

A  
Networks Perspective  
On  
Duplication And Divergence

By,  
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# Gene and genome duplications

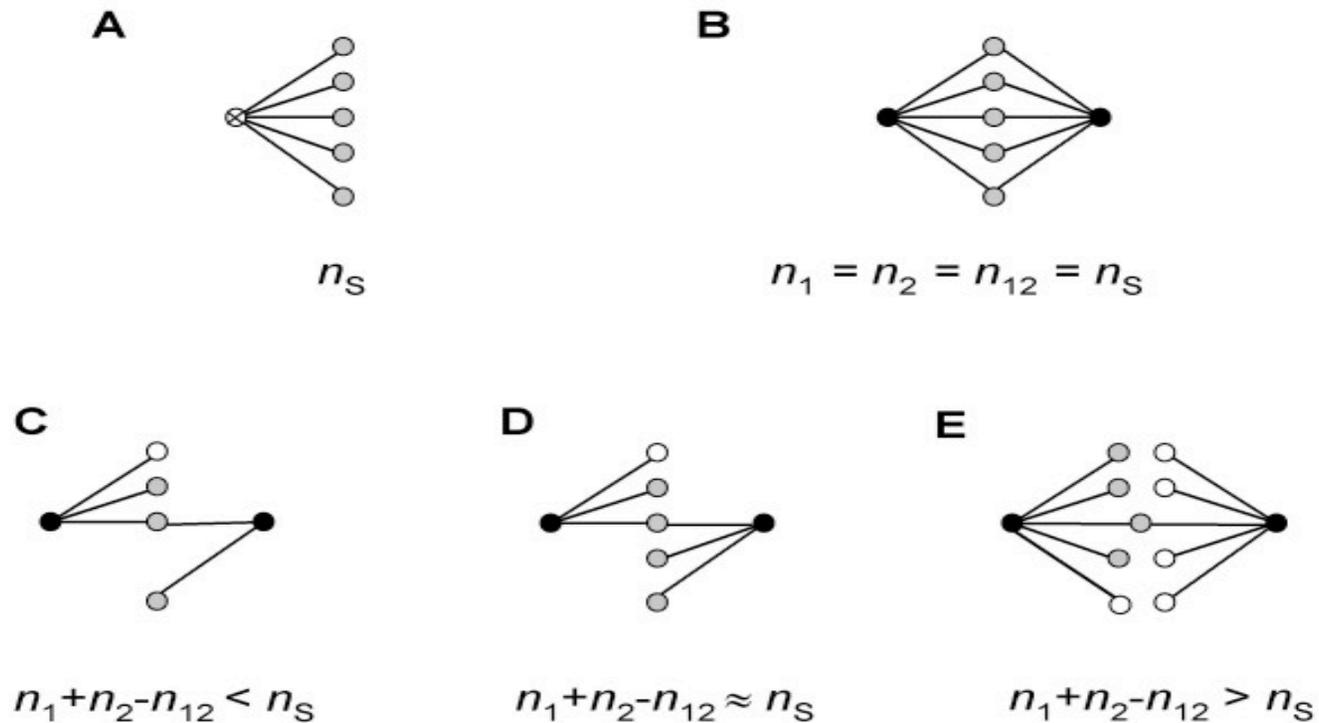
- Increase in the number of functionally different genes over the course of evolutionary history
- Increase in genome size from primitive organisms to more complex ones
- Source of genetic material on which evolution can work

# Rapid and Asymmetric Divergence of Duplicate Genes in the Human Gene Co-expression Network

(W Chung, R Albert, I Albert, A Nekrutenko, K Makova 2006)

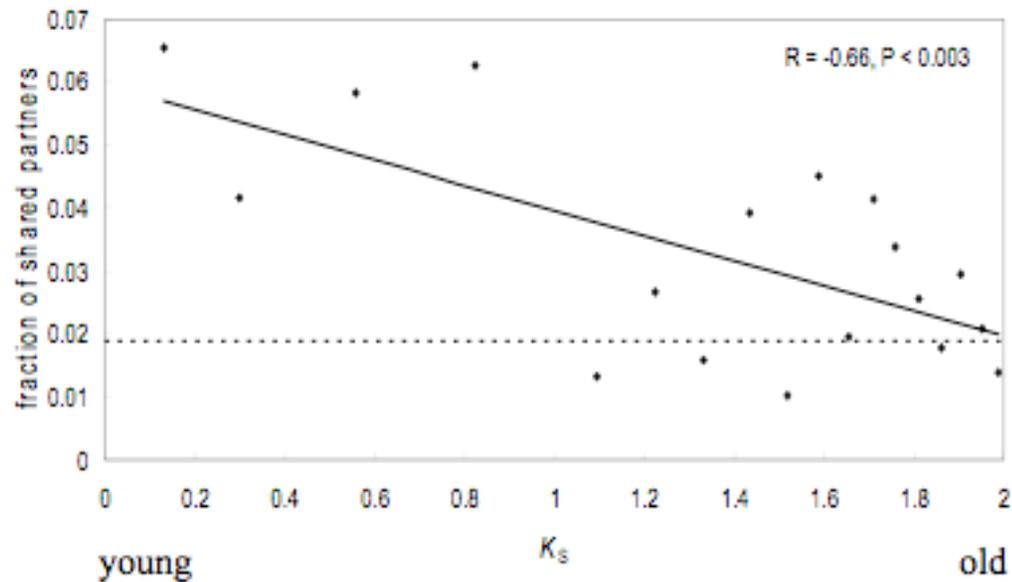
Aim : To study the fates of genes after duplication

# Schematic representation of duplicate gene evolution



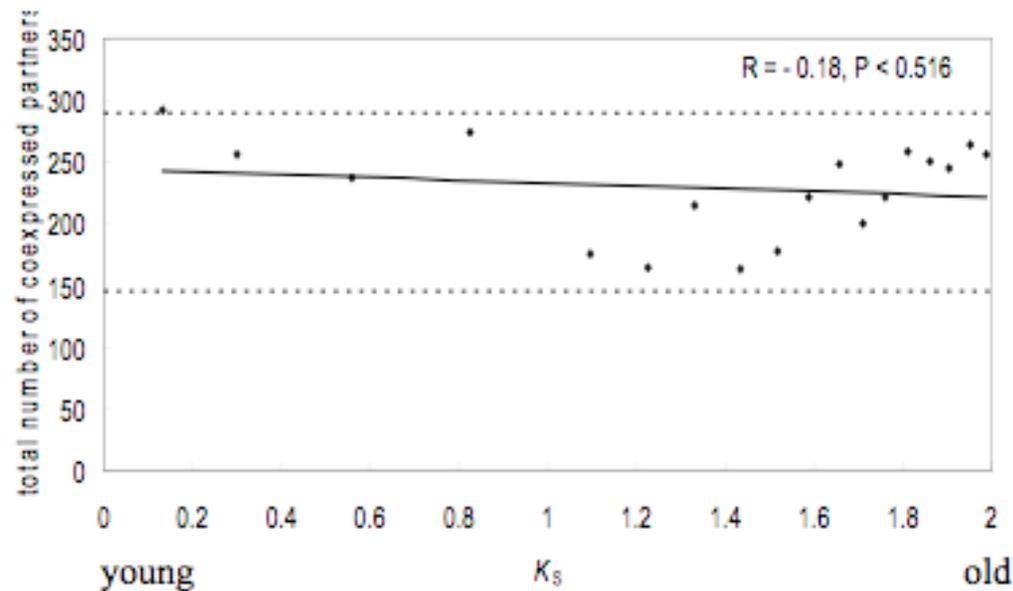
**(A) prior to duplication event, (B) immediately after duplication, (C, D, E) after some time following gene duplication.**

# Dynamics of loss and gain of co-expressed partners



Fraction of shared partners among all partners for each duplicate gene pair =  $n_{12}/(n_1 + n_2 - n_{12})$

## Dynamics of loss and gain of co-expressed partners (cont.)



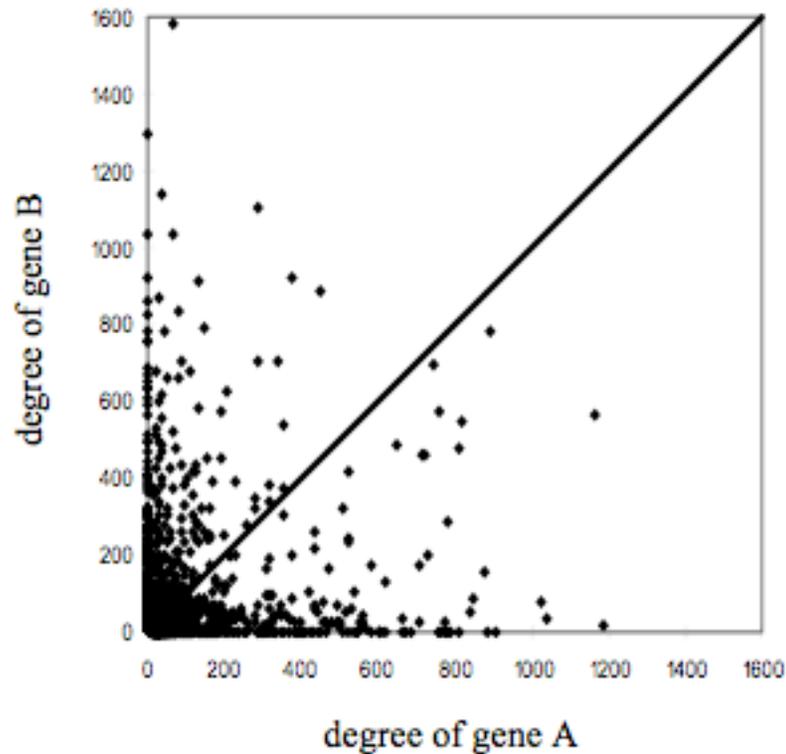
Change in the total number of partners of each duplicate gene pair =  $n_1 + n_2 - n_{12}$

At any time point examined,  $n_1 + n_2 - n_{12} > n_s$

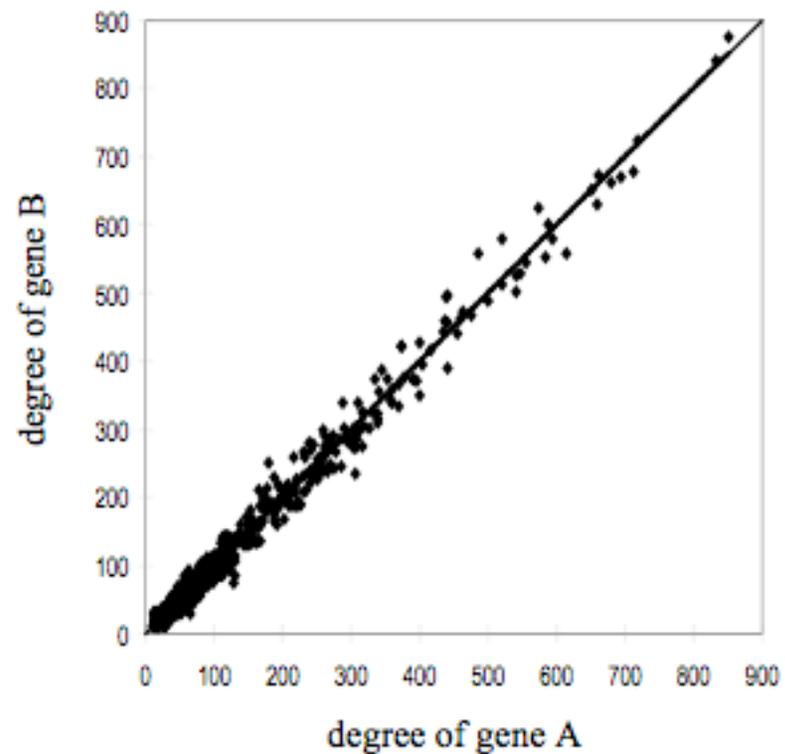
The gain of new partners is rapid

# Asymmetric expression divergence of duplicate genes

Observed:  
Asymmetric divergence



Simulation:  
Symmetric divergence



## Conclusions

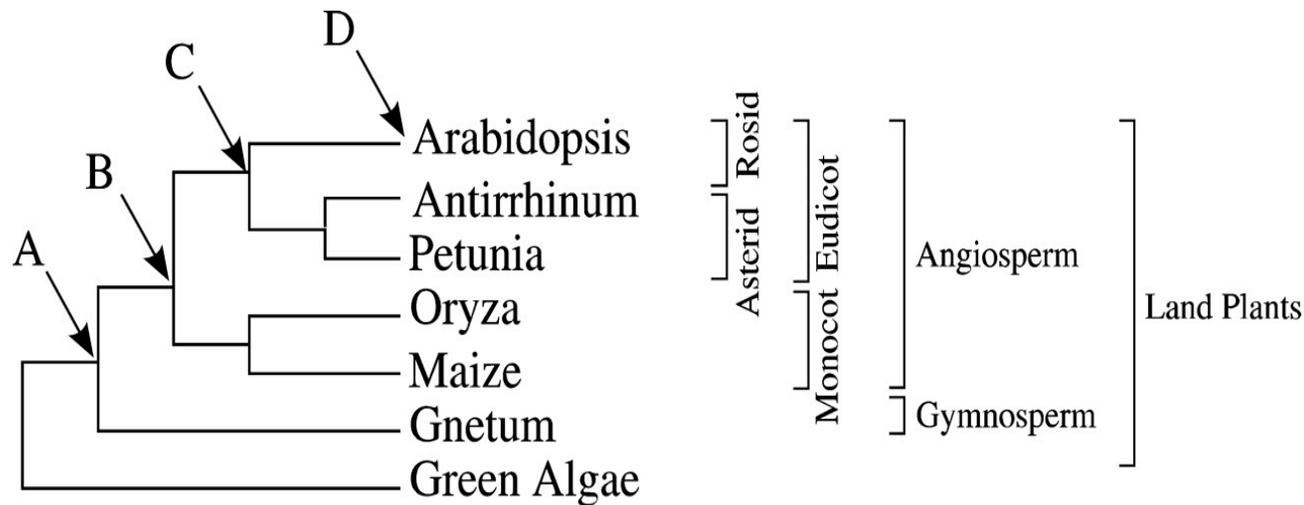
- Duplicate genes quickly lose similarity in gene expression profiles. As a result, except for immediately after duplication, they cannot be considered redundant parts in the network.
- The acquisition of new co-expressed partners is rapid and plays a prominent role in the evolution of duplicate genes.

# Evidence of Interaction Network Evolution by Whole-Genome Duplications: A Case Study in MADS-Box Proteins

(A.S. Veron, K. Kaufmann, and E. Bornberg-Bauer 2007)

Aim: To test the possible effects of Whole  
Genome Duplications (WGDs) on the growth  
and topology of interaction networks

# Phylogenetic relationship between the species studied



Phylogenetic relationship is used to infer the splits of the species and branches.

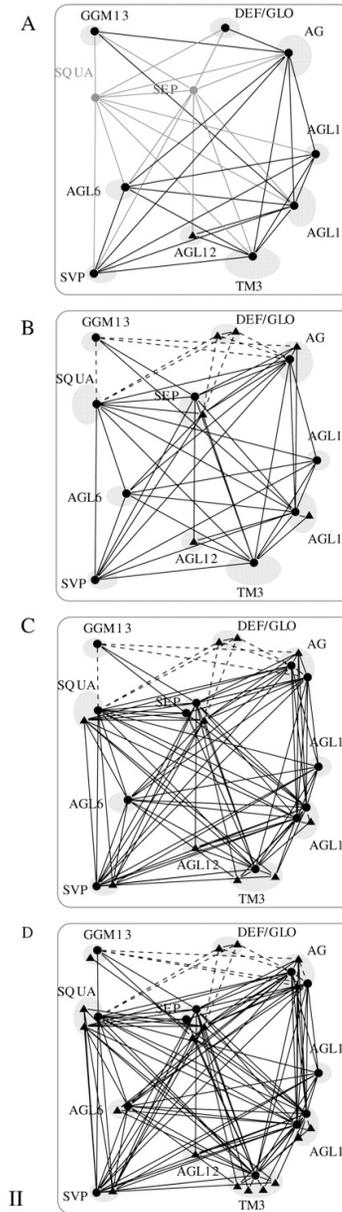
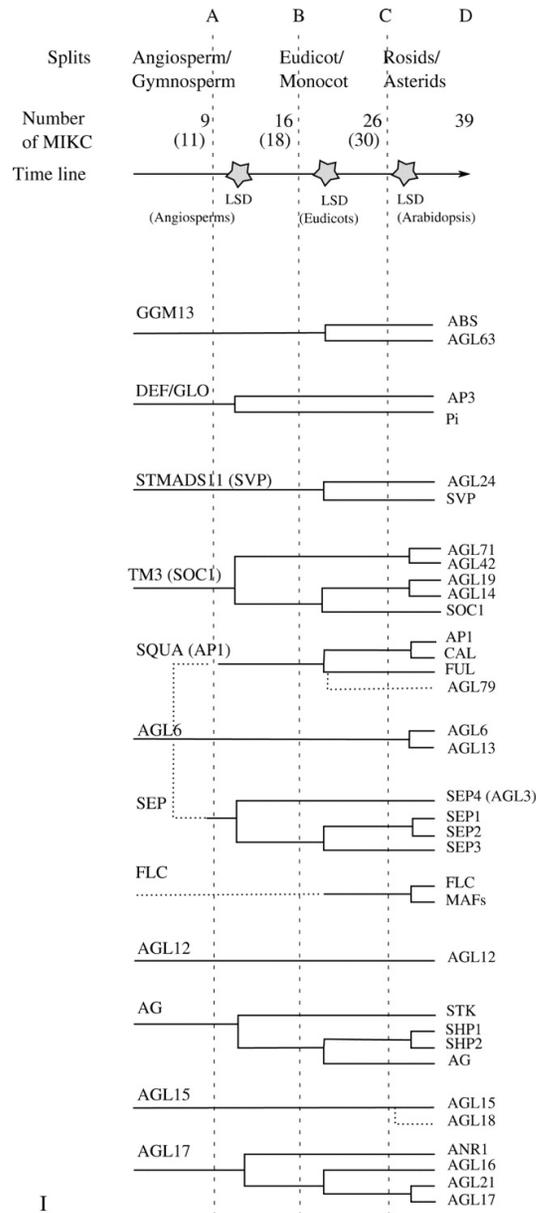
A: Angiosperm–gymnosperm split;

B: eudicot–monocot split;

C: rosid–asterid split; and

D: present time.

# Evolutionary model for the MIKC-type protein network



# Results and Conclusions

- The growth of the MIKC-type gene family corresponds with WGDs
- The 3 rounds of WGDs have added layers of interacting paralogs without modifying the original topology of the MIKC-type PPI networks
- The MIKC Interaction Network has a specific topology, characterized by a high number of shared interactors between paralogs, high interaction pattern conservation between orthologs, and high inter-subfamily connectivity.

# References

1. Chung WY, Albert R, Albert I, Nekrutenko A, Makova KD, *Rapid and asymmetric divergence of duplicate genes in the human gene coexpression network*, BMC Bioinformatics 2006, 7:46 (27 January 2006).
2. Veron AS, Kaufmann K, Bornberg-Bauer E, *Evidence of Interaction Network Evolution by Whole-Genome Duplications: A Case Study in MADS-Box Proteins*, Mol. Biol. Evol. 24(3):670-678. (2007)
3. Teichmann S, Madan Babu, *Gene regulatory network growth by duplication*, Nature genetics, 36(5) (May 2004)
4. Lynch, Conery, *The evolutionary fate and consequences of duplicate genes*, Science 290 (10 Nov 2000)