

Impact of microRNAs on Organization of Protein Interactions and Formation of Protein Complexes

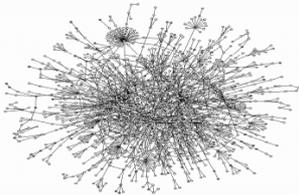
Limsoon Wong
29/9/2010

(Thanks: Wilson Goh, Guimei Liu, Judy Sng)



Motivation

- Typical PPI network
- Can a protein interact w/ so many proteins simultaneously?
- Big "hub" & its "spokes" should be decomposed into subclusters
 - A subcluster is a set of proteins that interact in the same space & time
 - Viz., a protein complex



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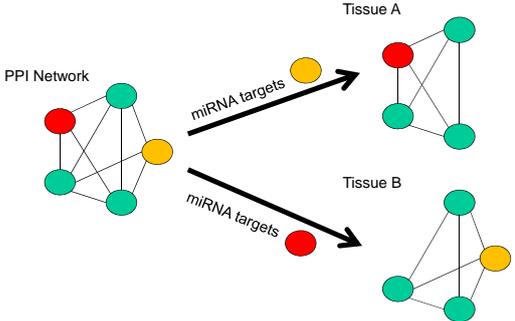
MicroRNAs

- MiRNAs are small regulatory molecules that act by mRNA degradation or via translational repression
- Do miRNAs have a role in controlling complex formation?
- E.g., diff expression of miRNAs across diff tissues can result in formation of diff protein complexes by repressing expression of some sub-components



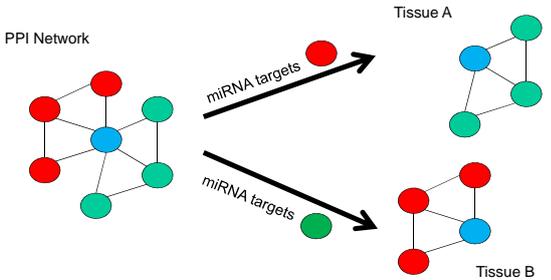
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Can this happen?



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Can this happen?



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Hypothesis

- MiRNAs w/ widely diff expression profiles (i.e., anti-coexpressed) control mutually exclusive bio processes; and so result in diff complexes

Results in progress...

- Verify some general properties implied by the Hypothesis
- Check some predictions in experiments



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Terminology

- “Hub” – proteins having ≥ 50 PPI partners
- “Hub spokes” – PPI partners of a hub
- “Hamming distance” – # of tissues two miRNAs are differentially expressed in
- “Anti-coexpressed” – two miRNAs with Hamming distance ≥ 35 (out of max of 40 tissues)
- “Co-expressed” – two miRNAs that tend to be expressed in the same tissues

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Data Sets

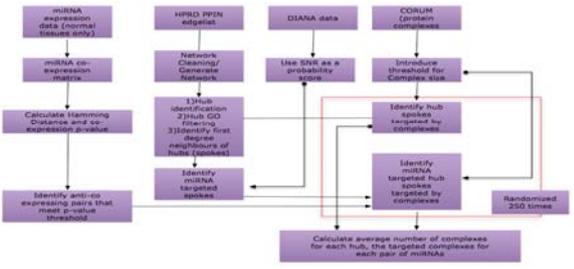
- Biological network info
 - Human Protein Reference Database
- MiRNA expression info
 - 40 normal tissues from Landgraf’s database
- Protein complex info
 - CORUM
- MiRNA target info
 - Prediction by Diana Micro-T

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Workflow

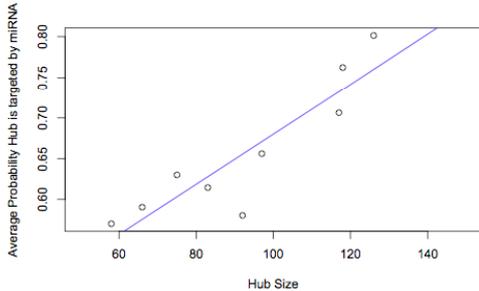


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- Size of hub (i.e., # of neighbors it has) is linearly correlated w/ ave prob of hub targeted by miRNA

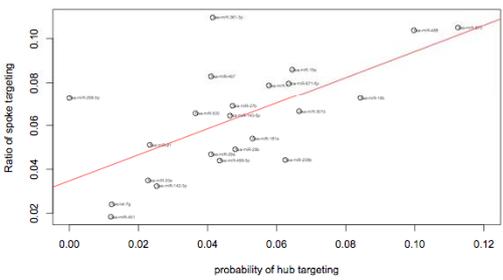


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- When a miRNA is more likely to target a hub, it is also more likely to target more of its spokes

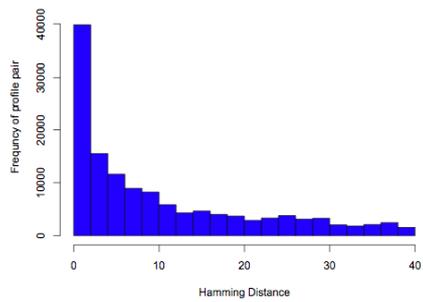


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- Freq distribution of Hamming distance based on all miRNA pairs shows that most miRNA pairs are co-expressed



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NUS

- Co-expressed miRNAs are more freq than anti-coexpressed miRNAs
- Are hub spokes preferentially targeted by them?

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NUS

- Anti-coexpressed MiRNAs target "hub spokes" more strongly than co-expressed miRNAs

Hamming Distz	Ave # of hub spokes targeted
0-1	24.5
2-10	28
11-20	28
21-30	29.5
>30	33.5

- Co-expressed miRNAs, despite much larger #, target far fewer hub-spokes than anti-coexpressed miRNAs
- ⇒ Anti-coexpressed miRNAs have propensity to regulate direct partners of hubs

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NUS

- Hub spokes are preferentially targeted by anti-coexpressed miRNAs
- Do they work "co-operatively" or "antagonistically"?

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- Overlap betw targeted spokes decreases with increasing anti-coexpression

$$J = \frac{|A \cap B|}{|A \cup B|}$$

Adjusted R-squared: 0.3042
p-value: 0.0002396

- Anti-coexpressed miRNAs avoid targeting same spokes
- ⇒ These miRNAs are likely to involve in opposed functions
- ⇒ May be tissue-specific & complexes formed resp. may be diff
- ⇒ Avoid targeting complex members of each other

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NUS

Spoke targeting by miRNAs is specific

- For a hub, if its spokes targeted by a miRNA (in an anti-coexpressed pair) are removed, can the remaining spokes form protein complexes?
- Yes! For every targeting miRNA (in an anti-coexpressed pair), 80-90% of the time, the remaining spokes can form protein complexes

⇒ Targeting miRNA affects small subset of protein complexes formed by hub spokes

⇒ Very specific mode of action?

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NUS

- Hub-Spoke targeting by anti-coexpressed miRNAs is specific

- In most complexes disrupted by anti-coexpression pairs, there is no third complex that can be formed from components of disrupted complexes
- ⇒ MiRNA disruption of complexes is a controlled and specific event

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- Anti-coexpressed miRNAs target different subsets of complexes controlled by hubs
- Do these disrupted complexes have something to do with maintaining tissue-specific function or regulating tissue-specific processes?

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Identification of miRNA-regulated complexes

- Examine complexes disrupted in a scenario where there is evidence for miRNA upregulation and mRNA downregulation
- A downregulated mRNA that is predicted to be targeted by an upregulated miRNA (in an anti-coexpressed pair) is considered to be a real target
- Check protein complexes involving real targets
 - Are these expected to be suppressed?

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VPA-Treated Mice

- Valporic Acid (VPA) prompts differentiation of hippocampal neural progenitor cells into neurons, but they prevent their differentiation into oligodendrocytes and astrocytes
- Tx of mice over a 2-day period w/ VPA indicated readjustment of miRNA levels. 136 miRNAs were over-expressed with 1000 targeted genes down regulated
- 236 genes are high-confidence miRNA targets

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The 236 Genes

- Genes in this set are involved in
 - Chromatin modification (n= 14, P = 2.12e-05)
 - Nervous system dev (n = 23, P = 0.00077)
 - Cell differentiation (n = 32, P = 0.00129)
- ⇒ These miRNA targets have role in epigenetic regulation in the maturation of neurons from progenitors

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Complexes Disrupted

- Check against CORUM shows 53 complexes got disrupted via elevated miRNA targeting
 - 15 of these contain HDAC 1 and/or 2.
 - 8 possess Swi/Snf components involved in neuronal differentiation and neurogenesis
 - 5 belong to polycomb family of complexes which are epigenetic regulators, play a role in cell fate transition and neuronal differentiation
 - 8 complexes are SMAD regulators. SMAD can induce proliferation and differentiation of hippocampal neurons

Caveat: These are the best-matching human complexes, not mouse!

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Complexes Disrupted

HDAC-containing	Switch-involved	SMADS	Others
Anti-HDAC2	BAF/pBAF	JUND-FOSB-SMAD3-SMAD4	BRAF-RAF1-14-3-3
BRM-SIN3A-HDAC	p300-CBP-p270-SWI/SNF	PHL-SMAD2/3-SARA	BRCC
BHC/BHC110	SWI-SNF_chromatin_remodeling-related-BRCA1	BSmad	HBO1
pRb2/p130	BRM-associated	SMAD3-E2F4/5-p107-DP1	ING5
SMAD3-ESK1-SIN3A	BRG1-associated	SMAD3-HEF1-APC10-CDH1	ING4
HDAC1	BRG1-associated	SMAD3-SMAD4-FOXO3-FOXG1	hPRC1L
BRG1-SIN3A	EBAFa,b		
CoREST-HDAC	WINAC	SMAD3-SMAD4-cJun-cFos	KCNQ1_macromolecular
BRAFS3-BRCA2	NUMAC_complex	SMAD3/4-E2F4/5-p107-DP1	p32-CBF-DNA
BRM-SIN3A	Polycomb	Others	MLL1-WDR5
TIPS-DNMT-HDAC1	BCOR	Ubiquitin_E3_ligase	MW1-eIF4F
anti-BHC110	CEN	SNARE_complex	MOF
LSO1	E2F-6	CRM1-RAN-PHAX-CBC_complex	
M-2/NuRD-MTA3	EED-EZH2	PQC1-SRp40-SRp55-SRp75	
Mi2/NuRD-BCL6-MTA3	Polycomb_repressive_complex_1,2,3	WIP-WASp-actin-myosin-IIIa	
LARC_complex		Mis12_centromere	

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Complexes Disrupted

HDAC-containing	Switch-involved	SHADS	Others
Anti-HDAC2	BAF/pBAF	JUND-FOSB-SMAD3-SMAD4	BRAF-RAF1-14-3-3
BRM-SIN3A-HDAC	p300-CBP-p270-SWI/SNF	PHL-SMAD2/3-SARA	BRCC
BHC/BHC110	SWI-SNF_chromatin_remodeling-related-BRCA1	RSmad	HBO1
pRb2/p130-multimolecular_complex	BRM-associated	SMAD3-E2F4/5-p107-DP1	ING5
SMAD3-cSKI-SIN3A-HDAC1	BRG1-associated	SMAD3-HEF1-APC10-CDH1	ING4
BRG1-SIN3A	EBAF <i>a,b</i>	SMAD3-SMAD4-FOXO3-FOXO1	HPRC1L
CoREST-HDAC	WINAC	SMAD3-SMAD4-FOXO3-FOXO1	KCNQ1_macromolecular
BRAF53-BRCA2	NUMAC	SMAD3-SMAD4-FOXO3-FOXO1	p32-CBF-DNA
BRM-SIN3A	Polycomb	SMAD3-SMAD4-FOXO3-FOXO1	MLL1-WDR5
TIF5-DNMT-HDAC1	BCOR	SMAD3-SMAD4-FOXO3-FOXO1	MNK1-eIF4F
anti-BHC110	CEN	SMAD3-SMAD4-FOXO3-FOXO1	MOF
LSD1	E2F-6	SMAD3-SMAD4-FOXO3-FOXO1	complex
Mi-2/NuRD-MTA2	EED-E2F2	SMAD3-SMAD4-FOXO3-FOXO1	75
Mi-2/NuRD-BCL6-MTA3	Polycomb	SMAD3-SMAD4-FOXO3-FOXO1	8
LARC_complex		Mis12_centromere	

BHC controls expression of neuron-specific genes and neuronal differentiation. The component that is miRNA repressed, PHF21A, is enriched in differentiating ES cells. Its repression is speculated to have the opposite effect - that is, maintain the cells in a non-differentiated state

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Complexes Disrupted

HDAC-containing	Switch-involved	SHADS	Others
Anti-HDAC2	BAF/pBAF	JUND-FOSB-SMAD3-SMAD4	BRAF-RAF1-14-3-3
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TIF5-DNMT-HDAC1	BCOR	SMAD3-SMAD4-FOXO3-FOXO1	MNK1-eIF4F
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LSD1	E2F-6	SMAD3-SMAD4-FOXO3-FOXO1	complex
Mi-2/NuRD-MTA2	EED-E2F2	SMAD3-SMAD4-FOXO3-FOXO1	75
Mi-2/NuRD-BCL6-MTA3	Polycomb	SMAD3-SMAD4-FOXO3-FOXO1	8
LARC_complex		Mis12_centromere	

The component in HPRC1L that is miRNA repressed (E3 ubiquitin-protein ligase RING2) is enriched in differentiating ES cells. Its repression is speculated to have opposite effect - that is, maintain the cells in a non-differentiated state

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Complexes Disrupted

HDAC-containing	Switch-involved	SHADS	Others
Anti-HDAC2	BAF/pBAF	JUND-FOSB-SMAD3-SMAD4	BRAF-RAF1-14-3-3
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SMAD3-cSKI-SIN3A-HDAC1	BRG1-associated	SMAD3-HEF1-APC10-CDH1	ING4
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anti-BHC110	CEN	SMAD3-SMAD4-FOXO3-FOXO1	MOF
LSD1	E2F-6	SMAD3-SMAD4-FOXO3-FOXO1	complex
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Mi-2/NuRD-BCL6-MTA3	Polycomb_repressive_complex_1,2,3	SMAD3-SMAD4-FOXO3-FOXO1	8
LARC_complex		Mis12_centromere	

npBAF complexes which contain ACTL6A/BAF53A and PHF10/BAF45A, are exchanged for homologous alternative ACTL6B/BAF53B and DPF1/BAF45B or DPF3/BAF45C subunits in neuron-specific complexes (nBAF). DPF1 is miRNA targeted.

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Conclusions

- miRNAs play impt role regulating formation of complexes
 - Anti-coexpressed miRNAs tend to regulate direct partners of hubs
 - MiRNA disruption of complexes is a controlled and specific event
- In VPA-treated mice, miRNAs disrupt neuron-specific and neuron-differentiating complexes
- The small # of disrupted complexes, and their precise roles, reaffirms miRNA action as precise

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Acknowledgements

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