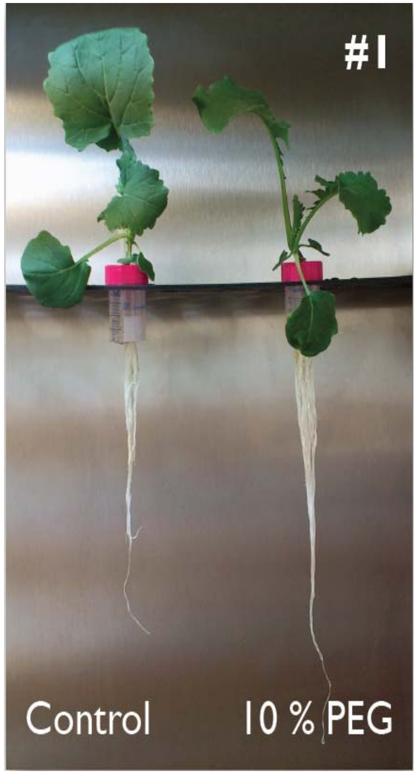
Adapted from Fernie & Schauer (2008)


Fernie AR, Schauer N (2008). Metabolomics-assisted breeding: a viable option for crop improvement? Trends in Genetics 25:39-48

# Stress tolerance and yield stability due to strong root system



- Better availability and acquisition of water and **nutrients**
- **Stress** (drought) and disease **resistance** (e.g. Verticillium), better crop stability
- Adequate **yield** (output) at lower input (fertilization, pesticides, etc.)



**Thanks:**

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**Prof. A. v. Tiedemann, U Göttingen (Germany)**

# Thank you for your attention!