CG020 Genomika

Přednáška 12

Nástroje systémové biologie

Modelové organismy, PCR a zásady navrhování primerů

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EVROPSKÁ UNIE esf MINISTERSTVO ŠKOLSTVÍ, MLÁDEŽE A TĚLOVÝCHOVY OP Vzdělávání pro konkurenceschopnost

INVESTICE DO ROZVOJE VZDĚLÁVÁNÍ

Tato prezentace je spolufinancována Evropským sociálním fondem a státním rozpočtem České republiky

Genomika 12

- Zdrojová literatura

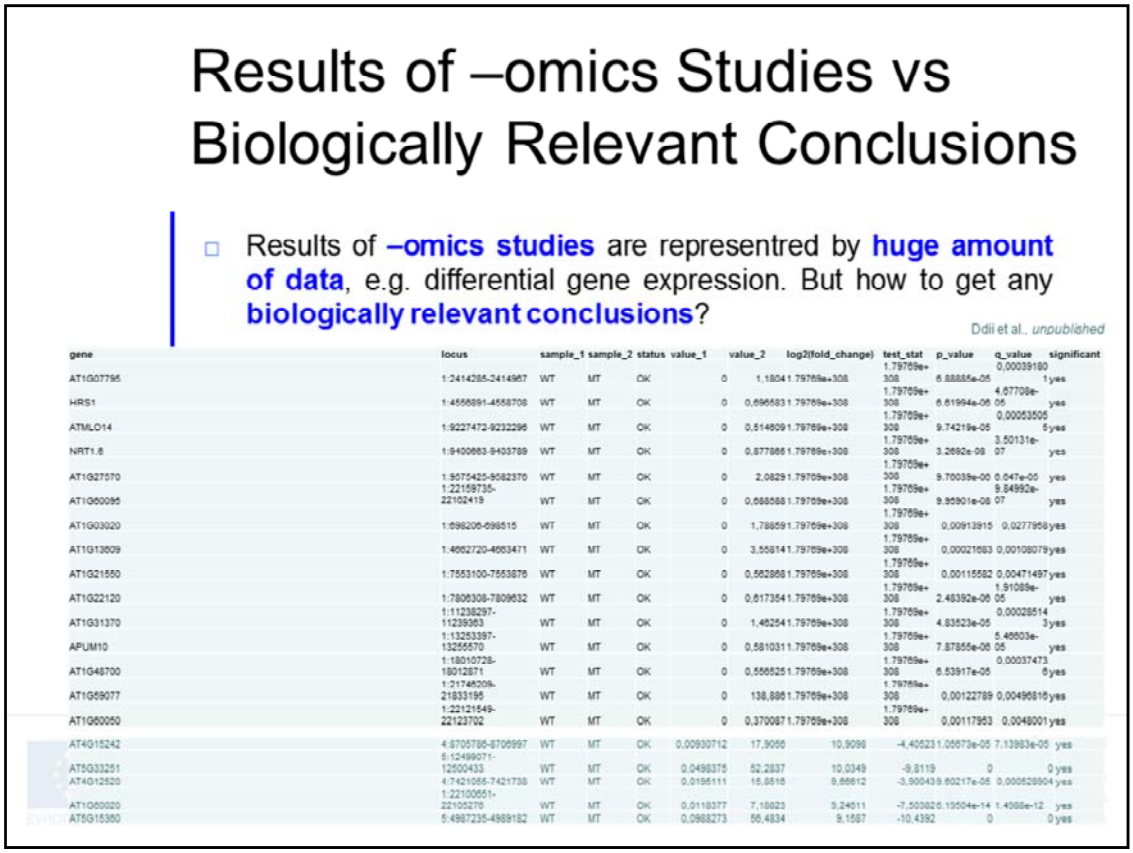
- Wilt, F.H., and Hake, S. (2004). Principles of Developmental Biology. (New York ; London: W. W. Norton)
- Roscoe B. Jackson Memorial Laboratory., and Green, E.L. (1966). Biology of the laboratory mouse. (New York: Blakiston Division) http://www.informatics.jax.org/greenbook/index.shtml
- Eden, E., Navon, R., Steinfeld, I., Lipson, D., and Yakhini, Z. (2009). GOrilla: a tool for discovery and visualization of enriched GO terms in ranked gene lists. BMC Bioinformatics 10, 48.
- The Arabidopsis Genome Initiative. (2000). Analysis of the genome sequence of the flowering plant Arabidopsis thaliana. Nature 408, 796-815.
- Gregory, S.G., Sekhon, M., Schein, J., Zhao, S., Osoegawa, K., Scott, C.E., Evans, R.S., Burridge, P.W., Cox, T.V., Fox, C.A., Hutton, R.D., Mullenger, I.R., Phillips, K.J., Smith, J., Stalker, J., Threadgold, G.J., Birney, E., Wylie, K., Chinwalla, A., Wallis, J., Hillier, L., Carter, J., Gaige, T., Jaeger, S., Kremitzki, C., Layman, D., Maas, J., McGrane, R., Mead, K., Walker, R., Jones, S., Smith, M., Asano, J., Bosdet, I., Chan, S., Chittaranjan, S., Chiu, R., Fjell, C., Fuhrmann, D., Girn, N., Gray, C., Guin, R., Hsiao, L., Krzywinski, M., Kutsche, R., Lee, S.S., Mathewson, C., McLeavy, C., Messervier, S., Ness, S., Pandoh, P., Prabhu, A.L., Saeedi, P., Smailus, D., Spence, L., Stott, J., Taylor, S., Terpstra, W., Tsai, M., Vardy, J., Wye, N., Yang, G., Shatsman, S., Ayodeji, B., Geer, K., Tsegaye, G., Shvartsbeyn, A., Gebregeorgis, E., Krol, M., Russell, D., Overton, L., Malek, J.A., Holmes, M., Heaney, M., Shetty, J., Feldblyum, T., Nierman, W.C., Catanese, J.J., Hubbard, T., Waterston, R.H., Rogers, J., de Jong, P.J., Fraser, C.M., Marra, M., McPherson, J.D., and Bentley, D.R. (2002). A physical map of the mouse genome. Nature 418, 743-750.
- Benitez, M. and Hejatko, J. Dynamics of cell-fate determination and patterning in the vascular bundles of Arabidopsis thaliana (submitted)

Osnova

- Nástroje **systémové biologie**
  - Analýza **genové ontologie**
  - **Modelování molekulárních regulačních sítí**
- Modelové organismy
  - *Mus musculus*
  - *Arabidopsis thaliana*
- Vybrané **metody molekulární biologie**
  - Příprava transgenních organismů
  - PCR
  - Design a příprava primerů (Dr. Hana Konečná)

Osnova

- Nástroje **systémové biologie**
  - Analýza **genové ontologie**



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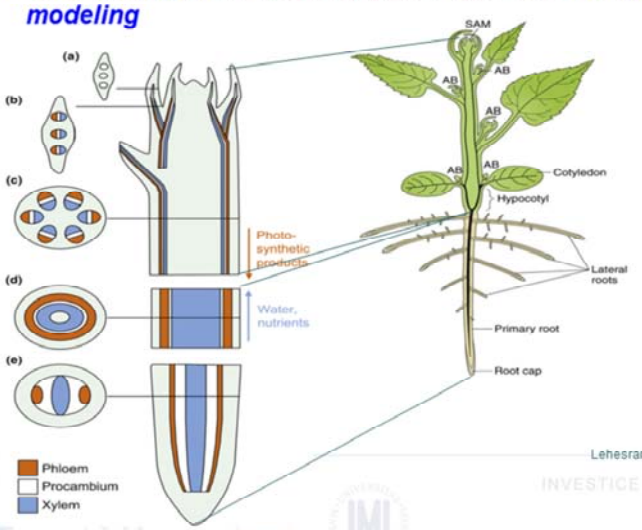
AT1G07795	1:2414285-2414967	WT	MT	OK	0	1,1804	1.79769e+308	1.79769e+308	6.88885e-05	0,00039180	1yes
HRS1	1:4556891-4558708	WT	MT	OK	0	0,696583	1.79769e+308	1.79769e+308	6.61994e-06	4,67708e-05	yes
ATMLO14	1:9227472-9232296	WT	MT	OK	0	0,514609	1.79769e+308	1.79769e+308	9.74219e-05	0,00053505	5yes
NRT1.6	1:9400863-9403789	WT	MT	OK	0	0,877885	1.79769e+308	1.79769e+308	3.2692e-09	3,50131e-07	yes
AT1G27570	1:9575425-9582370	WT	MT	OK	0	2,08291	1.79769e+308	1.79769e+308	9.76039e-06	6.647e-05	yes
AT1G60095	1:22159735-22162419	WT	MT	OK	0	0,685581	1.79769e+308	1.79769e+308	9.95901e-08	9,84992e-07	yes
AT1G03020	1:696206-696515	WT	MT	OK	0	1,78859	1.79769e+308	1.79769e+308	0,00913915	0,0277958	yes
AT1G13609	1:4662720-4663471	WT	MT	OK	0	3,55814	1.79769e+308	1.79769e+308	0,00021583	0,00108079	yes
AT1G21550	1:7553100-7553876	WT	MT	OK	0	0,562868	1.79769e+308	1.79769e+308	0,00115582	0,00471497	yes
AT1G22120	1:7806308-7809632	WT	MT	OK	0	0,617354	1.79769e+308	1.79769e+308	2.48392e-06	1,91089e-05	yes
AT1G31370	1:11238297-11239363	WT	MT	OK	0	1,46254	1.79769e+308	1.79769e+308	4.83523e-05	0,00028514	3yes
APUM10	1:13253397-13255570	WT	MT	OK	0	0,581031	1.79769e+308	1.79769e+308	7.87855e-06	5,46603e-05	yes
AT1G48700	1:18010728-18012871	WT	MT	OK	0	0,566525	1.79769e+308	1.79769e+308	6.53917e-05	0,00037473	6yes
AT1G59077	1:21746209-21833195	WT	MT	OK	0	138,886	1.79769e+308	1.79769e+308	0,00122789	0,00496816	yes
AT1G60050	1:22121549-22123702	WT	MT	OK	0	0,370067	1.79769e+308	1.79769e+308	0,00117953	0,0048001	yes
AT4G15242	4:8706786-8706997	WT	MT	OK	0,00930712	17,9066	10,9096	-4,40523	1.05673e-05	7.13983e-05	yes
AT5G33251	5:12499071-12500433	WT	MT	OK	0,0496375	52,2837	10,0349	-9,8119	0	0	yes
AT4G12520	4:7421055-7421738	WT	MT	OK	0,0195111	15,5516	9,66512	-3,90043	9.60217e-05	0,000528904	yes
AT1G60020	1:22100651-22100276	WT	MT	OK	0,0118377	7,18823	9,24511	-7,50382	5.19504e-14	1.4088e-12	yes
AT5G15360	5:4987235-4989182	WT	MT	OK	0,0983273	56,4834	9,1587	-10,4392	0	0	yes

Excample of an output of transcriptional profiling study using Illumina sequencing performed in our lab. Shown is just a tiny fragment of the complete list, copmprising about 7K genes revealing differential expression in the studied mutant.

Molecular Regulatory Networks Modeling

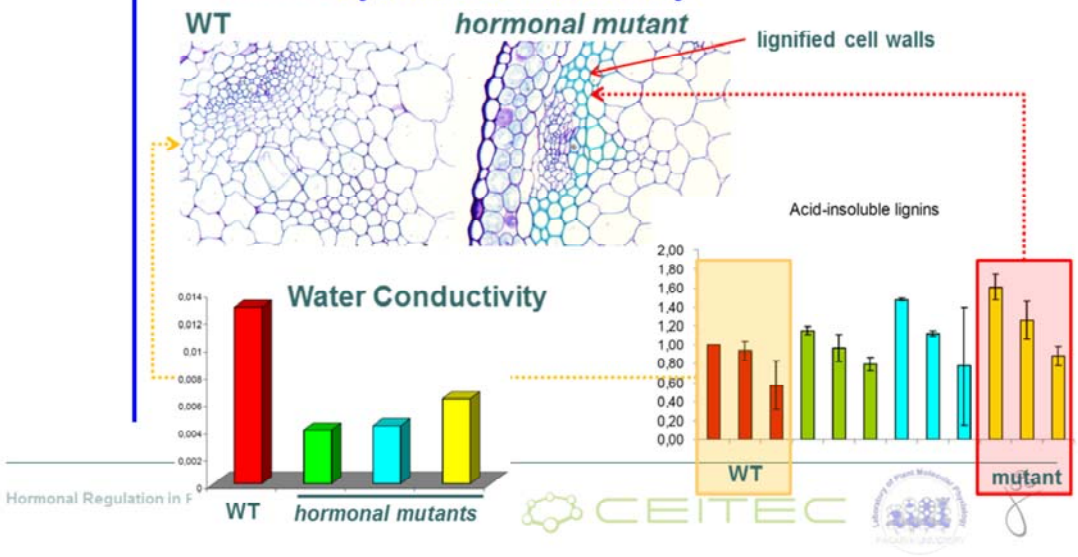
- ***Vascular tissue*** as a developmental model for ***GO analysis*** and ***MRN modeling***



Lehesranta etal., *Trends in Plant Sci* (2010)

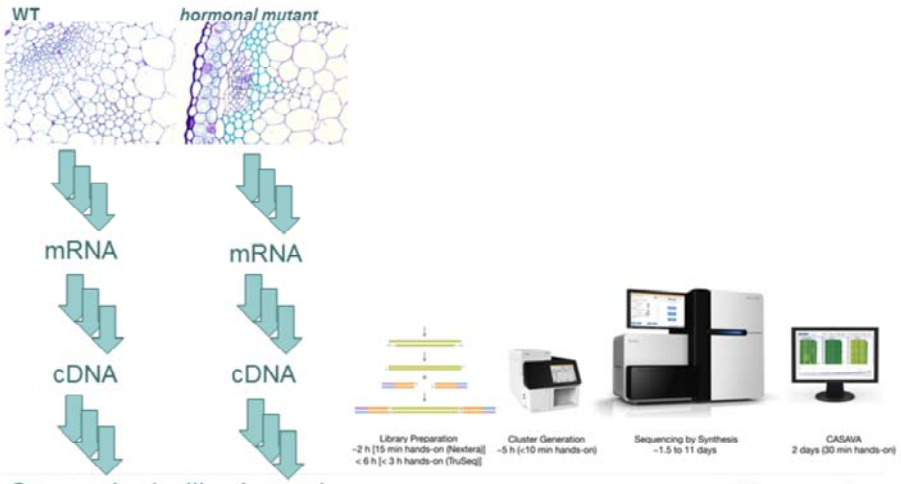
Hormonal Control Over Vascular Tissue Development

- Plant **Hormones Regulate Lignin Deposition** in Plant Cell Walls and **Xylem Water Conductivity**

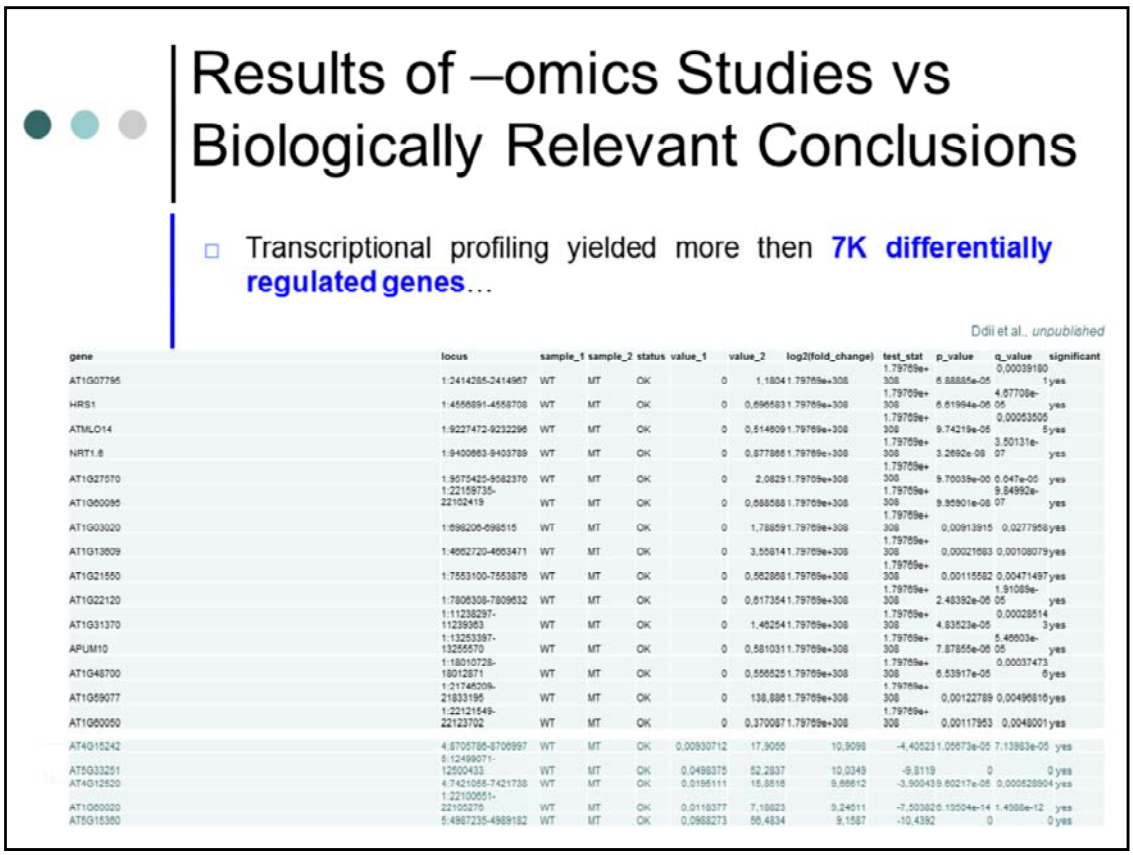


Hormonal Control Over Vascular Tissue Development

- ***Transcriptional profiling*** via ***RNA sequencing***



Sequencing by Illumina and
number of transcripts determination



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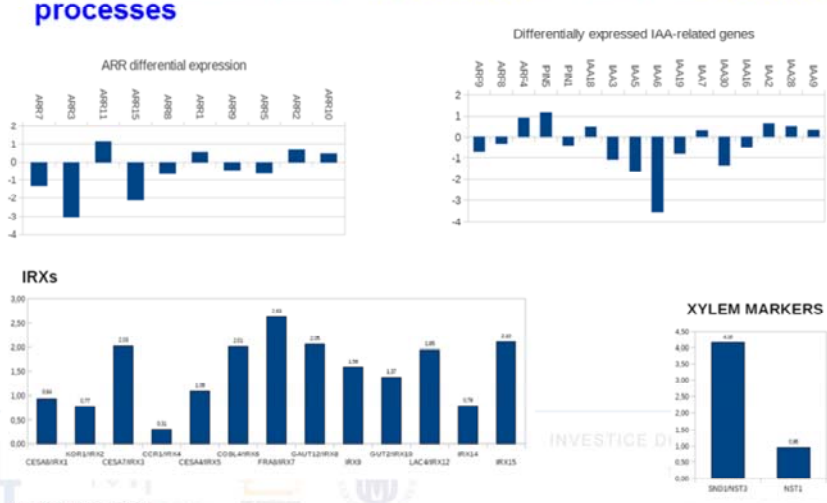
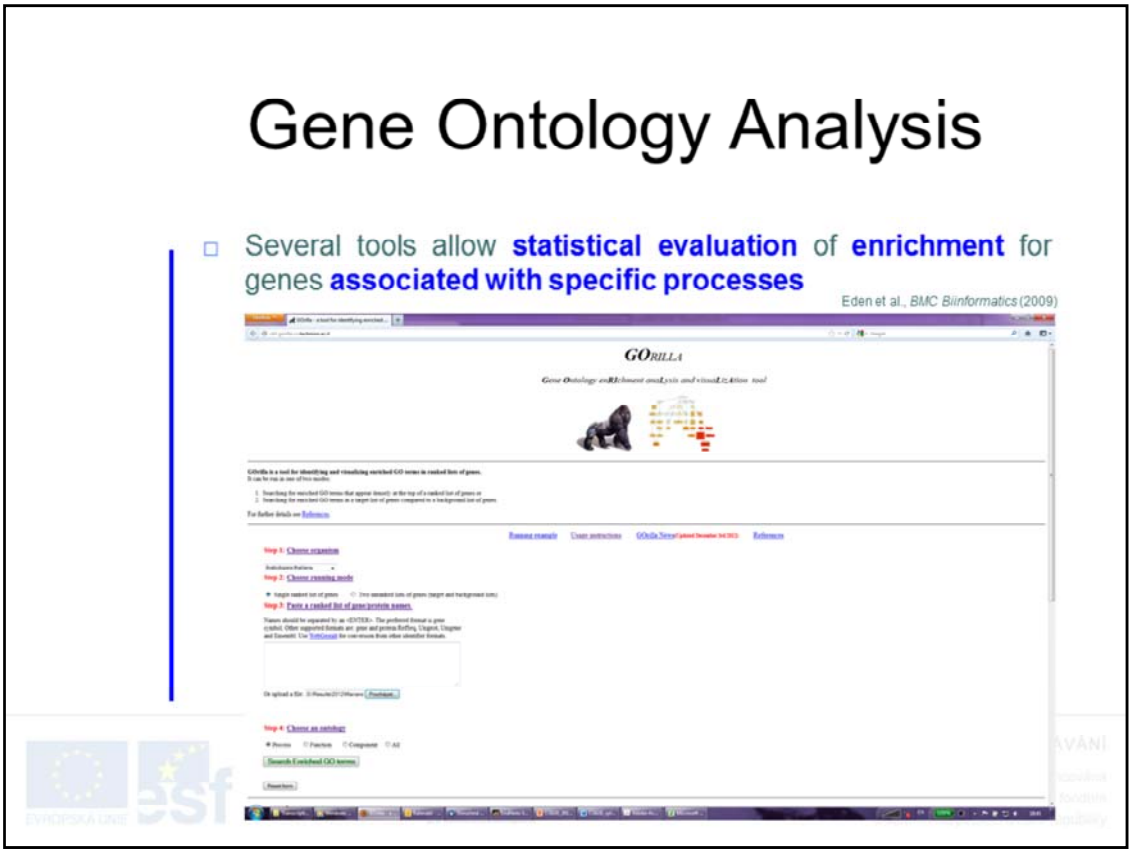
Excample of an output of transcriptional profiling study using Illumina sequencing performed in our lab. Shown is just a tiny fragment of the complete list, copmprising about 7K genes revealing differential expression in the studied mutant.

Gene Ontology Analysis

- One of the possible approaches is to study ***gene ontology***, i.e. previously demonstrated **association** of genes to **biological processes**



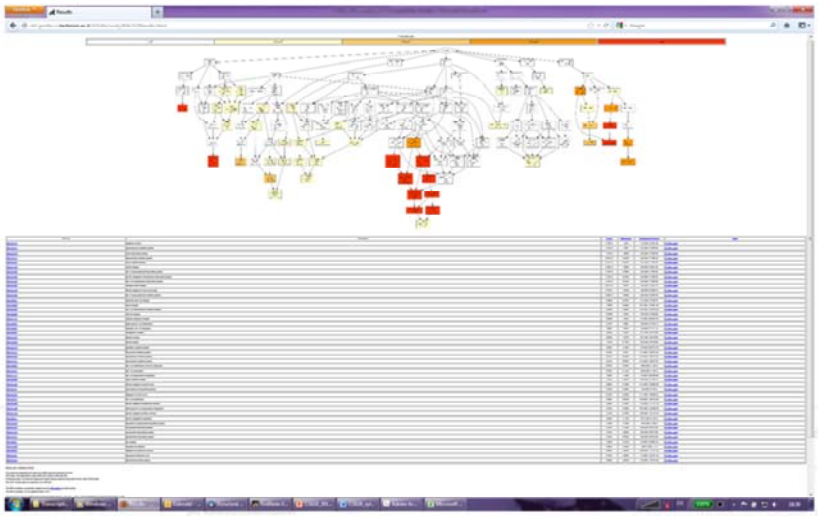
Ddii et al., *unpublished*



One of such recent and very useful tools is Gorilla software, freely available at http://cbl-gorilla.cs.technion.ac.il/.

Gene Ontology Analysis

- Several tools allow **statistical evaluation** of **enrichment** for genes **associated with specific processes**



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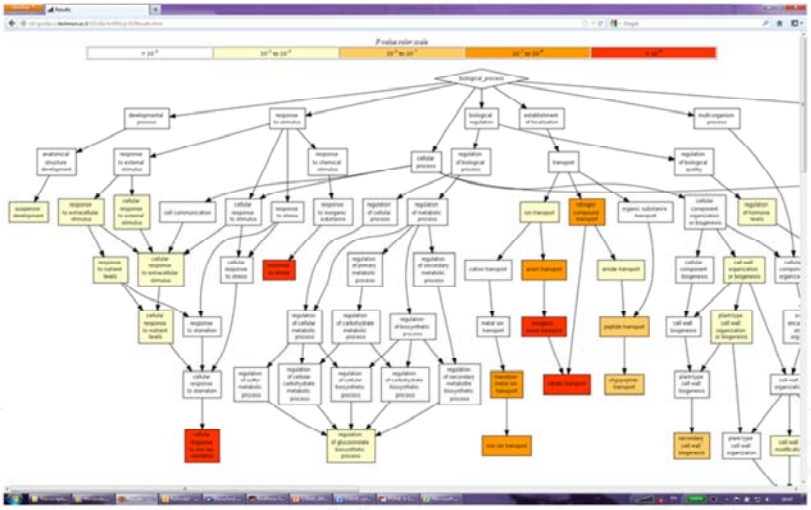

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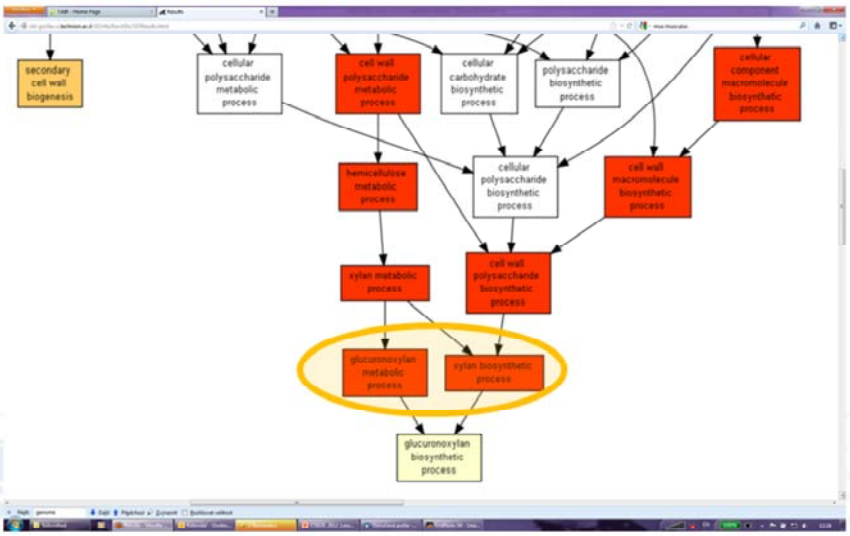

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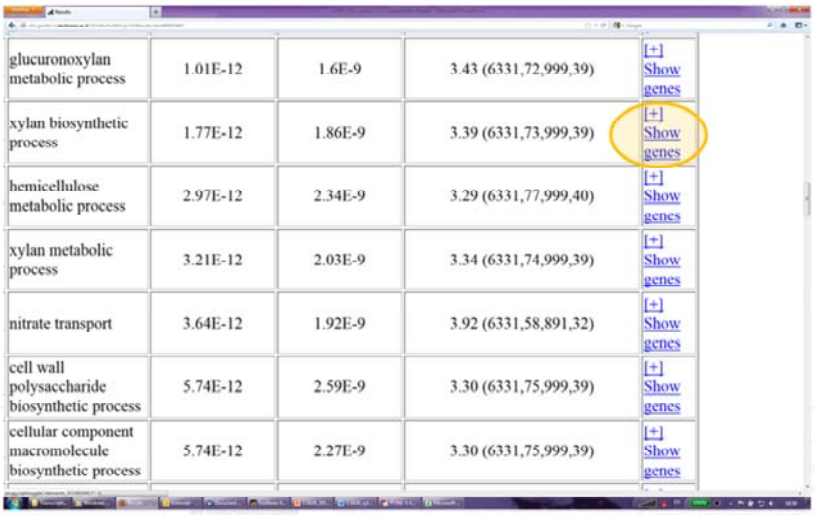
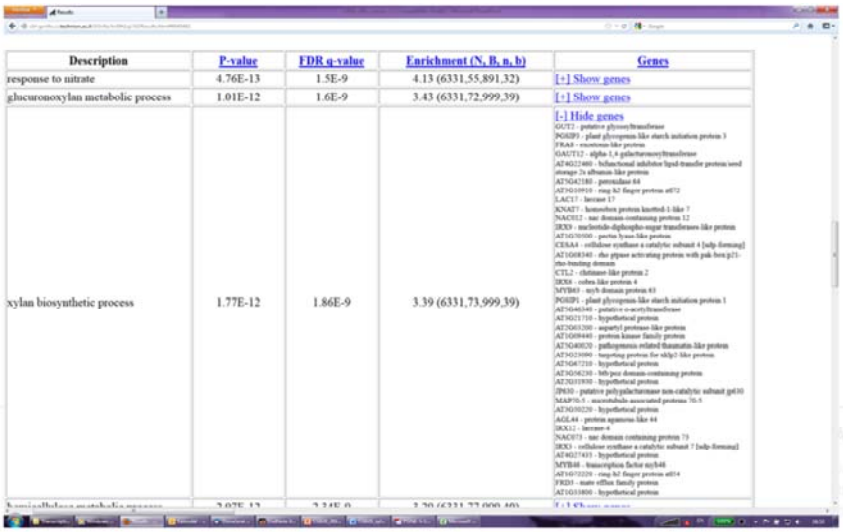


glucuronoxylan metabolic process	1.01E-12	1.6E-9	3.43 (6331,72,999,39)	[+] Show genes
xylan biosynthetic process	1.77E-12	1.86E-9	3.39 (6331,73,999,39)	[+] Show genes
hemicellulose metabolic process	2.97E-12	2.34E-9	3.29 (6331,77,999,40)	[+] Show genes
xylan metabolic process	3.21E-12	2.03E-9	3.34 (6331,74,999,39)	[+] Show genes
nitrate transport	3.64E-12	1.92E-9	3.92 (6331,58,891,32)	[+] Show genes
cell wall polysaccharide biosynthetic process	5.74E-12	2.59E-9	3.30 (6331,75,999,39)	[+] Show genes
cellular component macromolecule biosynthetic process	5.74E-12	2.27E-9	3.30 (6331,75,999,39)	[+] Show genes

Gene Ontology Analysis

- Several tools allow **statistical evaluation** of **enrichment** for genes **associated with specific processes**



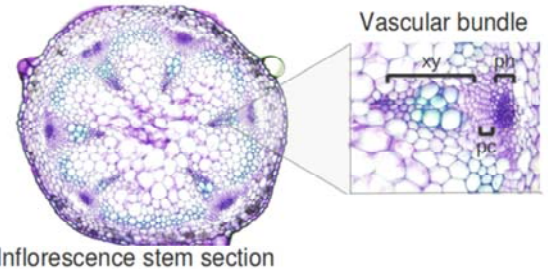
Description	P-value	FDR q-value	Enrichment (N, B, n, b)	Genes
response to nitrate	4.76E-13	1.5E-9	4.13 (6331,55,891,32)	[+] Show genes
glucuronoxylan metabolic process	1.01E-12	1.6E-9	3.43 (6331,72,999,39)	[+] Show genes
xylan biosynthetic process	1.77E-12	1.86E-9	3.39 (6331,73,999,39)	[-] Hide genes GUT2 - putative glycosyltransferase PGSIP1 - plant glycogenin-like starch initiation protein 3 FRA8 - exostosin-like protein GAUT12 - alpha-1,4-galacturonosyltransferase AT4G22480 - bifunctional inhibitor/lipid-transfer protein/seed storage 2s albumin-like protein AT5G42180 - peroxidase 64 AT2G30910 - ring/u2 finger protein e6f32 LAC17 - laccase 17 KNAT7 - homeobox protein knotted-1-like 7 NAC012 - nac domain-containing protein 12 IRX9 - nucleotide-diphospho-sugar transferases like protein AT1G70500 - pectin lyase-like protein CESA4 - cellulose synthase a catalytic subunit 4 [udp-forming] AT1G08540 - rho gtpase activating protein with pak-box/p21-rho-binding domain CTL2 - chitinase-like protein 2 IRX8 - cobra-like protein 8 MYB83 - myb domain protein 83 PGSIP1 - plant glycogenin-like starch initiation protein 1 AT5G46340 - putative o-acetyltransferase AT3G21710 - hypothetical protein AT2G03200 - aspartyl protease-like protein AT1G09440 - protein kinase family protein AT5G40020 - pathogenesis-related thaumatin-like protein AT4G21690 - targeting protein for xklp2-like protein AT5G47210 - hypothetical protein AT3G56230 - btb/poz domain-containing protein AT2G33830 - hypothetical protein PMI30 - putative polygalacturonase non-catalytic subunit pg030 MAP70-5 - microtubule-associated proteins 70-5 AT3G10220 - hypothetical protein AGL44 - protein agamous-like 44 IRX12 - laccase-4 NAC073 - nac domain containing protein 73 IRX3 - cellulose synthase a catalytic subunit 7 [udp-forming] AT4G27435 - hypothetical protein MYB46 - transcription factor myb46 AT1G72220 - ring/u2 finger protein e6f14 FRD3 - mate efflux family protein AT1G31800 - hypothetical protein
hemicellulose metabolic process	2.07E-12	2.24E-9	3.29 (6331,77,999,40)	[+] Show genes

Osnova

- Nástroje **systémové biologie**
  - Analýza **genové ontologie**
  - **Modelování molekulárních regulačních sítí**

Molecular Regulatory Networks Modeling

- ***Vascular tissue*** as a developmental model for ***MRN modeling***



Inflorescence stem section

Benitez and Hejatko, *submitted*

Molecular Regulatory Networks Modeling

- **Literature search** for published data and creating small database

Interaction	Evidence	References
A-ARRs –| CK signaling	Double and higher order type-A ARR mutants show increased sensitivity to CK.	[27]
	Spatial patterns of A-type ARR gene expression and CK response are consistent with partially redundant function of these genes in CK signaling.	[27]
	A-type ARRs decreases B-type ARR6-LUC.	[13]
	Note: In certain contexts, however, some A-ARRs appear to have effects antagonistic to other A-ARRs.	[27]
AHP6 –| AHP	ahp6 partially recovers the mutant phenotype of the CK receptor WOL.	[9]
	Using an in vitro phosphotransfer system, it was shown that, unlike the AHPs, native AHP6 was unable to accept a phosphoryl group. Nevertheless, AHP6 is able to inhibit phosphotransfer from other AHPs to ARRs.	[9]

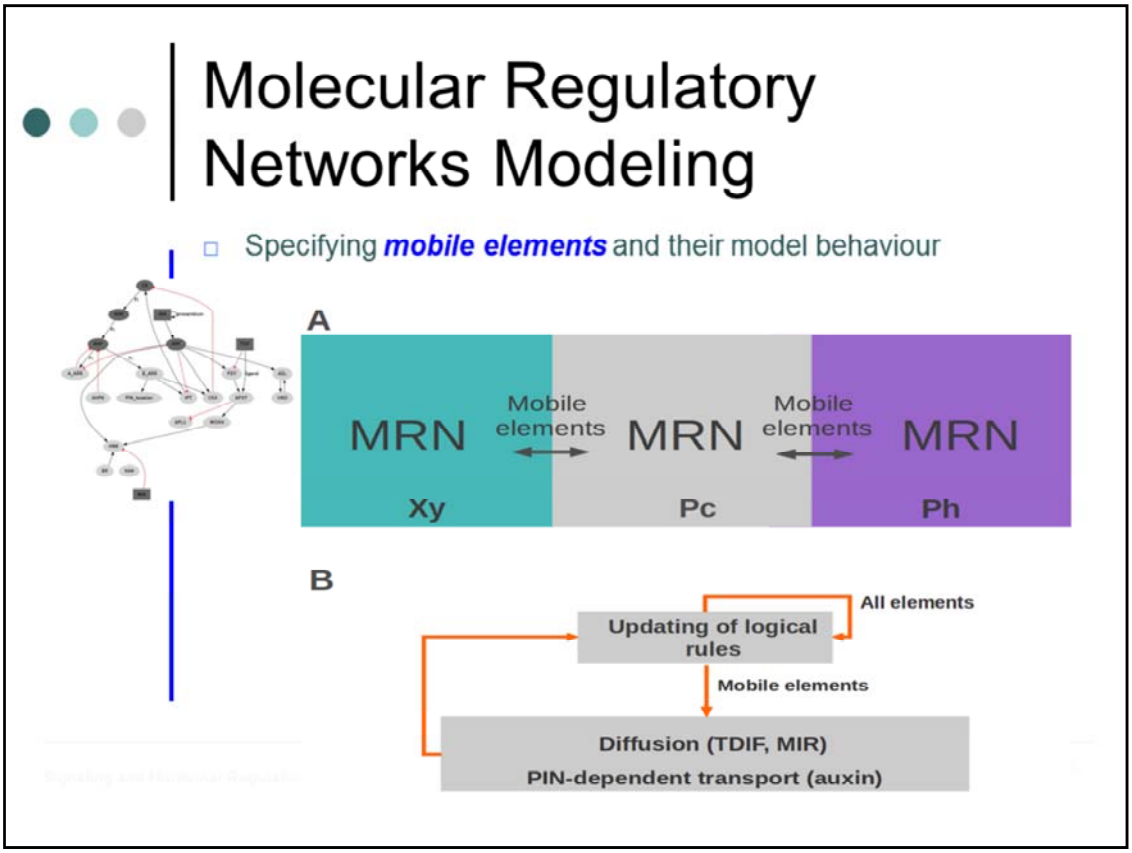
Benitez and Hejatko, *submitted*

Molecular Regulatory Networks Modeling

- Formulating ***logical rules*** defining the ***model dynamics***

Network node	Dynamical rule
CK	2 If ipt=1 and ckx=0 1 If ipt=1 and ckx=1 0 else
CKX	1 If barr>0 or arf=2 0 else
AHKs	ahk=ck
AHPs	2 If ahk=2 and ahp6=0 and aarr=0 1 If ahk=2 and (ahp6+aarr<2) 1 If ahk=1 and ahp6<1 0 else
B-Type ARRs	1 If ahp>0 0 else
A-Type ARRs	1 If arf<2 and ahp>0 0 else

Benitez and Hejatko, *submitted*



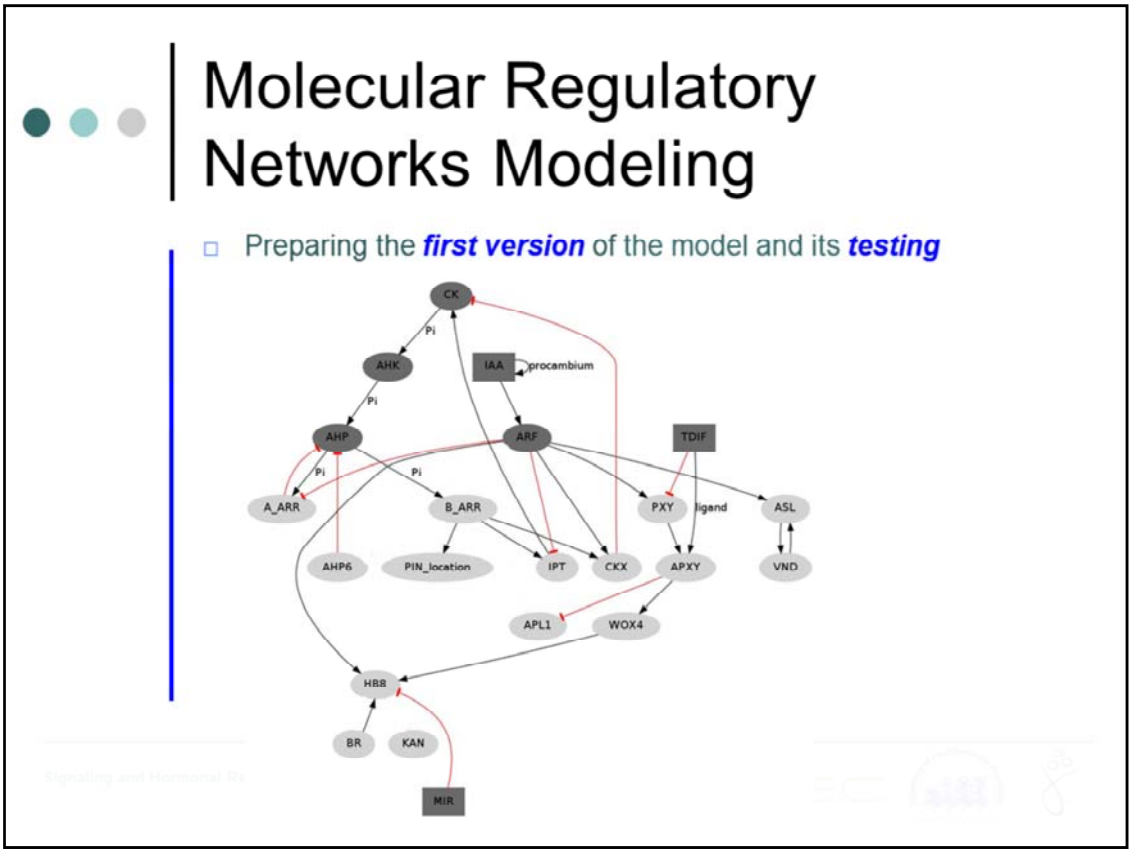
According to experimental evidence for the system under study, the hormone IAA, the peptide TDIF, and the microRNA MIR165/6 are able to move among the cells. In the case of TDIF and MIR165/6, the mobility is defined as diffusion and is given by the following equation:

$$g(t+1)T[i]= H(g(t)[i]+ D\ (g(t)[i+1]+g(t)[i-1] - N(g(t)[i]))-b) \quad (2),$$

where $g(t)T[i]$ is the total amount of TDIF or MIR165 in cell (i). D is a parameter that determines the proportion of g that can move from any cell to neighboring ones and is correlated to the diffusion rate of g. b is a constant corresponding to a degradation term. H is a step function that converts the continuous values of g into a discrete variable that may attain values of 0, 1 or 2. N stands for the number of neighbors in each cell. Boundary conditions are zero-flux. In the case of IAA, the mobility is defined as active transport dependent on the radial localization of the PIN efflux transporters and is defined by the equation:

$$iaa(t+1)T[i]=Hiaa(iaa(t)[i]+Diaa(pin(t)[i+1])(iaa(t)[i+1])+Diaa(pin(t)[i-1])(iaa(t)[i-1])-N(Diaa)(pin(t)[i])(iaa(t)[i])-biaa) \quad (3),$$

where *Diaa* is a parameter that determines the proportion of IAA that can be transported among cells. The transport depends on the presence of IAA and PIN in the cells and *biaa* corresponds to a degradation term. As in equation 2, H is a step function that converts the continuous values to discrete ones and N stands for the number of neighbors in each cell. Boundary conditions for IAA motion are also zero-flux.



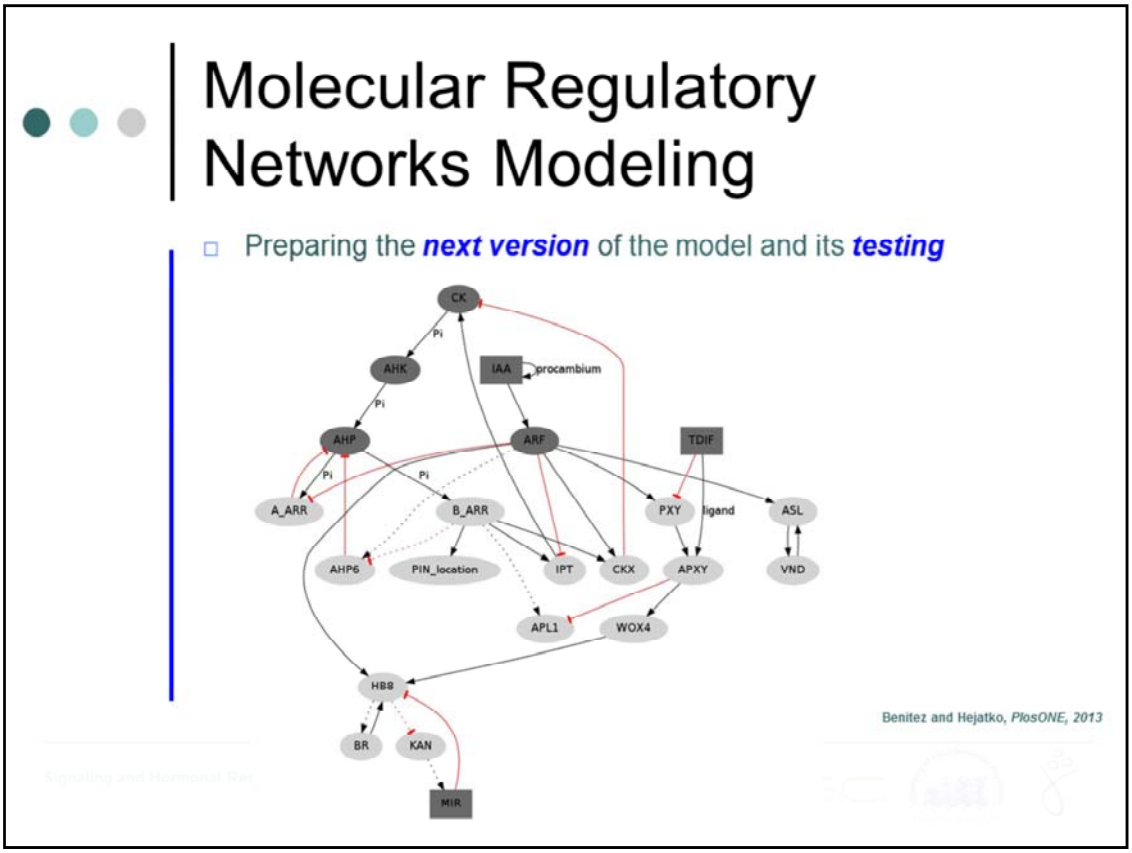
The proposed model considers data that we identified and evaluated through an extensive search (up to January 2012). It takes into account molecular interactions, hormonal and expression patterns, and cell-to-cell communication processes that have been reported to affect vascular patterning in the bundles of Arabidopsis. The model components and interactions are graphically presented in the figure above. In the network model, nodes stand for molecular elements regulating one another's activities. Most of the nodes can take only 1 or 0 values (light gray nodes in the figure), corresponding to "present" or "not present," respectively. Since the formation of gradients of hormones and diffusible elements may have important consequences in pattern formation, mobile elements TDIF and MIR, as well as members of the CK and IAA signaling systems, can take 0, 1 or 2 values (dark gray nodes in the figure above) Benitez and Hejatko, submitted.

Molecular Regulatory Networks Modeling

- Specifying of missing interactions via ***informed predictions***

Interaction	Evidence	References
CK → PIN7 radial localization	Predicted interaction (could be direct or indirect)	
	Informed by the following data:	
	During the specification of root vascular cells in Arabidopsis thaliana, CK regulates the radial localization of PIN7.	[18]
	Expression of PIN7:GFP and PIN7::GUS is upregulated by CK with no significant influence of ethylene.	[18,20]
	In the root, CK signaling is required for the CK regulation of PIN1, PIN3, and PIN7. Their expression is altered in wol, cre1, ahk3 and ahp6 mutants.	[19]
CK→ APL	Predicted interaction (could be direct or indirect)	
	Consistent with the fact that APL overexpression prevents or delays xylem cell differentiation, as does CKs.	[21]
	Partially supported by microarray data and phloem-specific expression patterns of CK response factors.	(TAIR, ExpressionSet:1005823559, [22])

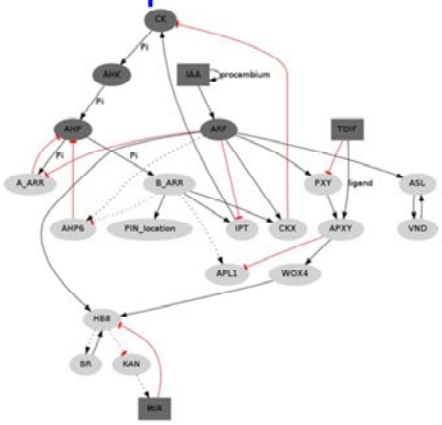
Signaling and Hormon:

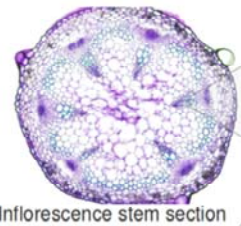


In comparison to the model shown on slide 21, the final version of the model contains the predicted interactions (dashed lines).

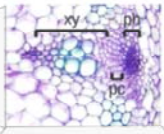
Molecular Regulatory Networks Modeling

- ***Good model*** should be able to ***simulate reality***





Inflorescence stem section



Xylem (xy)	Procambium (pc)	Phloem (ph)
VND ASL	WOX4	APL

Benitez and Hejatko, *PlosONE, 2013*

Molecular Regulatory Networks Modeling

- Formulating ***equations*** describing the ***relationships*** in the model

logical rule function

state in the time *t*

***Static* nodes:** $g_n(t+1)=F_n(g_{n1}(t),g_{n2}(t),\ldots, g_{nk}(t))$

state in the time *t+1*

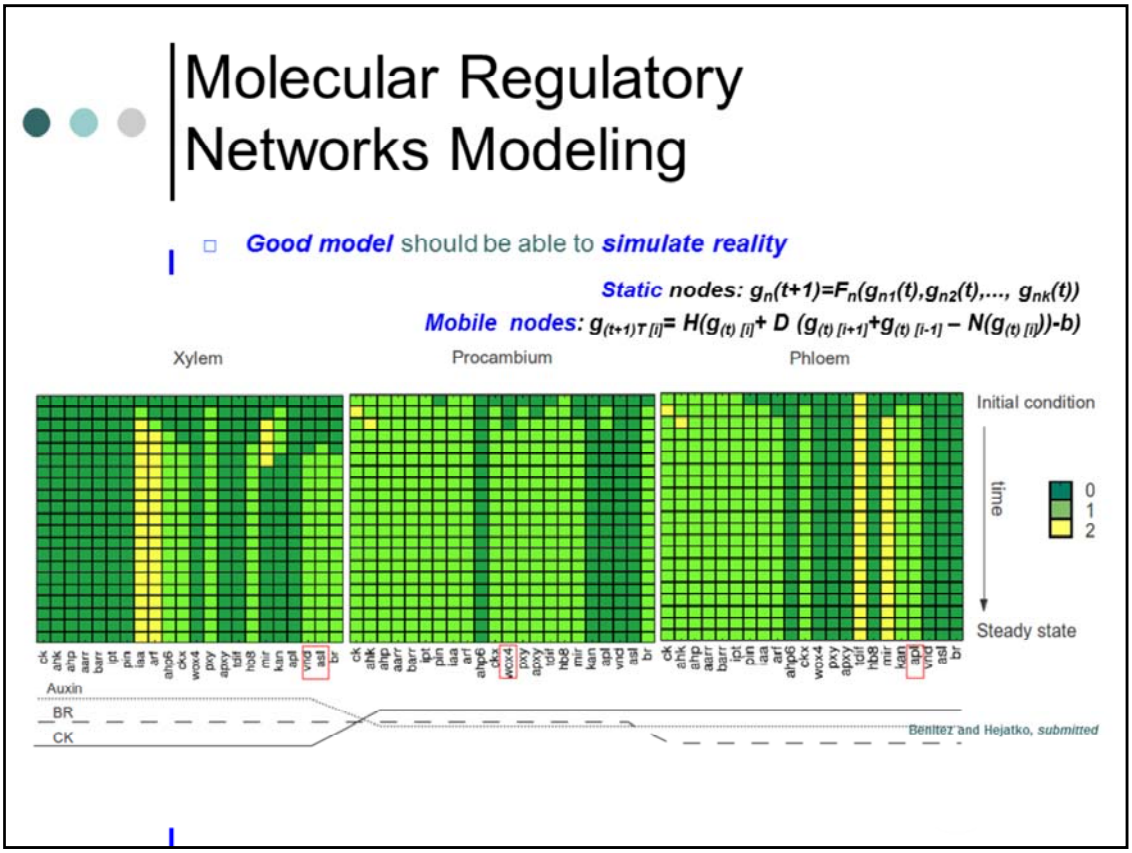
Amount if TDIF or MIR165 in cell *i*

***Mobile* nodes:** $g_{(t+1)T\,[i]}= H(g_{(t)\,[i]}+ D\,(g_{(t)\,[i+1]}+g_{(t)\,[i-1]} - N(g_{(t)\,[i]}))-b)$

state in the time *t+1*

constant corresponding to a degradation term

proportion of movable element



The initial conditions specify the initial state of some of the network elements (figure above) and are the following :

I) In the procambial position (central compartment), CK is initially available and there is an initial and sustained IAA input or self-upregulation. This condition is supported by several lines of evidence. Also *HB8*, a marker of early vascular development that has been found in preprocambial cells, is assumed to be initially present at this position. These conditions are not fixed, however. After the initial configuration, all the members of the CK and IAA signaling pathways, as well as *HB8*, can change their states according to the logical rules.

II) In the xylem and phloem positions, it is assumed that no element is initially active except for the CK signaling pathway and TDIF, both in the phloem position.The level of expression for a given node is represented by a discrete variable *g* and its value at a time *t+1* depends on the state of other components of the network (*g1*, *g2*, ..., *gN*) at a previous time unit. The state of every gene *g* therefore changes according to:

$gn(t+1)=Fn(gn1(t),gn2(t),\ldots, gnk(t))$ (1).

In this equation, *gn1, gn2,…, gnk* are the regulators of gene *gn* and *Fn* is a discrete function known as a logical rule (logical rules are grounded in available experimental data, for example see slide 20). Given the logical rules, it is possible to follow the dynamics of the network for any given initial configuration of the nodes expression state. One of the most important traits of dynamic models is the existence of steady states in which the entire network enters into a selfsustained configuration of the nodes state. It is thought that in developmental systems such self-sustained states correspond to particular cell types.

According to experimental evidence for the system under study, the hormone IAA, the peptide TDIF, and the microRNA MIR165/6 are able to move among the cells. In the case of TDIF and MIR165/6, the mobility is defined as diffusion and is given by the following equation:

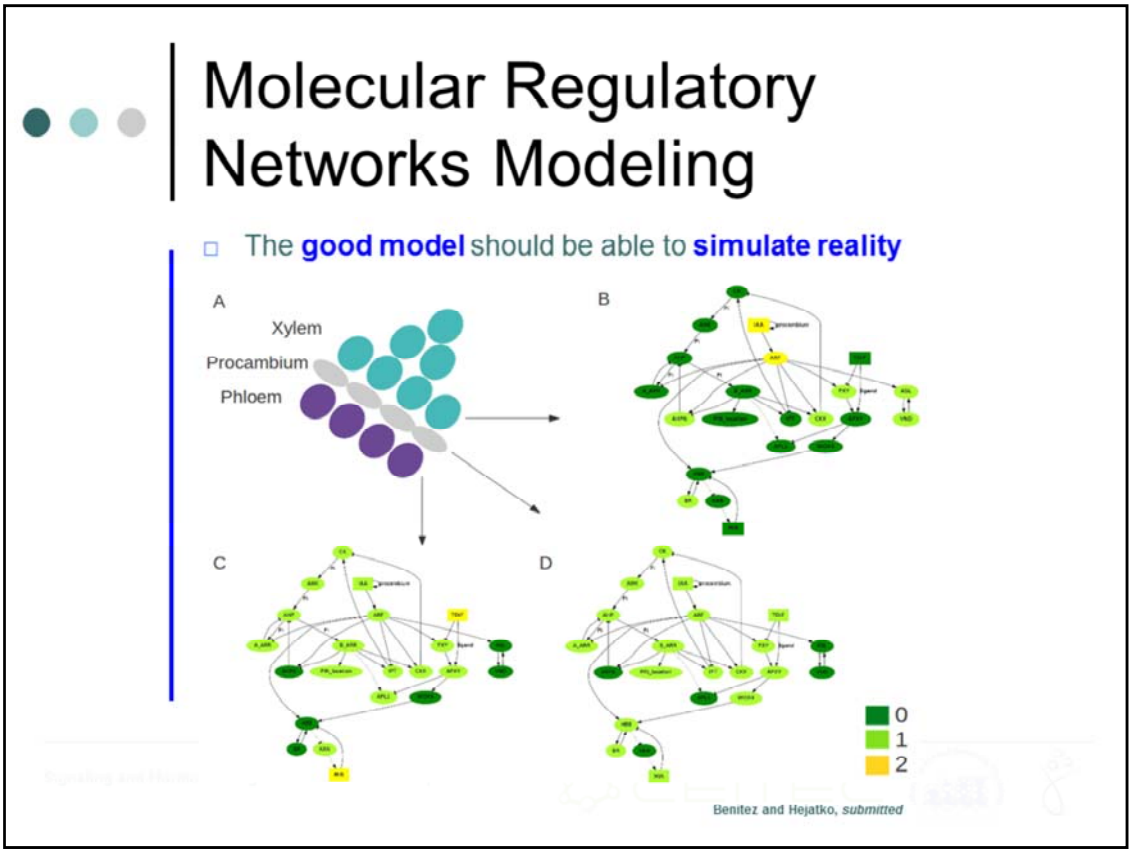
$g(t+1)T[i]= H(g(t)[i]+ D(g(t)[i+1]+g(t)[i-1] – N(g(t)[i]))-b)$ (2),

where *g(t)T[i]* is the total amount of TDIF or MIR165 in cell *(i)*. *D* is a parameter that determines the proportion of *g* that can move from any cell to neighboring ones and is correlated to the diffusion rate of *g*. *b* is a constant corresponding to a degradation term. *H* is a step function that converts the continuous values of *g* into a discrete variable that may attain values of 0, 1 or 2. *N* stands for the number of neighbors in each cell. Boundary conditions are zero-flux. In the case of IAA, the mobility is defined as active transport dependent on the radial localization of the PIN efflux transporters and is defined by the equation:

$iaa(t+1)T[i]=Hiaa(iaa(t)[i]+Diaa(pin(t)[i+1])(iaa(t)[i+1])+Diaa(pin(t)[i-1])(iaa(t)[i-1])-N(Diaa)(pin(t)[i])(iaa(t)[i])-biaa)$ (3),

where *Diaa* is a parameter that determines the proportion of IAA that can be transported among cells. The transport depends on the presence of IAA and PIN in the cells and *biaa* corresponds to a degradation term. As in equation 2, *H* is a step function that converts the continuous values to discrete ones and *N* stands for the number of neighbors in each cell. Boundary conditions for IAA motion are also zero-flux.

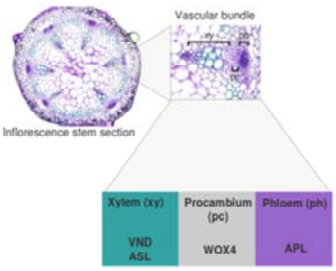
Using the logical rules, equations 1–3, and a broad range of parameter values (not shown here), it is possible fully to reproduce the results and analyses reported in the following sections (see the figure above for the simulation time course).

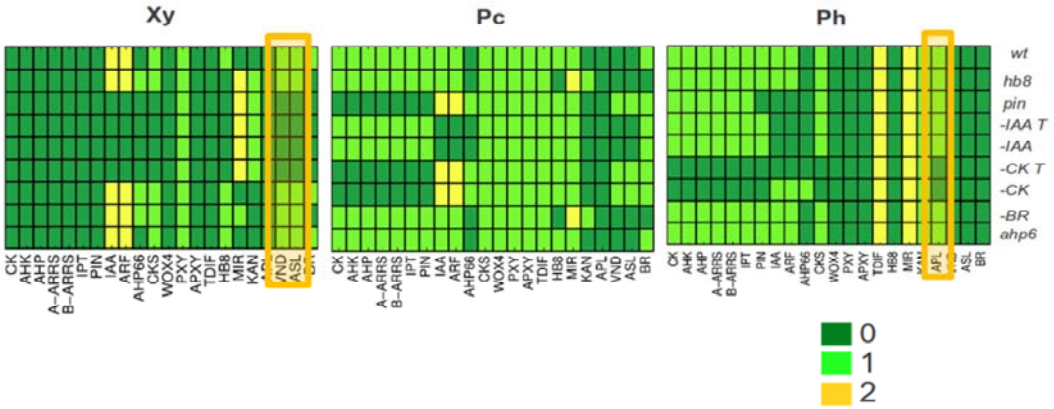


Another representation of the distinct expression profiles in the individual vascular bundle compartments (phloem, procambium and xylem).

Molecular Regulatory Networks Modeling

- Simulation of ***mutants***





Osnova

- Nástroje **systémové biologie**
  - Analýza **genové ontologie**
  - **Modelování molekulárních regulačních sítí**
- Modelové organismy
  - *Mus musculus*

Mus musculus

myš domácí, house mouse

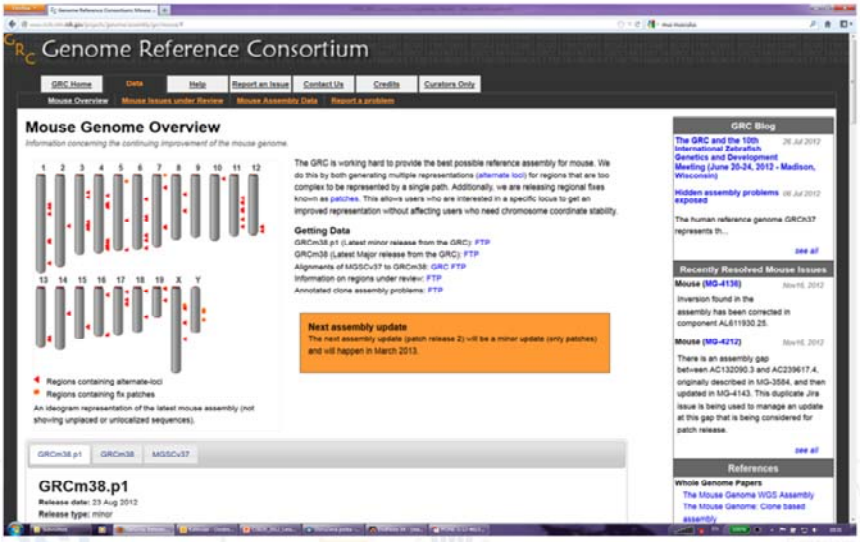
- malé nároky na chovnou plochu
- relativně velké množství mláďat (3-14, v průměru 6-8)
- velikost genomu se blíží velikosti genomu člověka (cca 3000 Mbp), podobně jako počet genů (cca 24K)
- 20 chromozomů (19+1)
- vhodná pro široké spektrum fyziologických experimentů (anatomicky i fyziologicky podobná člověku)
- možno poměrně snadno získávat K.O. mutanty i transgenní linie

More info about mouse at
http://www.informatics.jax.org/greenbook/index.shtml.

Mus musculus

myš domácí, house mouse

- Genom známý od roku 2002 (http://www.ncbi.nlm.nih.gov/projects/genome/assembly/grc/mouse/)



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Arabidopsis thaliana

huseníček polní, mouse-ear cress

- malé nároky na kultivační plochu
- velké množství semen (20.000/rostlinu a více)
- malý a kompaktní genom, (125 MBp, cca 25.000 genů, prům. velikost 3 kb)
- 5 chromozomů
- vhodná pro široké spektrum fyziologických experimentů
- velká přirozená variabilita (cca 750 ekotypů (Nottingham Arabidopsis Seed Stock Centre))

Columbia 0

Landsberg 0

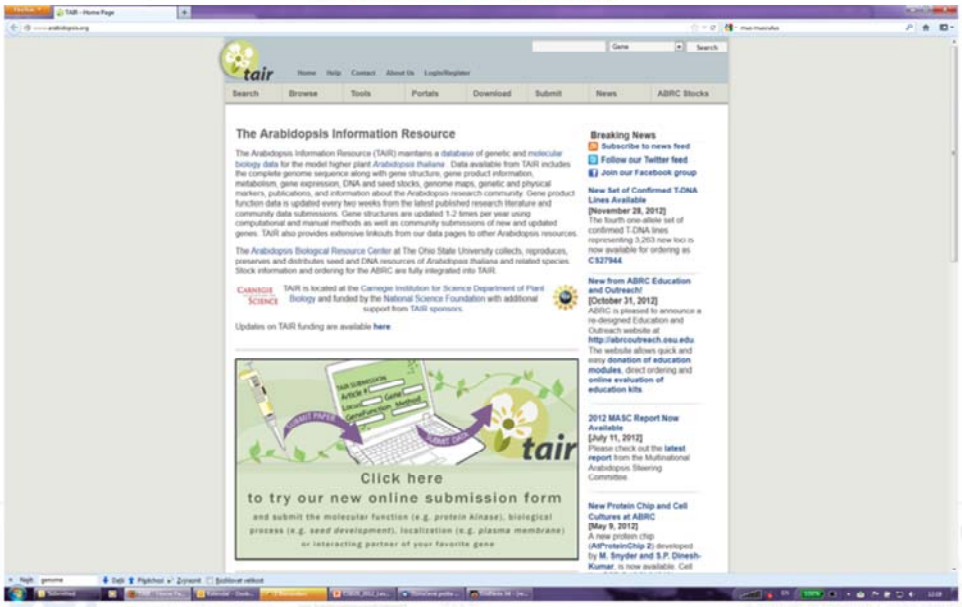
Wassilewskija 0

http://seeds.nottingham.ac.uk/

Arabidopsis thaliana

huseníček polní, mouse-ear cress

- Genom známý od roku 2000 (http://www.arabidopsis.org/)



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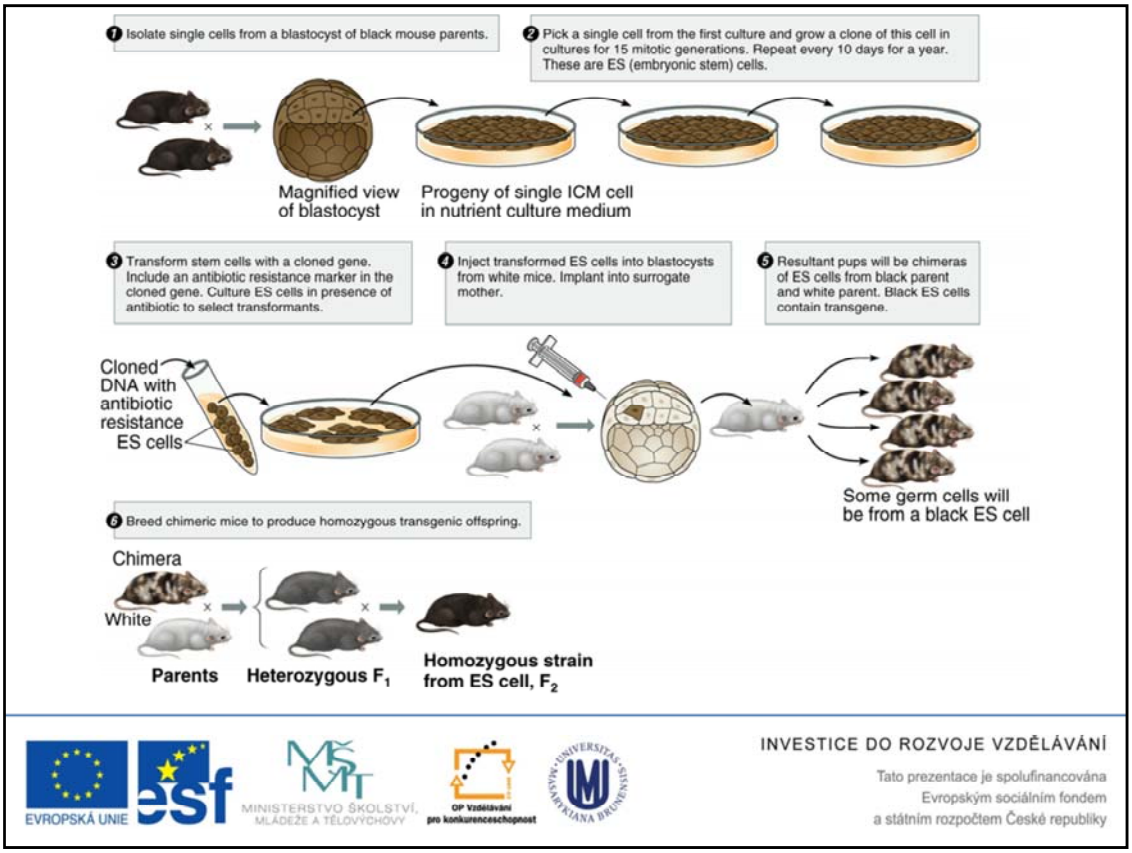
  - Příprava transgenních organismů



Individula ICM cells of the embryo could be isolated and later re-introgressed into the new embryo. These ICM cells are called **embryonic stem (ES) cells**. It is very important technique that allows production of transgenic mice.

The isolated ES cells are transformed via foreign DNA construct and it is injected within the embryo. The transformed cell becomes a part of the embryo and might result into formation of different tissue types, among them the spermatogonia or oogonia. i.e. the tissue that provides progenitor for sperm or egg cells in the resulting chimera. Thus, the progeny of those chimeras will inherit the modified cell with certain probability and these individuals will carry the transgene in every cell of their body. Thus, the trangenic mice will be produced.

This is very important mainly with regard of the knockout mutant (K.O.) production. In the modified ES, the genes might be specifically eliminated via DNA recombination. In that way, function of many of the mice genes was identified.

E.g. the gene *NODAL* is expressed in the anterior portion of the primitive streak that is equivalent to the Hensen's node. *nodal/nodal* embryos are lethal, they do not undergo gastrulation and from almost no mesoderm.

Transformace *Arabidopsis* prostřednictvím *Agrobacteria tumefaciens*

Crown gall of raspberry caused by *Agrobacterium tumefaciens*.

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UNIVERSITAS MASARYKIANA BRUNENSIS
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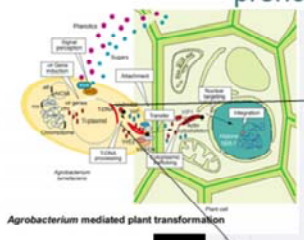
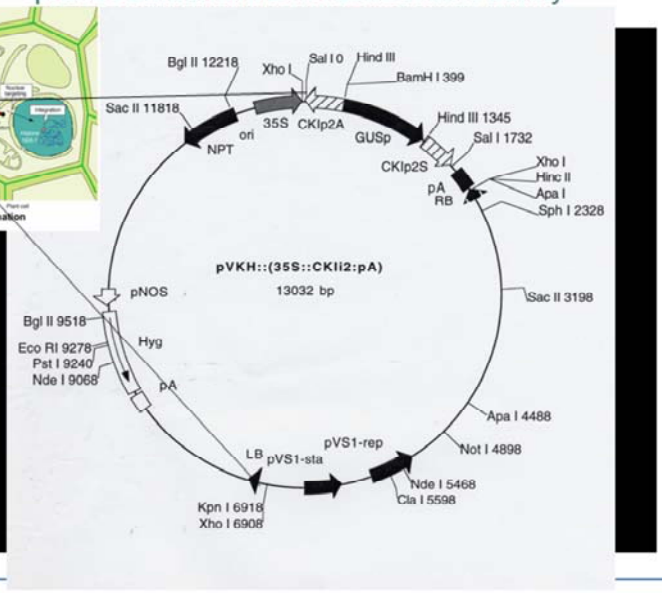
Transformace *Arabidopsis* prostřednictvím *Agrobacteria tumefaciens*

přenos bakteriální DNA do rostlinné buňky



Agrobacterium mediated plant transformation



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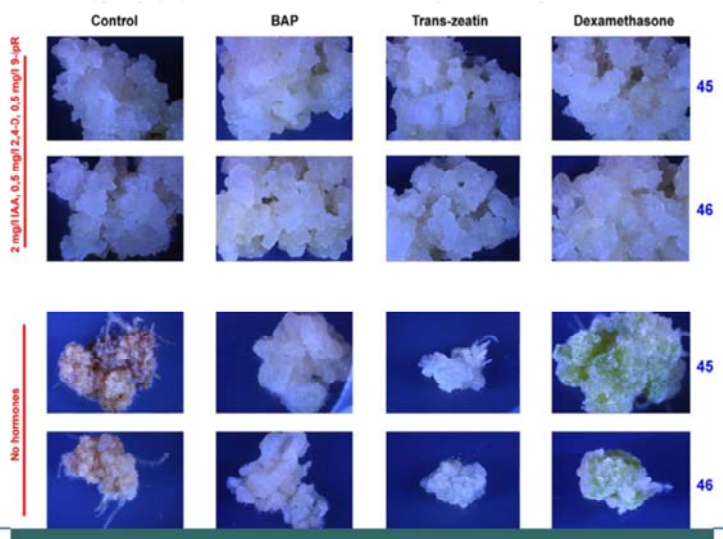
Transformace kokultivací listových disků

ÁVÁNÍ
ncována
i fondem
a státním rozpočtem České republiky

Transformace kokultivací kalusů



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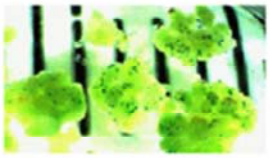
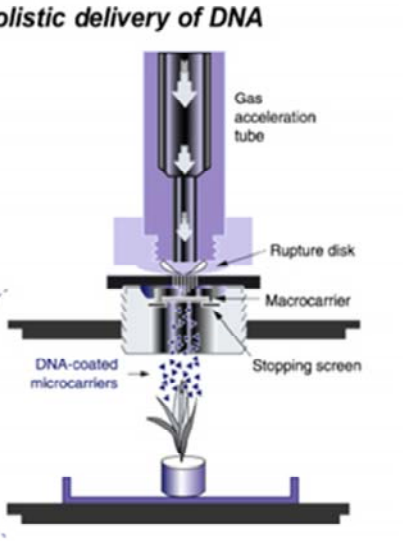
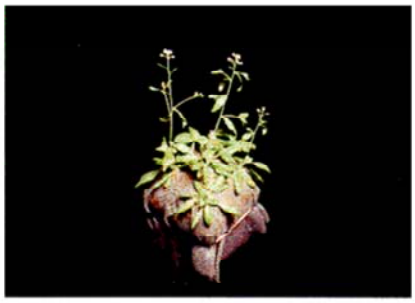
Transformace „nastřelováním“ DNA





Transformace květenství



When plants have primary bolts 5-15 cm they are ready to infiltrate. Clipping of primary bolts is not necessary.

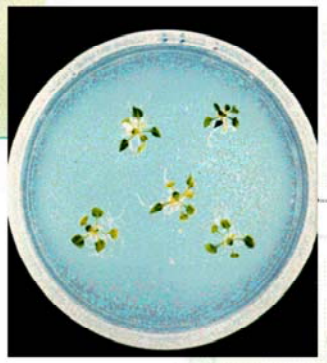
After infiltration, pots are placed on their sides to allow for drainage and are covered with plastic wrap. Plants are returned, in this state, to the growth chamber for 24 hours. After 24 hours, they are turned upright into a fresh flat.

http://www.bch.msu.edu/pamgreen/green.htm

Plants are allowed to grow to maturity. They are staked to avoid seed loss and facilitate plant harvesting.
NOTE: Leaves degenerate within 2 weeks of infiltration. This is normal and does not affect seed set.

Transformace květenství

Sterilize seed in bleach solution.



http://www.bch.msu.edu/pamgreen/green.htm

Plant transformed seedlings in soil.

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PCR

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  - Design a příprava primerů (Dr. Hana Konečná)

Shrnutí

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Diskuse

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