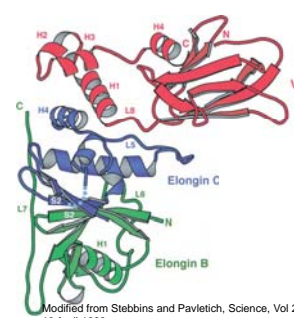
 CENTER FOR
PROTEIN FOLDING
MACHINERY

**Modulating VHL Proteostasis By
Manipulating TRiC**

Eric Jonasch, M.D.
UT MD Anderson Cancer Center

VHL Gene and Gene Product

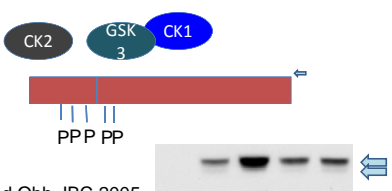
- Located on 3p25
- 213 amino acid protein
- 30 kDa Size
- Binds to Elongin C/B
- Forms "VBC complex"



Modified from Stebbins and Pavletich, Science, Vol 284
16 April 1999

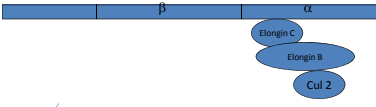
VHL Is Posttranslationally Modified

- S33, S38, and S43 are phosphorylated in the N-terminal acidic domain by casein kinase (CK) 2 and reduce fibronectin association.¹
- S68 and S72 in pVHL30 are phosphorylated by GSK3 and CK1 respectively, which inhibits microtubule stabilization and HIF2a binding.²



1. Lolkema and Ooh JBC 2005
2. Thoma and Krek MCB 2006

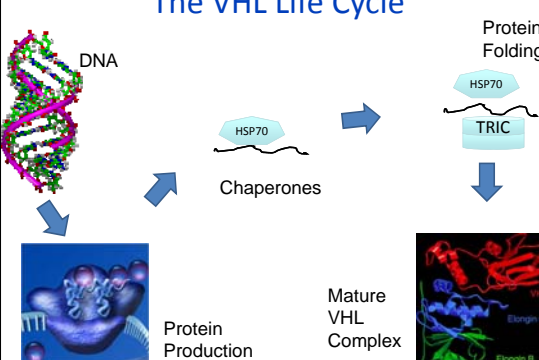
VHL: A Regulatory Hub



Extracellular Matrix Control Cell Cycle Regulation Primary Cilium Regulation Angiogenesis

Ohh et al, Natl Cell, Vol 1, 959-968, 1998
Kurland et al, Cancer Res 2000; 60: 151
Garnett et al, Oncogene 12:2421-2433, 1995
Kim et al, Clin Cancer Res 2005
Thoma et al, Nature Cell Biology Aug 2009
Kurland et al, Nat Cell Biol May 15, 2007
Pugh et al, Nature Medicine 2002
Kurland NEJM May 2008

The VHL Life Cycle



DNA Chaperones Protein Folding HSP70 TRiC Protein Production Mature VHL Complex

Over One Third of Mutations are Missense (Hereditary and Sporadic)

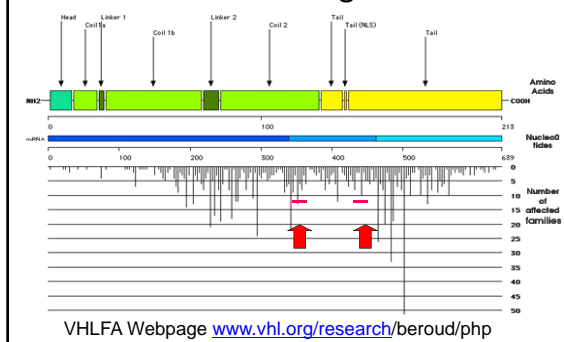
TABLE 2: Types of Mutation Found in von Hippel-Lindau Disease Without (Type 1) and With (Type 2) Pheochromocytoma*

VHL type	Number of families	Number of mutations found				
		Missense	Nonsense	Micro deletion (1-9 bp)	Insertion (1-8 bp)	Deletion (4-380 kb)
1	336	72	29	31	13	53
2	79	61	1	0	2	2
Total	414	133	30	31	15	55

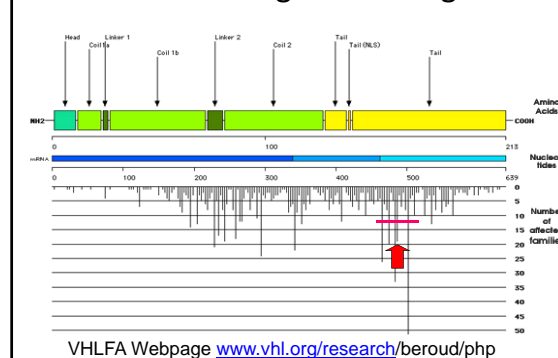
*Each type of mutation was tested by Fisher's exact test (2-tailed) for association with VHL types 1 or 2. Microdeletions/insertions ($P = 0.019$), nonsense ($P = 0.044$), and deletion mutations ($P = 0.012$) were predictive of VHL type 1. Missense mutations were significantly more common in VHL type 2 ($P = <0.001$). Fifty-three VHL families without information sufficient to classify into VHL1, VHL2 were excluded from this analysis.

Zhar et al: Human Mut 1996;8(4):348-57

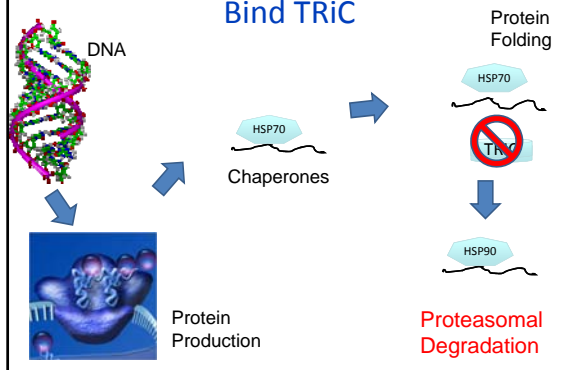
Disease Causing Mutations Occur in TRiC Binding Sites



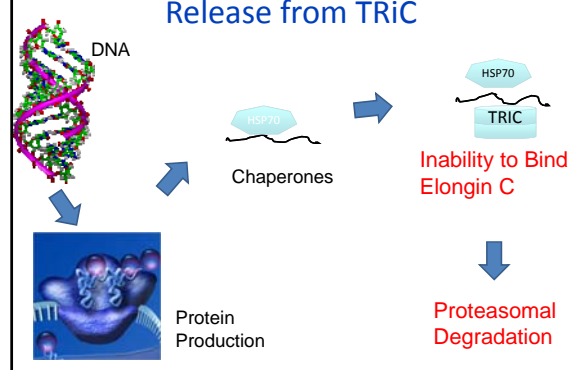
And In the Elongin C Binding Site



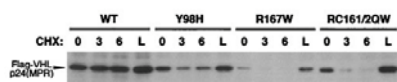
Mutated VHL May Fail to Bind TRiC



Mutated VHL May Fail to Release from TRiC

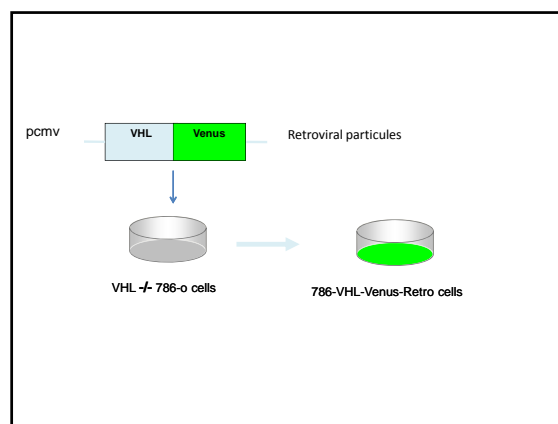


Point Mutations Destabilize pVHL

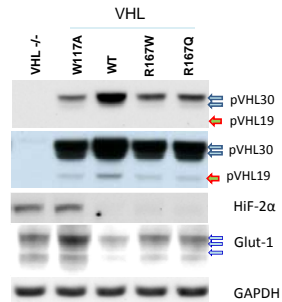


Flag tagged VHL transfected into 786-0 incubated with cycloheximide or lactacystin

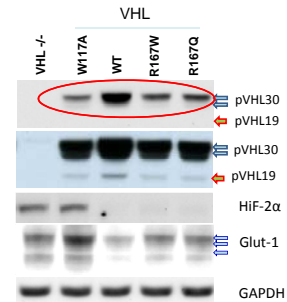
Schoenfeld and Burk PNAS 2000



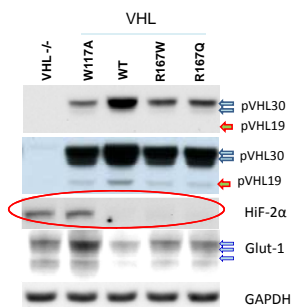
Comparison of mutated and the wild-type VHL protein level in 786-VHL-Venus-Retro cell lines



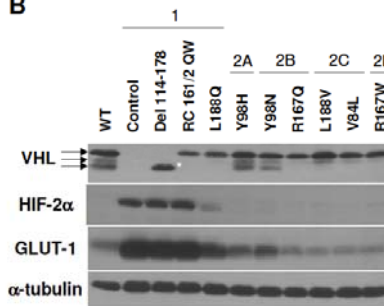
Comparison of mutated and the wild-type VHL protein level in 786-VHL-Venus-Retro cell lines



Comparison of mutated and the wild-type VHL protein level in 786-VHL-Venus-Retro cell lines

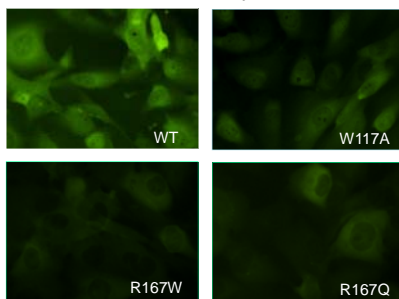


B



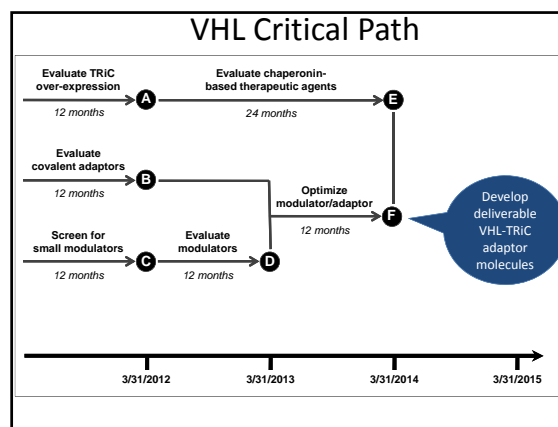
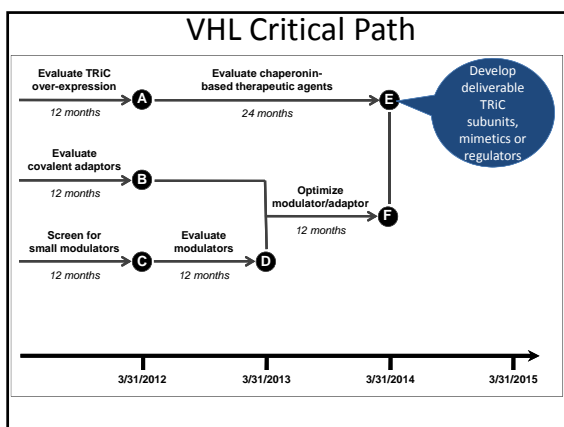
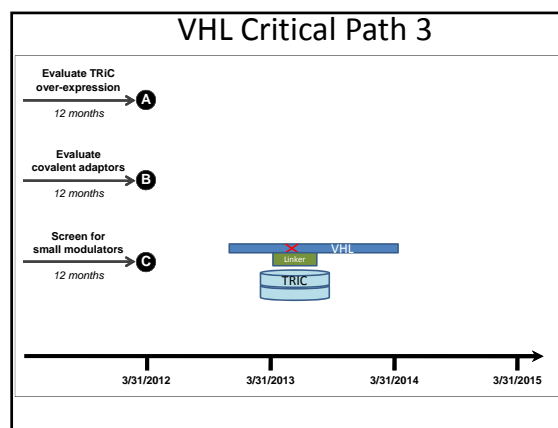
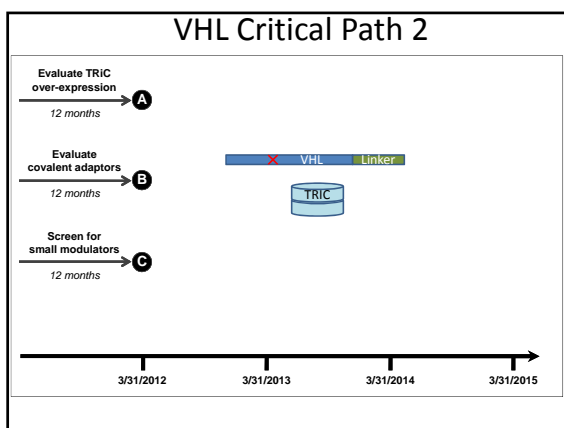
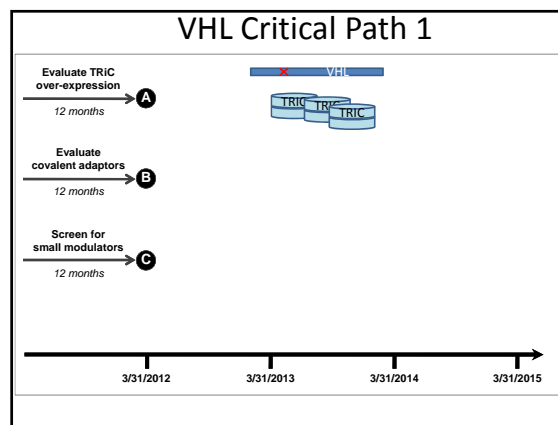
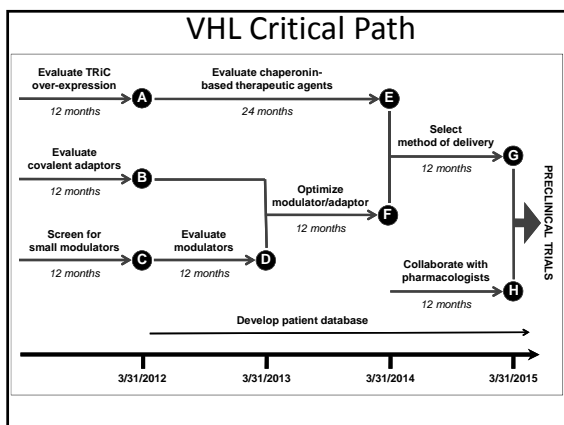
Bangiyeva *et al* BMC Cancer 2009

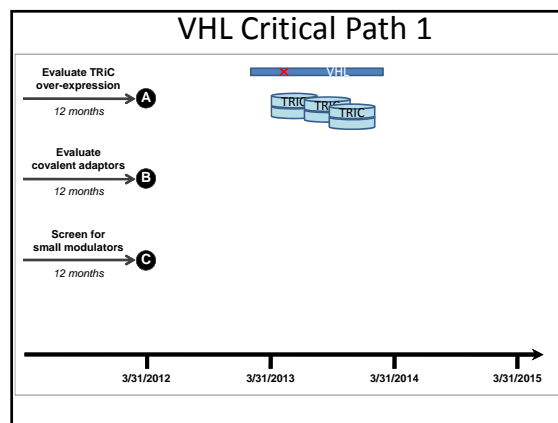
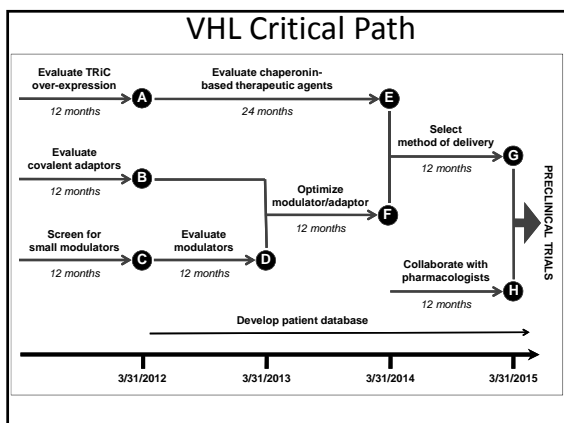
Differential Stability of VHL Can Be Measured in a Cellular System



How can we normalize function of point-mutated VHL?

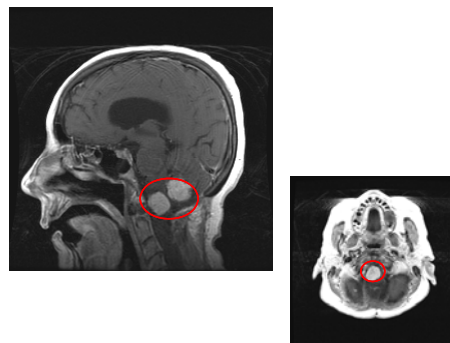
1. Raise the level of functional but unstable VHL protein
2. Refunctionalize point mutated, malformed VHL by facilitating refolding and appropriate ligand binding



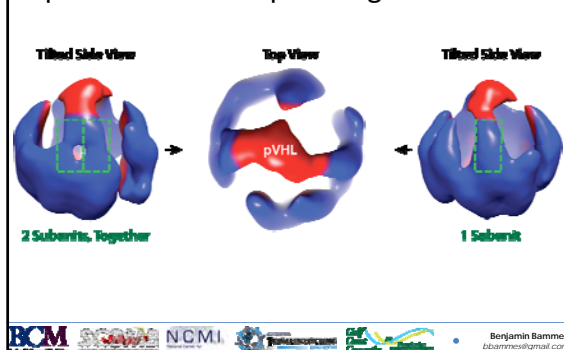


Rationale

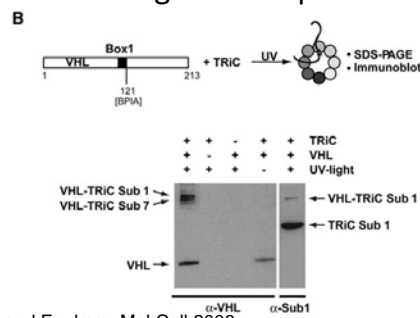
- By understanding the effect of TRiC up- and down-modulation on the stability of mutated pVHL, we will be able to assess the therapeutic value of introducing exogenous or TRiC subunits into VHL lesions.



pVHL Binds to 2 Apical Regions of TRiC

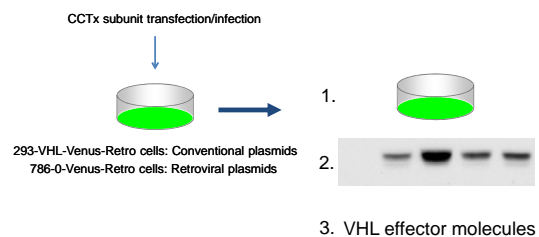


CCT1 and CCT7 are probable binding sites for pVHL



CCTx Knock-In

CCTx Knock-In: Strategy

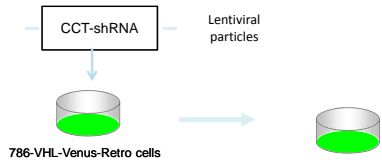


CCTx Knockdown

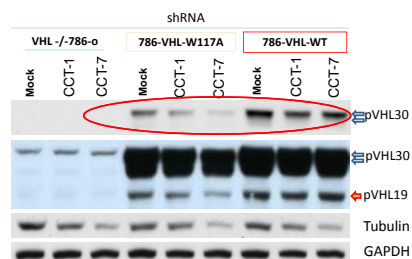
CCTx Knockdown: Rationale

- Downregulation of CCTx subunits in RCC lines will inform regarding relative dependence of VHL isoforms on TRiC stabilization.

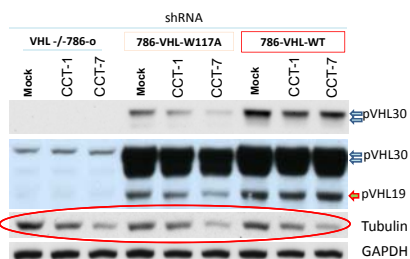
Strategy



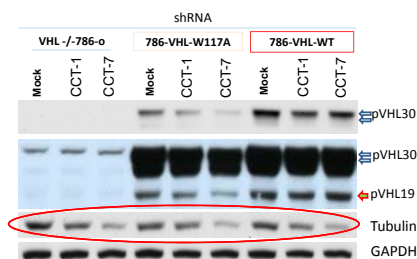
CCT1 or CCT7 Knock-Down



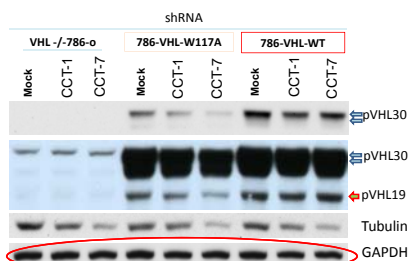
CCT1 or CCT7 Knock-Down



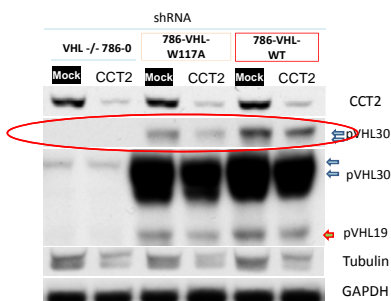
CCT1 or CCT7 Knock-Down



CCT1 or CCT7 Knock-Down



CCT2 Knock-Down



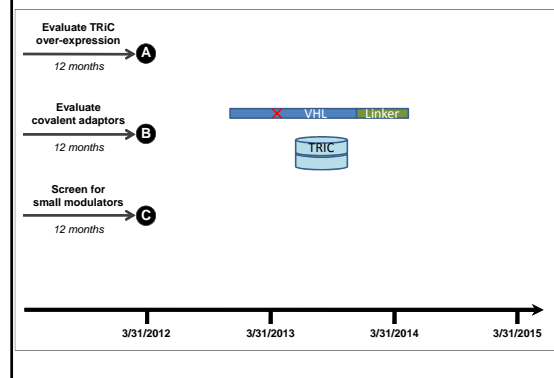
Next Steps

Further explore effect of CCTx knockdown on TRiC client and nonclient proteins in 786-O and other cell lines:

- Evaluate effect of CCTx knockdown on global TRiC levels
- Evaluate effect of multiple CCTx knockdown
- Generate box 1 plus 2 mutant VHL constructs

↕
CCTx knock-in studies

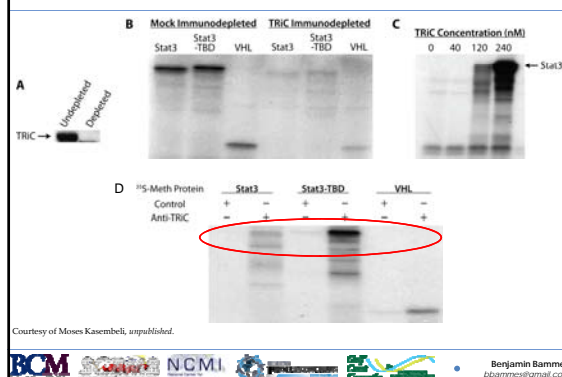
VHL Critical Path 2



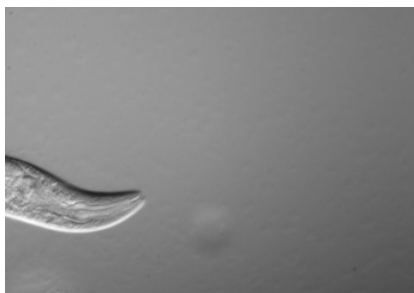
Rationale

- Covalent linkage of TriC binding domains (TBD) will provide information on ability of TBD to influence VHL isoform association with TriC.

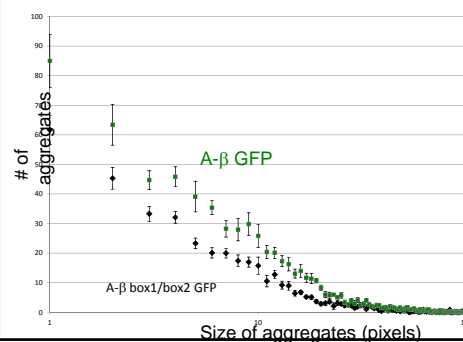
Stat3-TBD Interacts with TriC *in vitro*



C. elegans as an experimental system: Kaveh Ashrafi

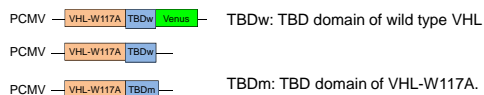


Engineering the box-1/box-2 domain into A-β GFP causes reduction of sizes of aggregates

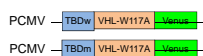


Strategy

TBD fused downstream of VHL mutant: Completed, pending analysis

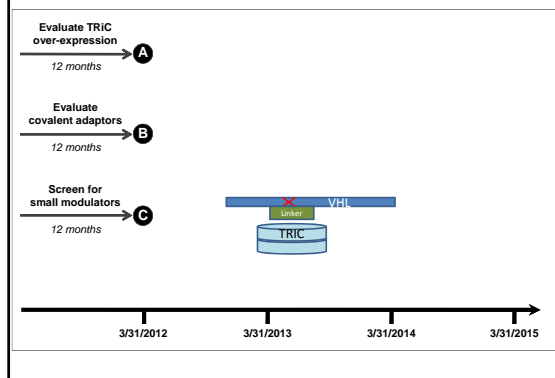


Fusions with TBD fused at the N-terminal of VHL:



We will compare the mRNA and protein levels of the two fusions in 786-O cells.

VHL Critical Path 3



Rationale

- Noncovalent modulators of TRiC-VHL interaction will potentially aid folding of mutant pVHL, and restore functionality.
- Once promising pharmacophores are discovered, further refinement will lead to development of therapeutics for VHL and RCC.

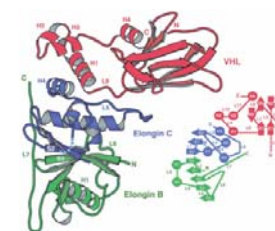
Strategy

1. Use in silico techniques to generate bivalent molecules that will bind to pVHL and to TRiC.
2. Perform unbiased search for compounds that restore VHL-TRiC interaction/restore functionality of pVHL
3. Develop a “molecular toolbox” to assess impact of candidates on VHL proteostasis, in particular the effect on VHL-TRiC interaction

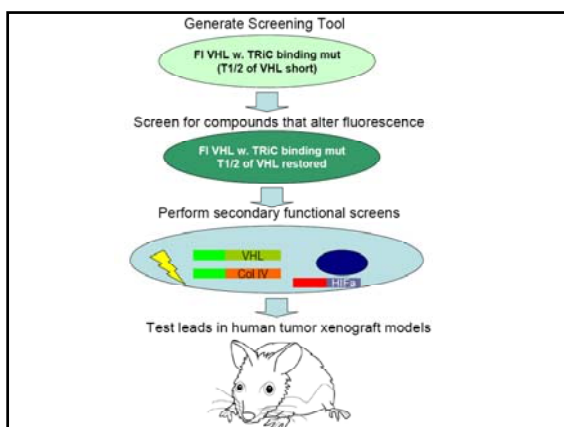
In Silico Design: Vijay Pande and Veena Thomas

Stapled peptide approach:

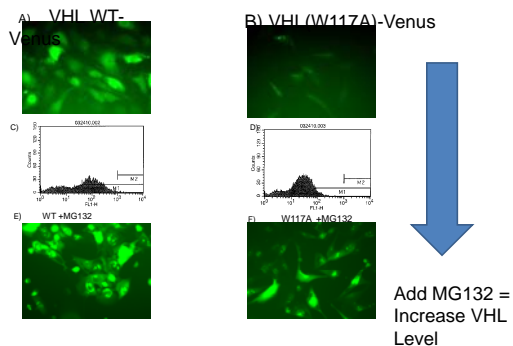
- H4 helix in Elongin C could be a suitable motif for a stapled peptide to recruit VHL.
- Design of TRiC binding end- being performed in parallel for Htt project.



Veena Thomas and Vijay Pande



Proteasome Inhibition Raises Mutant VHL Levels



Phase II Trial of Bortezomib for Patients With Advanced Renal Cell Carcinoma

G. Varuni Kondagunta, Beverly Drucker, Lawrence Schwartz, Jennifer Bacik, Stephanie Marion, Paul Russo, Madhu Mazumdar, and Robert J. Motzer

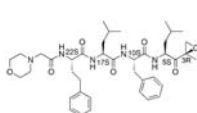
Results

Of the 37 assessable patients, the best response was a partial response in four patients (11%; 95% CI, 3% to 25%) and stable disease in 14 patients (38%; 95% CI, 23% to 55%). The four patients with partial response experienced response durations of 8, 8+, 15+, and 20+ months. Grade 2 or 3 sensory neuropathy was present in 10 patients (53%) overall. One patient in the 1.5 mg/m² group had grade 3 sensory neuropathy; no grade 3 sensory neuropathy was seen in the 1.3 mg/m² group.

New Mechanisms of Action for Therapies in VHL and RCC: An Unmet Need

- Antiangiogenic agents do not directly target tumor cell, and resistance eventually develops
- mTOR inhibitors are not highly efficacious

Carfilzomib (Onyx)



- Tetrapeptide ketoepoxide-based inhibitor specific for chymotrypsin-like active site of 20S proteasome.
- Better tolerated than bortezomib- only minimal peripheral neuropathy.
- Phase I study contained RCC patients- partial responses and disease stabilization seen in nearly half the patients.

Clinical and Preclinical Studies to be launched at MD Anderson

- Phase II study in clear cell (VHL deficient) RCC
 - Assess mutational state of patient tumors
 - test hypothesis activity of carfilzomib is highest in tumors with point-mutated pVHL
- Preclinical studies
 - Human xenograft tumors with various VHL mutations in nu/nu mice

Summary

- Ongoing research will further elucidate role of TRiC and proteostatic pathway regulation in modulating disease state in VHL deficiency.
- Phase 2 clinical trial to be launched within next six months on basis of data generated from Nanomedicine program.

Lab Team

Zhiyong Ding, Shanshan Bai, Meng Gao and Peter German



Acknowledgements

NIH Roadmap Team

- Richard Fisher
- Jeffrey Schloss
- Jennifer Mehren

Nanomedicine Group

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- Judith Frydman
- William Mobley
- Vijay Pande
- Tanja Kortemme

Lab

- Zhiyong Ding
- Peter German
- Shanshan Bai
- Meng Guo

Clinic

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- Marcia Holloway
- Maisha Amusa