CG920 Genomics

Lesson 4

Forward Genetics

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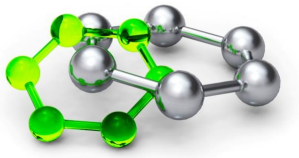


Outline

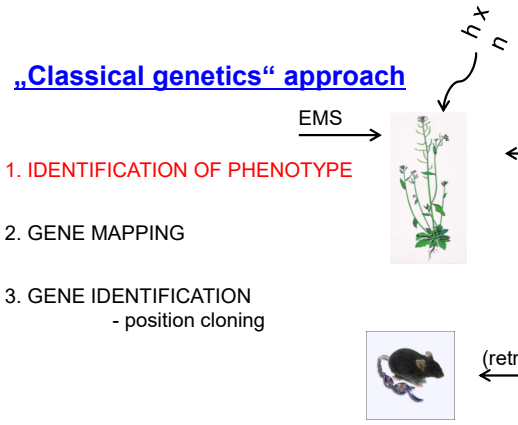
- Forward vs. Reverse Genetics
- Use of Libraries of Insertional Mutants in Forward Genetics
  - Searching in Libraries of Insertional Mutants According to:
    - anatomically or morphologically detectable phenotype
    - metabolic profile
    - expression of genes of interest
  - Identification of the Mutated Locus
    - plasmid rescue
    - iPCR
- Use of Libraries of Point Mutants in Forward Genetics
  - Positional Cloning
  - GWAS

Outline

- Forward vs. Reverse Genetics

„Classical“ genetics *versus* „reverse genetics“ approaches in functional genomics

RANDOM MUTAGENESIS



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    - anatomically or morphologically detectable phenotype

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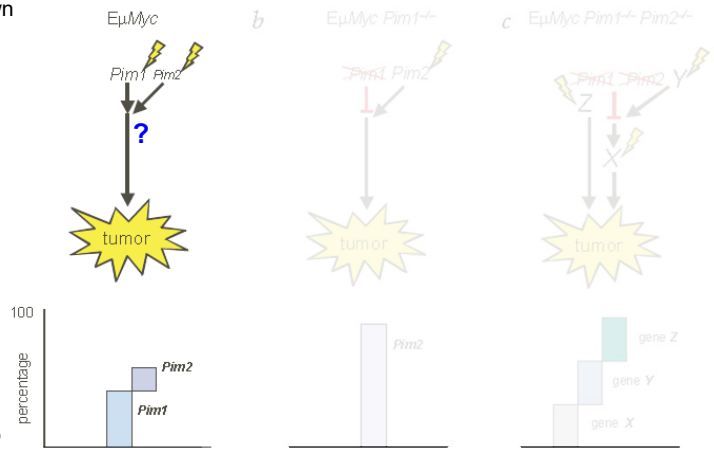
Insertional mutagenesis in forward genetics approaches

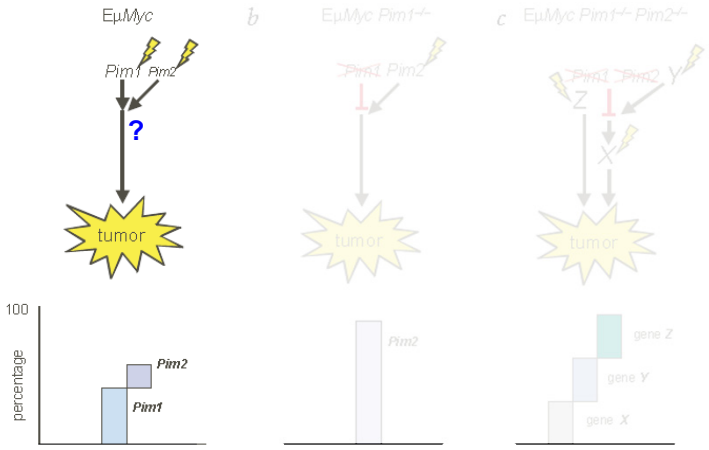
- Use of insertional mutagenesis for study of carcinogenesis
  - Infection of EμMyc mice by MoMuLV retrovirus leads to lymphomas formation, which arose due to activation of Pim kinases (40 % activation of Pim1, 15 % activation of Pim2), molecular targets of these kinases were unknown



Mikkers et al., Nature Gen (2002)

Insertional mutagenesis in forward genetics approaches

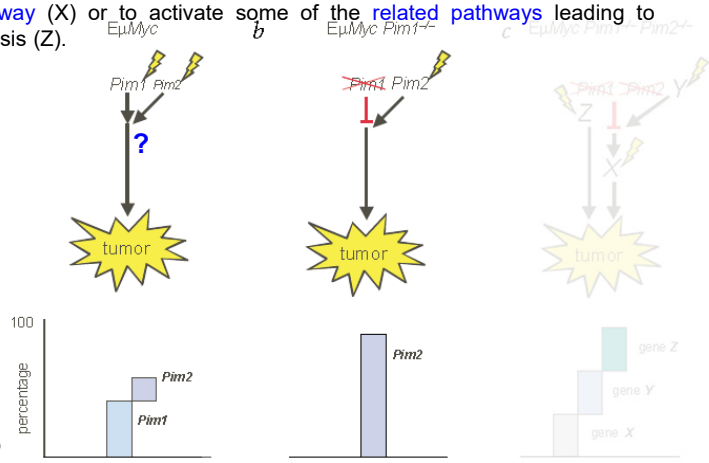
- Use of insertional mutagenesis for study of carcinogenesis
  - Infection of EμMyc *pim1* mutants by MoMuLV retrovirus leads to lymphomas formation, which in 90 % contain insertion nearby (activation) Pim2



Mikkers et al., Nature Gen (2002)

Insertional mutagenesis in forward genetics approaches

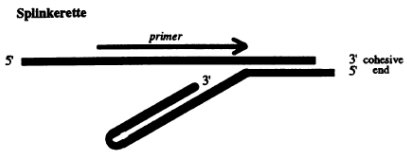
- Use of insertional mutagenesis for study of carcinogenesis
  - Infection of EμMyc double mutants *pim1, pim2* by MoMuLV retrovirus leads to lymphomas formation, which can be expected to activate either one of the signalling partner of Pim proteins (Y), one of the downsteram proteins of Pim signalling pathway (X) or to activate some of the related pathways leading to lymphomagenesis (Z).



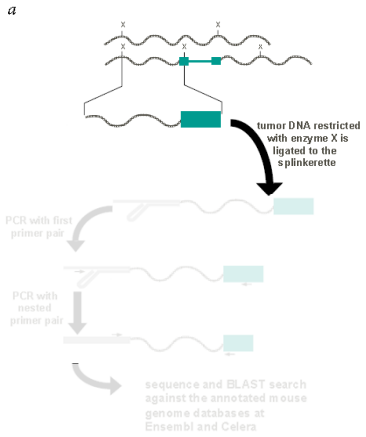
Mikkers et al., Nature Gen (2002)

Insertional mutagenesis in forward genetics approaches

- Isolation of genomic regions adjacent to the insertion site of the provirus
  - Cleavage of genomic DNA and ligation of special linkers, so-called *splincerettes* (increasing the specifity of amplification)



Devon et al., Nucl Acid Res (1994)



Mikkers et al., Nature Gen (2002)

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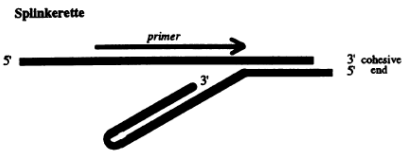
Insertional mutagenesis in forward genetics approaches

- Isolation of genomic regions adjacent to the insertion site of the provirus
  - First amplification using specific primers



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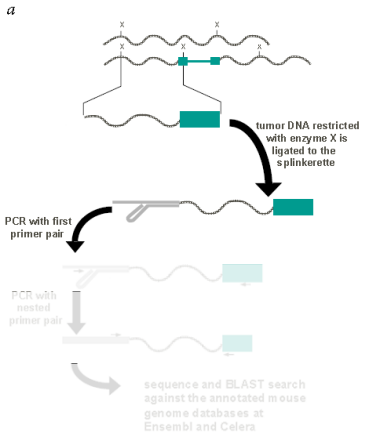

Mikkers et al., Nature Gen (2002)

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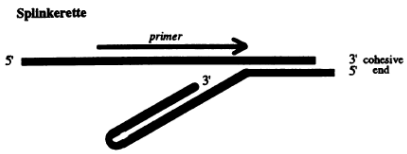
Insertional mutagenesis in forward genetics approaches

- Isolation of genomic regions adjacent to the insertion site of the provirus
  - Second amplification using nested primers (increasing the specifity)



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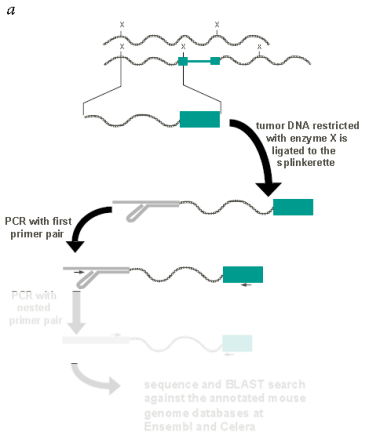

Mikkers et al., Nature Gen (2002)

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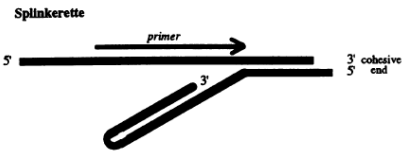
Insertional mutagenesis in forward genetics approaches

- Isolation of genomic regions adjacent to the insertion site of the provirus
  - Sequencing and localization of regions adjacent to provirus by searching in annotated databases of mouse genome



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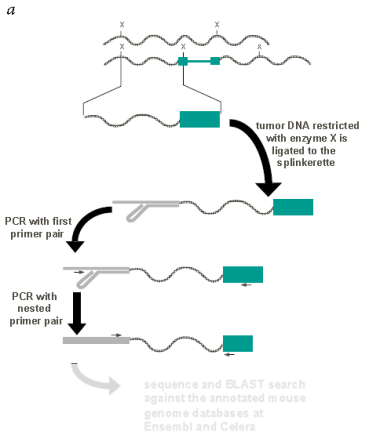

Mikkers et al., Nature Gen (2002)

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In case of splincerette, the primer is of the same sequence as the top strand and therefore it is unable to act as a primer until the complement of this strand has been synthesized (from the insert-specific primer at the right-hand side).

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    - metabolic profile

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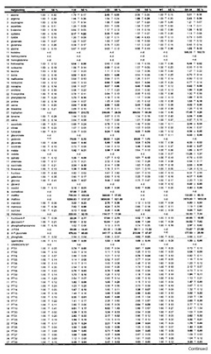
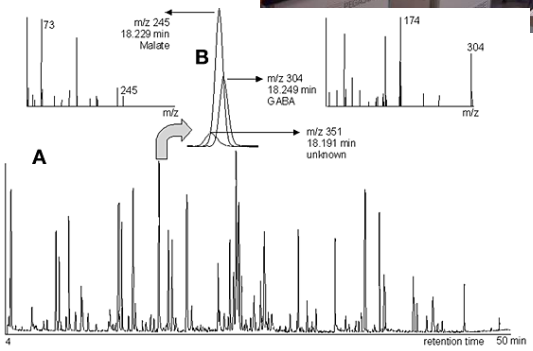
Metabolic profiling

- Metabolic profiling of plants
  - Automated analysis of metabolites (up to 25.000) by GC-MS techniques in libraries of T-DNA mutants





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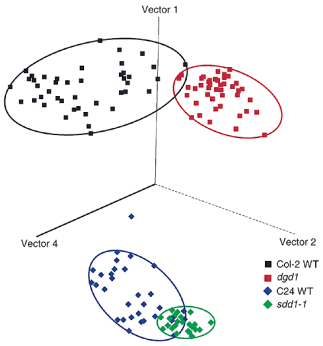
Metabolic profiling

- Metabolic profiling of plants
  - Automated analysis of metabolites (up to 25.000) by GC-MS techniques in libraries of T-DNA mutants
  - Identification of interesting (even comercially interesting) mutants



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Metabolic profiling

- Metabolic profiling of plants
  - Automated analysis of metabolites (up to 25.000) by GC-MS techniques in libraries of T-DNA mutants
  - Identification of interesting (even comercially interesting) mutants
  - Fast and easy isolation of genes through identification of sequences adjacent to T-DNA

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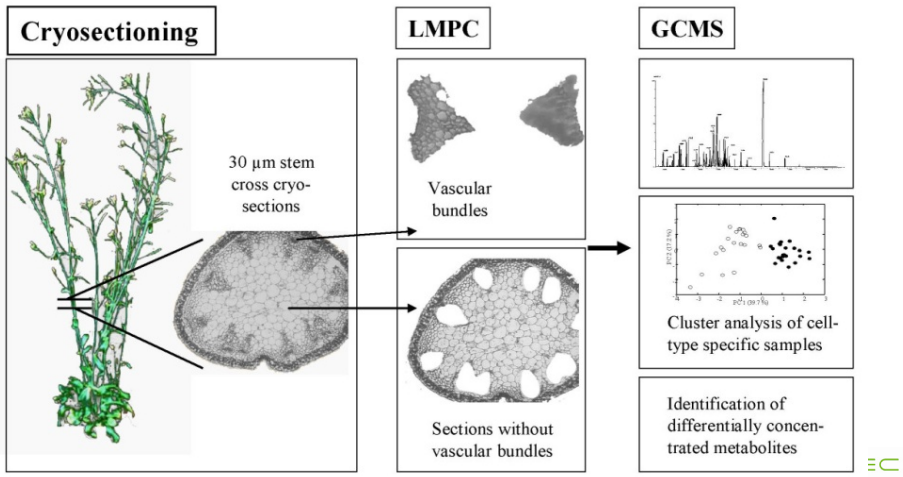
Metabolic profiling

- Metabolic profiling of plants
  - Possibility to use special techniques, e.g. microdissection



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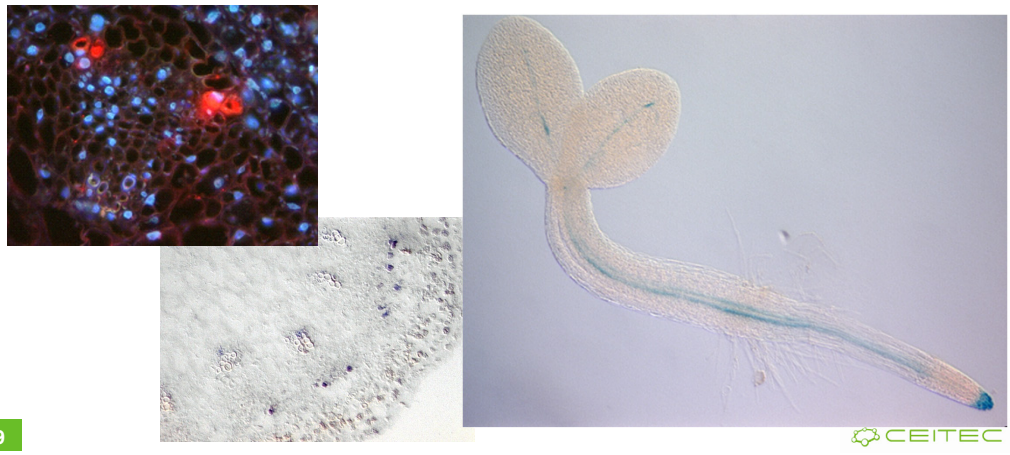
Expression profile

- Identification of mutants with a change in the expression profile
  - Analysis of *expression profile* (*pattern*) of the gene and identification of mutants with altered expression pattern



Expression profile

- Identification of mutants with a change in the expression profile
  - Analysis of *expression profile* (*pattern*) of the gene and identification of mutants with altered expression pattern
  - Possibility of partial automation (virtual digital microscopy)

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Automated Microscopy Screening

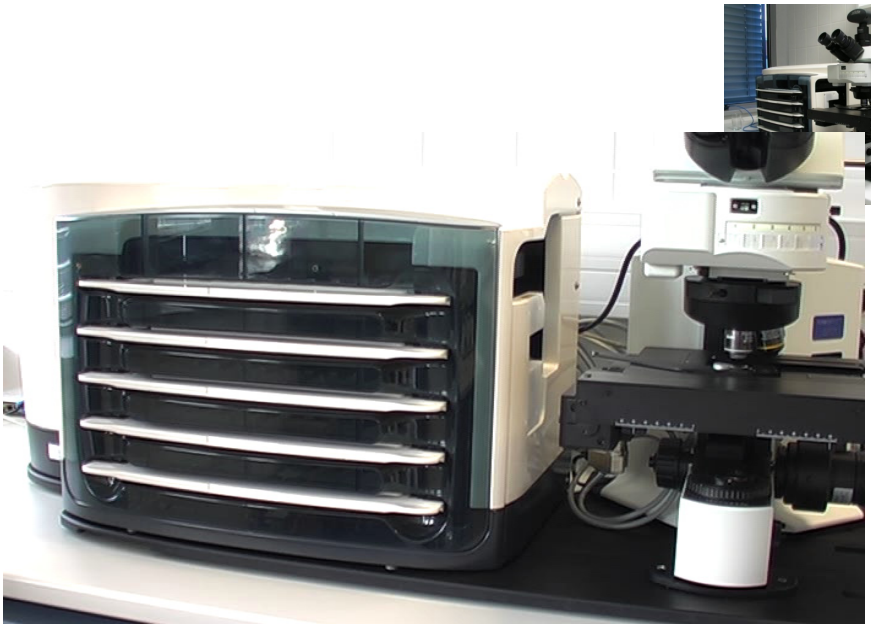

image.vsi

Dobisova and Hejatko, *Methods in Mol Biol, 2014*

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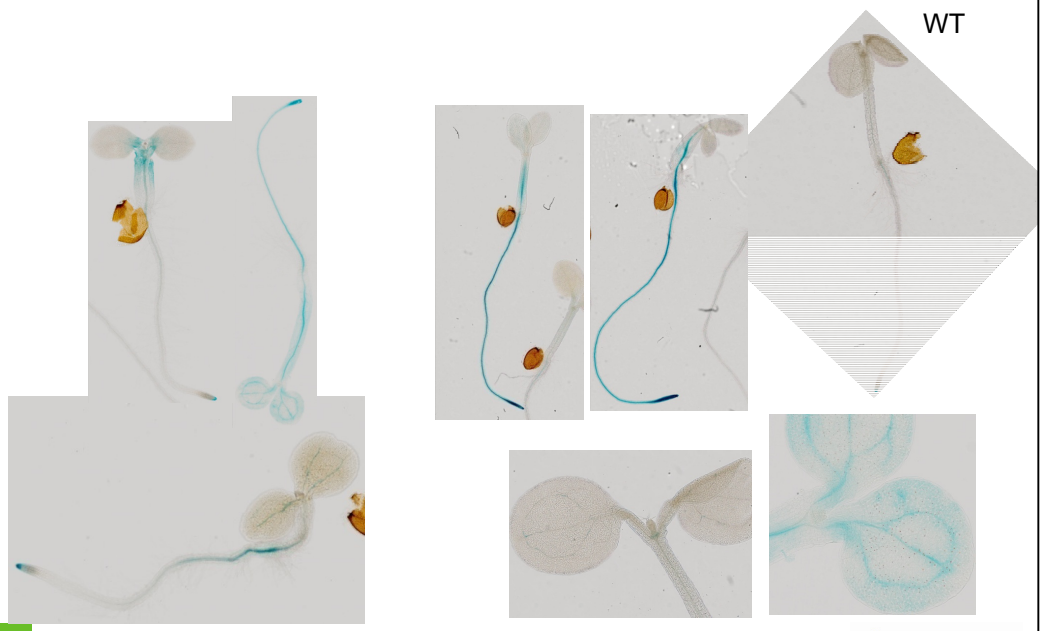
Tady by mohla být reference zpět na CEITEC, jaké skvělé vybavení v něm je a jak dobře se vám s tím pracuje

Pokud tam nezůstane video, ikonu bych dala pryč

Expression profile



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    - iPCR

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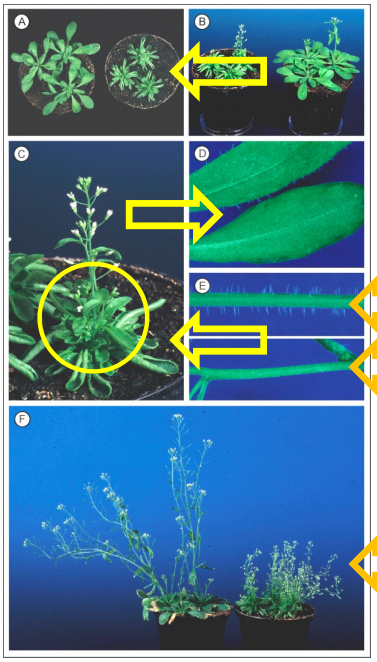
Identification of mutated locus

- Identification of chromosomal rearrangements responsible for bushy phenotype of *Arabidopsis*
  - Description of phenotype

Identification of mutant



- Crinkled leaves
- Bushy phenotype (branching defective)
- No trichomes on leaves and stems
- Late senescence

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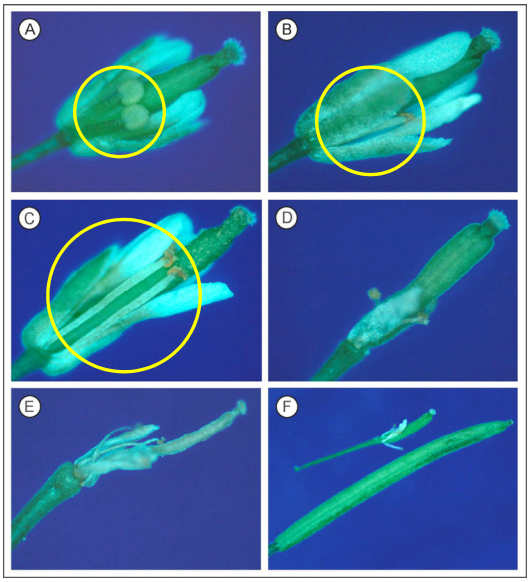
Identification of mutant



- Male sterility, defects in stamen filament elongation (A,B)

(compare with wild type C)

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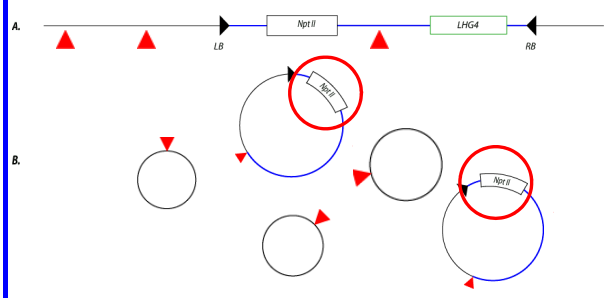
Identification of mutated locus

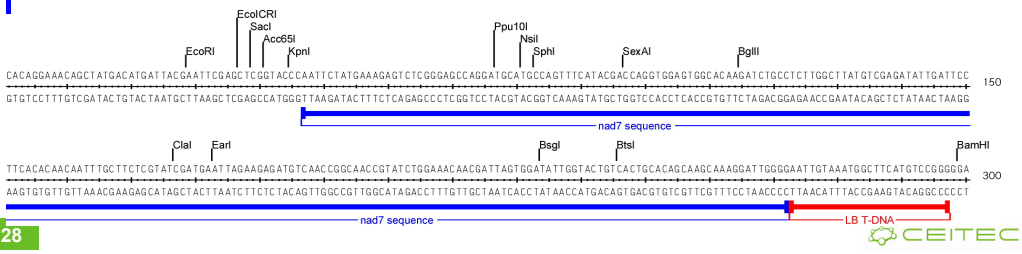
- Identification of chromosomal rearrangements responsible for bushy phenotype of *Arabidopsis*
  - Description of phenotype
  - Identification of T-DNA mutated region

Identification of mutated locus

1. Identification of region of genomic DNA adjacent to the ***left border*** using ***plasmid rescue***



- Restriction digestion (*EcoRI*) of mutant genomic DNA
- Religation and transformation of *E. coli*
- Isolation of plasmid DNA from positively selected clones
- Identified sequence was identical to gene for *NAD7* coded by mtDNA



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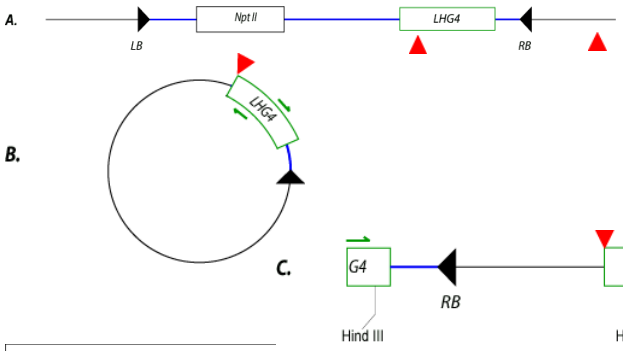
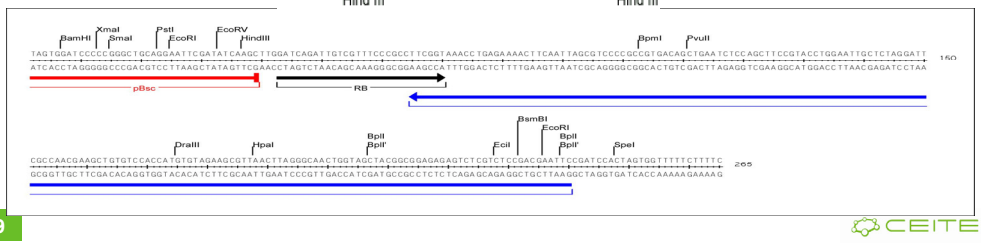
Identification of mutated locus

2. Identification of region of genomic DNA adjacent to the ***right border*** using ***inversion PCR*** **(iPCR)**



- Restriction digestion (*EcoRI)* of mutant genomic DNA
- Purification, religation and PCR using T-DNA specific primers
- Cloning and sequencing
- Identified sequence was not homologous to any sequences with known function



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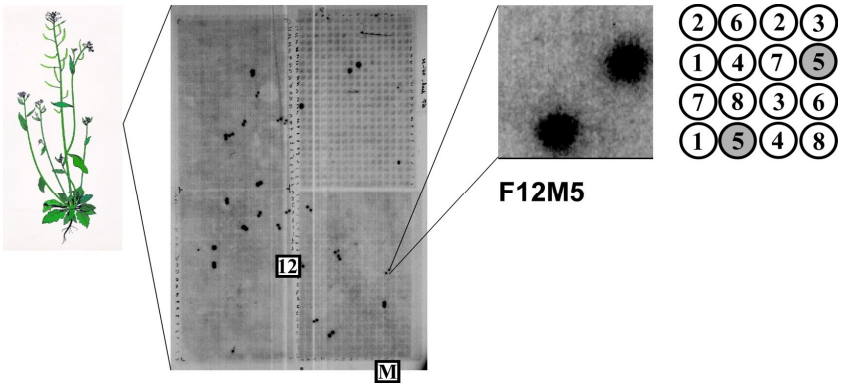
Identification of mutated locus

- Identification of chromosomal rearrangements responsible for bushy phenotype of *Arabidopsis*
  - Description of phenotype
  - Identification of T-DNA mutated region
  - Localization of T-DNA insertion site in *Arabidopsis* genome

Searching in library IGF-BAC

- Genome library containing 10.752 clones with an average size of an insert of 100 kb
- Bacterial clones arranged in the microtiter plates
- Library loaded onto nylon filters for hybridization with the radiolabeled probe



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Mapping with IGF-BAC database

I. Sequences adjacent to the left border of T-DNA

- 28 positively hybridizing clones in total
- 19 of them located on chromosome 2
- 18 of them similar with mtDNA

II. Sequences adjacent to the right border of T-DNA

- 6 positively hybridizing clones in total
- all of them located on chromosome 2

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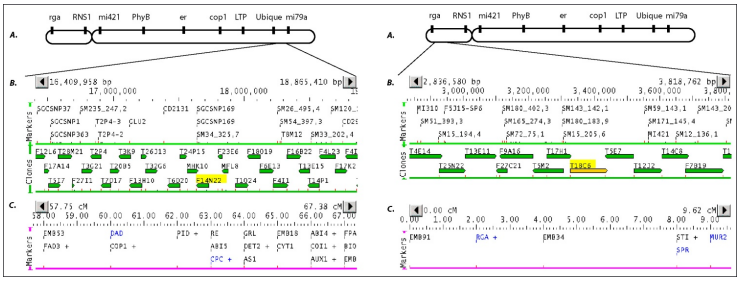
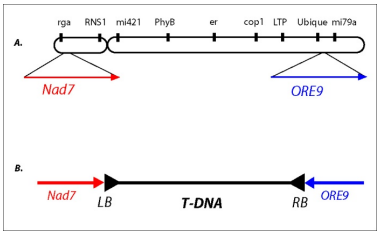
Localization of genomic T-DNA adjacent to both left and right T-DNA borders on chromosome 2

Sequences adjacent to ***right*** and ***left*** border of T-DNA



- There was probably an inversion of almost entire chromosome 2



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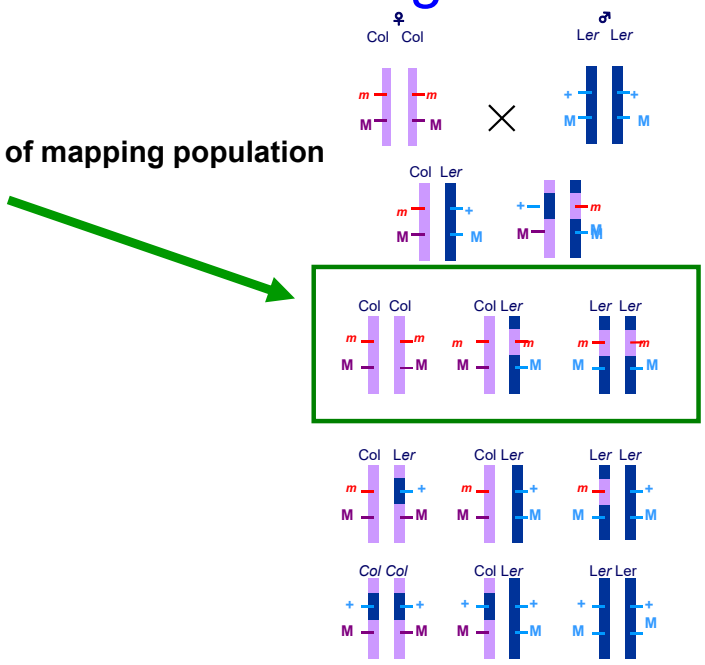
Identification of mutated locus

- Positional cloning
  - Principle: co-segregation analysis of segregating population (mostly of offspring of backcrosses) with molecular markers
    - **SSLP** (Simple Sequence Length Polymorphism)
      - Polymorphism of genome (PCR products) length, amplified using specific primers
    - **RFLP** (Restriction Fragment Length Polymorphism)
      - Detection by Southern blot (PCR after digestion of the genomic DNA and ligation of adapters)
    - **CAPS** (Cleaved Amplified Polymorphic Sequence)
      - Restriction fragment length polymorphism, genome segments amplified by PCR
    - **RAPD** (Randomly Amplified Polymorphic DNA)
      - Polymorphism of length of randomly amplified genome segments, using short 8-10bp primers

Positional cloning

Preparation of mapping population



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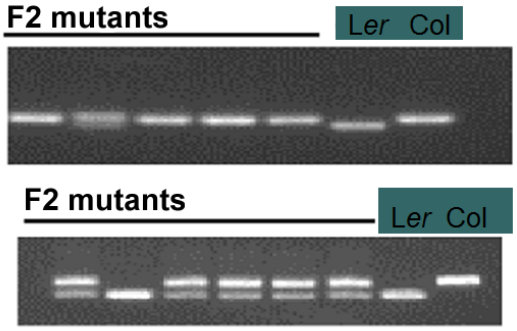
Recombinant analysis – determining the percentage of recombination between mutation and molecular marker

r [%] = number of chromosomes of *Col* / number of all the chromosomes × 100



marker I – linked
5 mutants
1/10 × 100 = 10%

marker II - no linkage
6 mutants
7/12 × 100 = 58%

- Analysis of approximately 2000 mutant plants
- Determining the closest (still segregating) marker
- Identification of mutation by sequencing

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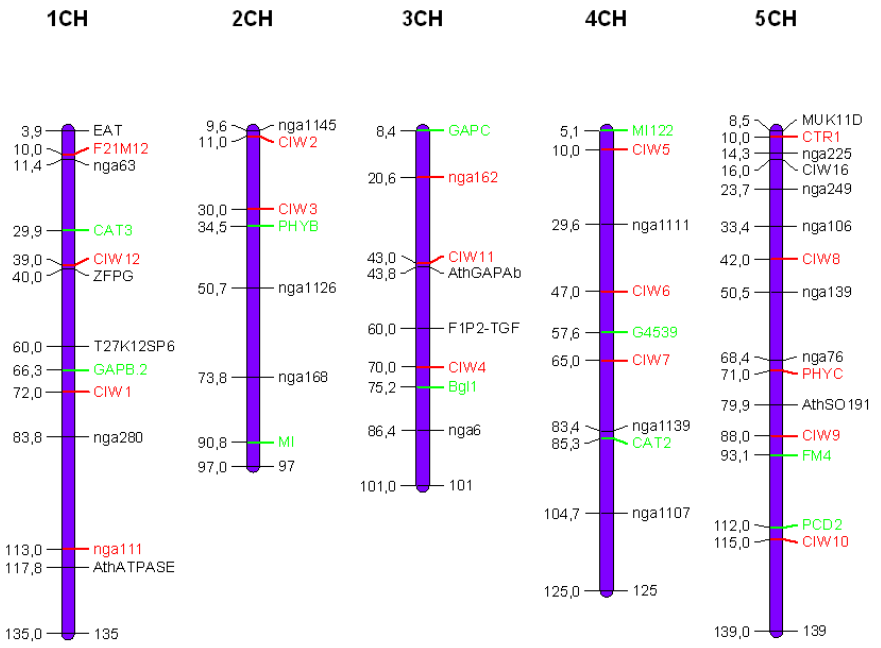
Map of DNA molecular markers



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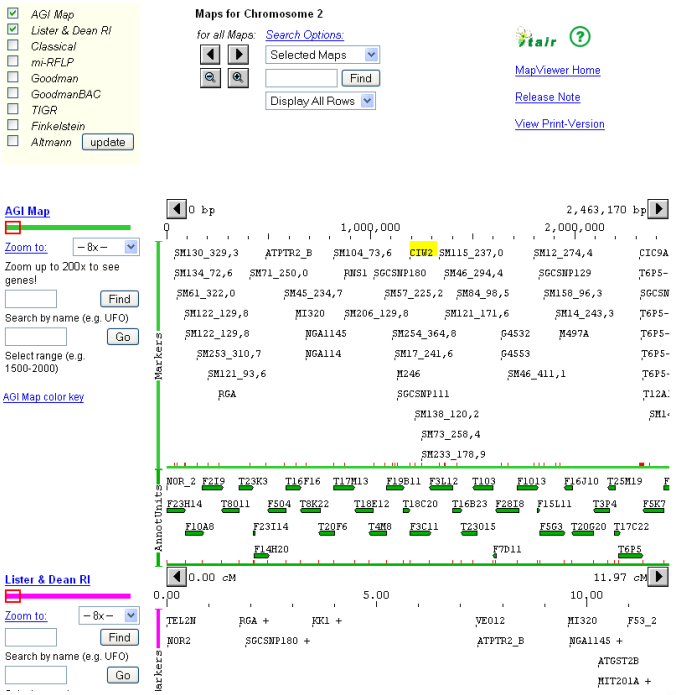
Markers for fine mapping



CIW2

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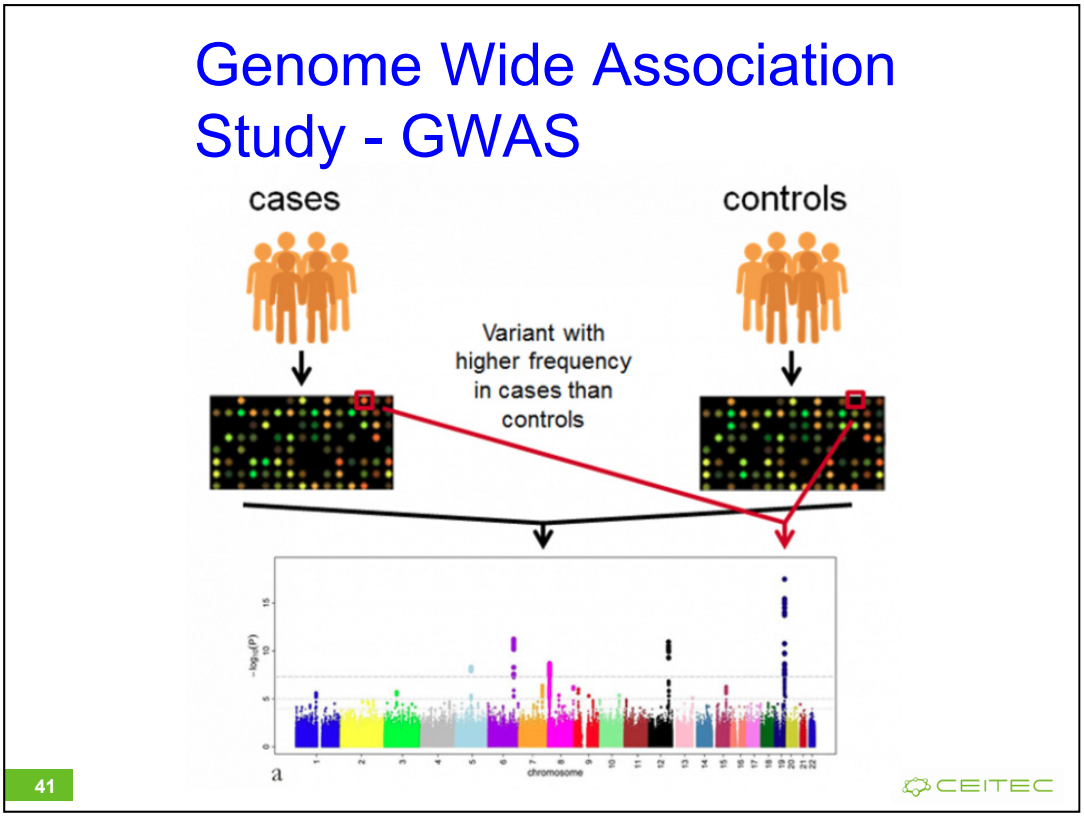

https://www.ebi.ac.uk/training-beta/online/courses/gwas-catalogue-exploring-snp-trait-associations/what-is-gwas-catalog/what-are-genome-wide-association-studies-gwas/

A typical GWAS study collects data to find out the common variants in a number of individuals, both with and without a common trait (e.g. a disease), across the genome, using genome wide SNP arrays. Variants associated with the disease, or within the same haplotype as a variant associated with a disease, will be found at a higher frequency in cases than in controls. Statistical analysis is carried out to indicate how likely a variant is to be associated with a trait.

As GWAS analyse common variants, usually typed on commercial SNP arrays (Figure 3), they do not generally identify causal variants. GWAS identify common variants which tag a region of linkage disequilibrium (LD) containing causal variant(s). Additional or follow-on studies are usually required to narrow the region of association and identify the causal variant

Key Concepts

- Forward genetics allows targeted screening for interesting phenotypes, whose association with a given gene/locus is unknown
  - Employs both insertional mutagenes as well as point mutations
    - **Inserional mutation**
      - (mostly) loss-of-function mutation
        - Identification via
          - iPCR
          - plasmid rescue
    - **Point mutation**
      - Both loss-of-function as well as
      - gain-of-function mutations
        - Identification via
          - map-based cloning
          - GWAS

Discussion