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# ERANET-PG ASSYST: "Associative expression and systems analysis of complex traits in oilseed rape/canola"



# ASSYST Consortium

## JLU Giessen, Germany

- **Rod Snowdon:** Coordination, global expression (seedlings)

## NRC-PBI & AAFC, Saskatoon, Canada

- **Isobel Parkin, Pierre Fobert:** Global expression (seeds)
- **Sue Abrams:** Hormone profiling (seeds/seedlings)
- **Andrew Sharpe:** SNP platform development, genotyping

## John Innes Centre, Norwich, UK

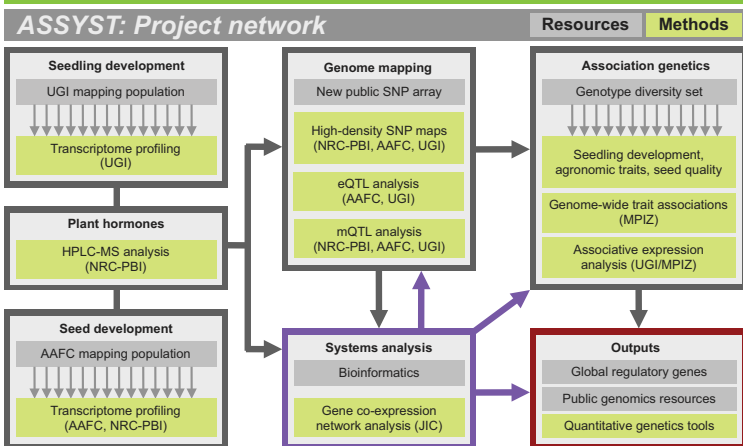
- **Ian Bancroft, Janet Higgins:** Systems analysis

## MPI for Breeding Research, Cologne, Germany

- **Benjamin Stich:** "Associative gene expression"



# ASSYST Network



# ASSYST: Project aims

- **Ultra-deep expression analysis** in seeds and seedlings: Digital gene expression profiling via Illumina SuperSAGE
- Integration of global gene expression data with phenotype, metabolite and yield data ("**associative systems analysis**")
- Identification of **key regulatory genes for complex traits** via **eQTL** and **gene-co-expression network analysis**
- Generation and genotyping of a large public **diversity set** (approx. 450 lines) for **association studies** in *B. napus*
- 454-based EST-SNP discovery and development of a new, **public SNP array**



# Background



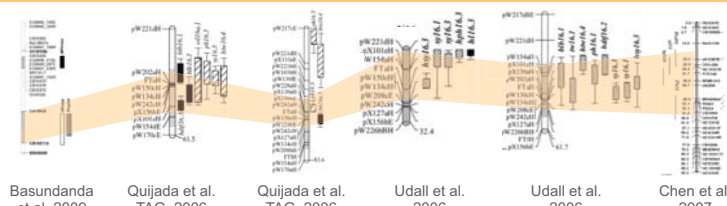
## DFG Priority Program: "Heterosis in Plants"

- Comparative QTL analysis of heterosis for seedling biomass traits, plant height, seed weight, pod traits and seed yield in different crosses

# Multi-trait QTL "hotspots"

- Hotspots of QTL for multiple traits are often found in the same chromosome regions in very different genetic backgrounds
- Similar heterotic QTL clusters (biomass, metabolites) have also been reported in *Arabidopsis* (Meyer et al. 2008, Lysec et al. 2009)

## Example: Major QTL cluster on Bn chromosome N16 in six diverse backgrounds



Basundanda et al. 2009    Quijada et al. TAG, 2006    Quijada et al. TAG, 2006    Udall et al. 2006    Udall et al. 2006    Chen et al. 2007



## Multi-trait gene regulation

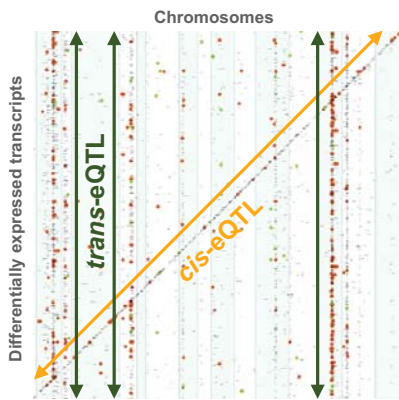


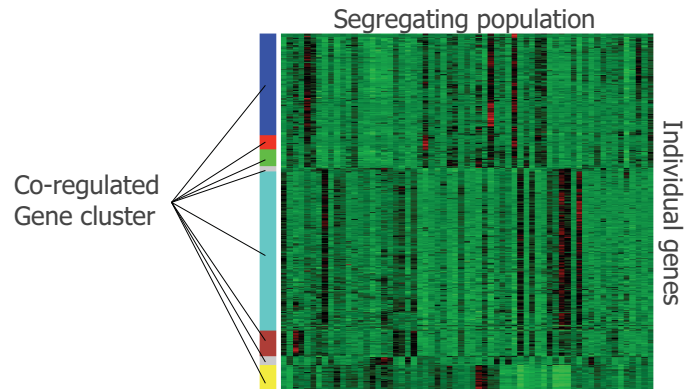
Image: Zou et al. BMC Bioinformatics 2007

### Hypothesis:

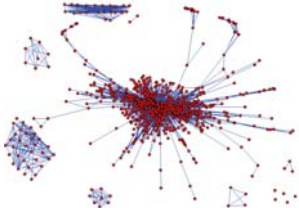
- Key QTL hotspots for heterosis, biomass, yield, may be caused by global regulatory genes that are active in different processes throughout the entire plant development
- Global transcription factors should show up as as major **trans-eQTL**



## Gene co-regulation (trans-eQTL) Correlated expression = Gene cluster



## Identification of regulatory genes: “Gene co-expression network analysis”

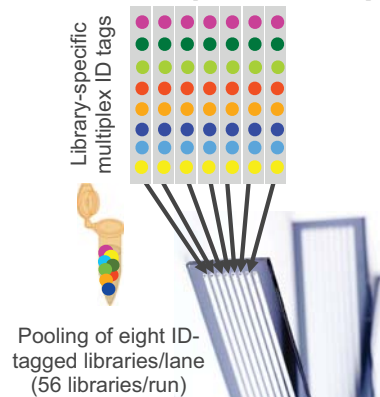


- Important hubs in a network recognizable by their number and strength of interactions
- Some important hubs may be more or less unknown
- Ultradeep transcriptome sequencing (Illumina GAII): Quantification of known and unknown transcripts



## Digital Gene Expression

### Global expression analysis: Illumina SuperSAGE

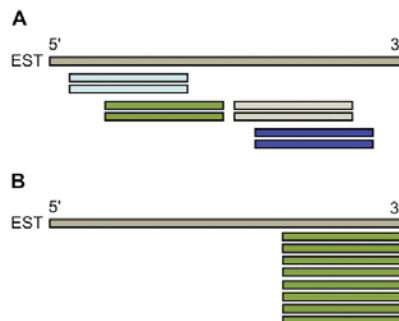


- 60 million tag sequences per Illumina run
- > 1 million 26bp EST tags per SuperSAGE library
- Accurate quantification of gene expression, even for very low-abundance transcripts and unknown genes



## B. napus SNP discovery

- 454 sequencing of anchored 3'-ESTs
- SNP discovery in panel of diverse lines including mapping parents
- Release of public array with 1536 SNPs on target for early 2010
- Two new B. napus SNP maps with extensive QTL data



Eveland et al. Plant Physiol (2008)



## B. napus diversity set

- 450 genetically diverse inbred lines
- Spring, winter, Asian oilseed types, fodder rape, vegetable forms, resynthesised B. napus



- Seed production complete, genotyping with genome-wide SSRs in progress (genome-wide SNPs in 2010)
- 2009/2010 field trials (winter-type materials) sown at 5 sites, greenhouse and growth chamber tests in progress



## Transnational research

- Longstanding German-French cooperation in Brassica genomics, GABI-Canada cooperation since 2005
- Considerable synergy (technology platforms, expertise)
- ERANET-PG ASSYST: Much more than just additive benefits
- Close ties to Multinational Brassica Genome Project (MBGP)

 [brassica.info](http://brassica.info)



## Cooperations & support

