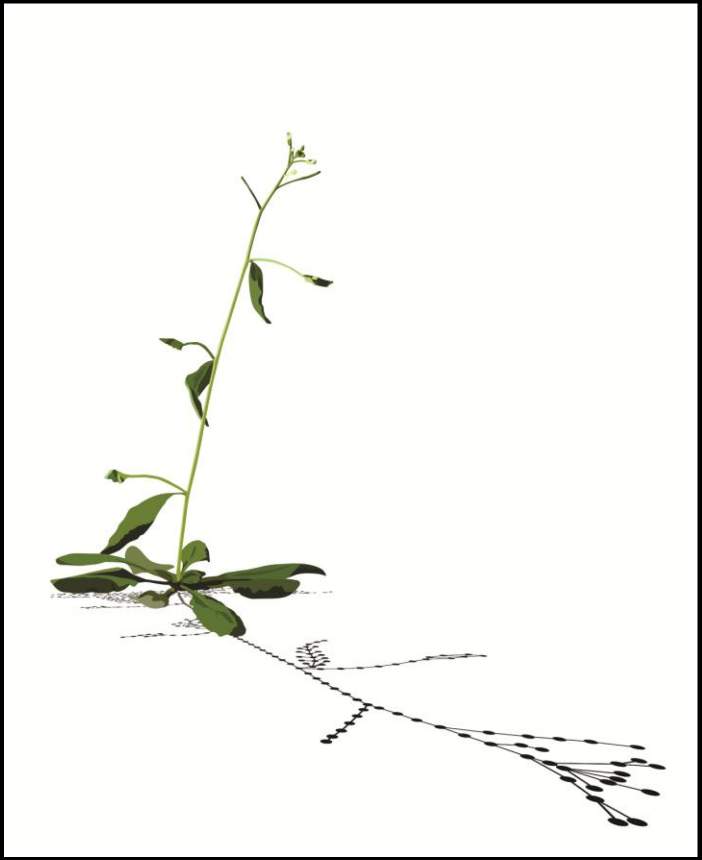
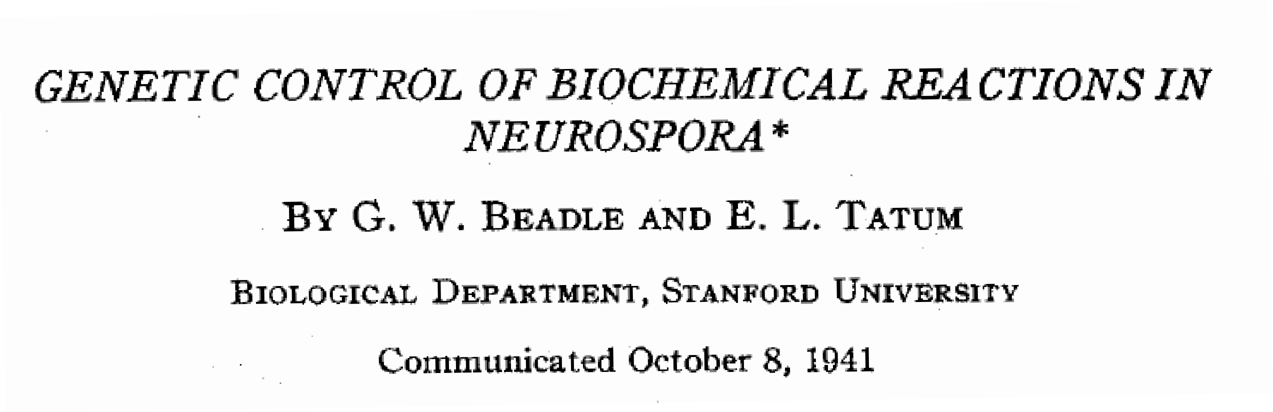
Evolution, systems organization and pathogen attack of a plant interactome network

DFCI Center for Cancer Systems Biology
Harvard Medical School

Center for Food and Life Sciences
Technical University of Munich (TUM)





*GENETIC CONTROL OF BIOCHEMICAL REACTIONS IN NEUROSPORA**

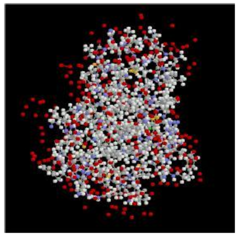
BY G. W. BEADLE AND E. L. TATUM

BIOLOGICAL DEPARTMENT, STANFORD UNIVERSITY

Communicated October 8, 1941

Nature Reviews | Genetics

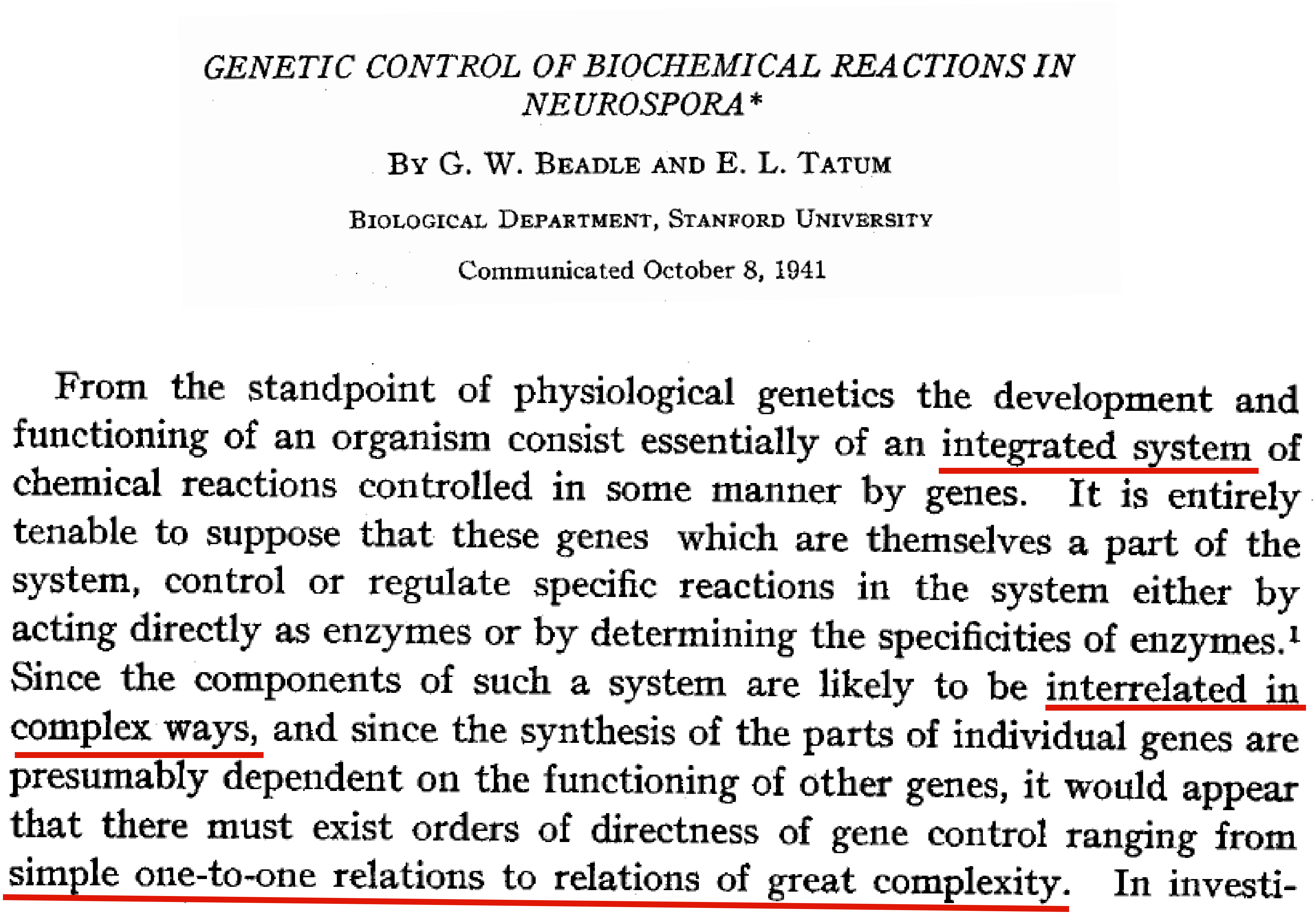
1 gene



Insulin

1 protein
(enzyme)

1 trait



*GENETIC CONTROL OF BIOCHEMICAL REACTIONS IN NEUROSPORA**

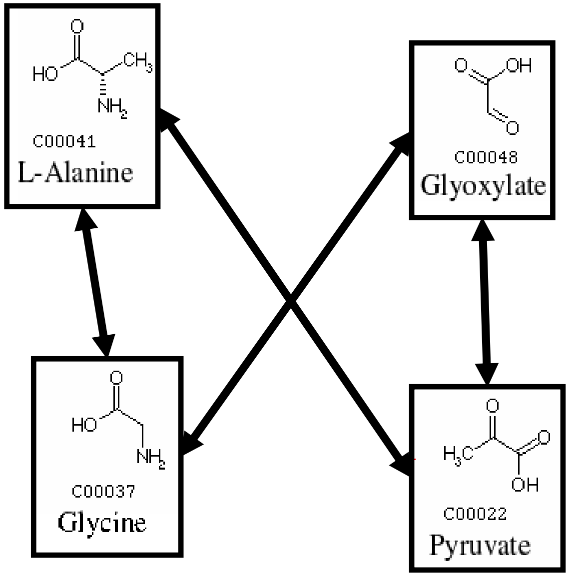
By G. W. Beadle and E. L. Tatum

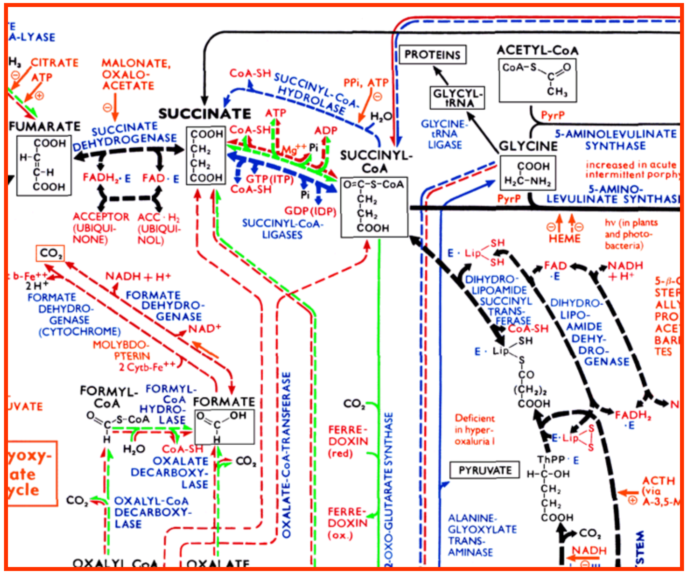
Biological Department, Stanford University

Communicated October 8, 1941

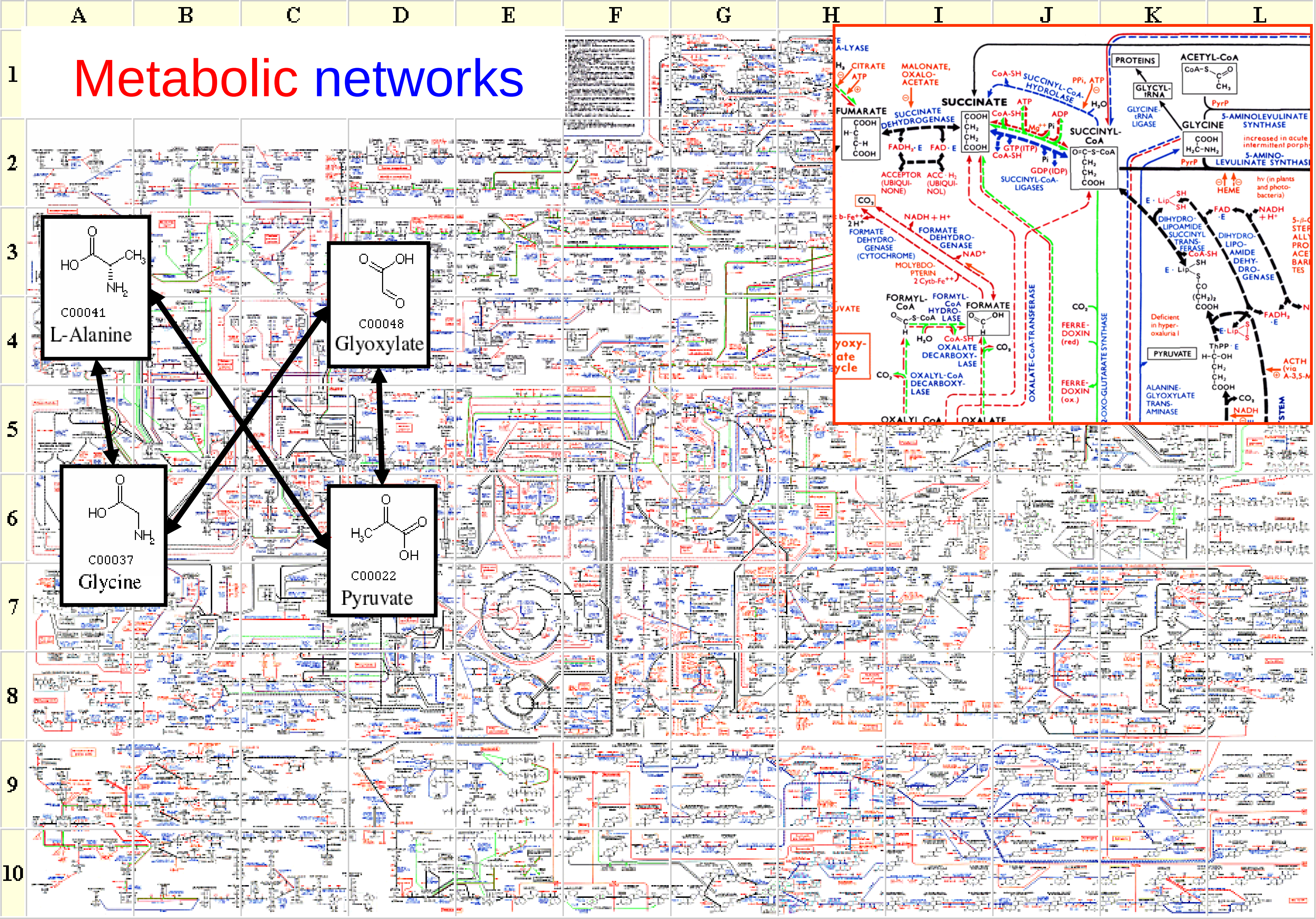
From the standpoint of physiological genetics the development and functioning of an organism consist essentially of an integrated system of chemical reactions controlled in some manner by genes. It is entirely tenable to suppose that these genes which are themselves a part of the system, control or regulate specific reactions in the system either by acting directly as enzymes or by determining the specificities of enzymes.[1] Since the components of such a system are likely to be interrelated in complex ways, and since the synthesis of the parts of individual genes are presumably dependent on the functioning of other genes, it would appear that there must exist orders of directness of gene control ranging from simple one-to-one relations to relations of great complexity. In investi-

Metabolic pathways

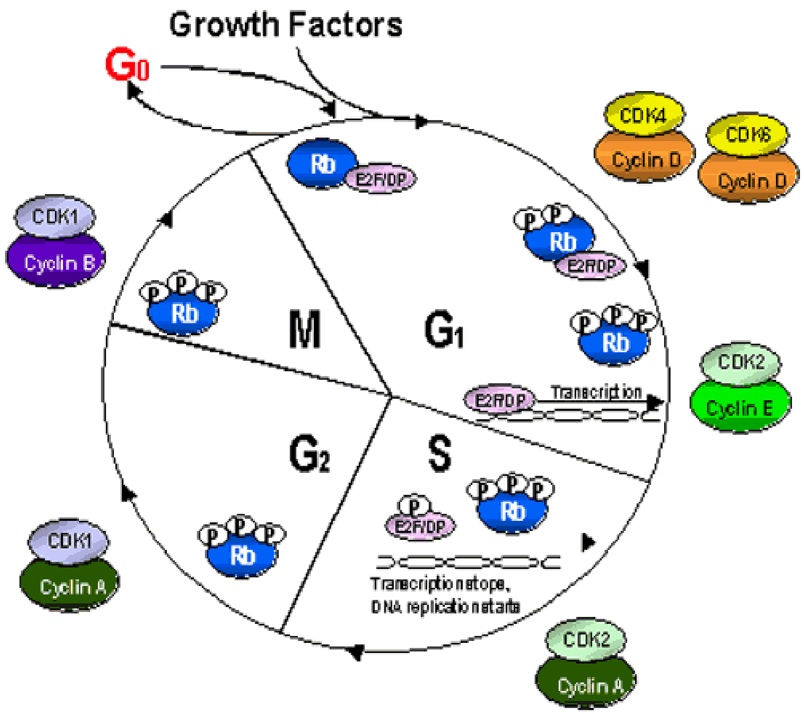




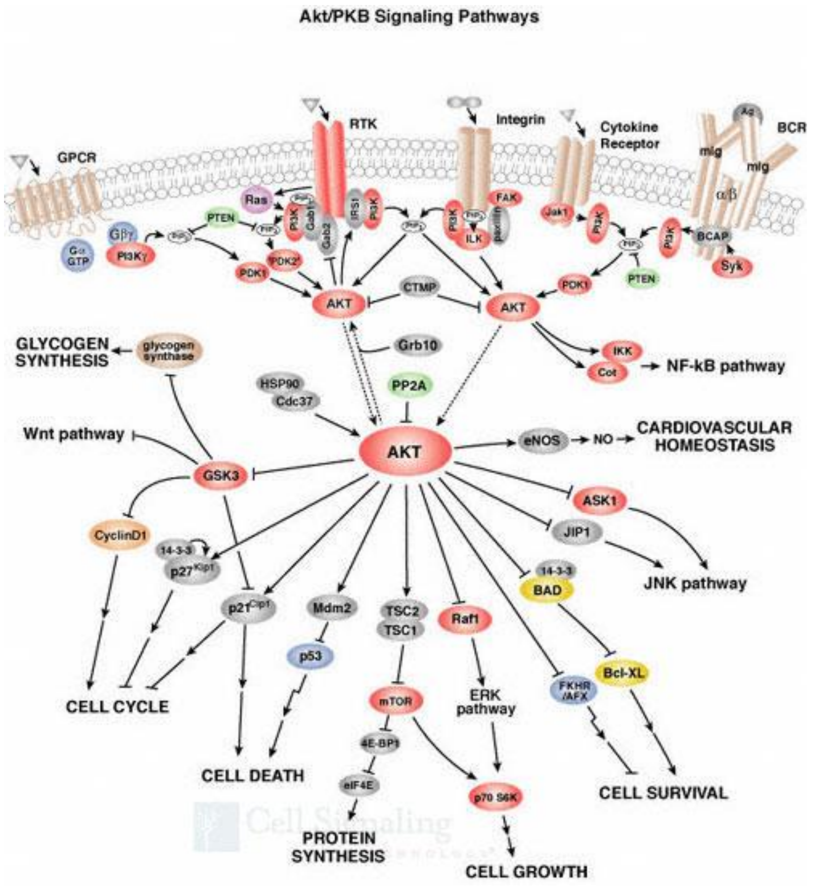
Metabolic networks



… description of pathways



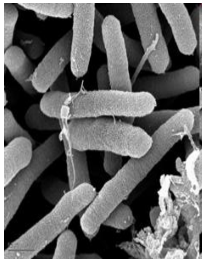
The eukaryotic cell cycle



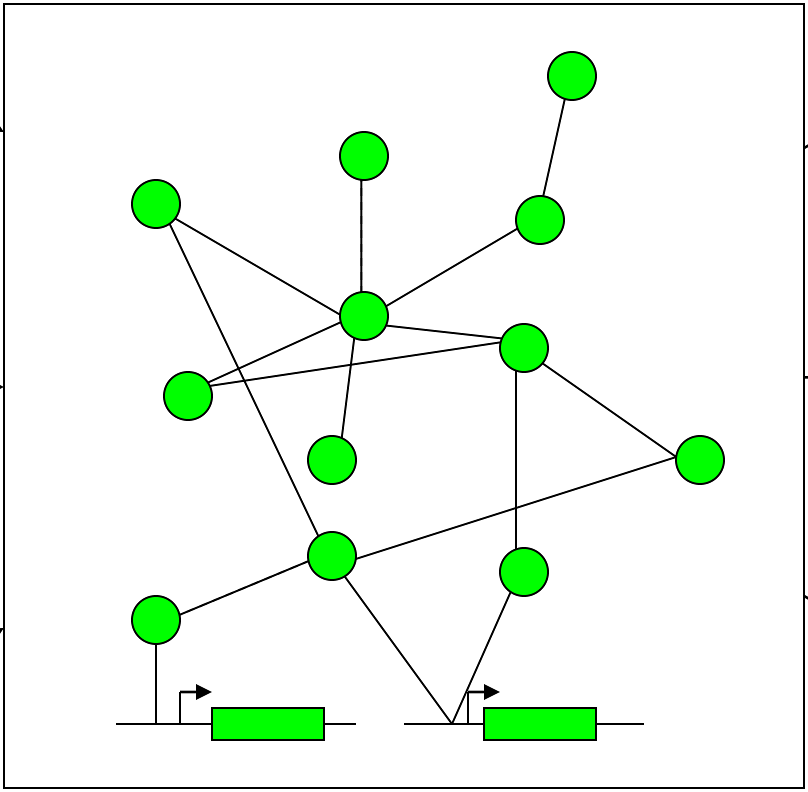
Understanding (and manipulating) phenotypes

Genome

Genetic variation

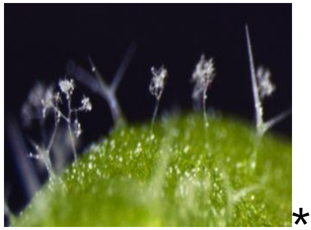


Environmental perturbations



Germination*

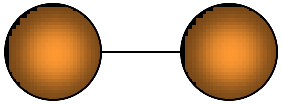
Flowering**



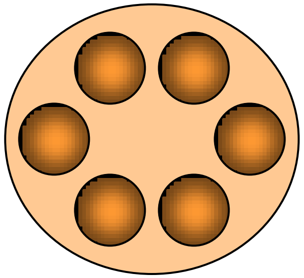
Infection***

* G. Leubner, Freiburg, Ger
** http://www.topnews.in
*** P. Epple, J Dangle, UNC, USA

Experimental approaches to interaction mapping

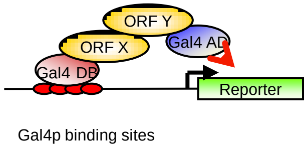


Binary protein
interaction analysis

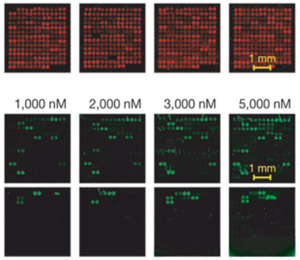


Protein complex analysis

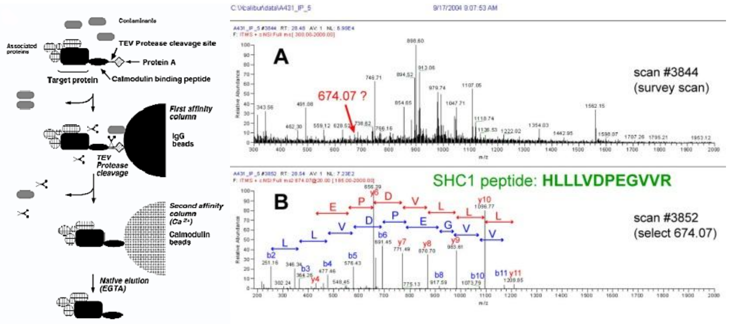
Y2H



Protein
arrays

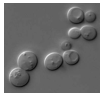


AP-MS

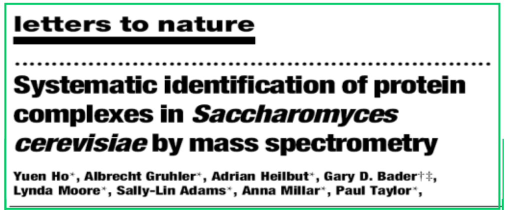


e.g. J.C. Gavin (EMBL)

Protein interaction datasets for *S. cerevisiae*



Affinity-Purification Mass spectrometry (AP-MS)



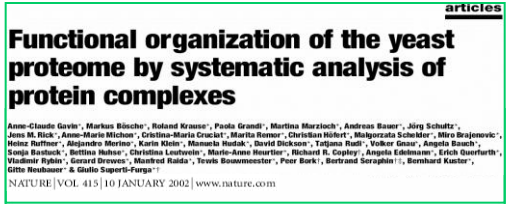
letters to nature

Systematic identification of protein complexes in *Saccharomyces cerevisiae* by mass spectrometry

Yuen Ho*, Albrecht Gruhler*, Adrian Heilbut*, Gary D. Bader†‡, Lynda Moore*, Sally-Lin Adams*, Anna Millar*, Paul Taylor*,

Global landscape of protein complexes in the yeast *Saccharomyces cerevisiae*

Nevan J. Krogan[1,2]*†, Gerard Cagney[1,3]*, Haiyuan Yu[4], Gouqing Zhong[1], Xinghua Guo[1], Alexandr Ignatchenko[1], Joyce Li[1], Shuye Pu[5], Nira Datta[1], Aaron P. Tikuisis[1], Thanuja Punna[1], José M. Peregrín-Alvarez[5],



articles

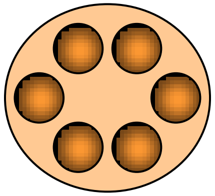
Functional organization of the yeast proteome by systematic analysis of protein complexes

Anne-Claude Gavin*, Markus Bösche*, Roland Krause*, Paola Grandi*, Martina Marzioch*, Andreas Bauer*, Jörg Schultz*, Jens M. Rick*, Anne-Marie Michon*, Cristina-Maria Cruciat*, Marita Remor*, Christian Höfert*, Malgorzata Schelder*, Miro Brajenovic*, Heinz Ruffner*, Alejandro Merino*, Karin Klein*, Manuela Hudak*, David Dickson*, Tatjana Rudi*, Volker Gnau*, Angela Bauch*, Sonja Bastuck*, Bettina Huhse*, Christina Leutwein*, Marie-Anne Heurtier*, Richard R. Copley†, Angela Edelmann*, Erich Querfurth*, Vladimir Rybin*, Gerard Drewes*, Manfred Raida*, Tewis Bouwmeester*, Peer Bork†, Bertrand Seraphin†‡, Bernhard Kuster*, Gitte Neubauer* & Giulio Superti-Furga*†

NATURE | VOL 415 | 10 JANUARY 2002 | www.nature.com

Proteome survey reveals modularity of the yeast cell machinery

Anne-Claude Gavin[1]*†, Patrick Aloy[2]*, Paola Grandi[1], Roland Krause[1,3], Markus Boesche[1], Martina Marzioch[1], Christina Rau[1], Lars Juhl Jensen[2], Sonja Bastuck[1], Birgit Dümpelfeld[1], Angela Edelmann[1], Marie-Anne Heurtier[1], Verena Hoffman[1], Christian Hoefert[1], Karin Klein[1], Manuela Hudak[1], Anne-Marie Michon[1], Malgorzata Schelder[1], Markus Schirle[1], Marita Remor[1], Tatjana Rudi[1], Sean Hooper[2], Andreas Bauer[1], Tewis Bouwmeester[1], Georg Casari[1], Gerard Drewes[1], Gitte Neubauer[1], Jens M. Rick[1], Bernhard Kuster[1], Peer Bork[2], Robert B. Russell[2] & Giulio Superti-Furga[1,4]



Yeast-2-Hybrid (Y2H)

A comprehensive two-hybrid analysis to explore the yeast protein interactome

Takashi Ito*†, Tomoko Chiba*, Ritsuko Ozawa‡, Mikio Yoshida§, Masahira Hattori‡, and Yoshiyuki Sakaki‡¶

*Division of Genome Biology, Cancer Research Institute, Kanazawa University, Kanazawa 920-0934, Japan; ‡Human Genome Research Group, RIKEN Genomic Sciences Center, Yokohama 230-0045, Japan; §INTEC Web and Genome Informatics Corporation, Tokyo 136-0075, Japan; and ¶Human Genome Center, Institute of Medical Science, University of Tokyo, Tokyo 108-8639, Japan

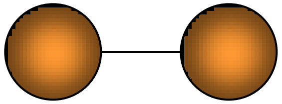
Communicated by Satoshi Omura, The Kitasato Institute, Tokyo, Japan, January 22, 2001 (received for review December 4, 2000)

A comprehensive analysis of protein–protein interactions in *Saccharomyces cerevisiae*

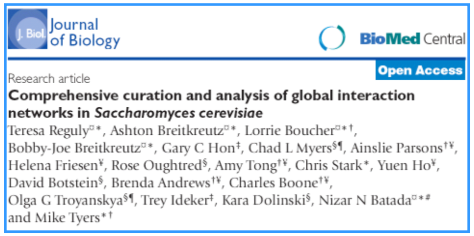
Peter Uetz*†, Loic Giot*‡, Gerard Cagney†, Traci A. Mansfield‡, Richard S. Judson‡, James R. Knight‡, Daniel Lockshon†, Vaibhav Narayan‡, Maithreyan Srinivasan‡, Pascale Pochart‡, Alia Qureshi-Emili†§, Ying Li‡, Brian Godwin‡, Diana Conover†§, Theodore Kalbfleisch‡, Govindan Vijayadamodar‡, Meijia Yang‡, Mark Johnston†¶, Stanley Fields†§ & Jonathan M. Rothberg‡

‡ CuraGen Corporation, 555 Long Wharf Drive, 11th Floor, New Haven, Connecticut 06511, USA

† Departments of Genetics and Medicine and § Howard Hughes Medical Institute, University of Washington, Box 357360, Seattle, Washington 98195-7360, USA



Literature curation (LC)



Journal of Biology

BioMed Central

Open Access

Research article

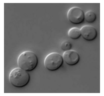
Comprehensive curation and analysis of global interaction networks in *Saccharomyces cerevisiae*

Teresa Reguly¤*, Ashton Breitkreutz¤*, Lorrie Boucher¤*†, Bobby-Joe Breitkreutz¤*, Gary C Hon‡, Chad L Myers§¶, Ainslie Parsons†¥, Helena Friesen¥, Rose Oughtred§, Amy Tong†¥, Chris Stark*, Yuen Ho¥, David Botstein§, Brenda Andrews†¥, Charles Boone†¥, Olga G Troyanskya§¶, Trey Ideker‡, Kara Dolinski§, Nizar N Batada¤*# and Mike Tyers*†

1 paper/dataset: 🟥 🟦 🟩

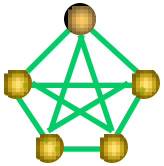
>1 paper/dataset: ▨ ▨ ▨

Computational analysis



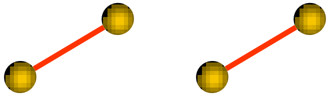
Haiyuan Yu

A. GS from complexes:



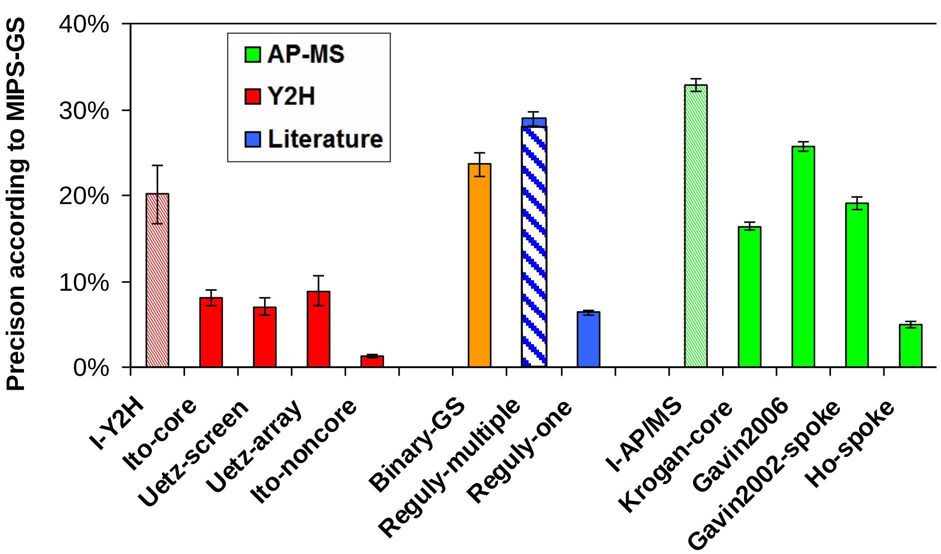
1. Consider all pairs within a certain complex (i.e., “matrix” model)
2. 9793 interactions among 1058 proteins

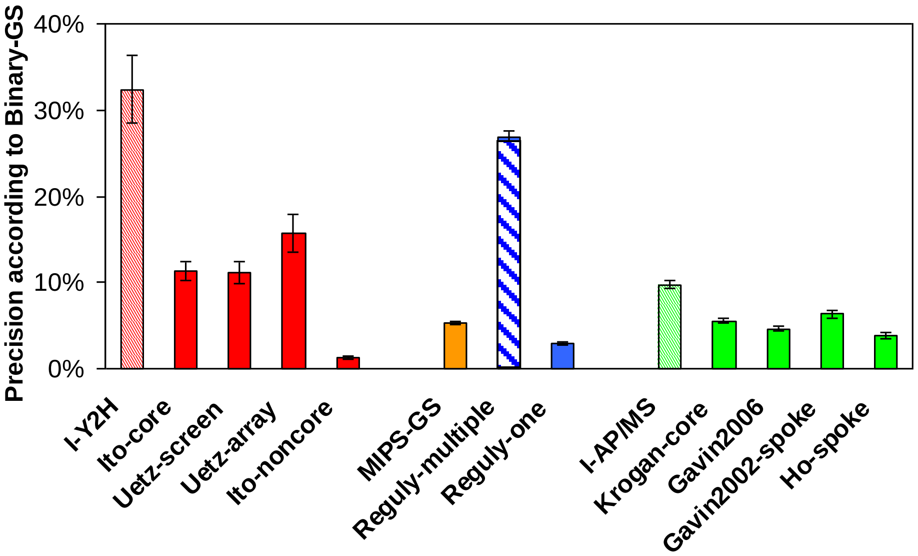
B. GS from binary interactions:



1. Consider only binary physical interactions
2. 1318 interactions among 1090 proteins

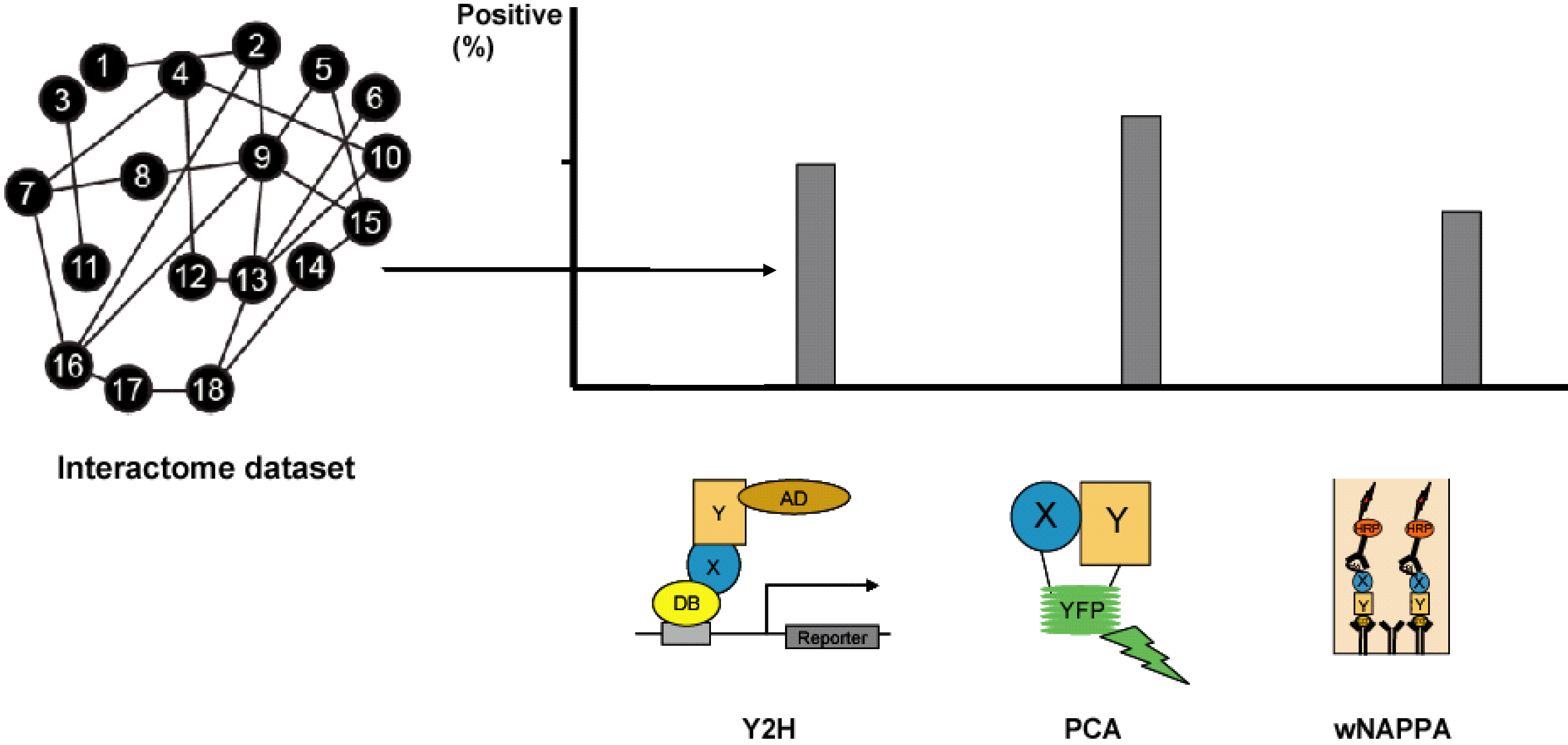
Precision = # of TPs / Total # of interactions in the dataset



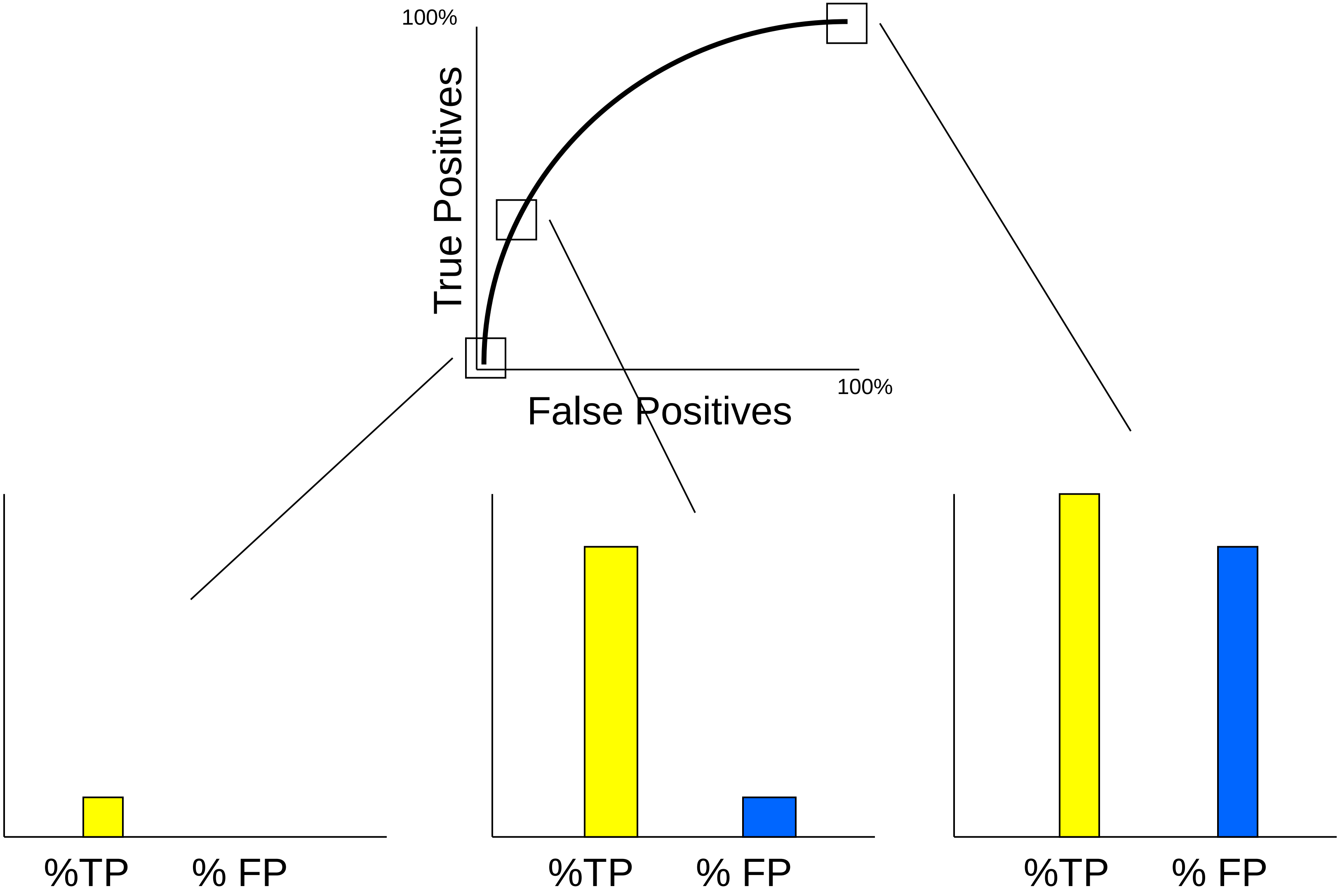


Measuring *specificity* of datasets

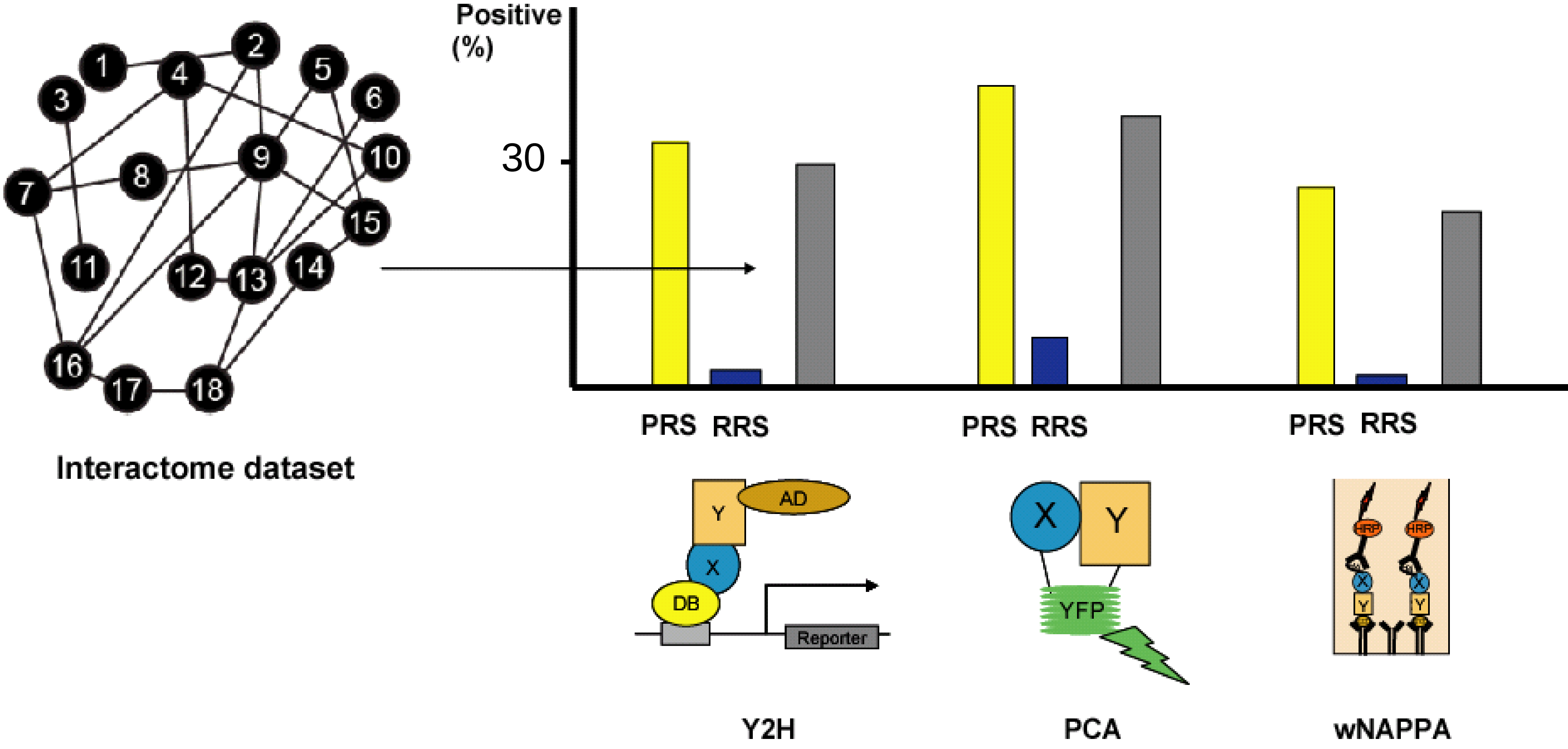
(false discovery rate)

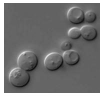


Stringency affects retest and false detection rate

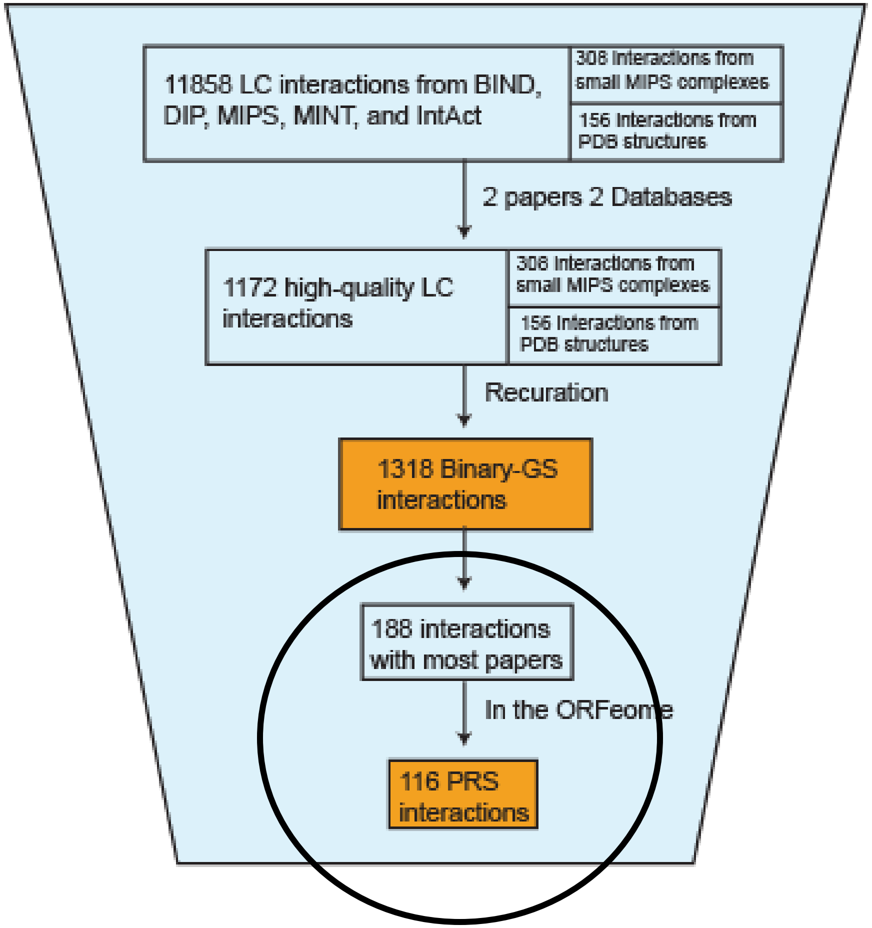


Measuring *specificity* of datasets





Interaction reference sets



11858 LC interactions from BIND, DIP, MIPS, MINT, and IntAct

308 Interactions from small MIPS complexes

156 Interactions from PDB structures

2 papers 2 Databases

1172 high-quality LC interactions

308 Interactions from small MIPS complexes

156 Interactions from PDB structures

Recuration

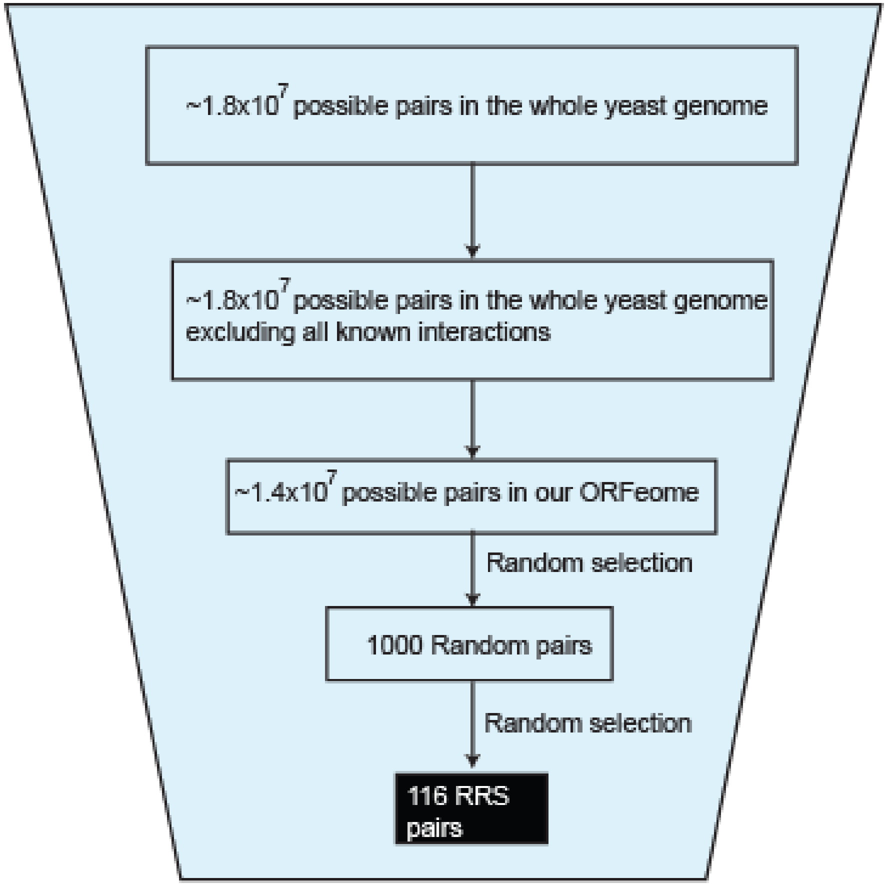
1318 Binary-GS interactions

188 interactions with most papers

In the ORFeome

116 PRS interactions

Yeast Positive Reference Set (PRS)



~1.8x10^7 possible pairs in the whole yeast genome

~1.8x10^7 possible pairs in the whole yeast genome excluding all known interactions

~1.4x10^7 possible pairs in our ORFeome

Random selection

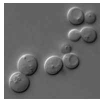
1000 Random pairs

Random selection

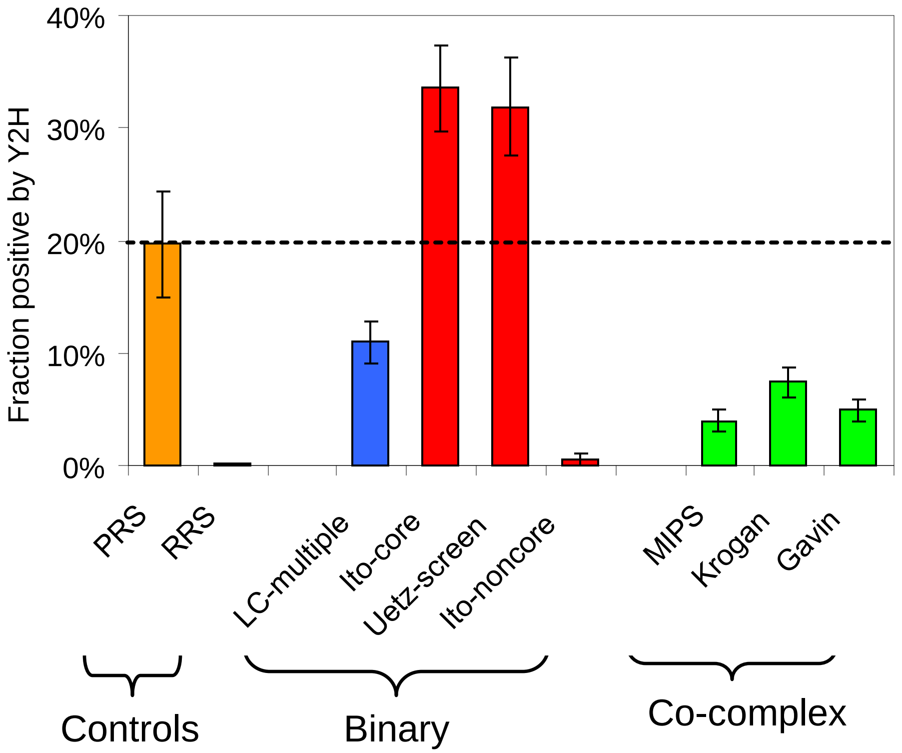
116 RRS pairs

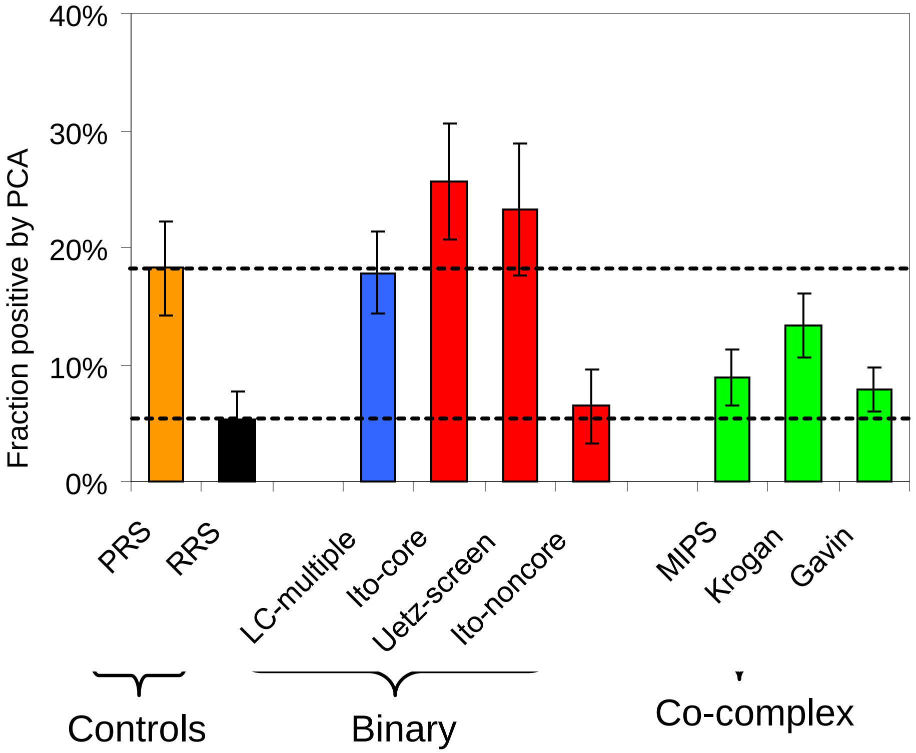
Yeast Random Reference Set (RRS)

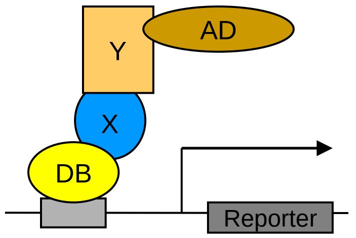
Cusick *et al.*, *Nat. Meth. 2009*

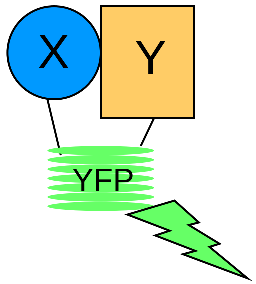


Retest by Y2H and PCA



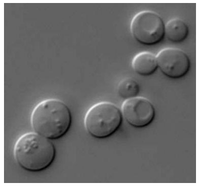


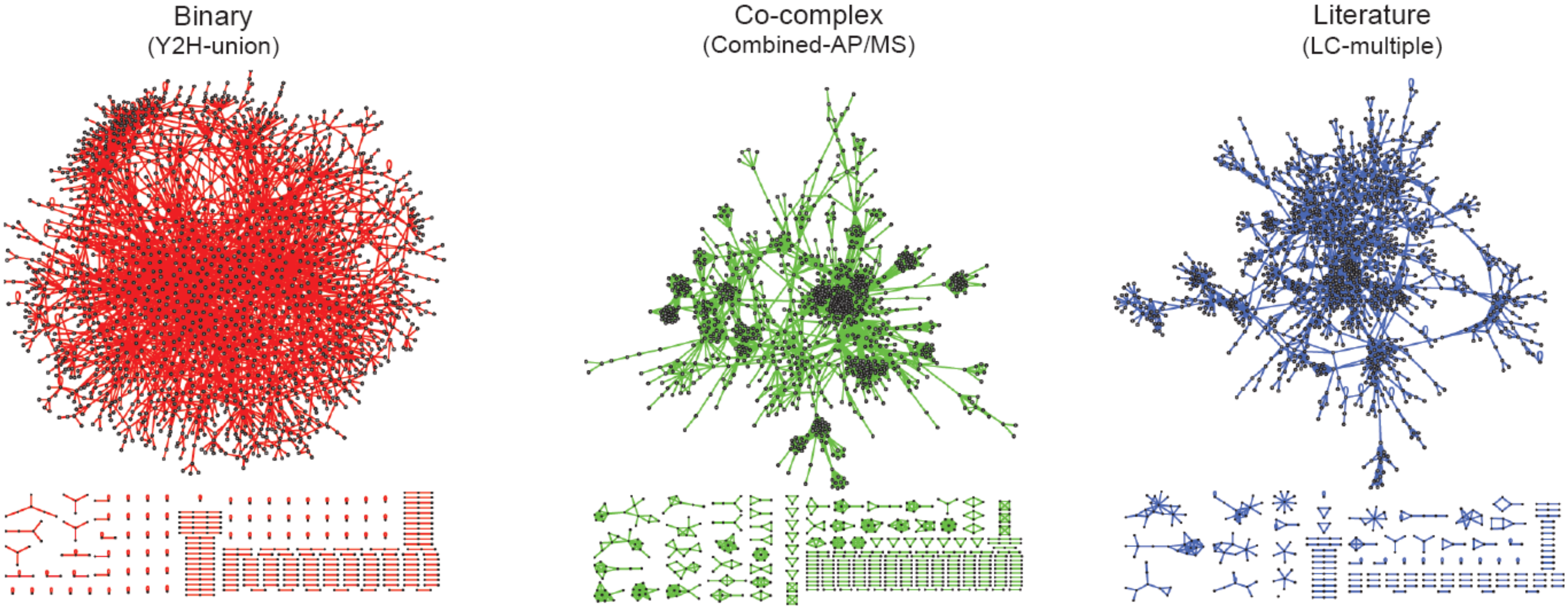




Yu *et al.*, *Science* (2008)

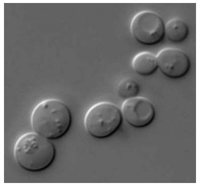
Topological comparison of datasets





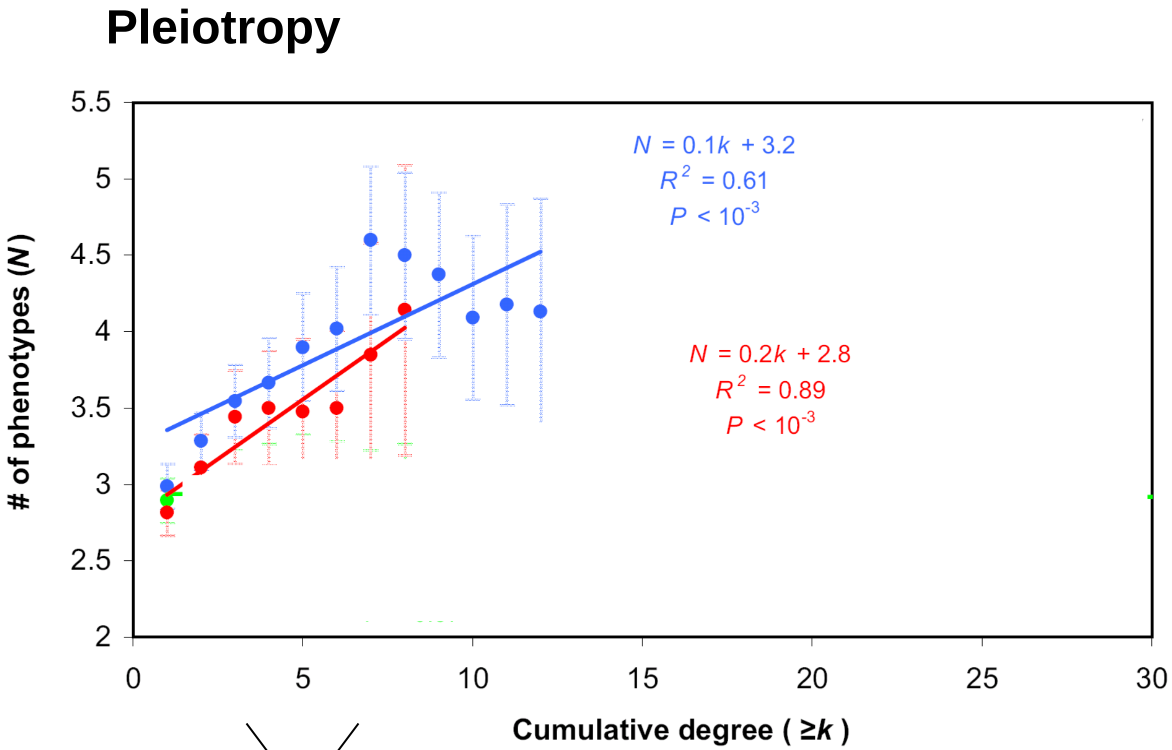
Yu, Braun, Yildirim *et al.*, *Science* 2008

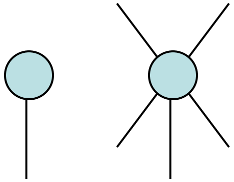
Binary network hubs tend to be pleiotropic



	cond1	…	cond n
KO1	-	+	+
KO2	+	+	+
KO3	-	-	-
…			
KO6000	-	+	-
wt	+	+	+

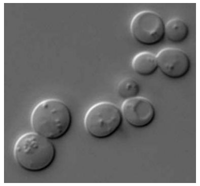
+ Growth
- No growth

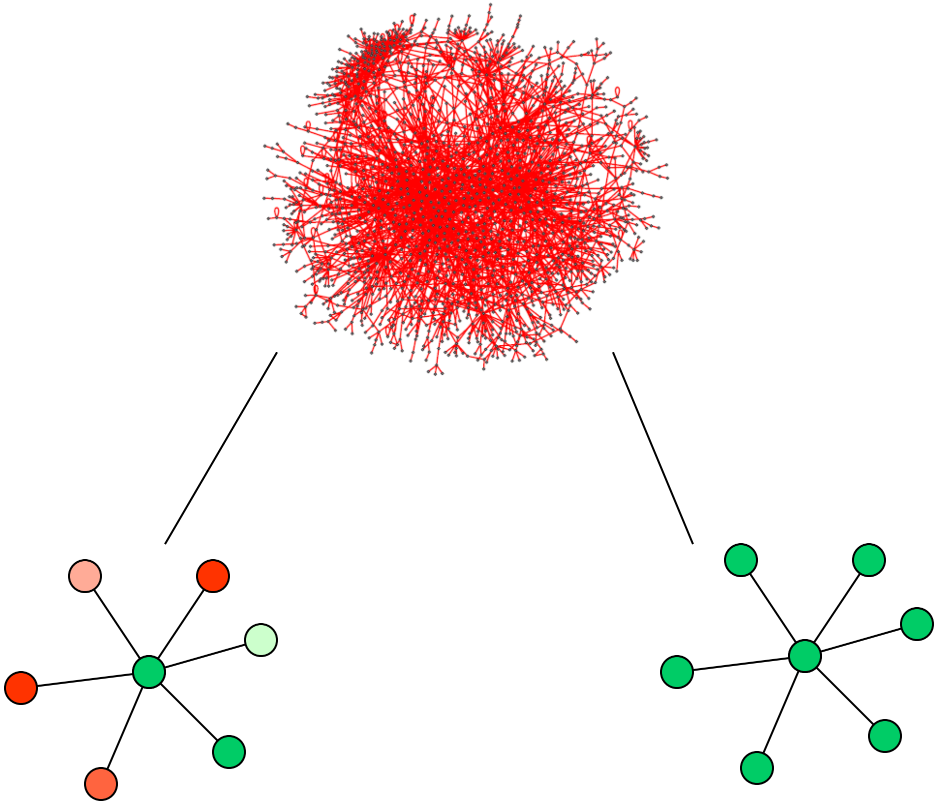




Yu, Braun, Yildirim *et al.*, *Science* 2008

Different types of hubs



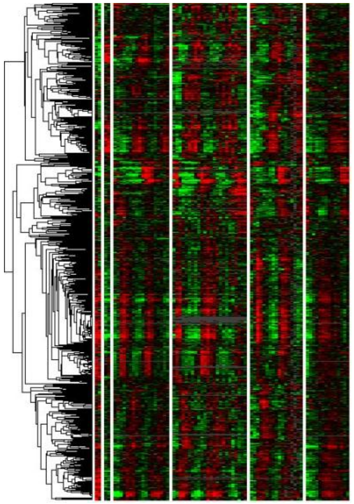


Date hubs

not correlated expression

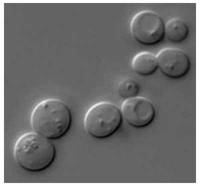
Party hubs

correlated expression

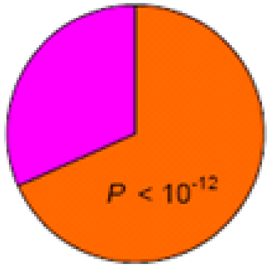


Han *et al.*, *Nature* 2004

Network hubs

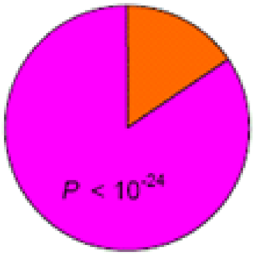


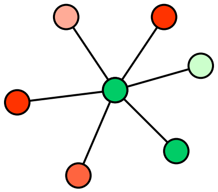
Binary Interaction Network (Y2H)



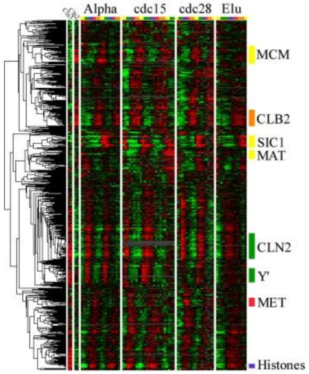
🟧 Date hubs
🟪 Party hubs

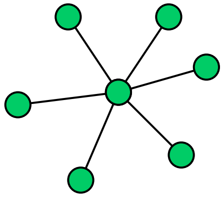
Protein Complex Network (AP/MS)





Date hubs

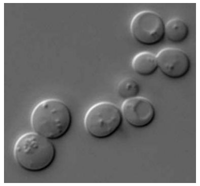


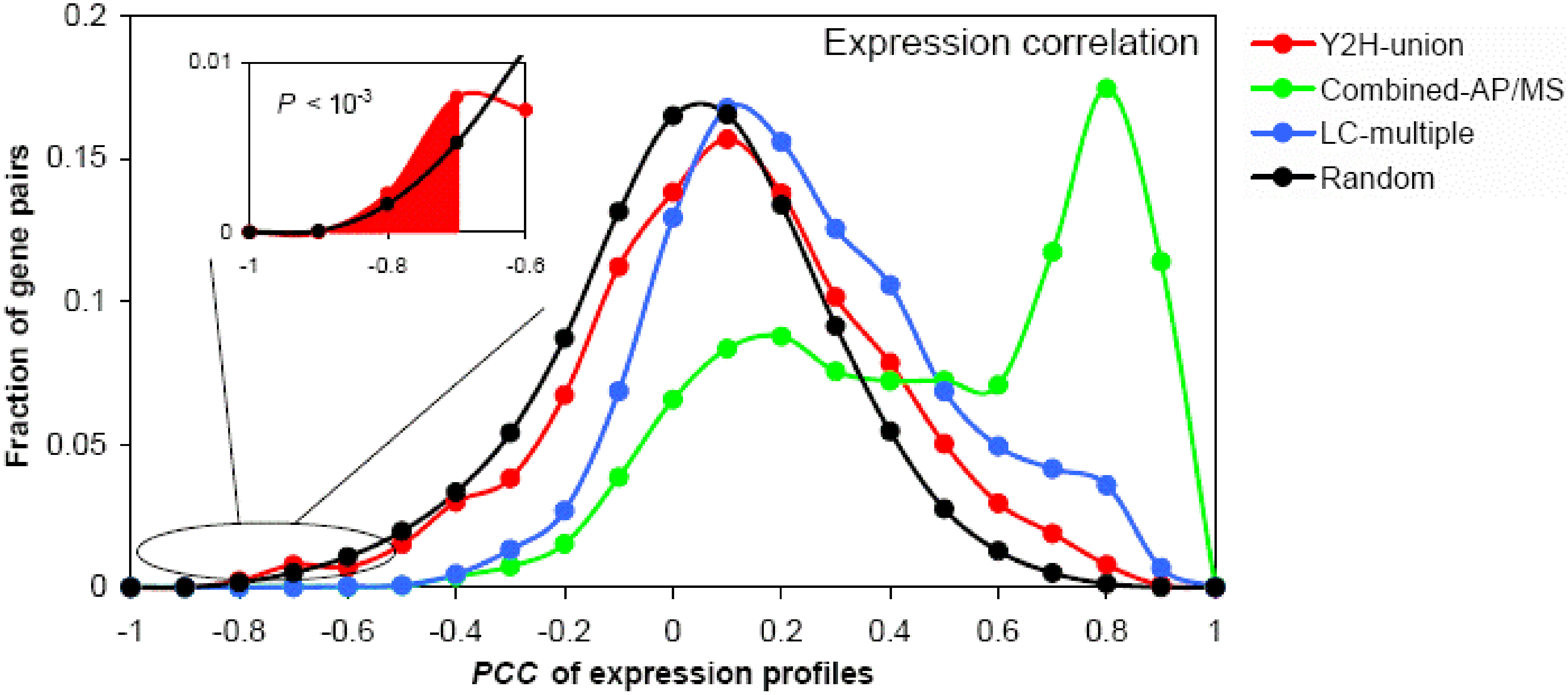


Party hubs

Yu, Braun, Yildirim *et al.*, *Science* 2008

Expression correlation



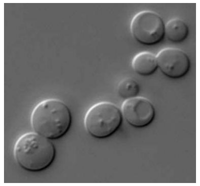


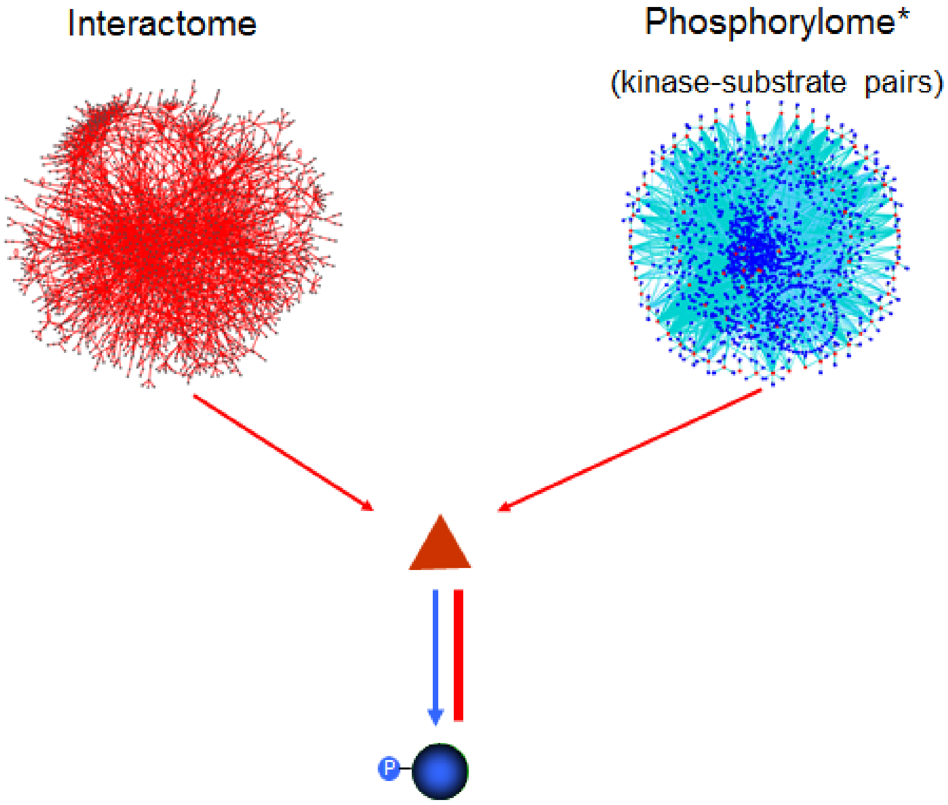
DANA-FARBER CANCER INSTITUTE

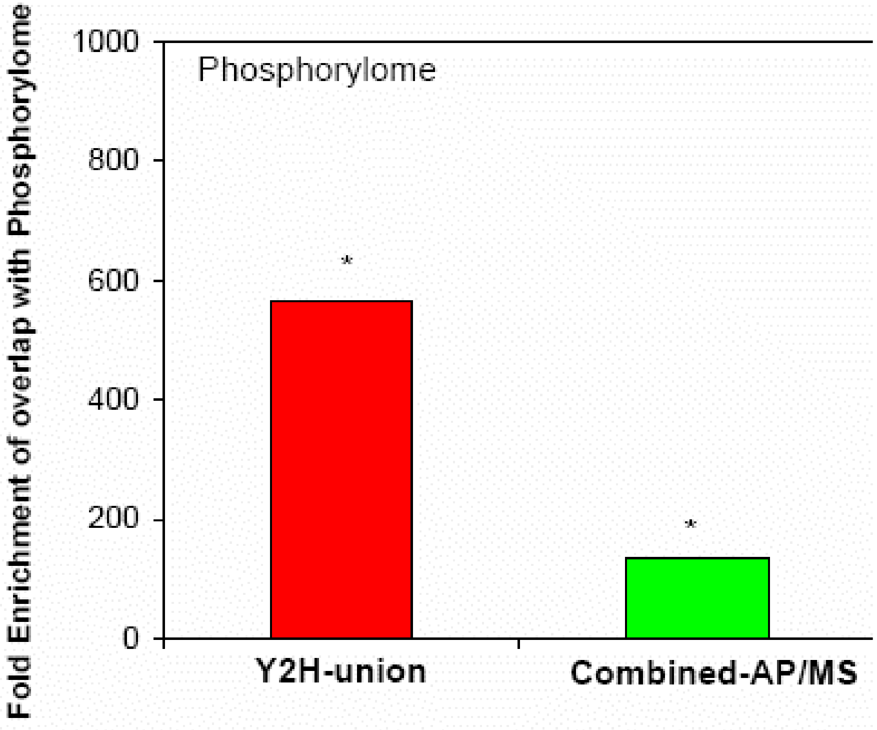
CCSB CENTER FOR CANCER SYSTEMS BIOLOGY

HARVARD MEDICAL SCHOOL

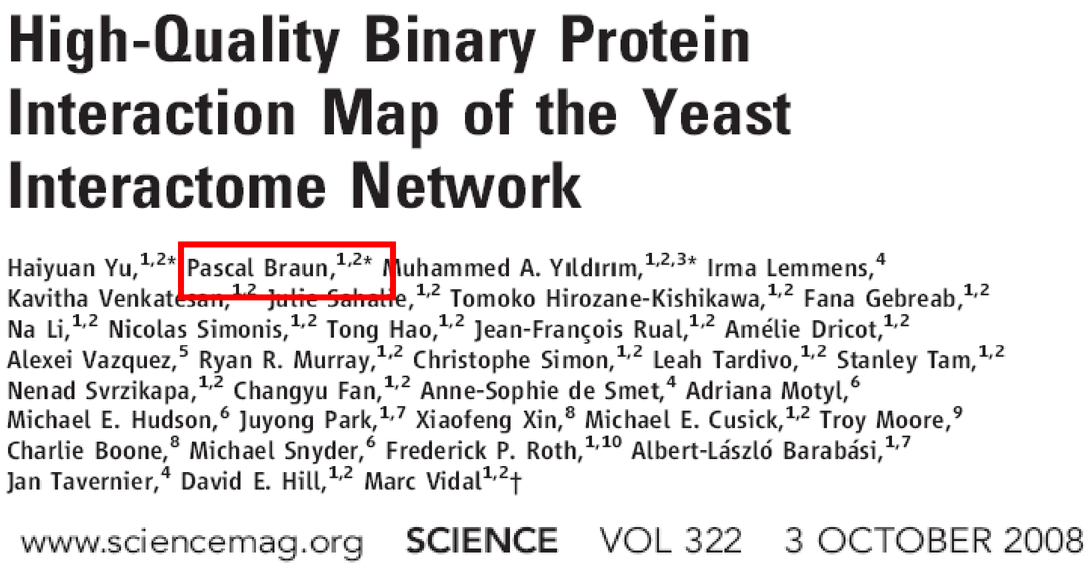
Interactome vs. phosphorylome







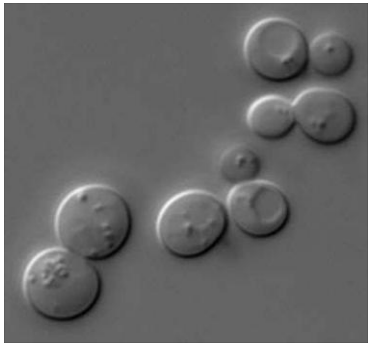
* Ptacek *et al.*, Nature. 2005

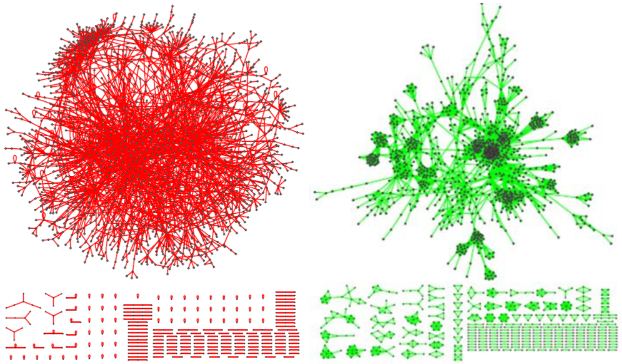


High-Quality Binary Protein Interaction Map of the Yeast Interactome Network

Haiyuan Yu,[1,2*] Pascal Braun,[1,2*] Muhammed A. Yıldırım,[1,2,3*] Irma Lemmens,[4]
Kavitha Venkatesan,[1,2] Julie Sahalie,[1,2] Tomoko Hirozane-Kishikawa,[1,2] Fana Gebreab,[1,2]
Na Li,[1,2] Nicolas Simonis,[1,2] Tong Hao,[1,2] Jean-François Rual,[1,2] Amélie Dricot,[1,2]
Alexei Vazquez,[5] Ryan R. Murray,[1,2] Christophe Simon,[1,2] Leah Tardivo,[1,2] Stanley Tam,[1,2]
Nenad Svrzikapa,[1,2] Changyu Fan,[1,2] Anne-Sophie de Smet,[4] Adriana Motyl,[6]
Michael E. Hudson,[6] Juyong Park,[1,7] Xiaofeng Xin,[8] Michael E. Cusick,[1,2] Troy Moore,[9]
Charlie Boone,[8] Michael Snyder,[6] Frederick P. Roth,[1,10] Albert-László Barabási,[1,7]
Jan Tavernier,[4] David E. Hill,[1,2] Marc Vidal[1,2]†

www.sciencemag.org SCIENCE VOL 322 3 OCTOBER 2008





- HT Y2H and AP-MS datasets are both of very high quality but of different nature.

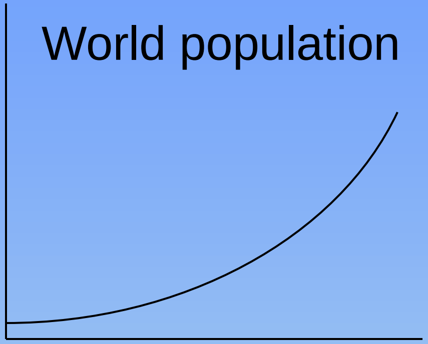
- Integrated Y2H-union network has ~3,000 binary interactions

- Binary and co-complex based networks have different topological and biological properties.

Plants and humans

Climate

Temp.
Droughts
Floods
Pathogens



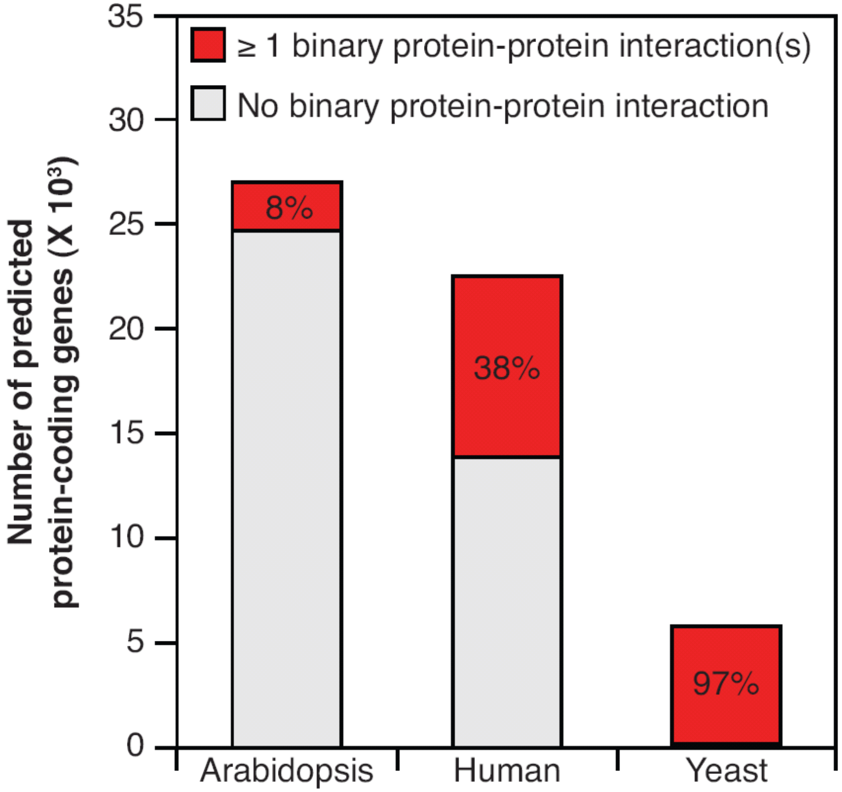
Food

Food-borne
pathogens

Fiber

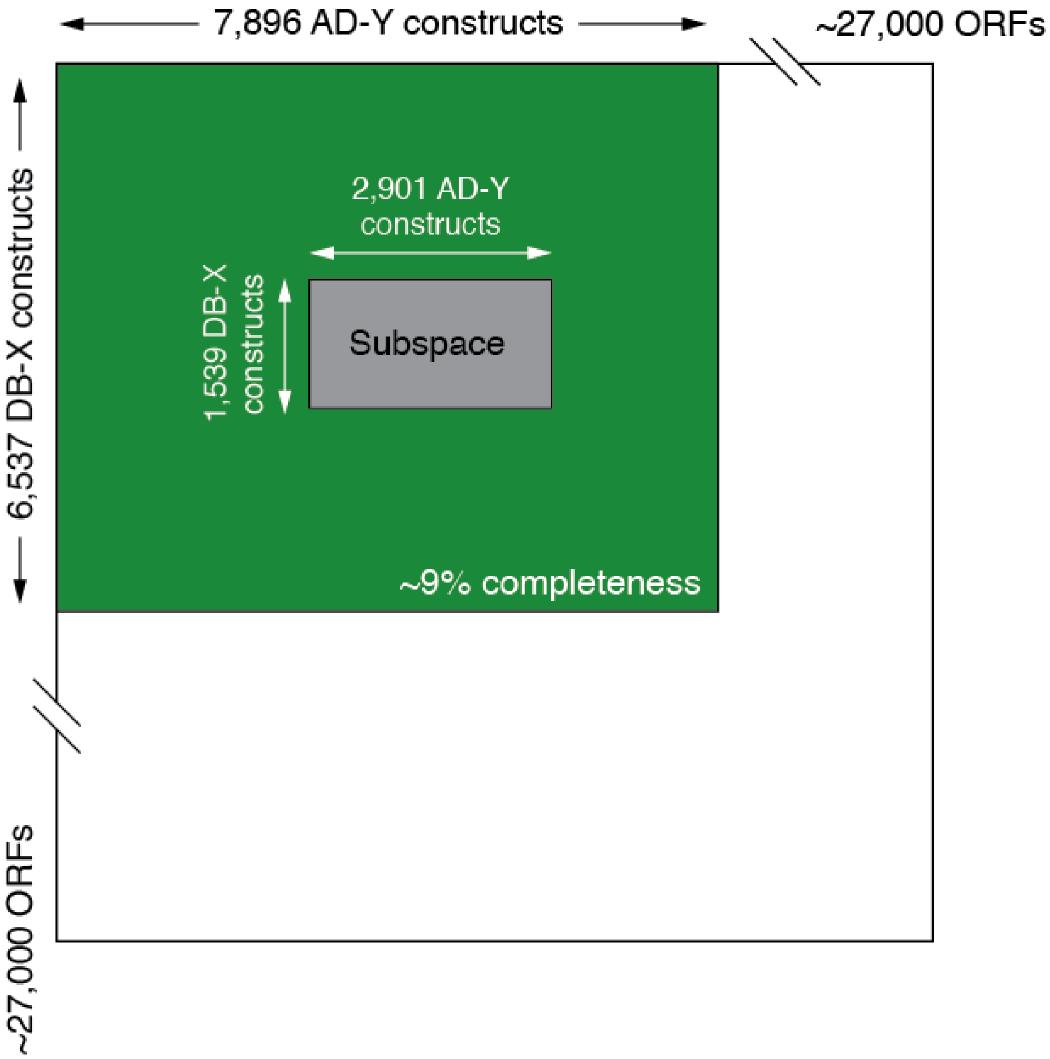
Fuel

Limited network information for plants

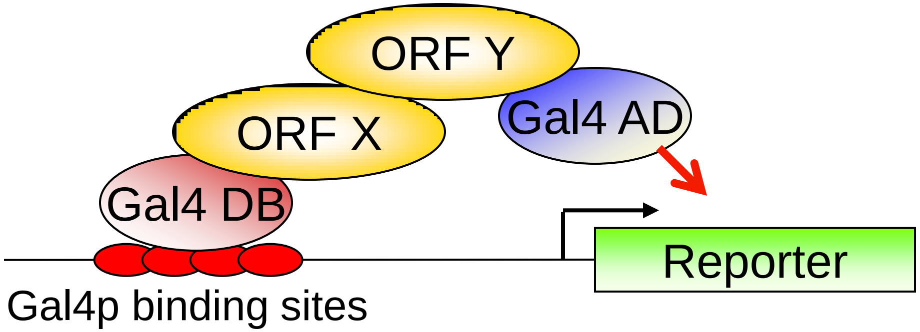


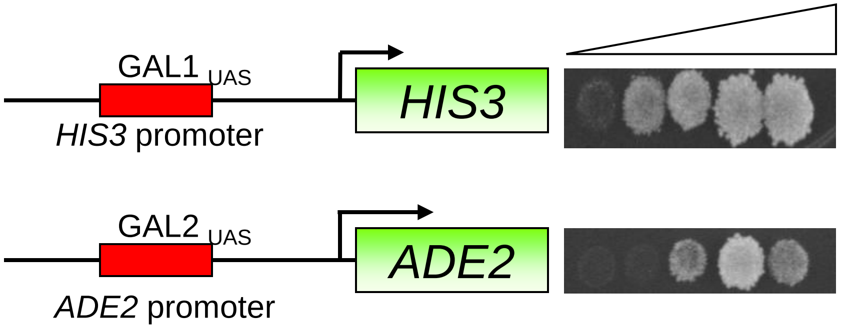
IntAct, April 2010

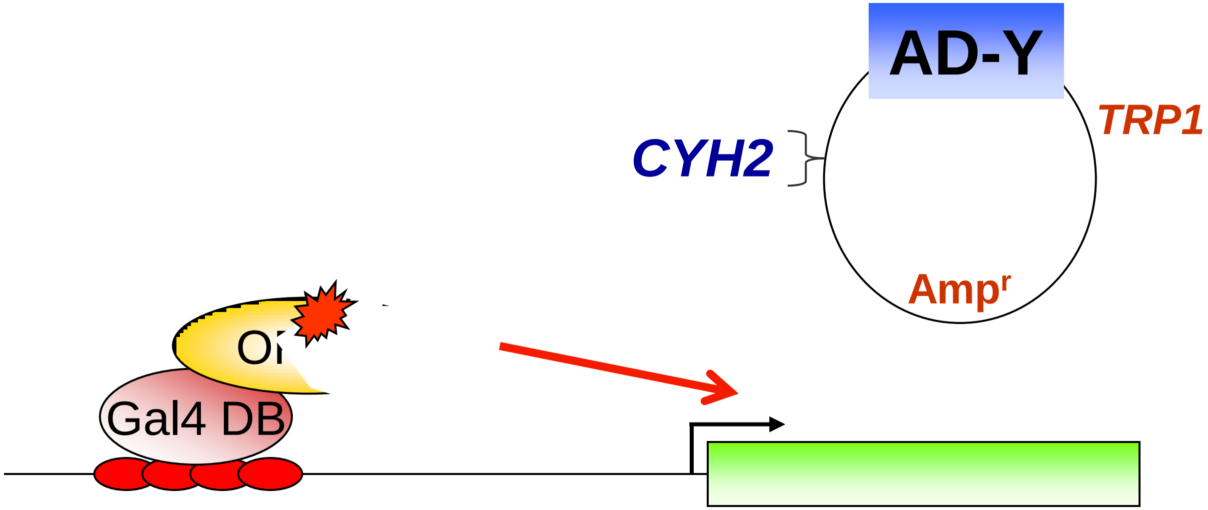
Arabidopsis ORFeome and search space – 10% completeness



High quality yeast-2-hybrid (Y2H)



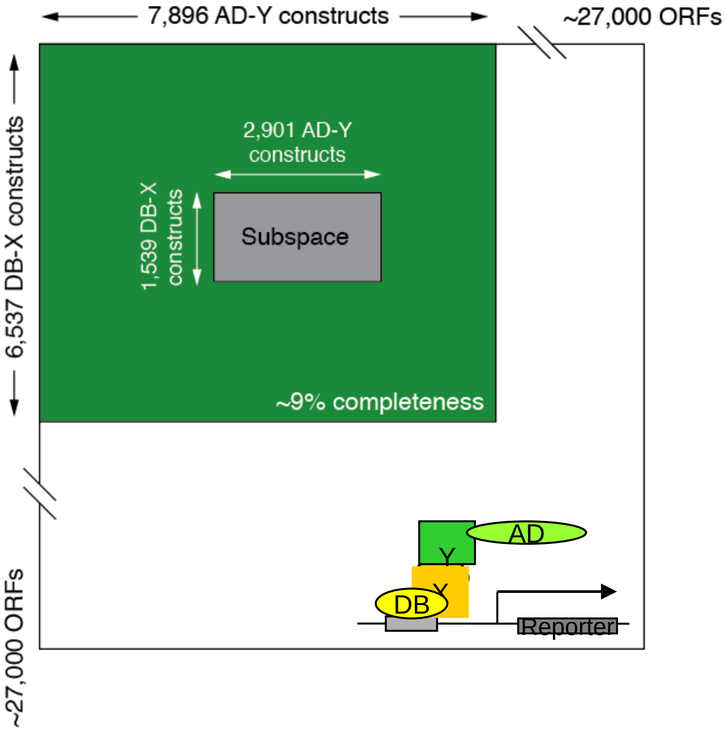


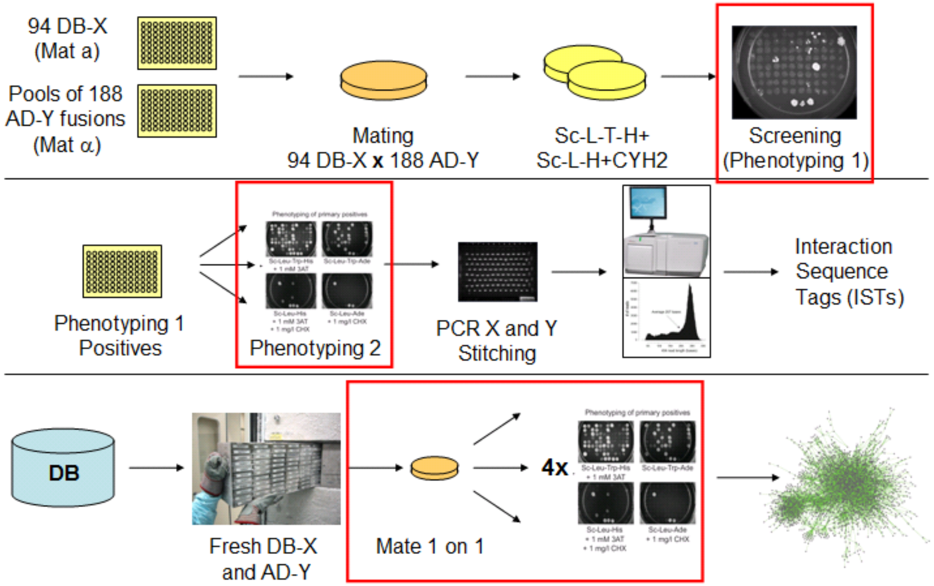


~~DB-X* de *novo* auto-activator!~~

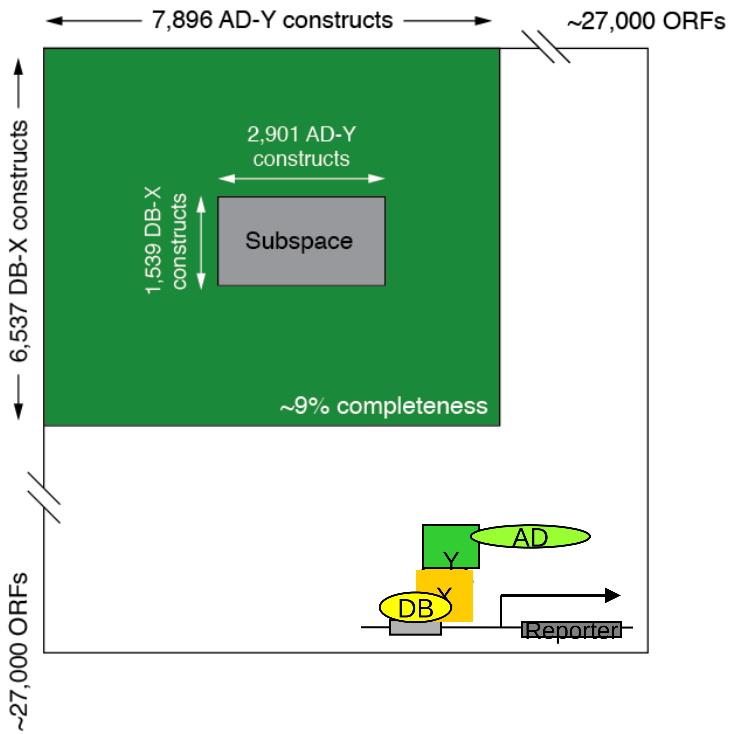
(Walhout & Vidal, Gen Res, 1999)

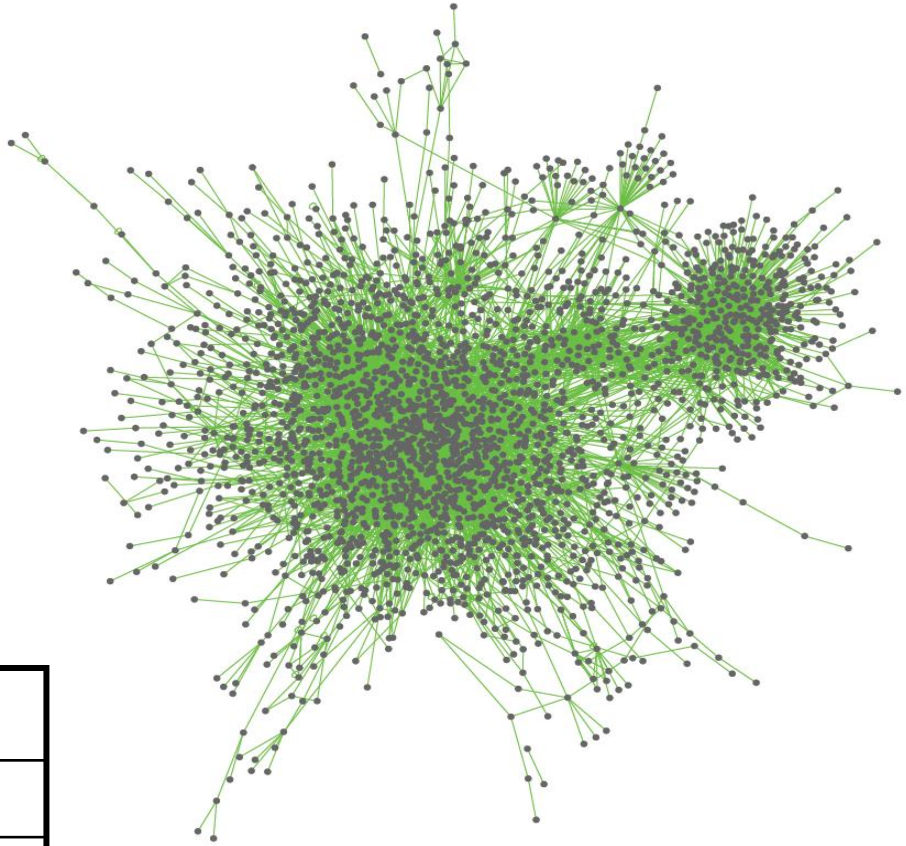
Arabidopsis ORFeome and search space – 10% completeness





Arabidopsis ORFeome and search space – 10% completeness

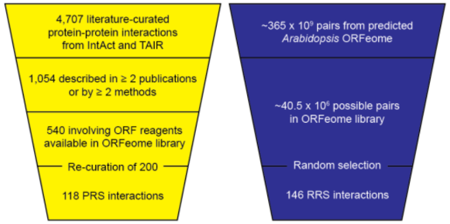




	Nodes	Edges
$\text{AI-1}_{\text{MAIN}}$	2,661	5,664
$\text{AI-1}_{\text{REPEAT}}$	673	1,066
AI-1	**2,774**	**6,205**

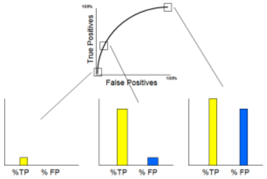
High quality of AI-1$_{\text{MAIN}}$

At-PRS At-RRS

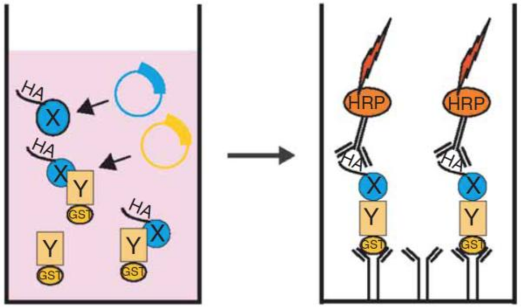


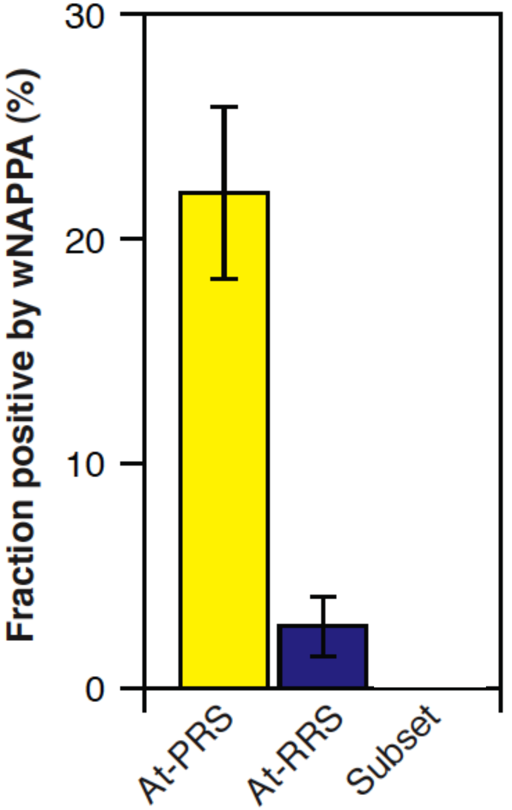
Arabidopsis Positive Reference Set (At-PRS)

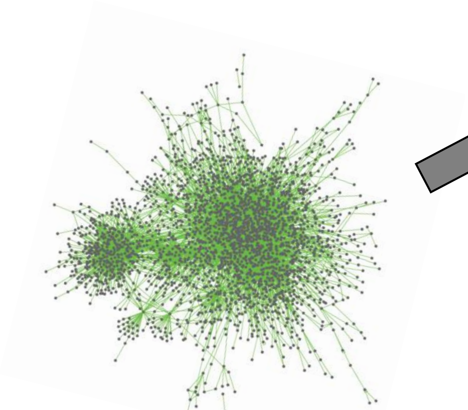
Arabidopsis Random Reference Set (At-RRS)



well-Nucleic Acid Protein Programmable Array (wNAPPA)



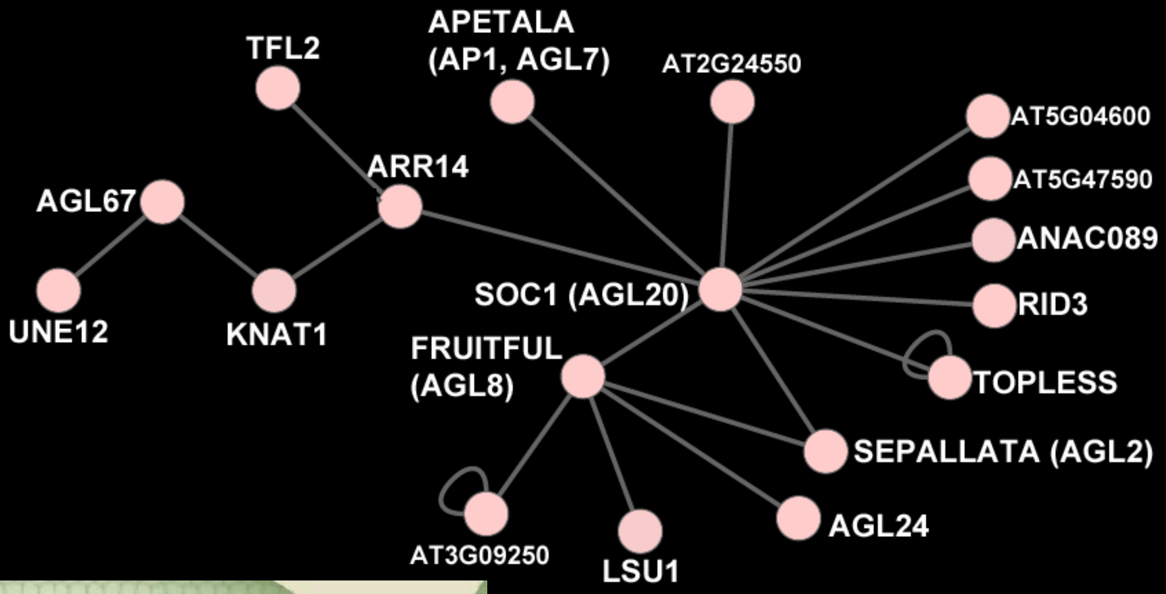


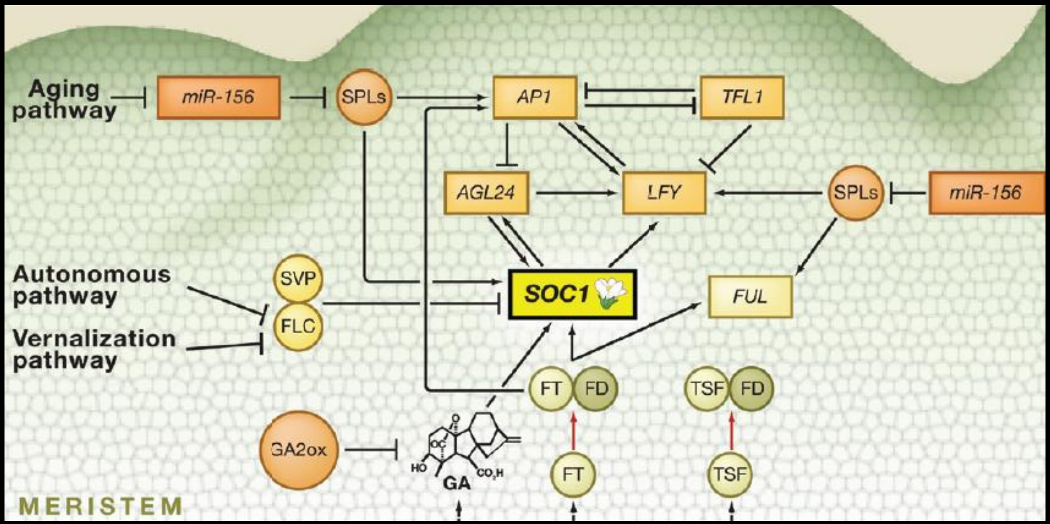


Random subset
(260 interactions)

Mary Galli, Ecker lab
Murat Tasan, Roth lab

Agamous-like transcription factors



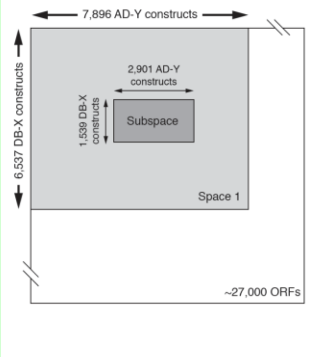


SnapShot: Control of flowering in Arabidopsis.
Fornara *et al*., *Cell* 2010

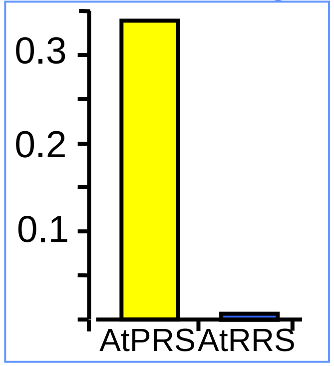
— AI-1 protein interaction
● *A. thaliana* protein

Scratching the surface of the Arabidopsis Interactome

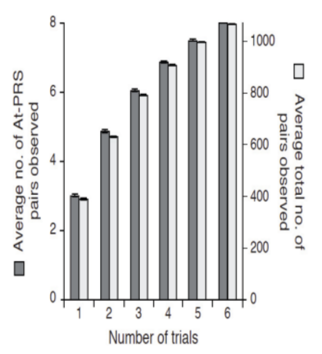
Completeness



Assay-sensitivity

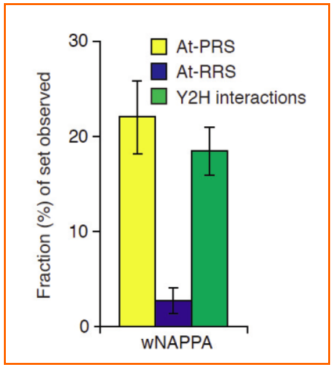


Sampling-sensitivity



Overall completion

Precision



Quality

10%

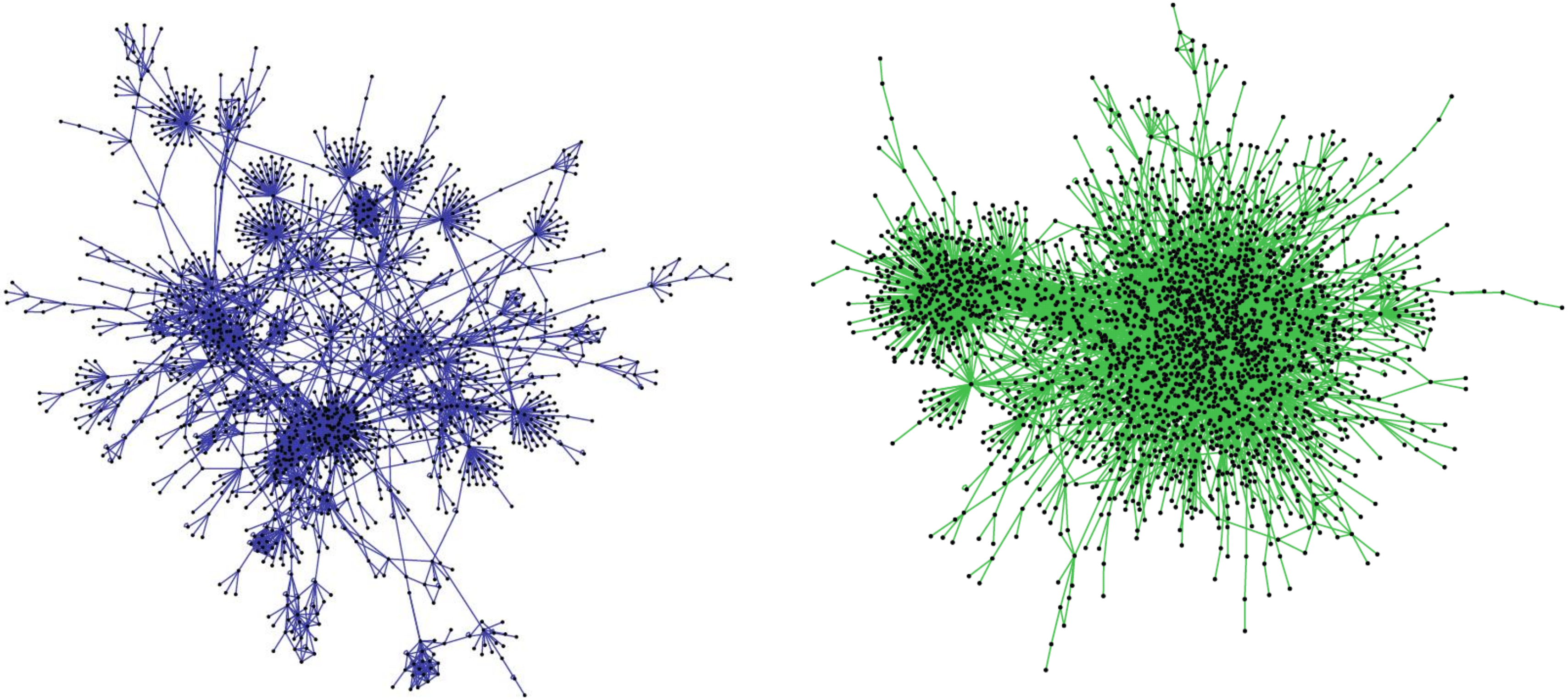
~25%

~40%

~80%

The *Arabidopsis thaliana* interactome contains
~300.000 binary protein-protein interactions

Comparison of AI-1 to literature curated interactions (LCI)



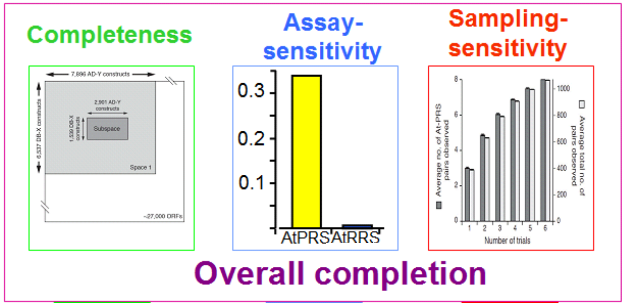
● Protein

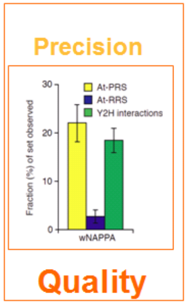
Protein-protein interaction in:

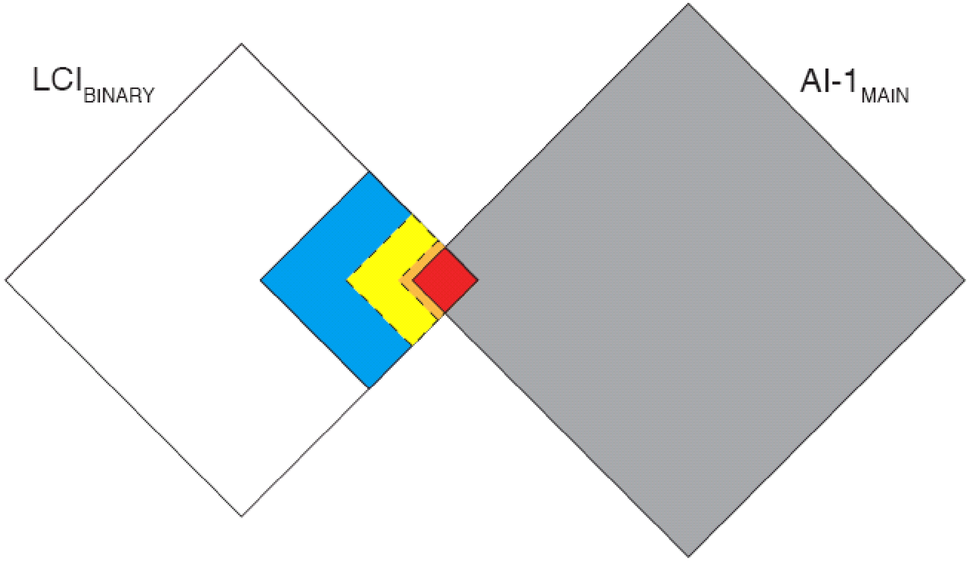
🟦 LCI$_{\text{BINARY}}$

🟩 AI-1$_{\text{MAIN}}$

Comparison of AI-1 to literature curated interactions (LCI)







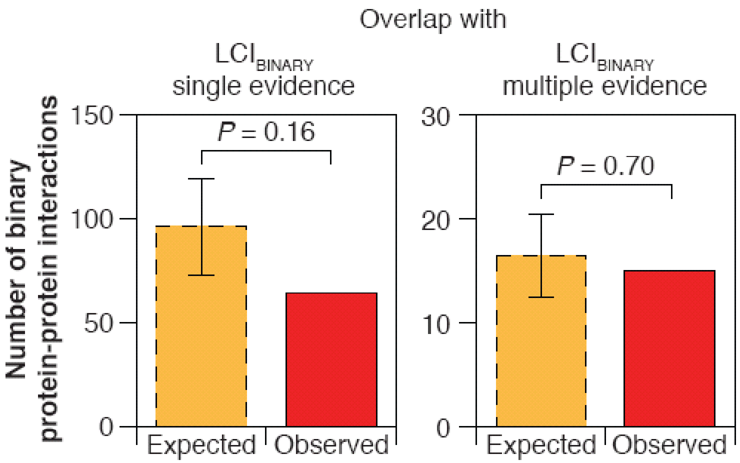
☐ LCI_{BINARY} outside of space 1

🟦 Proportion not detectable given assay sensitivity

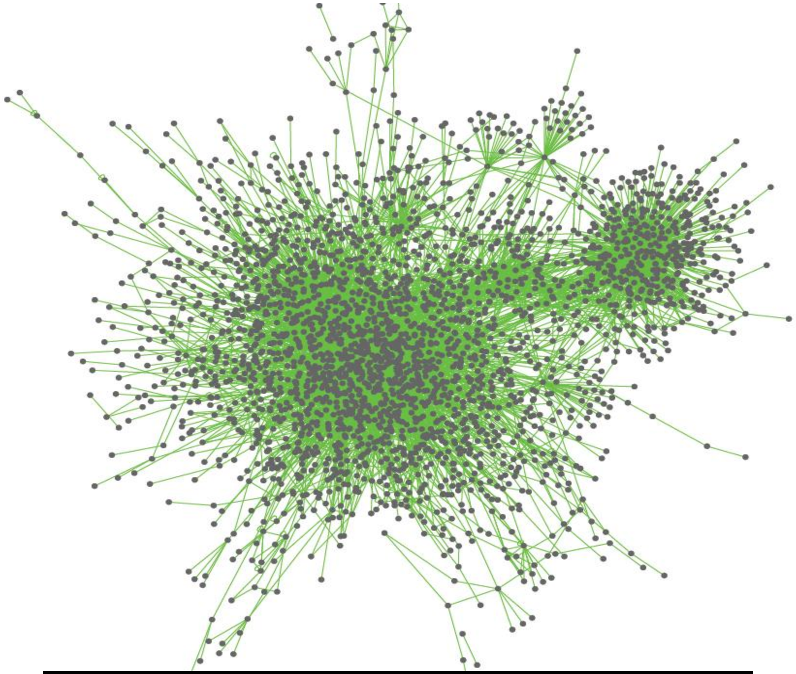
🟨 Proportion not detectable given sampling sensitivity

🟧 Expected overlap

🟥 Observed overlap

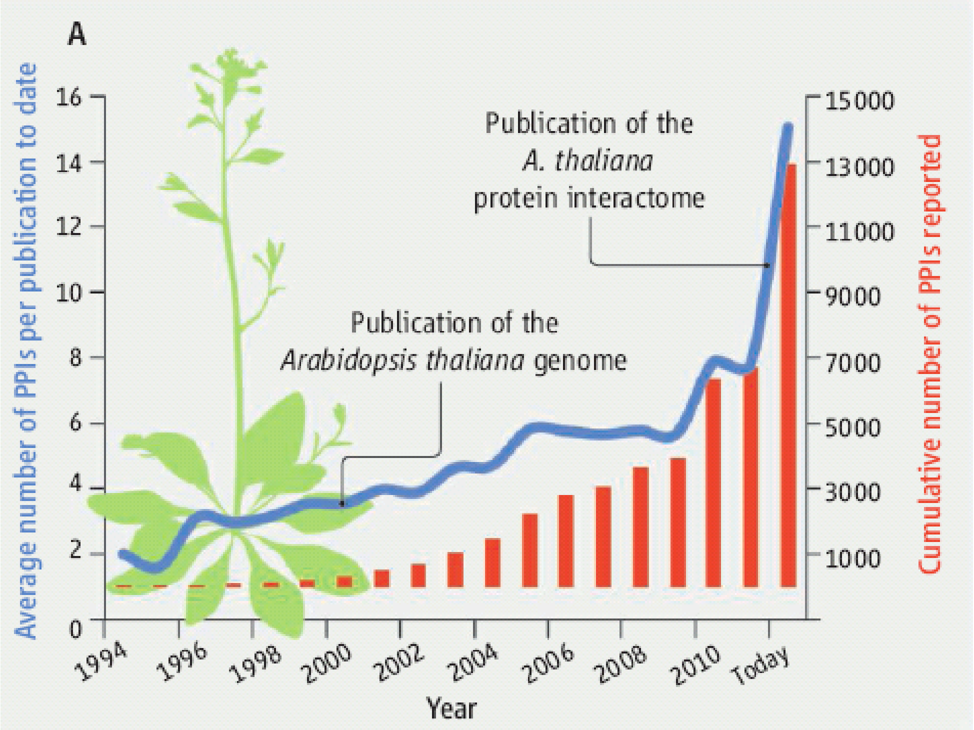


Construction and validation of Arabidopsis Interactome 1 (AI-1)



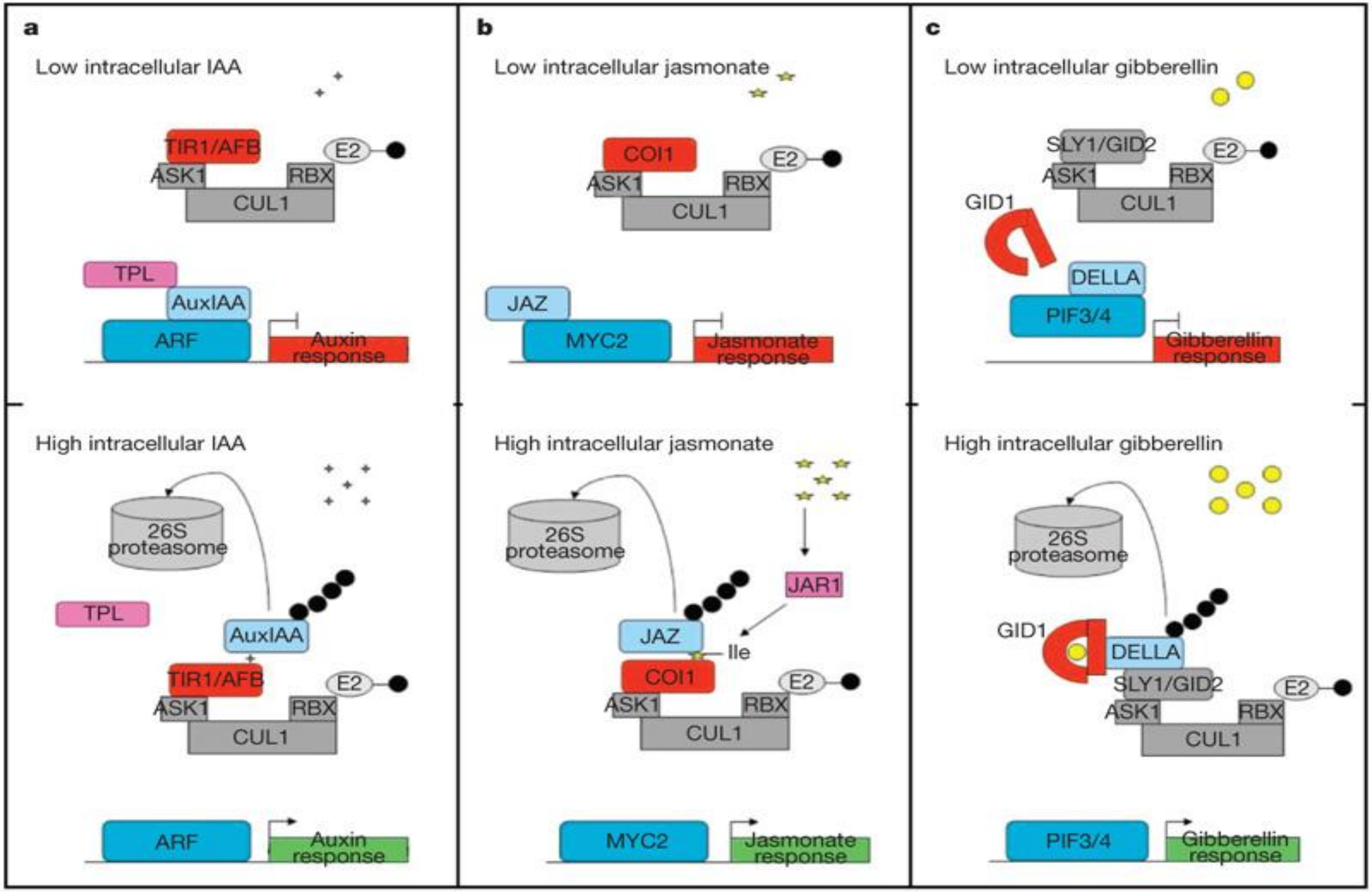
	Nodes	Edges
AI-1$_{\text{MAIN}}$	2,661	5,664
AI-1$_{\text{RPT}}$	673	1,066
AI-1	**2,774**	**6,205**

Arabidopsis Interactome Mapping consortium, *Science*, 29 Jul 2011



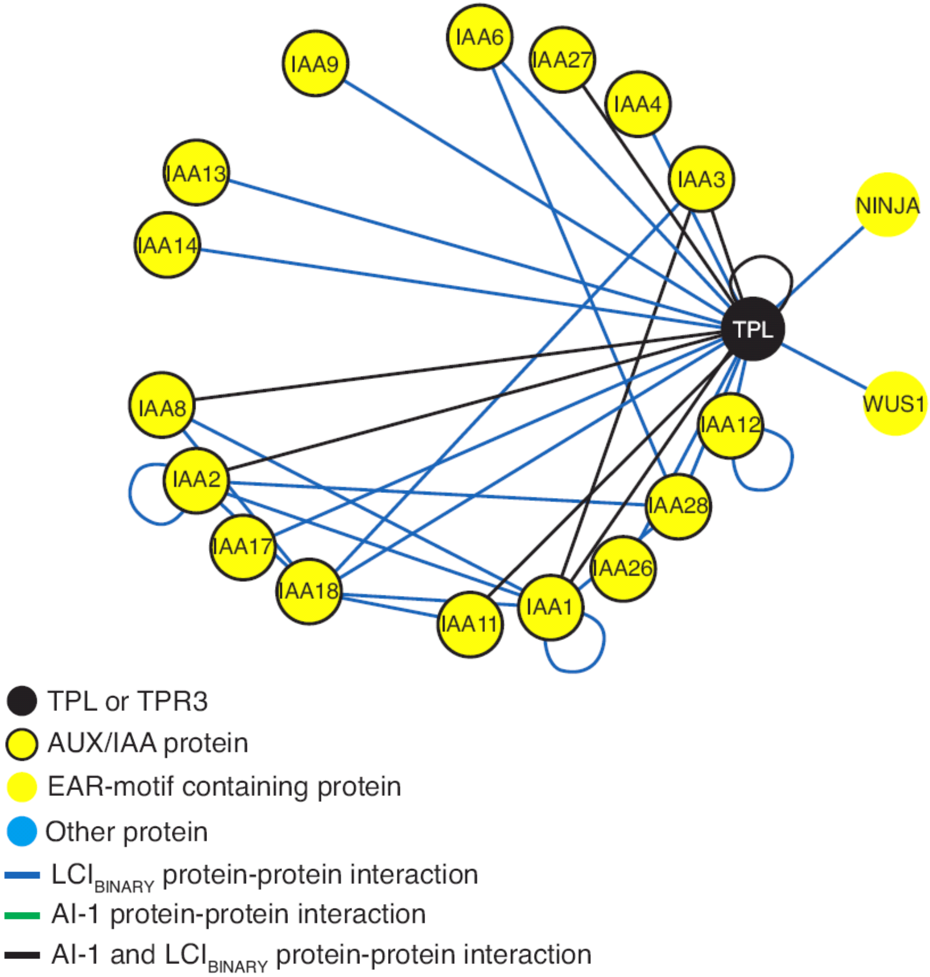
Perspective: A cellular roadmap for the plant kingdom. Landry, CR. *Science* 29 Jul 2011

Co-repressors targeted by hormone induced ubiquitination

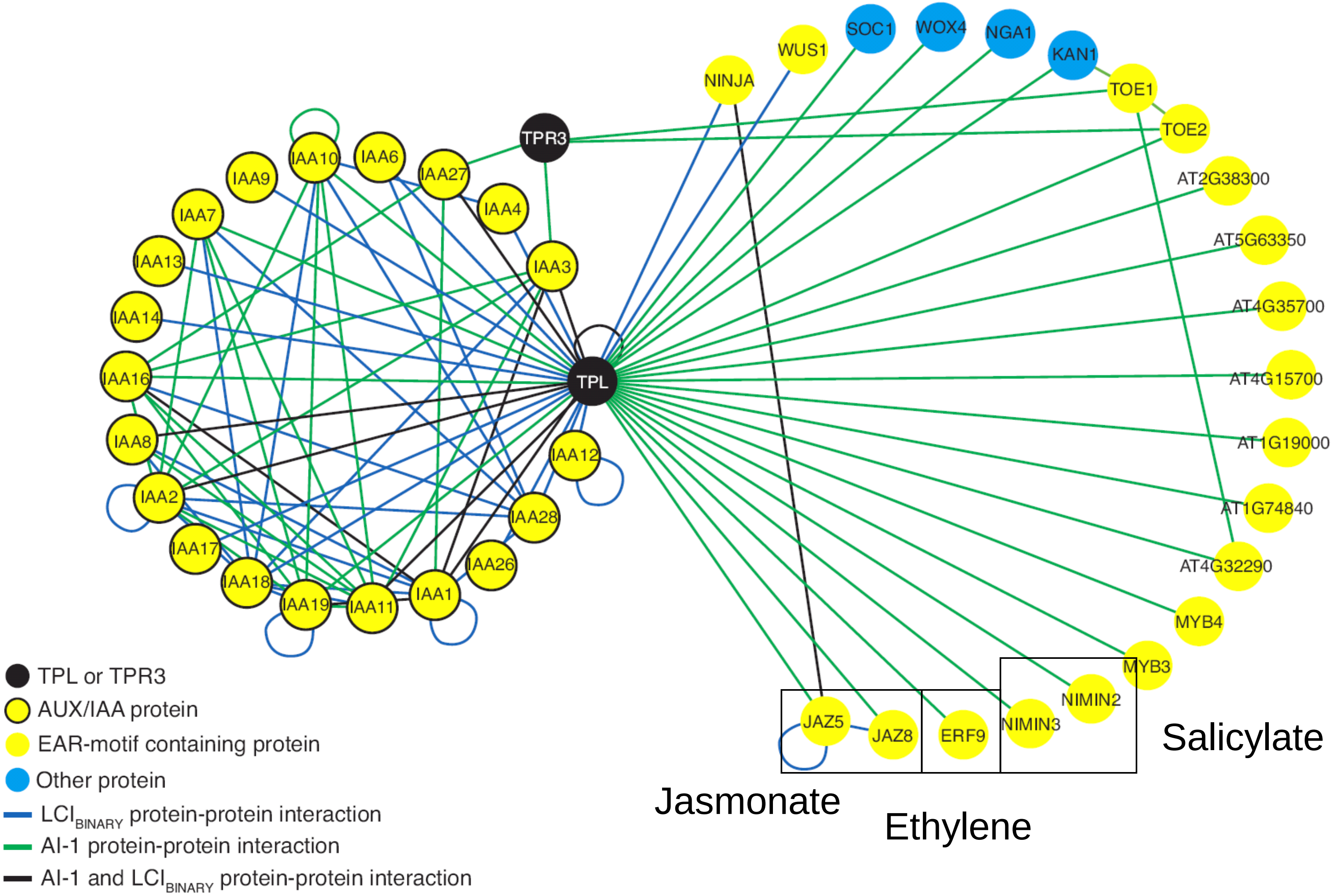


Santner & Estelle, *Nature* (2009)

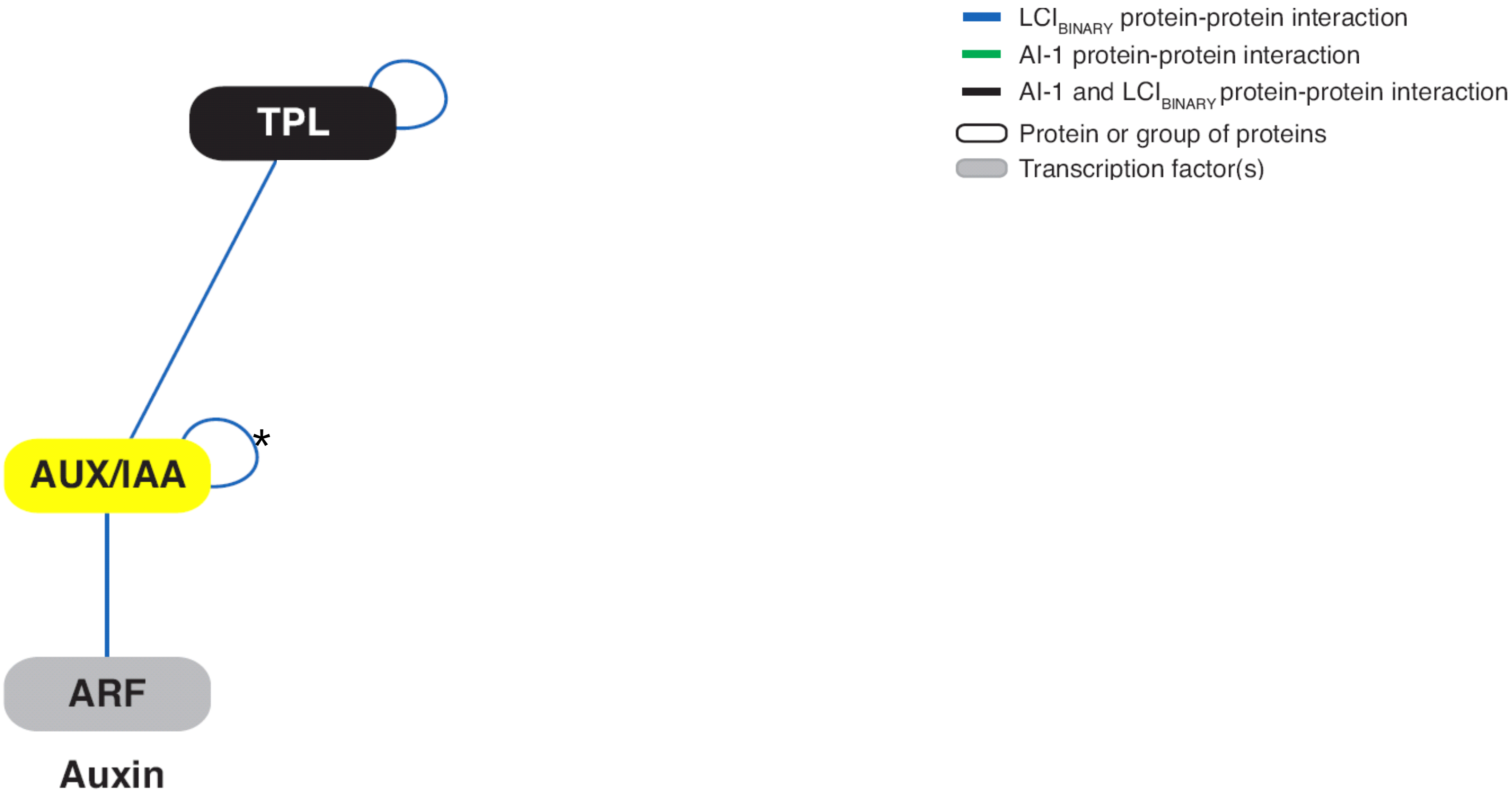
Complexity in hormone co-repressor protein interactions – JAZ TPL interactions



Complexity in hormone co-repressor protein interactions – JAZ TPL interactions

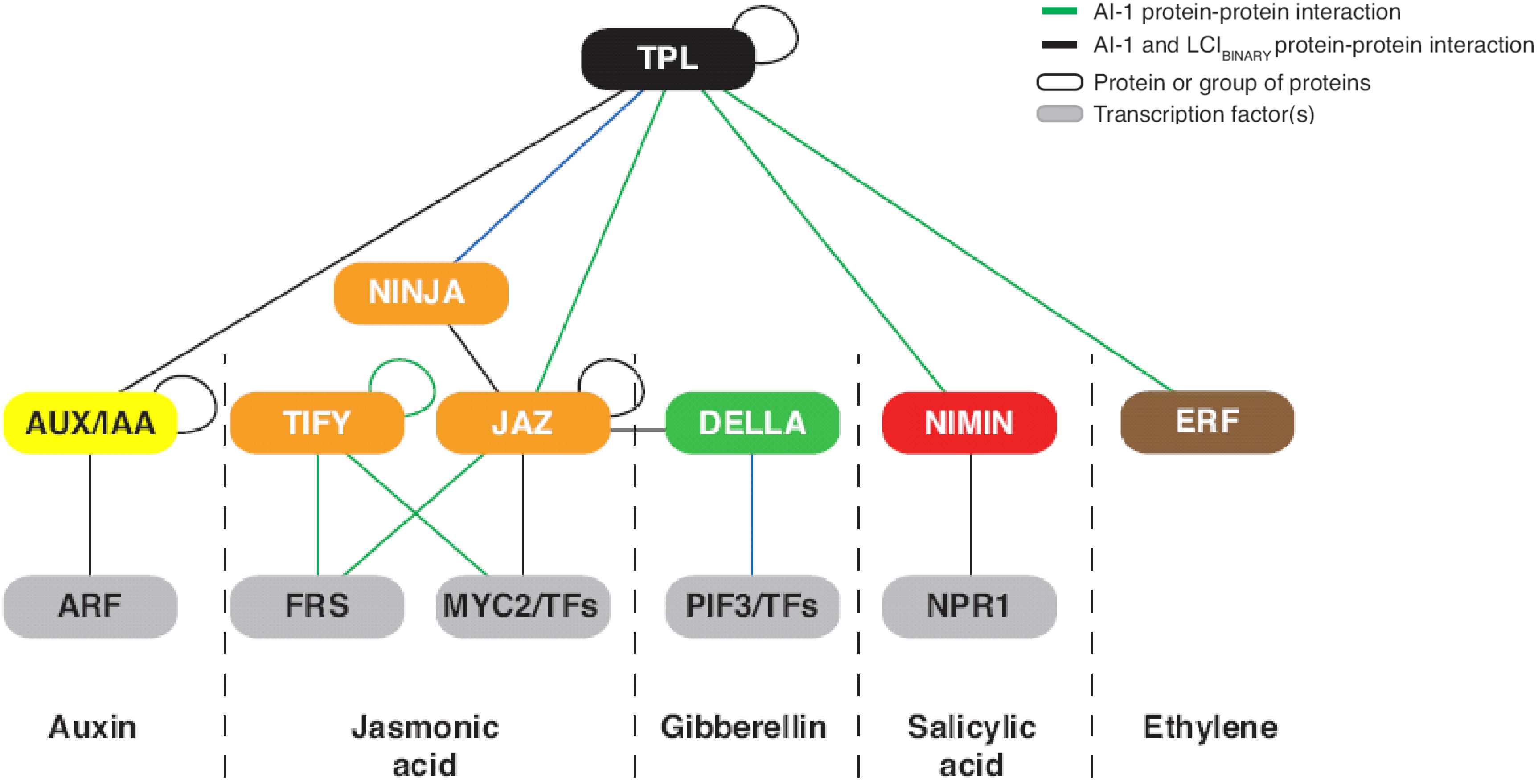


AI-1 reveals hormone transcriptional regulator interconnectivity



* Pauwels *et al.*, *Nature* 2010

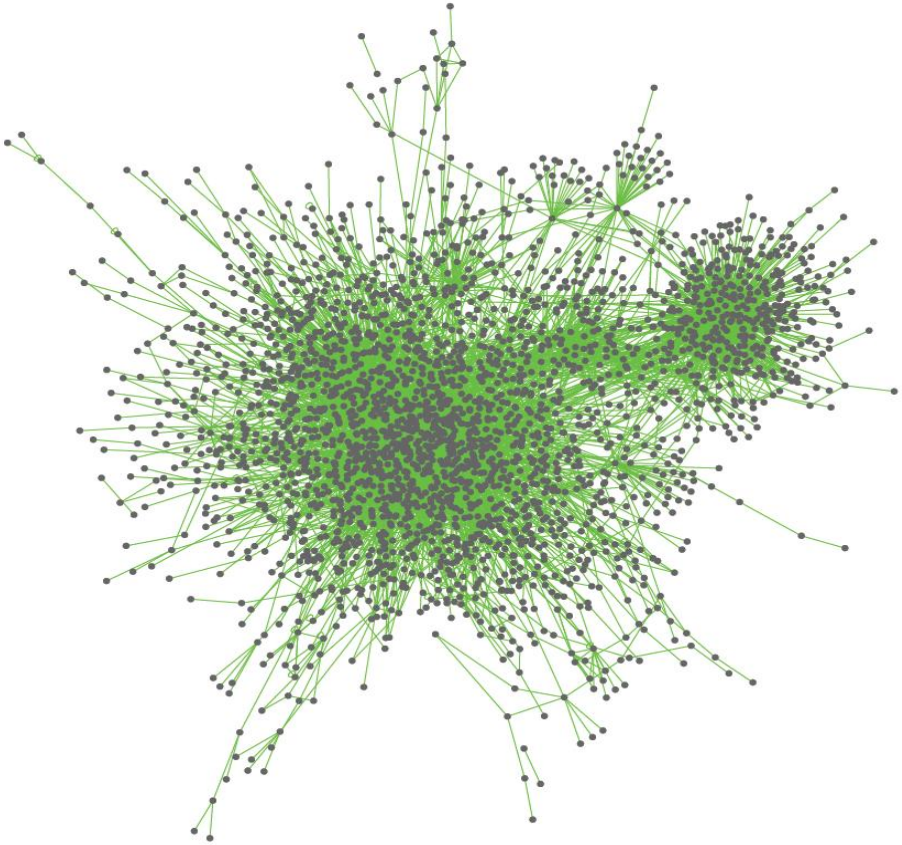
AI-1 reveals hormone transcriptional regulator interconnectivity



* Pauwels *et al.*, *Nature* 2010

Ab initio network analysis

A “countyside” highschool social network



Bearman et al, *Am. J Soc.* 2004

Ab initio network analysis

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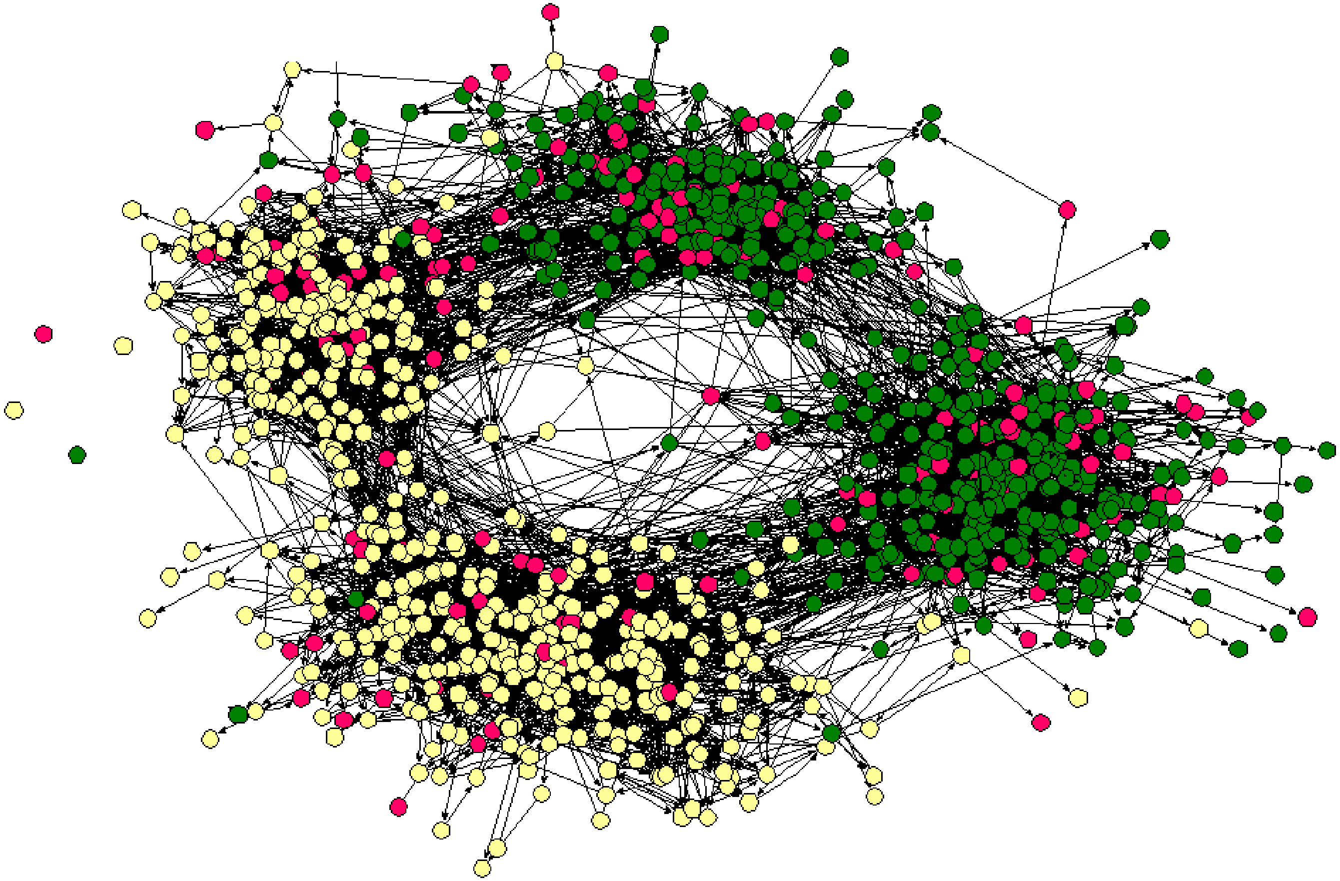
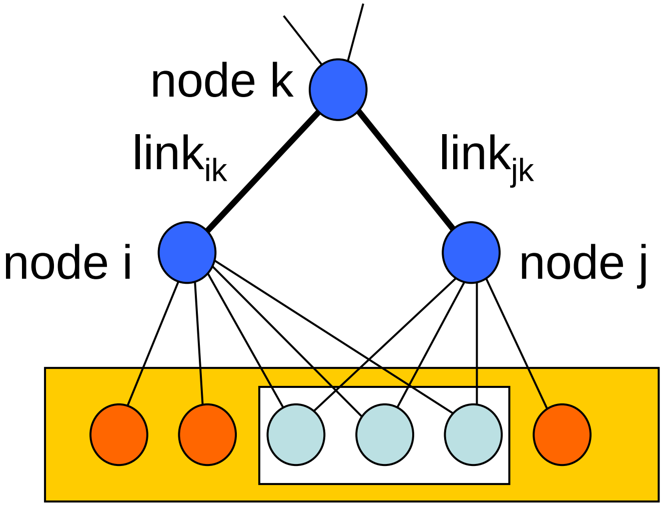
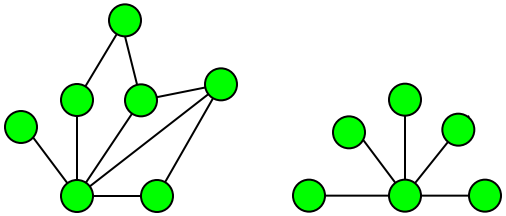


Bearman et al, *Am. J Soc.* 2004

Community detection by link analysis



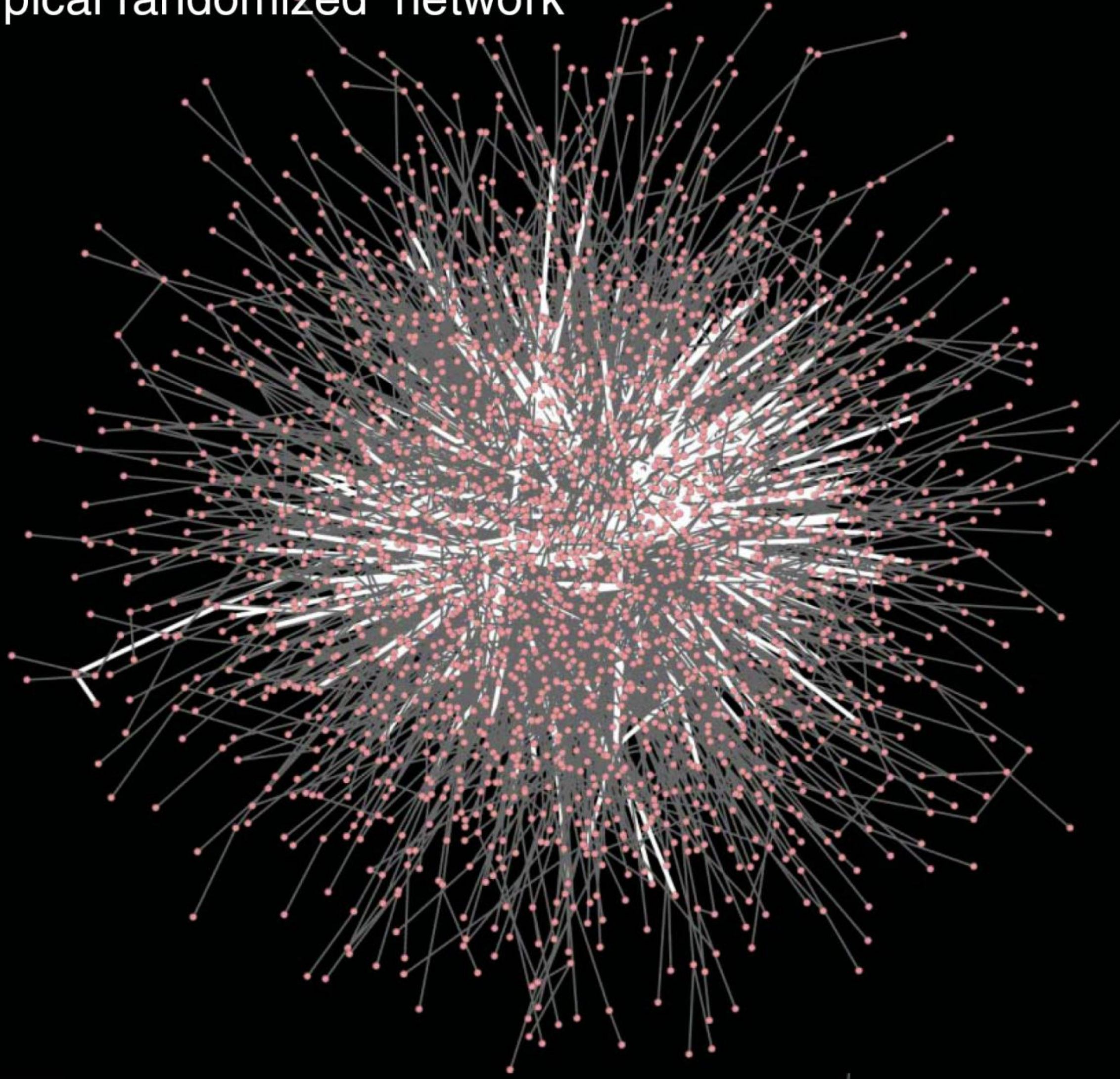
Ahn *et al.*, *Nature* 2010

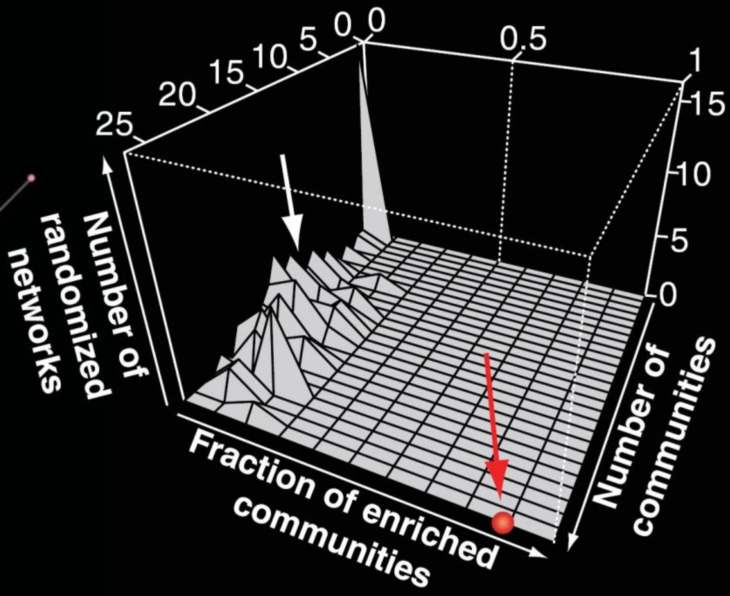


Size >5 nodes	Density >0	Density =0
GO enriched	23	29
Not enriched	3	53

Odds ratio= 13, p = 0.000002

Typical randomized network





Protein-protein interaction assigned to community:

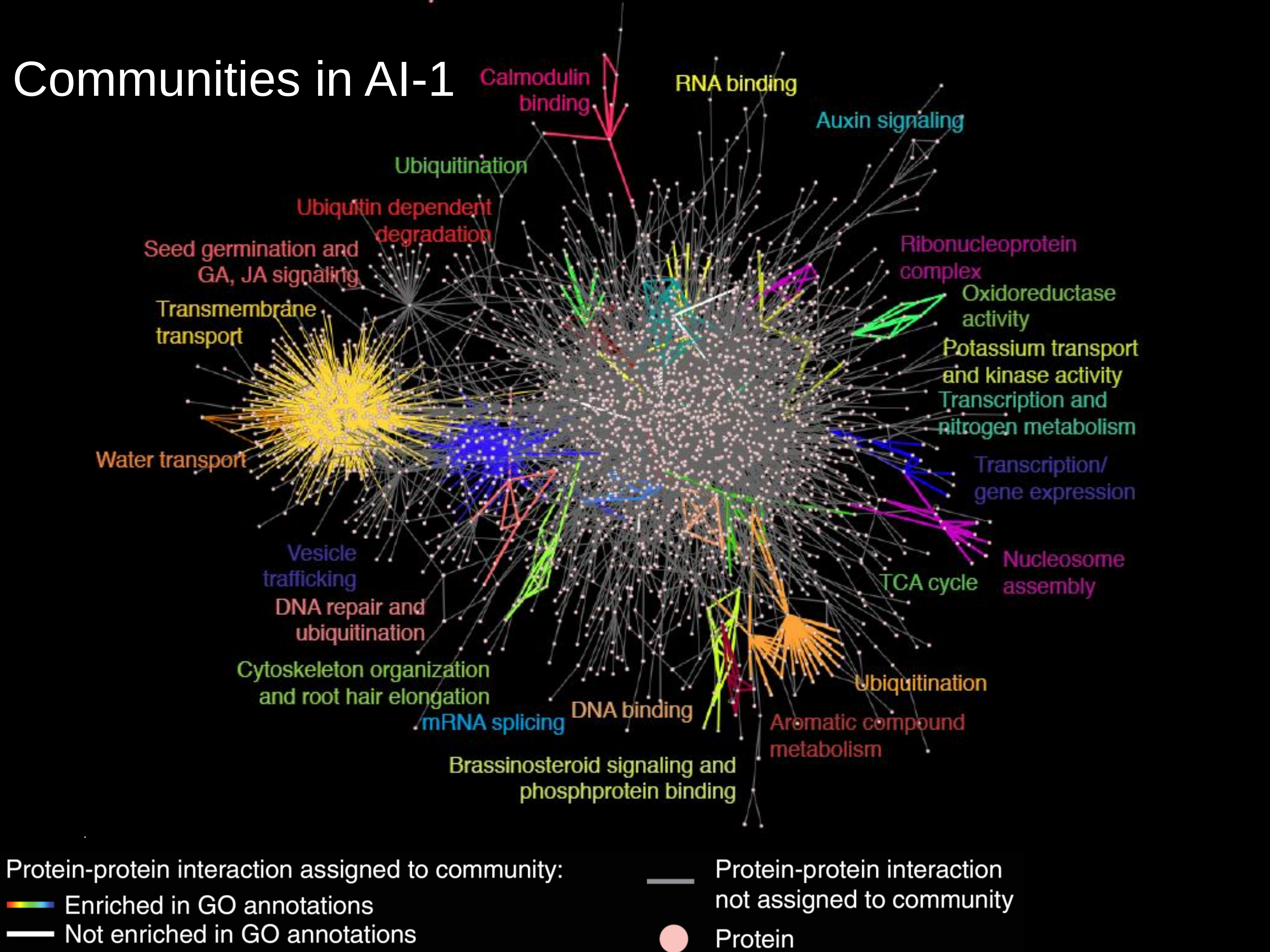
🌈 Enriched in GO annotations

━ Not enriched in GO annotations

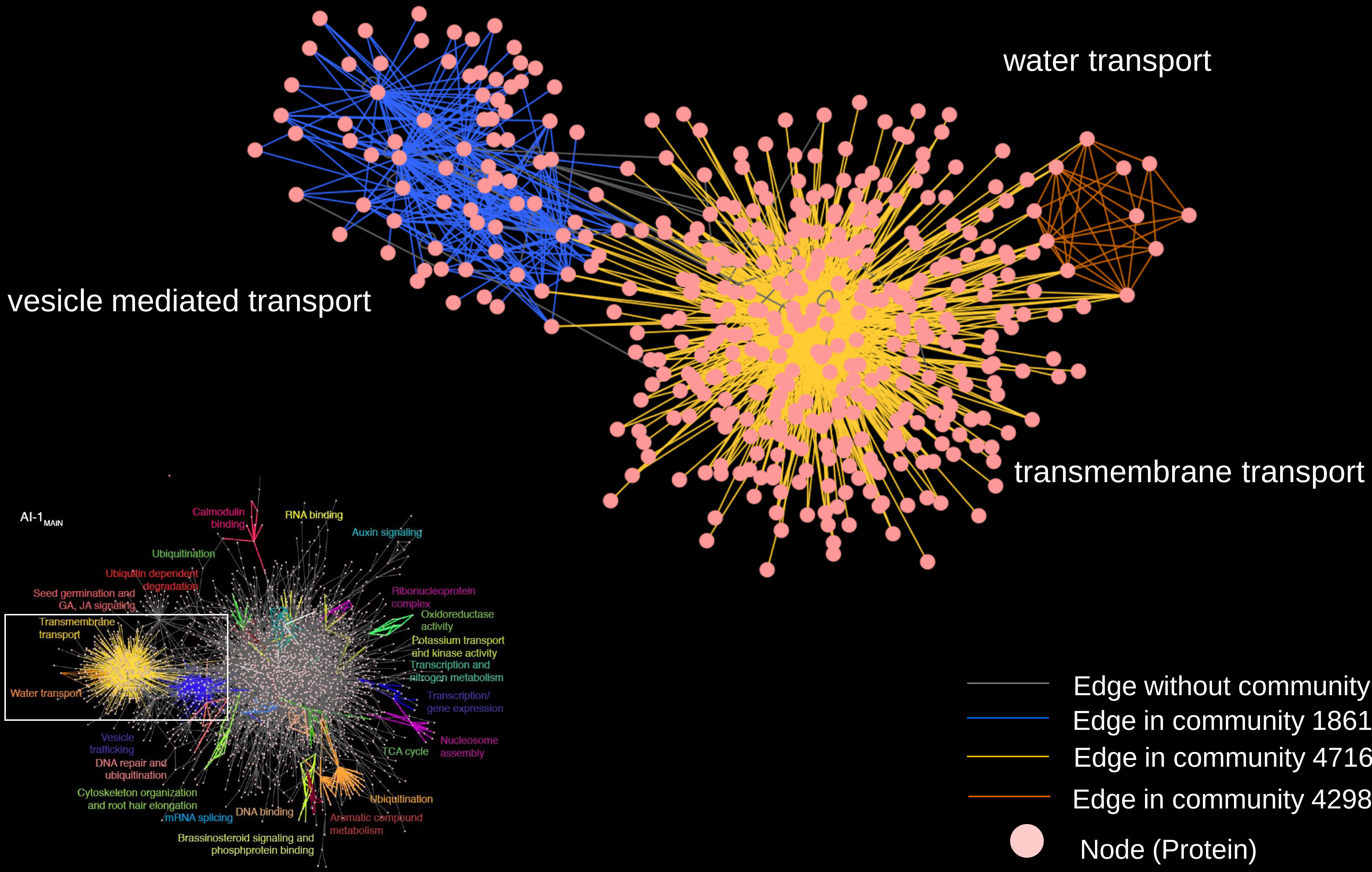
━ Protein-protein interaction not assigned to community

● Protein

Communities in AI-1

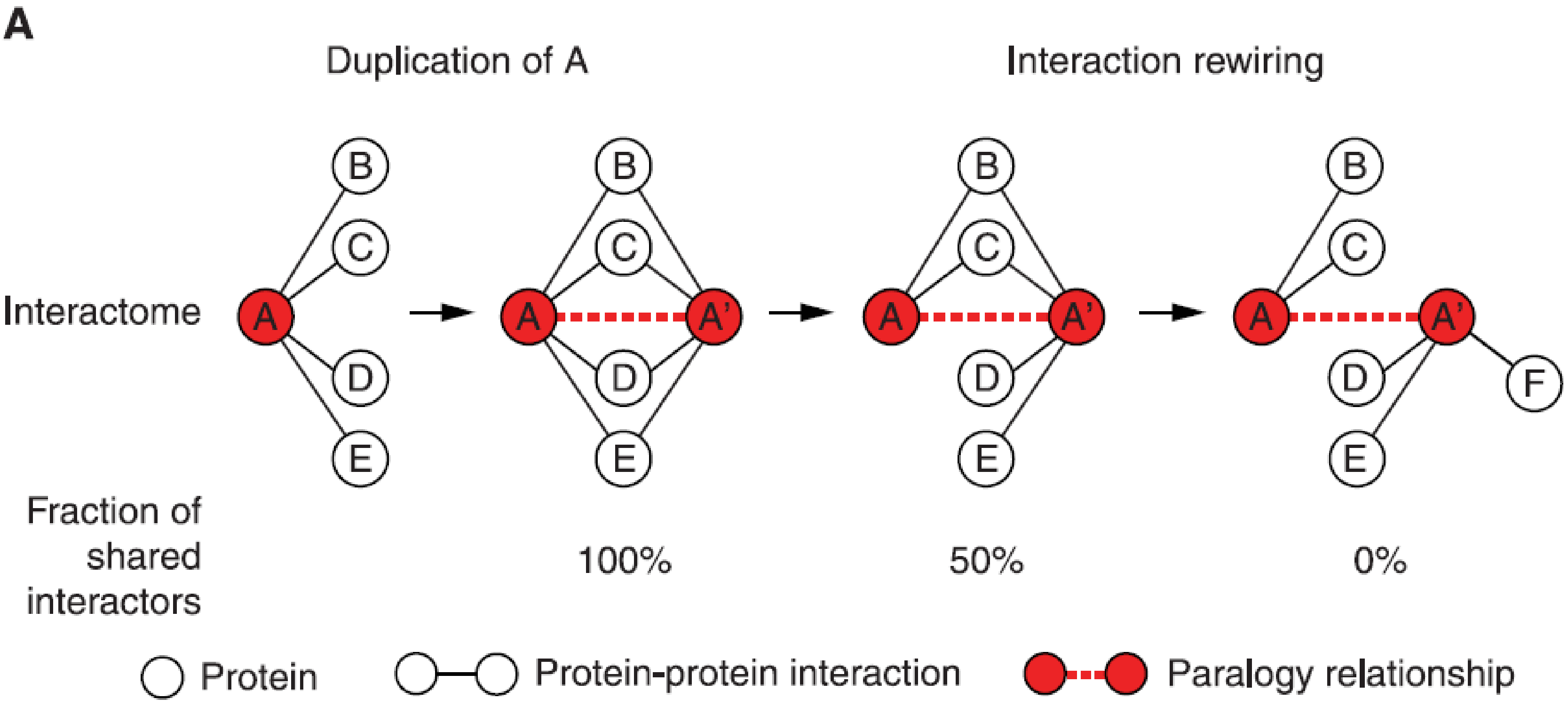


Connected communities in AI-1



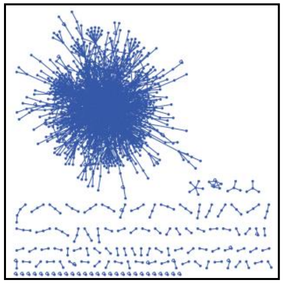
— Edge without community
— Edge in community 1861
— Edge in community 4716
— Edge in community 4298
● Node (Protein)

Duplication divergence model



AI-1 contains 1,882 pairs of paralogous proteins

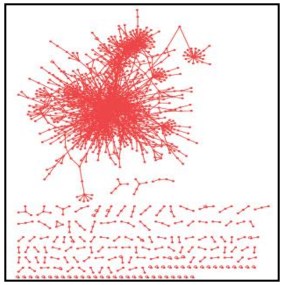
1,549 proteins



human

Rual *et al*., 2005

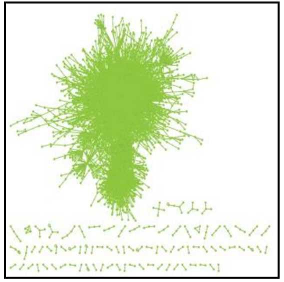
1,278 proteins



yeast

Yu *et al*., 2008

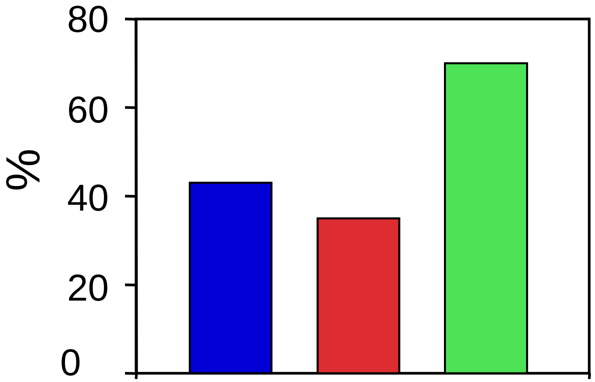
2,661 proteins



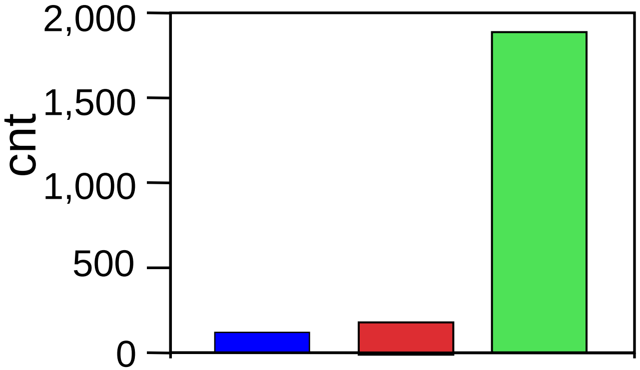
Arabidopsis

to be published

🟦 Human
🟥 Yeast
🟩 Arabidopsis



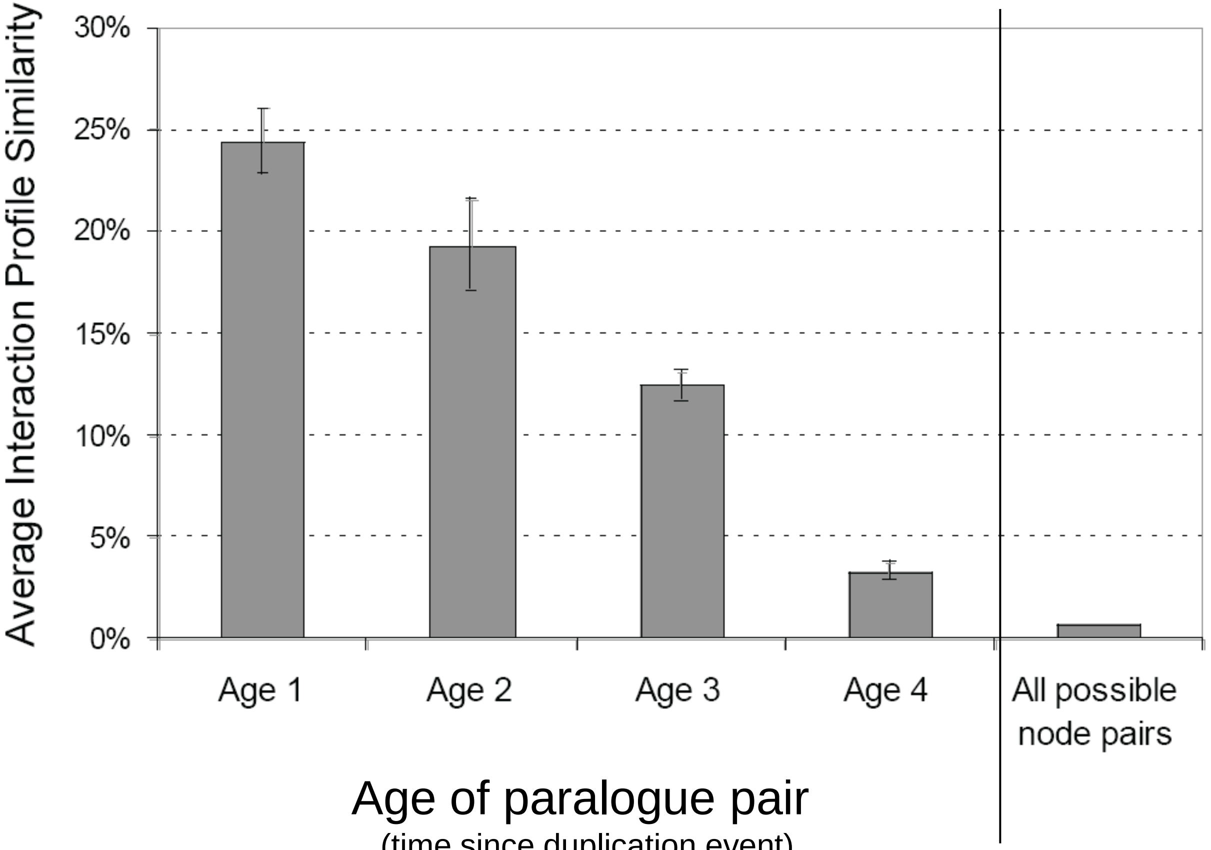
Fraction of genes with a paralog in the genome.



Number of genes with paralog in AI-1

Paralogy relationships: Villella *et al. Genome Research* 2008; ;Gramene.org; Ensembl.org

Interaction profile similarity of paralogues decreases over evolutionary time



Age of paralogue pair

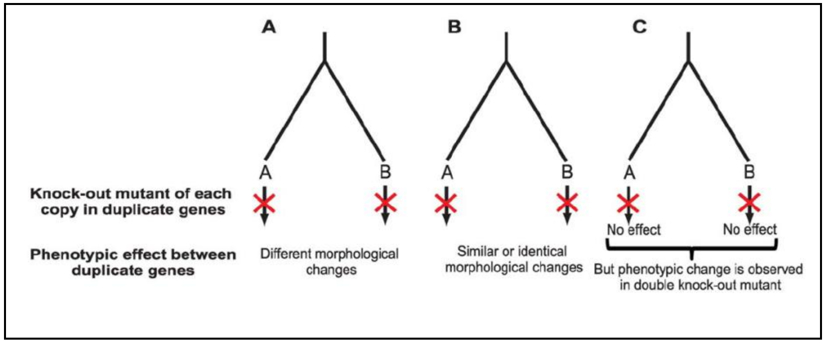
(time since duplication event)

Interaction profile correlates with functional divergence

OPEN ACCESS Freely available online PLoS GENETICS

Increased Expression and Protein Divergence in Duplicate Genes Is Associated with Morphological Diversification

Kousuke Hanada[1,2]*, Takashi Kuromori[1], Fumiyoshi Myouga[1], Tetsuro Toyoda[2], Kazuo Shinozaki[1]

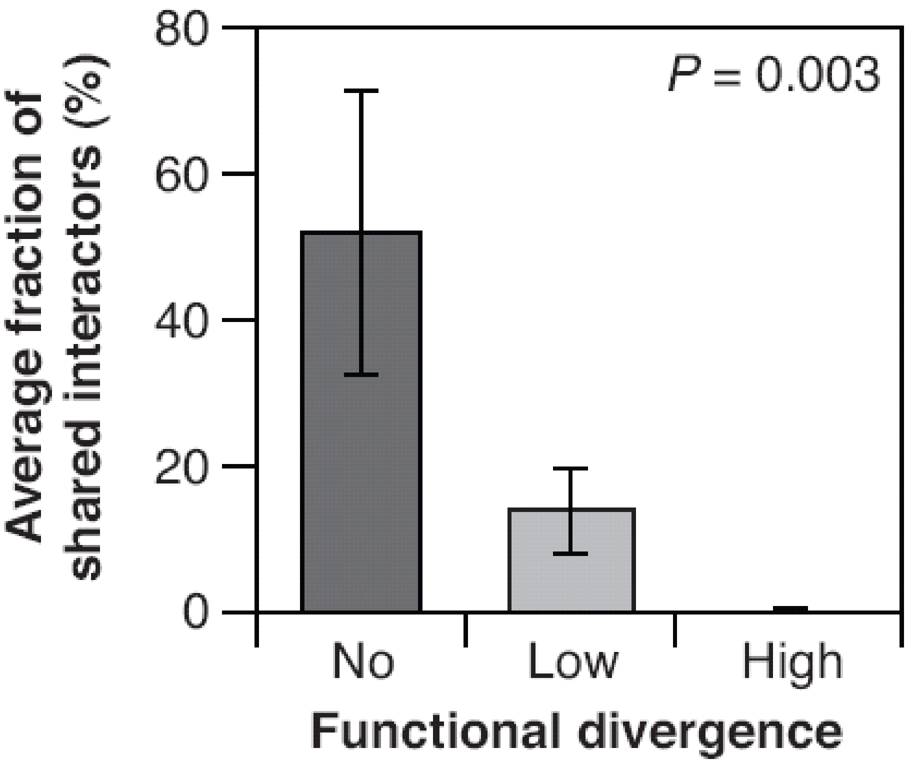


Functional divergence

High

Some

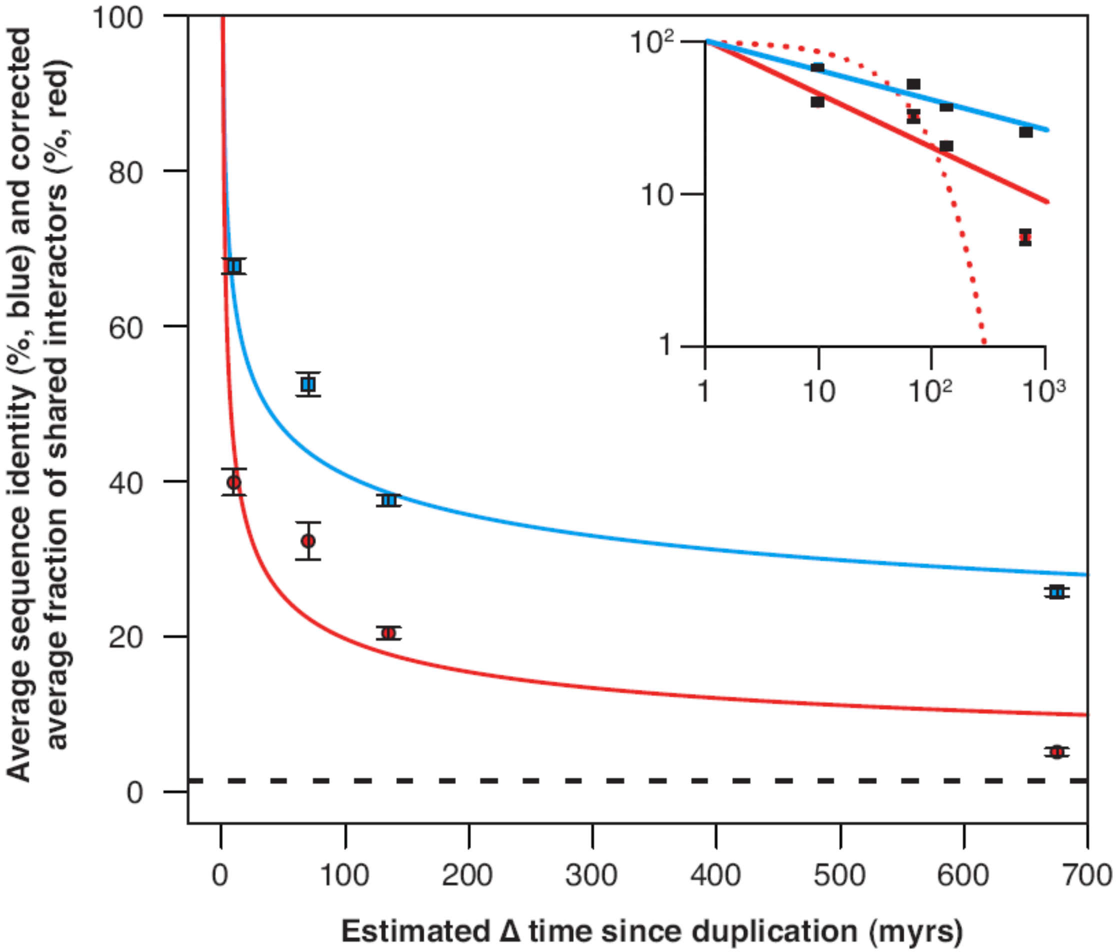
No



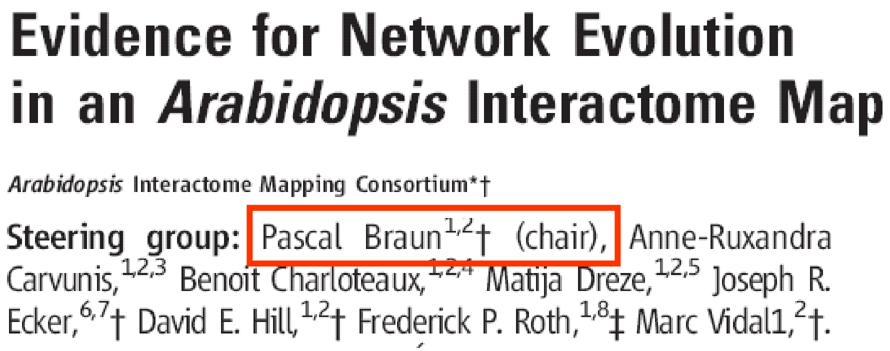
Rapid then slow divergence

— Sequence similarity

— Interaction profile



Arabidopsis thaliana interactome network papers

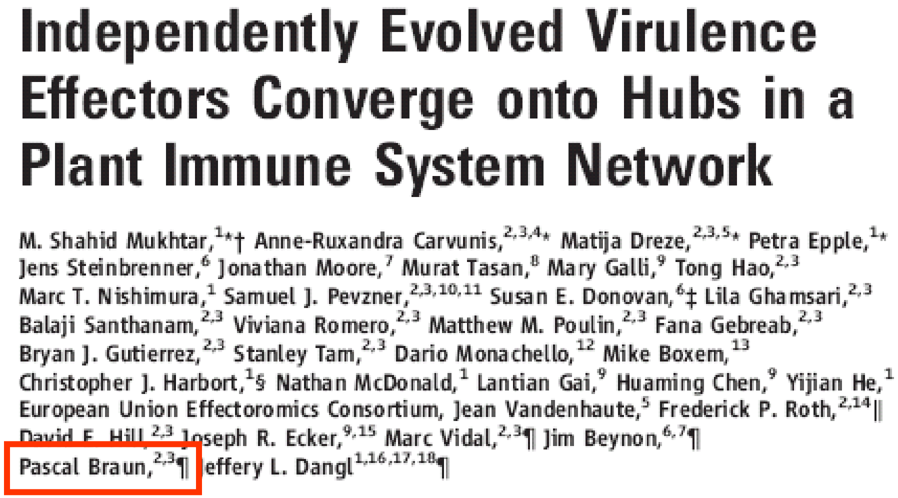


Evidence for Network Evolution in an *Arabidopsis* Interactome Map

Arabidopsis Interactome Mapping Consortium*†

Steering group: Pascal Braun[1,2]† (chair), Anne-Ruxandra Carvunis,[1,2,3] Benoit Charloteaux,[1,2,4] Matija Dreze,[1,2,5] Joseph R. Ecker,[6,7]† David E. Hill,[1,2]† Frederick P. Roth,[1,8]‡ Marc Vidal1,[2]†.

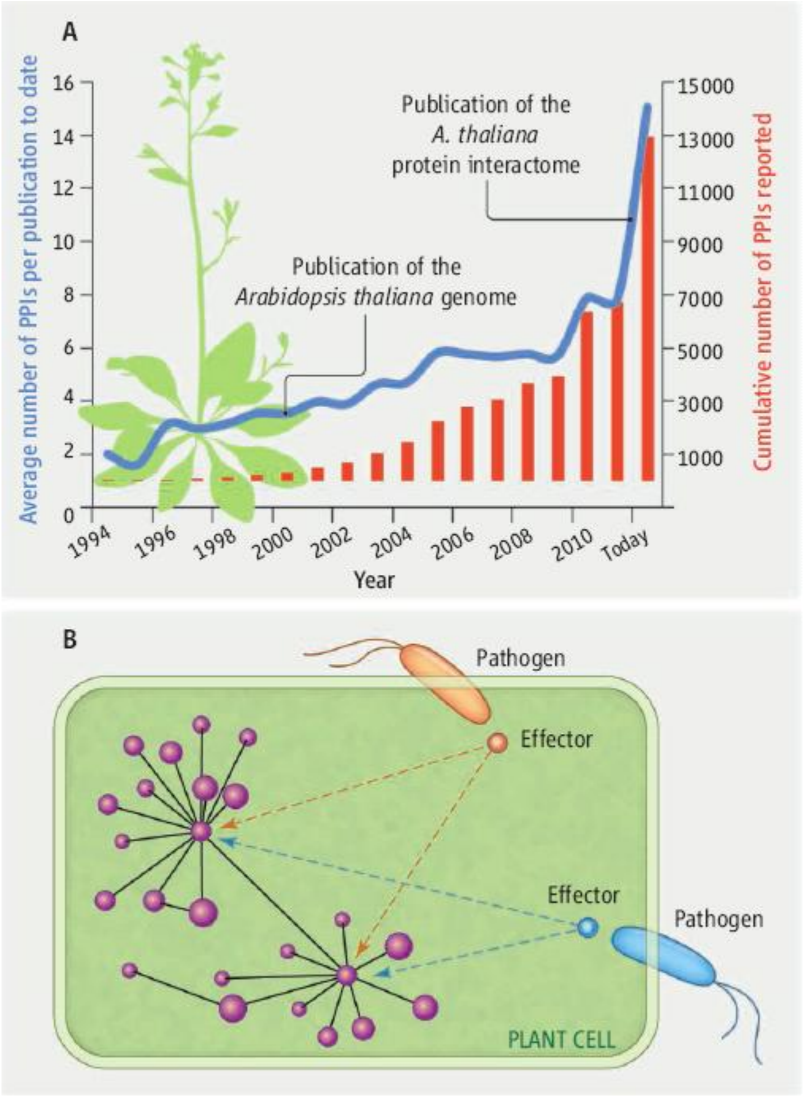
Science, 29 July 2011: 601-607



Independently Evolved Virulence Effectors Converge onto Hubs in a Plant Immune System Network

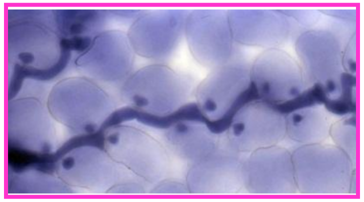
M. Shahid Mukhtar,[1]*† Anne-Ruxandra Carvunis,[2,3,4]* Matija Dreze,[2,3,5]* Petra Epple,[1]* Jens Steinbrenner,[6] Jonathan Moore,[7] Murat Tasan,[8] Mary Galli,[9] Tong Hao,[2,3] Marc T. Nishimura,[1] Samuel J. Pevzner,[2,3,10,11] Susan E. Donovan,[6]‡ Lila Ghamsari,[2,3] Balaji Santhanam,[2,3] Viviana Romero,[2,3] Matthew M. Poulin,[2,3] Fana Gebreab,[2,3] Bryan J. Gutierrez,[2,3] Stanley Tam,[2,3] Dario Monachello,[12] Mike Boxem,[13] Christopher J. Harbort,[1]§ Nathan McDonald,[1] Lantian Gai,[9] Huaming Chen,[9] Yijian He,[1] European Union Effectoromics Consortium, Jean Vandenhaute,[5] Frederick P. Roth,[2,14]‖ David E. Hill,[2,3] Joseph R. Ecker,[9,15] Marc Vidal,[2,3]¶ Jim Beynon,[6,7]¶ Pascal Braun,[2,3]¶ Jeffery L. Dangl[1,16,17,18]¶

Science, 29 July 2011: 596-601.



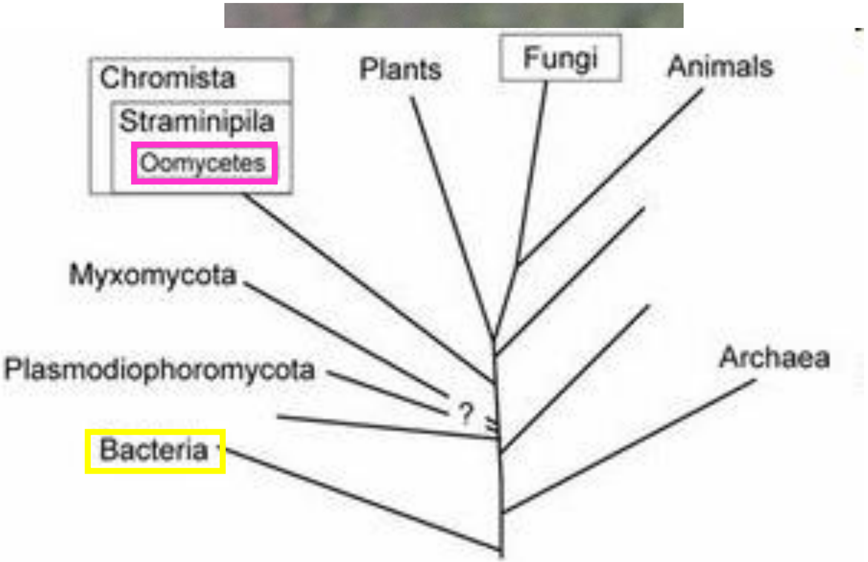
Perspective: A cellular roadmap for the plant kingdom. Landry, CR. *Science* 29 Jul 2011

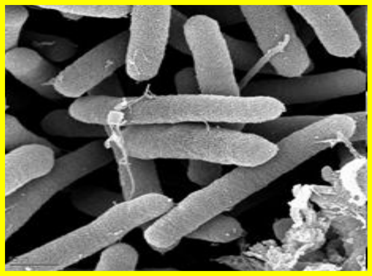
Plant pathogens



Hyaloperonospora arabidopsidis (Hpa)

1 Ga





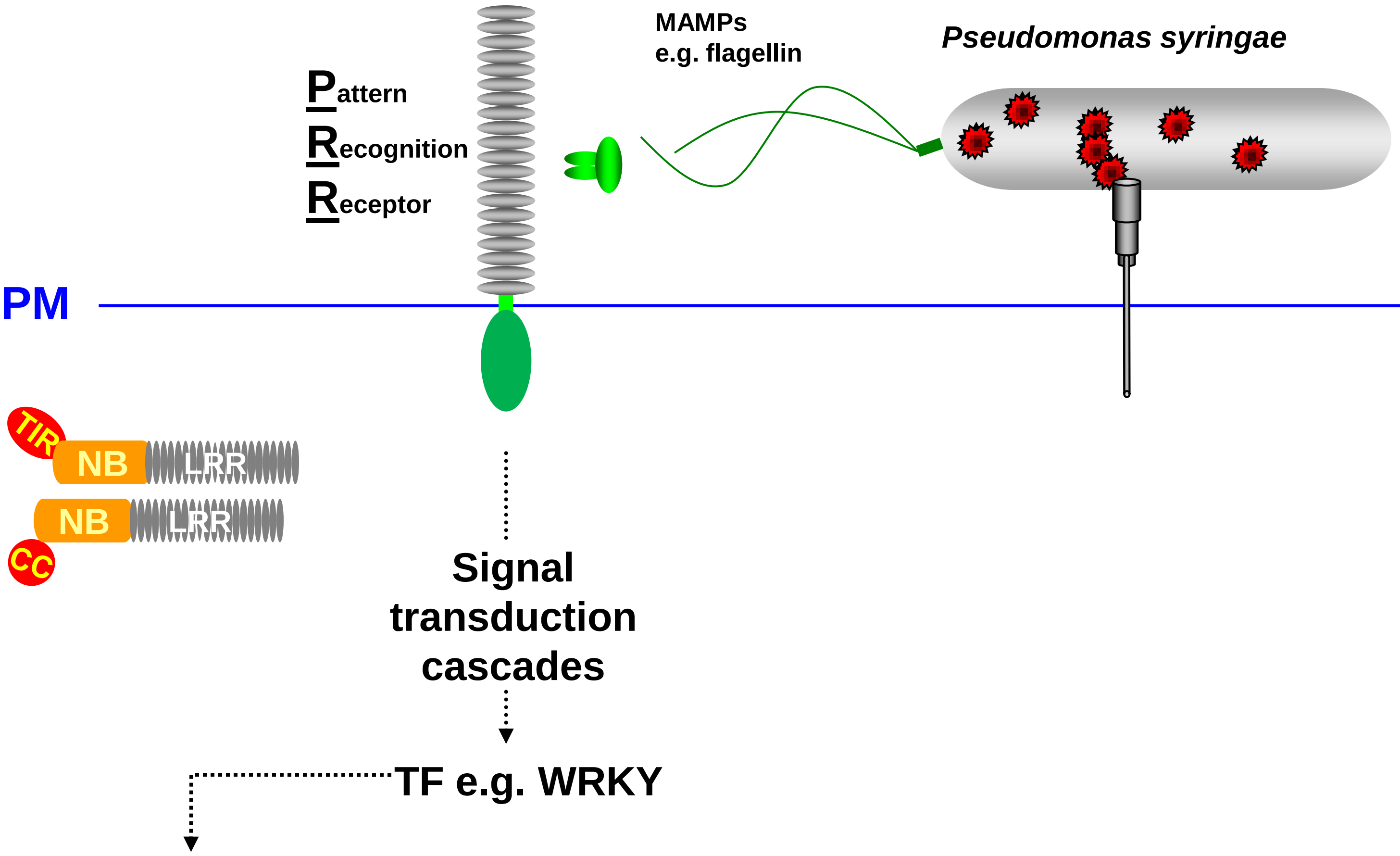
Pseudomonas syringae (Psy)

Hpa* infected *A. thaliana

Psy* infected *A. thaliana

Collaboration with Jeff Dangl (UNC), Jim Beyon (Warwick U.)

Molecular basis of disease resistance in Arabidopsis



Pattern
Recognition
Receptor

MAMPs
e.g. flagellin

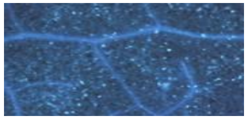
Pseudomonas syringae

PM

Signal transduction cascades

TF e.g. WRKY

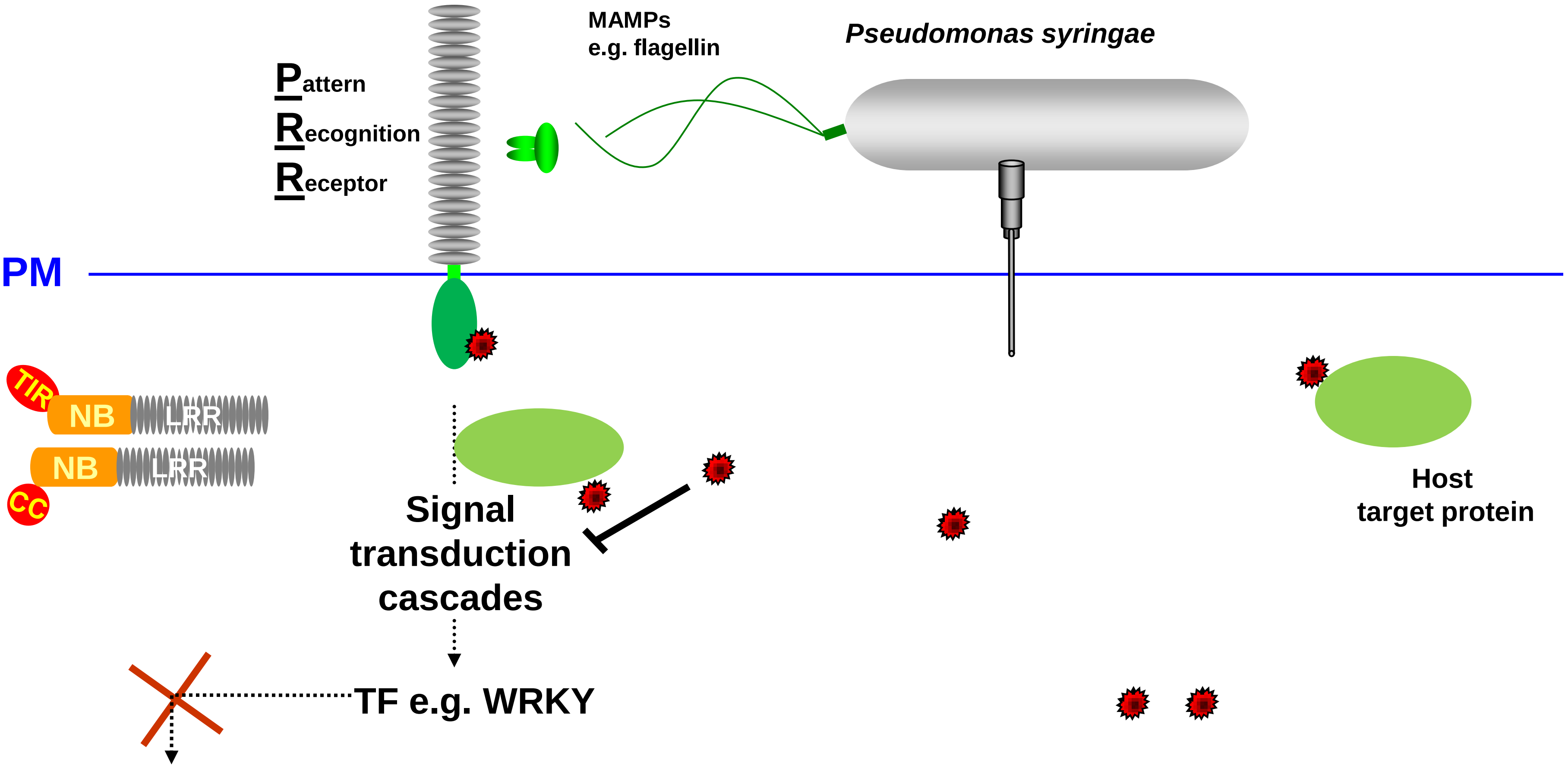
MAMPs-
Triggered
Immunity



S. Mukhtar, Dangl lab

Dangl and Jones (2006), modified

Molecular basis of disease resistance in Arabidopsis



Pattern
Recognition
Receptor

MAMPs
e.g. flagellin

Pseudomonas syringae

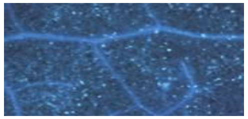
PM

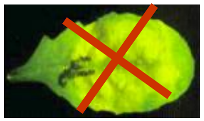
Signal transduction cascades

TF e.g. WRKY

Host
target protein

MAMPs-
Triggered
Immunity



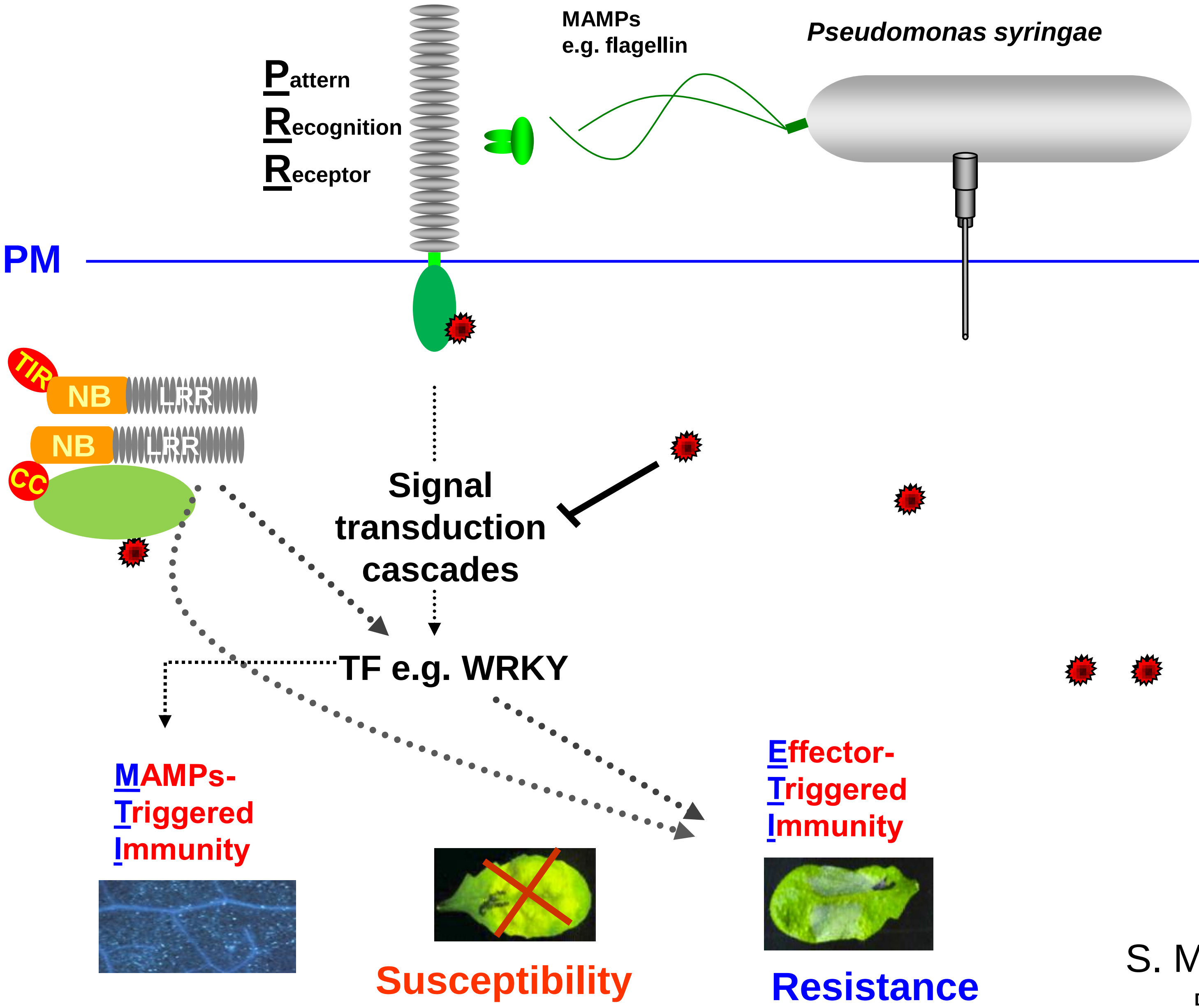


Susceptibility

S. Mukhtar, Dangl lab

Dangl and Jones (2006), modified

Molecular basis of disease resistance in Arabidopsis



Pattern
Recognition
Receptor

MAMPs
e.g. flagellin

Pseudomonas syringae

PM

Signal transduction cascades

Host target protein

TF e.g. WRKY

MAMPs-Triggered Immunity

Susceptibility

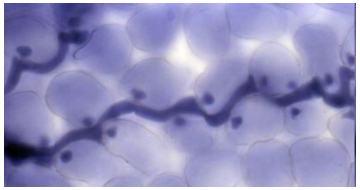
Effector-Triggered Immunity

Resistance

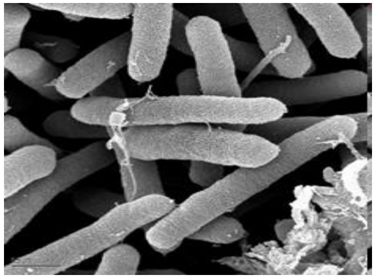
S. Mukhtar, Dangl lab

Dangl and Jones (2006), modified

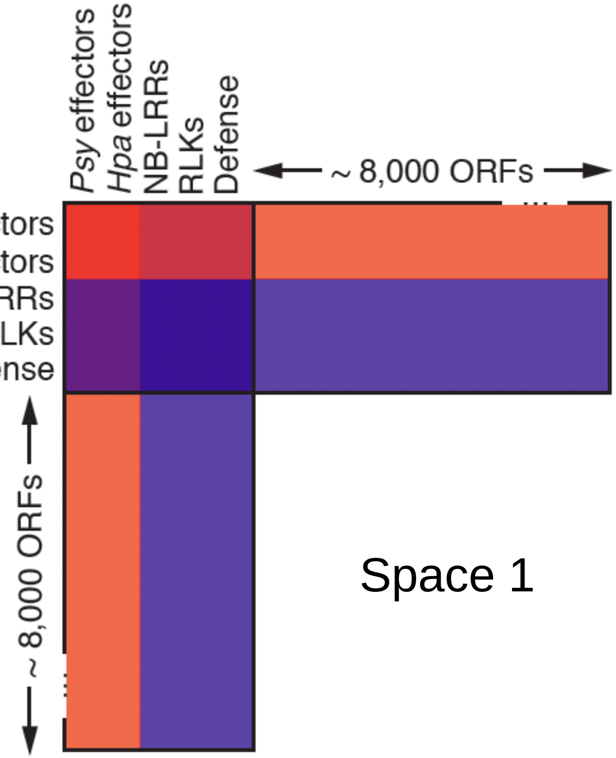
Experimental immune network



Hyaloperonospora arabidopsidis (Hpa)
(64 effectors)



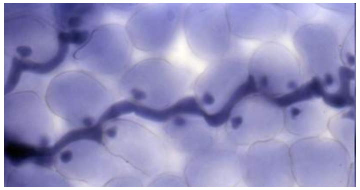
Pseudomonas syringae (Psy)
(44 effectors)



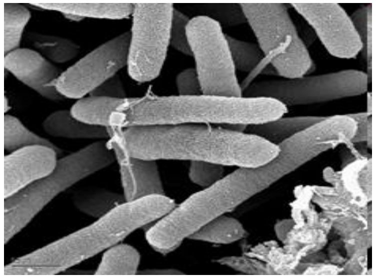
Hpa* infected *A. thaliana

Psy* infected *A. thaliana

Experimental immune network



Hyaloperonospora arabidopsidis (Hpa)
(64 effectors)



Pseudomonas syringae (Psy)
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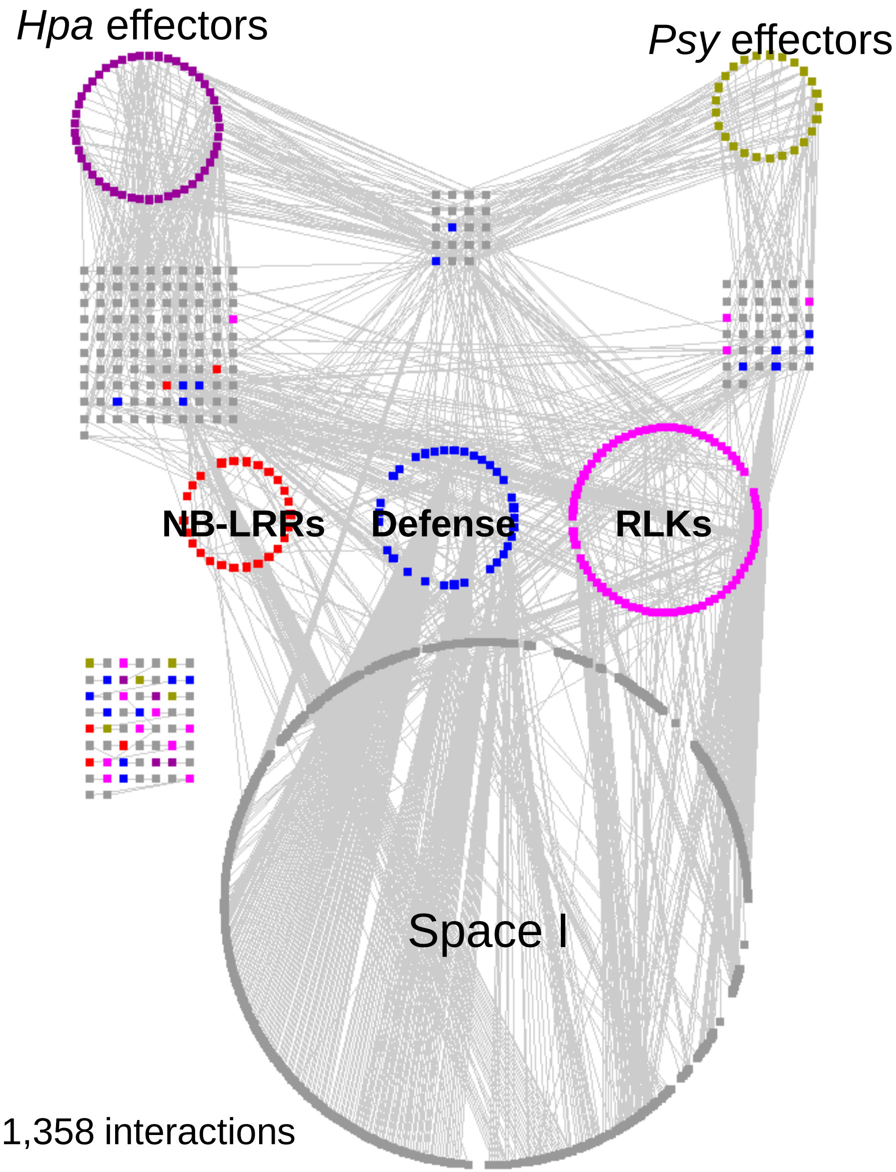


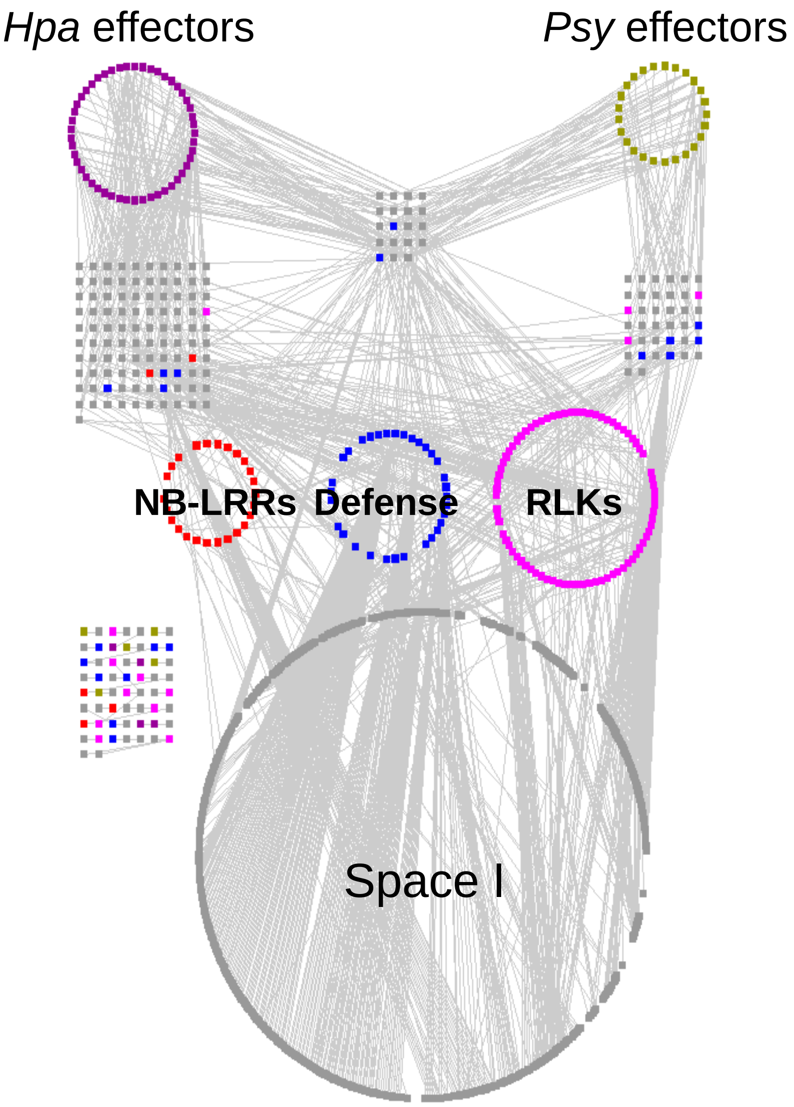
Hpa* infected *A. thaliana

Psy* infected *A. thaliana

— 1,358 interactions

● 926 proteins

Evolutionary distant pathogens converge on common targets



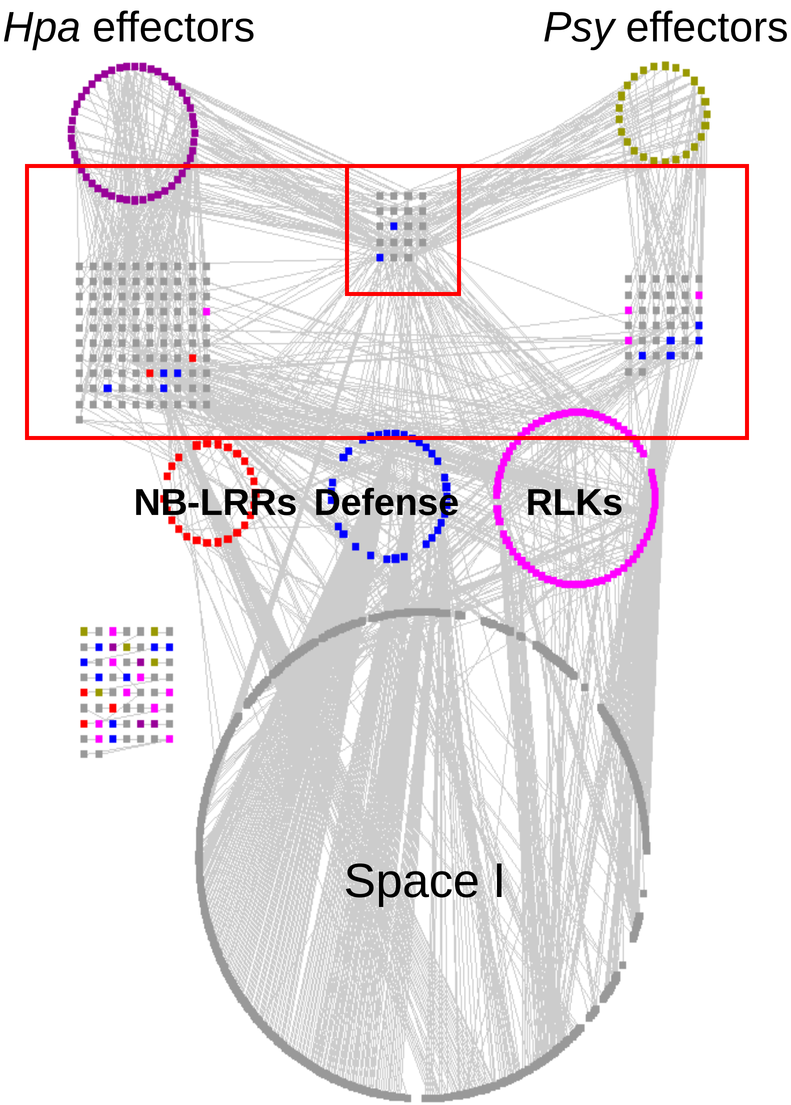
Pathogen Effectors

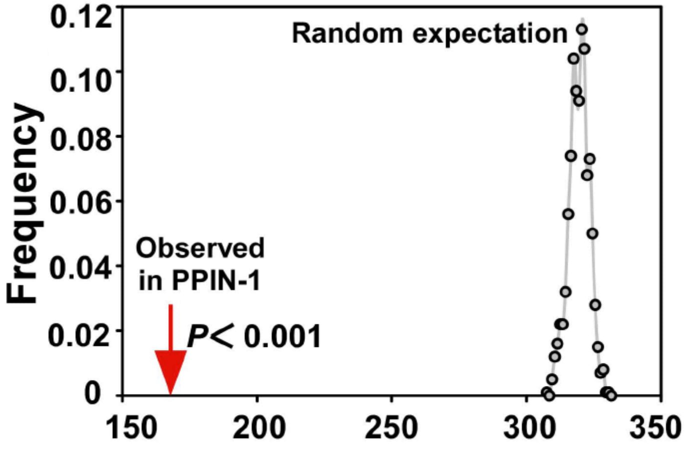
Effector targets (Arabidopsis)

Immune proteins (Arabidopsis)

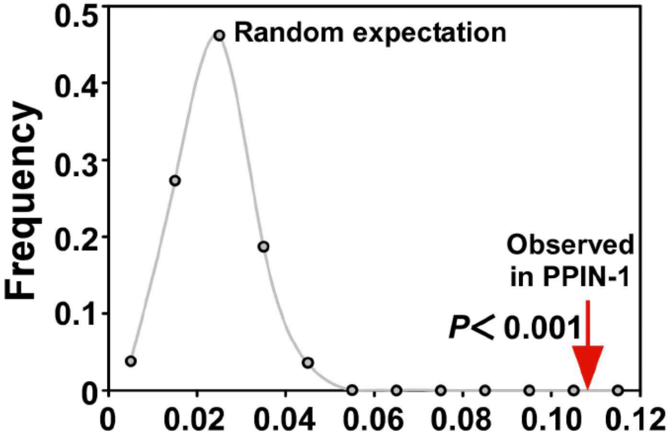
Other Arabidopsis proteins

Evolutionary distant pathogens converge on common targets



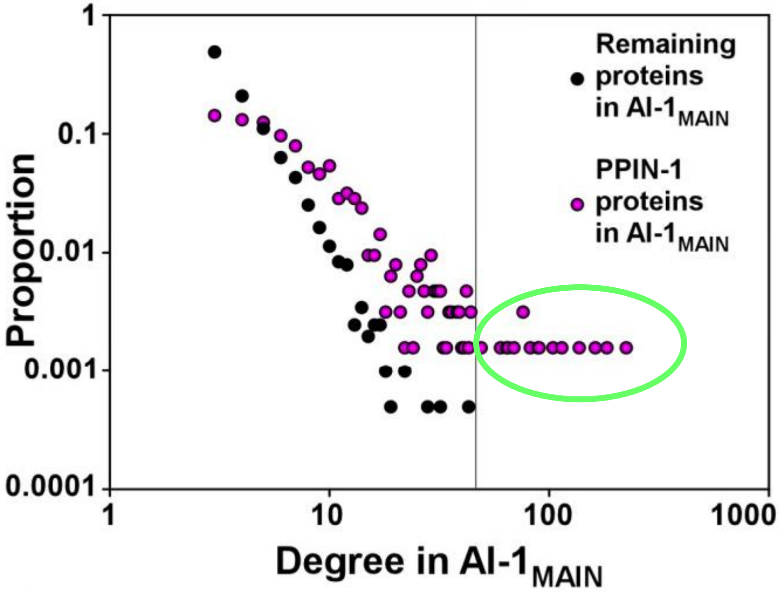


Total number of targets



Proportion shared targets

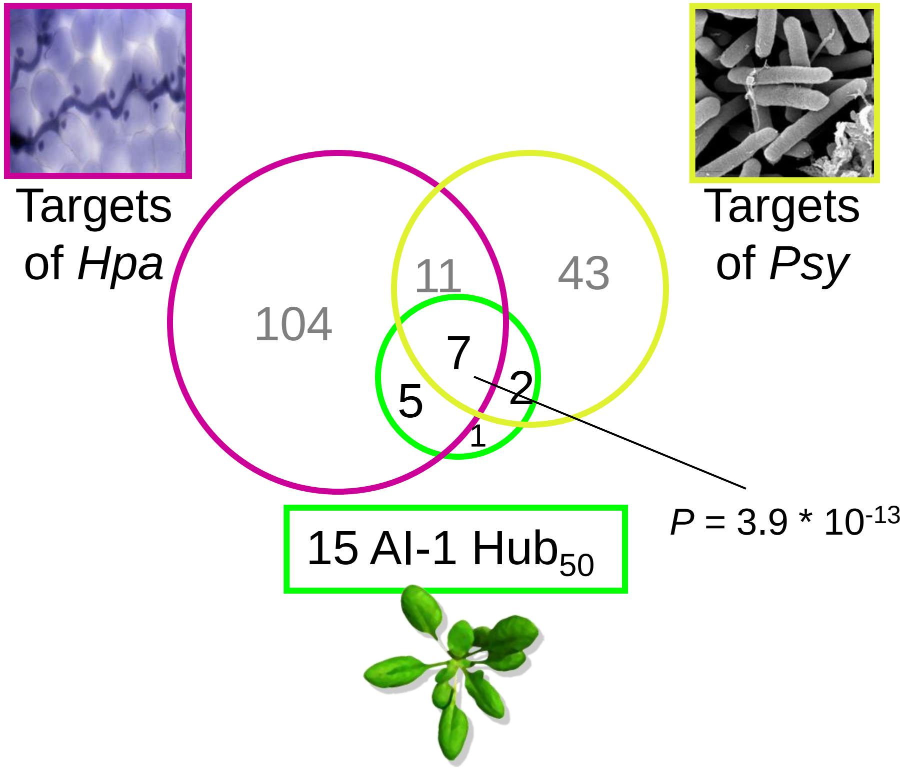
Evolutionary distant pathogens attack network hubs



Error and attack tolerance of complex networks

Réka Albert, Hawoong Jeong & Albert-László Barabási

NATURE | VOL 406 | 27 JULY 2000 |



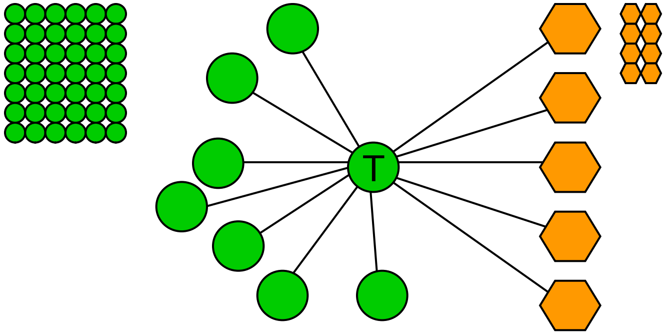
Targets of *Hpa*

Targets of *Psy*

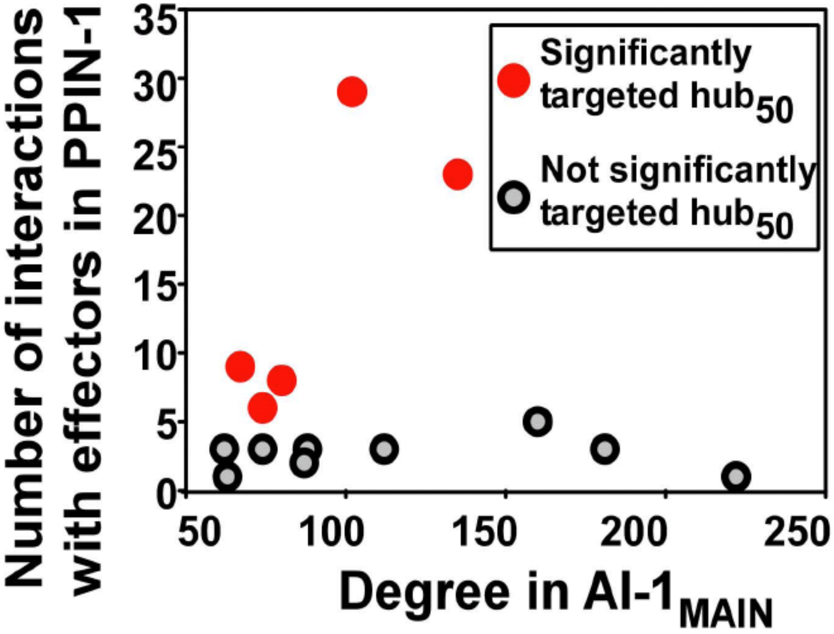
$P = 3.9 * 10^{-13}$

15 AI-1 Hub_{50}

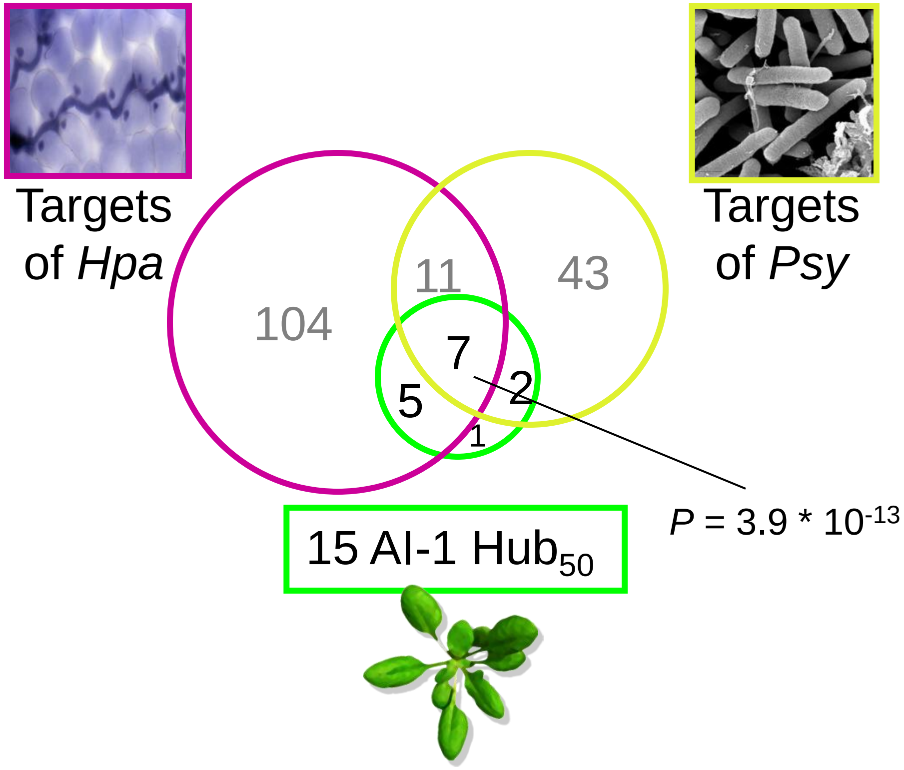
Some hubs are targeted significantly



🟢 Arabidopsis protein
Ⓣ Effector target
⬢ Pathogen effector protein



Evolutionary distant pathogens attack network hubs



Targets of *Hpa*

Targets of *Psy*

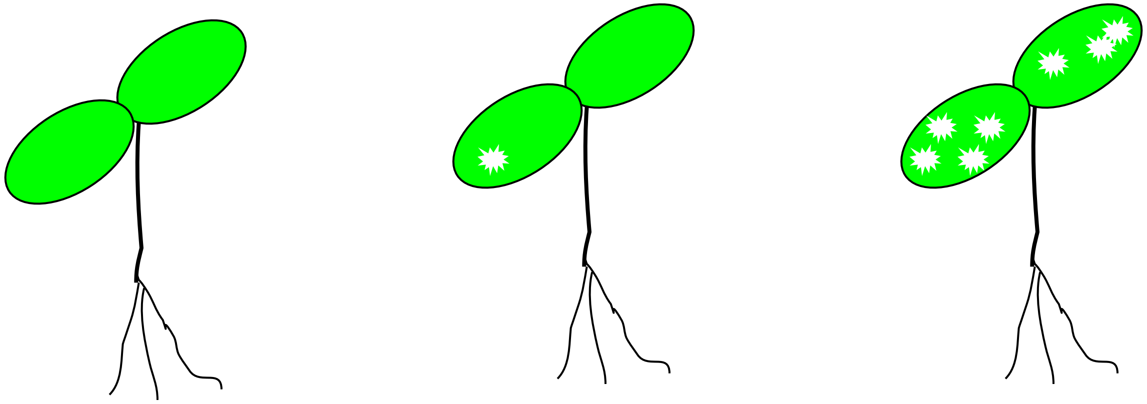
$P = 3.9 * 10^{-13}$

15 AI-1 Hub_{50}

Genetic validation of common effector targets

Enhanced
Disease
Susceptibility

Infection of Col-0 with
Hpa EMWA1 and EMOY2



uninfected

wt

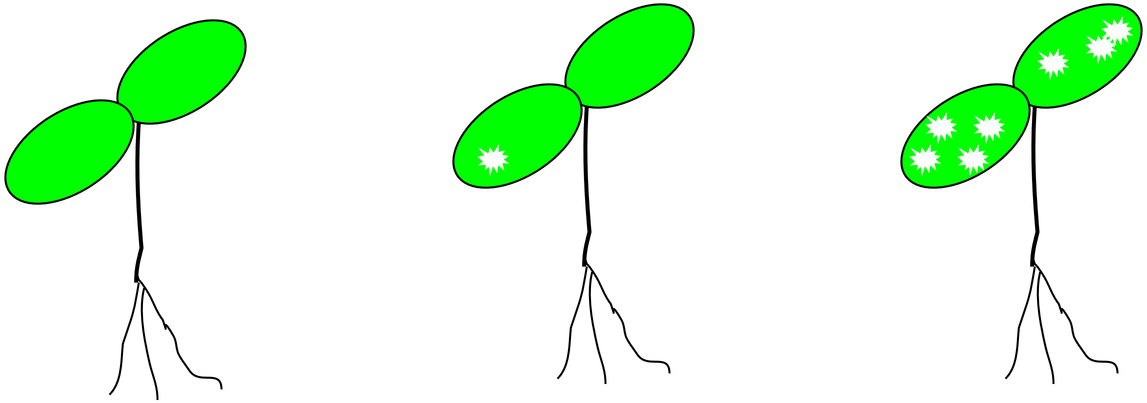
Mutants
(EDS)

H. arabidopsidis
infected leaf

Genetic validation of common effector targets

Enhanced
Disease
Susceptibility

Infection of Col-0 with
Hpa EMWA1 and EMOY2



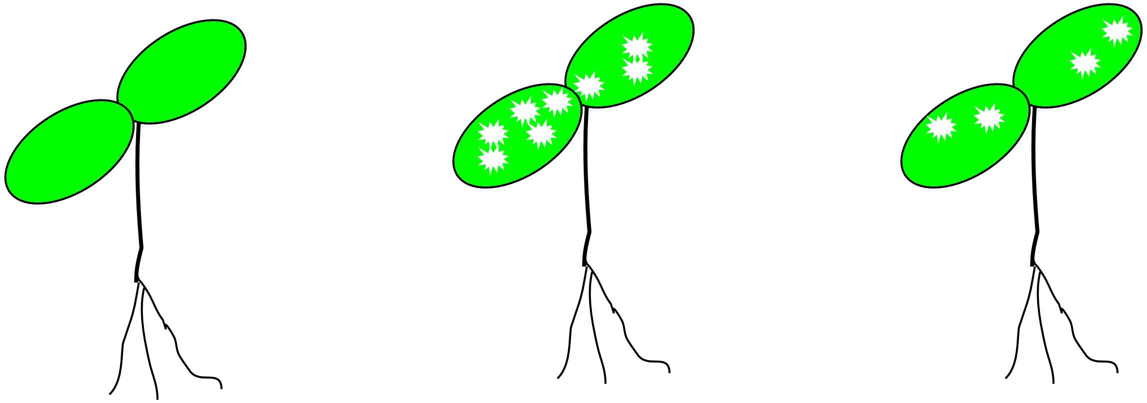
uninfected

wt

Mutants
(EDS)

Enhanced
Disease
Resistance

Infection of A.t. Col-0 with
Hpa NOCO-2



uninfected

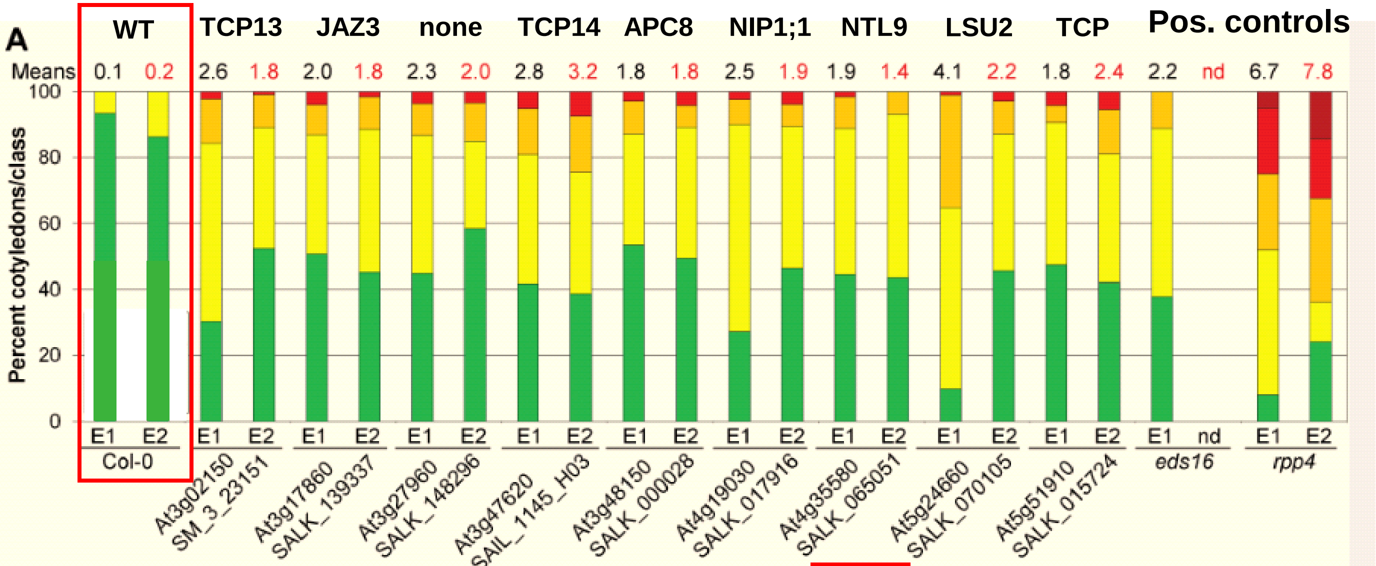
wt

Mutants
(EDR)

17/18 common effector targets have an immune system phenotype

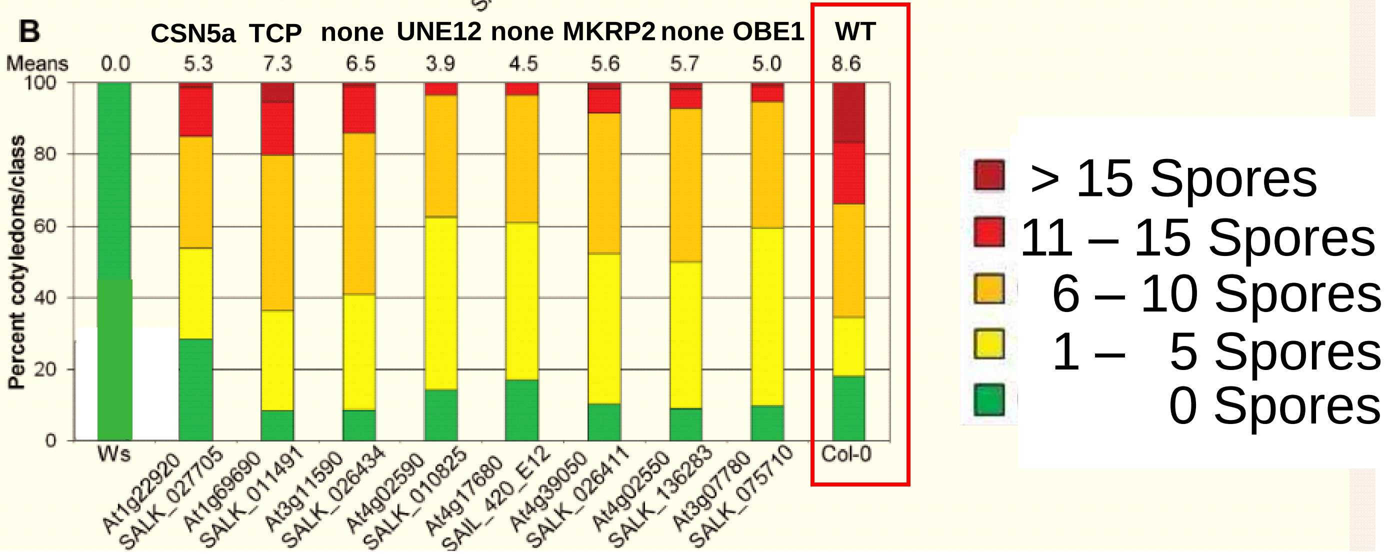
Enhanced Disease Susceptibility

Infection of Col-0 with *Hpa* EMWA1 and EMOY2



Enhanced Disease Resistance

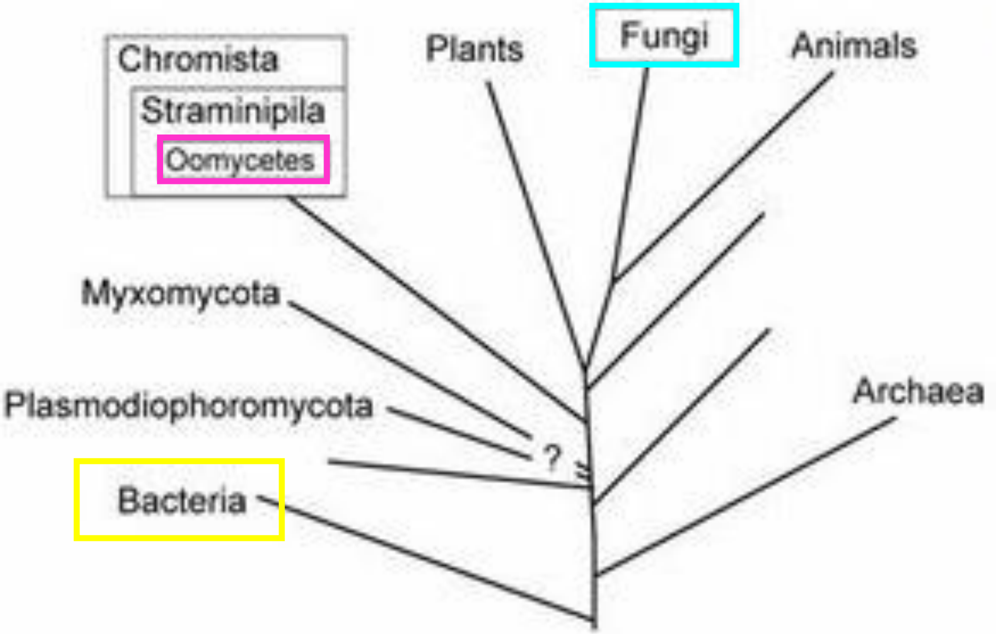
Infection of A.t. Col-0 with *Hpa* NOCO-2

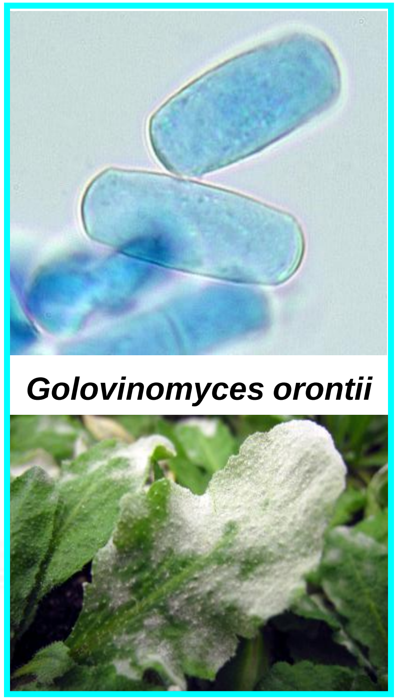


🟥 > 15 Spores
🟥 11 – 15 Spores
🟧 6 – 10 Spores
🟨 1 – 5 Spores
🟩 0 Spores

Challenge 'convergent-attack' model

Hyaloperonospora arabidopsidis





Golovinomyces orontii

Pseudomonas syringae

Collaboration with Jeff Dangl (UNC), Jim Beyon (Warwick U.), Paul Schulze-Lefert (MPIZ, Cologne), Ralph Panstruga (RWTH Aachen)

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Jim Beynon

TUM Dept. Plant Systems Biology
Technische Universität München

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