Exploiting genetic resources of the genus *Beta* to broaden the genetic variation in beet breeding

Christian Jung
Structure

• Gene bank at the PBI Kiel
• Structured populations
• Genes controlling life cycle regime
• *B. corolliflora* addition lines
• Procumbentes species as donors for cyst nematode resistance
# Accessions of the genus Beta available at the PBI Kiel

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<th>Species name</th>
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Haplotype variation of flowering time genes of sugar beet and its wild relatives and the impact on life cycle regimes

major flowering time regulators $BTC1$, $BvBBX19$, $BvFT1$ and $BvFT2$

$Beta$ diversity panel

Haplotype analysis of $BTC1$, $BvBBX19$, $BvFT1$ and $BvFT2$

accessions from northern latitudes flowered significantly later → strong impact of latitude of origin on life cycle

We identified sequence variation which may impact life cycle adaptation in beet.

importance of $BTC1$ in the domestication process of cultivated beets

distribution and adaptation of $Beta$ species to different life cycle regimes in response to different environments.
Cloning the Rhizomania resistance gene Rz2

*B. vulgaris* ssp. *maritima* population of 200 wild beets, sampled in their natural habitat

mapping-by-sequencing: generating a draft genome sequence of the wild beet

*Rz2* encodes a CC-NB-LRR protein, verified by RNAi

great potential of wild beets for rapid gene discovery

MBS with two pools of homozygous resistant and susceptible wild beet

wild beet population of *B. vulgaris* ssp *maritima* located along the coastal line of the Kalundborg fjord in Denmark
B. vulgaris x maritima  F2-populations

93161 x 960037

960037 x 070325

93161 x 980319

960037 x 000358
Sugar beet x *B. corolliflora* monosomic addition lines

trisomic sugar beet  \( \times \)  \( B. corolliflora \)

\[ \begin{align*}
\text{VV (2n=18+1)} & \times \quad \text{CCCC (2n=36)} \\
\Rightarrow & \quad \text{VVCC (2n=4x=36)} \\
& \quad \text{X} \quad \text{VV (2n=18)} \\
& \quad \text{VV (2n=18)} \\
\Rightarrow & \quad \text{VVC (2n=27)} \\
& \quad \text{(2n=18)} \\
\Rightarrow & \quad 2n = 18, 19* ........27
\end{align*} \]

- I. 970005/8
- II. 970025/2
- III. M12/2
- IV. 970015/32
- V. 983x44/13
- VI. 970014/58
- VII. 970001/4
- VIII. 970026/39
- IX. 98-6812/12

\* frequency of monosomic additions: 10.4%


**H. schachtii** resistance and tolerance genes

- All cultivated beets are susceptible against *H. schachtii*
- Wild beets of genus *Patellifolia*
  - complete resistance: no cyst formation
  - J2 larvae invade roots, no females (catch crops)
  - small syncytia can be found
- Tolerance: *B. vulgaris* ssp. *maritima* WB242

Wild beet chromosomes carrying genes for nematode resistance or tolerance

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<td><em>B. vulgaris</em> ssp. <em>maritima</em> WB242$^1$</td>
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Nematode resistant plant materials

Wild beets
- *P. procumbens*
- *P. patellaris*
- *(B. webbiana)*

Resistant sugar beet
- 2n=19 (Monosomic addition lines)
- 2n=19 (Monosomic fragment addition lines)
- 2n=18 (Translocation lines)
- Segregating populations
The *P. procumbens* translocation TR520 in sugar beet

In situ hybridization with two YACs as probes, pachytene chromosomes

Features of the TR520 translocation:
- **Size**: 2.2 Mbp (0.3% beet genome)
- **Number of ORFs**: 320
  - Retrotransposons: 13%
  - unclassified proteins: 24%
  - similarity to known proteins: 32%
  - no significant similarity: 31%
Selection of new mutants derived from the translocation line TR520

- Doses for gamma irradiation: 100gy, 200gy, 400gy
- Number of seeds irradiated: 4700
- Number of M2 families screened: 1400
- Markers assisted selection:
- Features of new translocation mutants:
  - susceptible against the BCN
  - smaller-sized translocation as compared to the resistant ones
Current work to clone the second nematode resistance gene *Hs1*-2

NGS of the resistant line TR520 → complete sequence available

Translocation breakpoint identified

Sequence annotation within the critical region → candidate genes identified

Functional analysis: hairy root transformation in combination with CRISPr-Cas mutation induction

Alignment of wild beet translocations on sugar beet chromosome 9 after physical mapping and whole genome sequencing

*Patellifolia procumbens*

- *Susceptible*
- *resistant*

*Beta vulgaris*

‘critical region’: present only in resistant translocation lines → genome region housing *Hs1*-2