**Degradation of Epigenetic Machinery for the Treatment of Cancer** Helai Mohammad, Ph.D. VP, Head of Biology SK Life Science Labs Keystone Symposia, Epigenetic Mechanisms and Cancer Treatment Feb 7, 2024

## Packaging the genome and positioning genes for transcriptional outcomes requires tightly controlled interplay of epigenetics Machinery can read, write, erase, and remodel



- DNMTs methylate CpG dinucleotides, frequently in the context of CpG rich regions
- Histone modifying enzymes catalyze the addition or removal of a variety of post-translational modifications (PTMs) including acetylation, phosphorylation, methylation, and many more
  - Epigenetic readers, including proteins that contain bromodomains or chromodomains, interpret the histone PTMs
- Chromatin access requires the activity of SWI/SNF ATP dependent remodeling complexes



# Packaging the genome and positioning genes for transcriptional outcomes requires tightly controlled interplay of epigenetics Machinery can read, write, erase, and remodel

Not for Distribution



life science labs

- DNMTs methylate CpG dinucleotides, frequently in the context of CpG rich regions
- Histone modifying enzymes catalyze the addition or removal of a variety of post-translational modifications (PTMs) including acetylation, phosphorylation, methylation, and many more
  - Epigenetic readers, including proteins that contain bromodomains or chromodomains, interpret the histone PTMs
- Chromatin access requires the activity of SWI/SNF ATP dependent remodeling complexes

3

### **Targeted protein degradation**

Ternary complex formation can enhance selectivity





**Discovery and Characterization of Orally Bioavailable p300 Selective Degraders** As of Dec 2023 Not for Distribution 5

# p300 and CBP are Paralogous HAT Enzymes with High Sequence Similarity

### Dual Targeting has Faced Challenges in Clinical Development due to Hematopoietic Toxicity



MV Karamouzis et al., Cell Research (2007), AR Waddell et al., Cancers (2021)

- DNA is packaged into nucleosomes that are comprised of the DNA itself wrapped around histones
- The 'tails' of histones can be modified by epigenetic machinery to permit or prevent access to transcription factors
- p300 and CBP are HAT (histone acetyl transferase) enzymes that mark histones with an acetyl group to activate expression of genes that are important in normal and cancer cell biology
- p300 and CBP share high sequence similarity across functional domains
- This has posed an unresolved challenge in discovery of selective functional domain targeted inhibitors; therefore, only dual inhibitors have entered the clinic despite narrow therapeutic margins



## p300 Depletion Is Synthetic Lethal with CBP Mutation

Synthetic Lethality Offers Tumor-Specific Vulnerability and Improved Tolerability



- CBP deleterious mutations confer sensitivity to p300 depletion
- p300 knock-down is synthetically lethal in presence of CBP mutations allowing for selective growth inhibition in this tumor-specific context
- CBP mutations are present in up to 15% of hematological malignancies and solid tumors
- Mutations in CBP present a predictive biomarker for a p300 selective degrader



## p300 Degraders Show Potent and Selective Degradation

p300 Degraders Show Low nM Potency with Minimal Impact on CBP



	P300		CBP	
	D <sub>max</sub> (%)	DC <sub>50</sub> (nM)	D <sub>max</sub> (%)	DC <sub>50</sub> (nM)
Compound 1	85	6.5	13	> max
Compound 2	85	2.0	27	> max
Dual Degrader	84	1.0	79	1.5

 Selectivity of degradation measured by HiBiT knock-in of either p300 (left) or CBP (right) in A549 cells



 Dose response by western blot confirms selectivity for p300 in H1299 cells expressing endogenous and untagged proteins



## p300 Selective Degraders are UPS Dependent

UPS (ubiquitin proteasome system) Inhibitors Block p300 Degradation



 Pretreatment with inhibitors of neddylation (MLN-4924, 1µM), cereblon (CC-220, 1µM) or proteasome (MG-132, 1µM) attenuates protein degradation



## p300 Degradation Impacts Target Pharmacology

Complete Suppression of Histone Acetylation Can be Achieved in CBP KO Cells



- CRISPR mediated genome editing was used to KO (knock-out) p300 or CBP in H1299 cells
- In-cell western blot was established to evaluate histone H3K27Ac (Histone H3, lysine 27 acetylation) in each cell line
- While a clinical stage dual p300/CBP inhibitor suppresses H3K27Ac in all contexts, p300 degraders lead to robust decrease in H3K27Ac with attenuated impact in wild-type or p300 knock-out cells, demonstrating selective pharmacology



# p300 Degraders Result in Selective Growth Inhibition in Synthetic Lethal Context

Potent Growth Inhibition is Observed in CBP KO Cells



- Engineered cell lines were utilized to investigate effects on cell growth in 6-day proliferation assay
- While a clinical stage dual p300/CBP inhibitor inhibits growth in all contexts, p300 degraders lead to growth inhibition in CBP knock-out cell line minimal impact to growth of p300 knock-out or wild-type parental cell line



mCRPC Translational Biology As of Dec 2023 Not for Distribution 12

# AR Positive Prostate Cancer may Show Exquisite Sensitivity to p300 Degraders

### Prostate Cancer Cells Depend on p300 for Growth



- Depletion of p300, but not CBP, results in growth inhibition of AR (androgen receptor) dependent prostate cancer cells through modulation of AR target genes
- Dual inhibitor shows efficacy in vivo in mCRPC (metastatic castration-resistant prostate cancer) cell line
- Dual CBP/p300 inhibitors have shown some promising clinical activity, however, therapeutic margin may be limited



## p300 Degraders Result in Suppression of AR-Mediated Gene Signatures

Selective Degrader Impact on Gene Expression is Equivalent to a Dual Inhibitor



- mCRPC cell line was treated for 48 h with p300 degraders or clinical stage dual inhibitor
- GSEA dot plot and heat map of heat map of differentially expressed genes within the androgen response signature confirms that p300 selective degraders can suppress AR target gene signatures
- AR positive prostate cancer cell growth is clinically correlated to unabated AR dependent gene expression, therefore, perturbation of this pathway can lead to meaningful clinical response



## p300 Degraders Exhibit Selective Growth Inhibition of AR Positive Prostate Cancer Cells

CBP Perturbation is not Required for Cell Growth Inhibition





- Treatment of AR positive prostate cancer cells with a p300 degrader results in cell growth inhibition superior to what is observed with a clinical stage dual p300/CBP inhibitor
- AR null DU145 cells show no response to p300 degraders indicating growth inhibition is selective for AR positive cells



## p300 Degrader is Efficacious in AR Positive Prostate Cancer Models

### Orally Administered p300 Degrader Induces Tumor Regression



Compound 1, 10 mpk, in vivo

 Oral administration (once daily) of Compound 1 to mice with H1703 xenografts demonstrates >90% reduction of p300 within tumor cells



 Oral administration (once daily) of Compound 1 to mice with prostate cancer xenografts demonstrates substantial tumor growth inhibition at pharmacologically relevant doses



## p300 Degraders Show Limited Activity in Hematopoietic Progenitor Ex Vivo Toxicity Study

p300 Degraders Show Less Potency than Dual Inhibitor or Dual Degrader



- Bone marrow derived hematopoietic stem cells were differentiated ex vivo for toxicity assessment
- Dual degrader and dual inhibitor inhibit the growth of myeloid progenitor cells
- p300 selective degraders show markedly less potency in bone marrow toxicity assay suggesting a better therapeutic index

## **Summary**

Discovery of p300 Selective Heterobifunctional Degraders for CBP Mutant Cancer and mCRPC



## **Acknowledgements**

### p300 Project Team

#### Biology

Mike Russell Cassandra Lowenstein Jianing Song Timothy Dougherty Harshil Dhruv Clemente Aguilar Nathan Kendsersky

## **Biochemistry and Structural Biology**

Elham Behshad Sudeep Banjade Peter Orth Cory Rice

#### **Chemistry Xuqing Zhang** Jeremy Roach Qiaolin Deng

DMPK Rakesh Nagilla

**CMC** Winston Wu

#### **Discovery Leadership**

Corey Strickland Helai Mohammad Larry Jolivette Scott Priestley Winston Wu Zhihua Sui

#### **Project Management**

Christine Stuhlmiller



**Discovery and Characterization of Orally Bioavailable SMARCA2 Selective Degraders** As of Dec 2023 Not for Distribution 20

# SWI/SNF ATP-dependent chromatin remodeling is critical for nucleosome positioning



SWI/SN Chromatin alteration ATP ADP Repositioning Irregular spacing or Nucleosome ejection or Histone dimer eviction

- ATPase function within the SWI/SNF complex is only provided by the mutually exclusive SMARCA2/4 paralogous subunits
- ATPase role of SMARCA is indispensable for the function of the SWI/SNF complex



# Non-essential role of SMARCA2 and SMARCA4 BRD provides opportunity for driving selectivity through degradation

### BRD domain targeting does not impact cell growth



- The essential role of SMARCA2/4 provides a clear mechanistic basis for the synthetic lethal relationship between the paralogs
- ATPase domain is druggable however inhibitors have faced selectivity challenges
- SMARCA2 bifunctional degraders can leverage BRD binding to retain cellular selectivity and minimize systemic toxicity



### **Discovery of potent, selective, and rapid degraders of SMARCA2**

Multiple orthogonal assays are utilized to characterize degraders



- SKLSL heterobifunctional degraders exhibit rapid kinetics
- Maximal degradation is achieved by 6 hours in HiBiT assay (HT1080 cells)



- HiBiT knock-in cell line utilized to determine degradation potency and selectivity
- Parental cell line exhibits similar response as HiBit degrader profiling cell line to confirm



# Structurally diverse molecules demonstrate proteasome dependent degradation of SMARCA2 and 4

UPS mechanism is confirmed with various inhibitors of the complex



- Cmpd9 and Cmpd16 are two chemically diverse degraders
- Pre-incubation with neddylation inhibitor MLN4924 or proteasome inhibitor MG132 prevents degradation of SMARCA2 and 4
- Cmpd9 and Cmpd16 degradation of SMARCA2 and 4 exhibit cullin ring E3 ubiquitin ligase and proteasome dependence



# SMARCA2 selective or dual degrader molecules allow for investigation of biology and in vitro to in vivo correlation

Cmpd17 represents an example of a dual mechanism while Cmpd9 is selective



	SMARCA2		SMARCA4	
	D <sub>max</sub> (%)	DC <sub>50</sub> (nM)	D <sub>max</sub> (%)	DC <sub>50</sub> (nM)
Cmpd17	97	0.1	98	0.6
Cmpd9	97	1	65	67

- HT1080 HiBit assay utilized to evaluate degradation
- Cmpd17 and 9 exhibit differences in degradation potency and selectivity
- Cmpd9 is a potent and selective SMARCA2 degrader
- Cmpd17 and Cmpd9 exhibit equivalent plasma clearance and tumor exposure



# SMARCA2 degradation selectivity leads to selective in vitro anti-proliferative activity

SMARCA4 LoF cells are sensitive to selective degraders while wild-type cells are unaffected



- 6-day proliferation assay used to investigate biological impact of SMARCA degradation
- Cmpd9 is a selective SMARCA2 degrader while Cmpd17 degrades SMARCA4 with similar potency
- Selective SMARCA2 degraders exhibit selective anti-proliferative activity on SMARCA4 LoF cells



# In vitro SMARCA2 potency and selectivity translates to in vivo protein degradation

Degradation in wild-type xenograft tumor model confirms in vitro results



- HT1080 xenograft model established for in vivo assessment of degradation
- SMARCA2 and SMARCA4 degradation in tumors was assessed after single administration of Cmpd17 or Cmpd9
- Cmpd17 shows greater reduction of SMARCA2 at 1mpk but shows similar degradation of both SMARCA2/4 at 10mpk
- Cmpd9 maintains greater selectivity than Cmpd17 even at the higher dose level thereby correlating with in vitro results



# Treatment with Cmpd18 leads to anti-tumor efficacy in SMARCA4 LoF NSCLC tumor model

Plasma and Tumor PK Average Tumor Volume (mm<sup>3</sup>) 30 mg/k Cmpd4 Vehicle 1000-10 ma/ka 10000-Plasma ng/ml 📥 30 mg/kg Concentration Tumor ng/g Cmpd18 1000 -Cmpd18 treatment 500-▼ 100 10 15 10 20 24 48 Day Hrs post dose

Sustained tumor exposure leads to efficacy with once weekly administration

- Cmpd18 selectively degrades SMARCA2 over SMARCA4 in vitro and in vivo
- NCI-H838 SMARCA4 LoF xenograft model was established for in vivo evaluation of SMARCA2 degrader efficacy
- Cmpd18 demonstrates sustained tumor exposure in NCIH838 xenograft model
- Cmpd18 treatment leads to potent anti-tumor efficacy effect in SMARCA4 LoF tumor model



# Cmpd101 demonstrates potent and selective SMARCA2 degradation in vitro and in vivo



### Cmpd101 is orally bioavailable

- Selective degradation evident in Hela HiBit assay
- Potent and selective antiproliferative activity on SMARCA4 LoF cells



- High circulating exposure and low clearance after Cmpd101 IV (1 mg/kg) and PO (3 mg/kg) administration
- Robust SMARCA2 degradation after single 3 mg/kg oral administration by 3 hours that persists through 24 hours



## Two structurally unique series of SMARCA2 degraders demonstrate oral bioavailability

Cmpd103 and Cmpd104 represent exemplars from each series



- SKLSL series of degraders exhibit oral bioavailability in mice ranging from 7-58 %F
- Rat oral bioavailability ranges from 9-31 %F
- Orally bioavailable degraders exhibit selective degradation of SMARCA2 and growth inhibition of SMARCA4 LoF cells



### Summary

Orally Available SMARCA2 Selective Heterobifunctional Degrader for SMARCA4 Mutant Cancer



### **Acknowledgements**

### SMARCA Project Team

#### **SK Life Science Labs**

#### Biology & Computational Biology

Jose C. Clemente Debangshu Samanta Timothy Dougherty Clemente Aguilar Nathan Kendsersky Shreyas Joshi

#### Chemistry & Computational Chemistry Lal Harikrishnan Zhenwu Li Steve Knight Matt Tudor Qiaolin Deng

Biochemistry & Structural Biology Elham Behshad Peter Orth

#### DMPK Rakesh Nagilla

Project Management Christine Stuhlmiller

#### **Discovery Leadership**

Corey Strickland Helai Mohammad Larry Jolivette Scott Priestley Winston Wu Zhihua Sui

#### **University of Michigan**

#### Prof. Shaomeng Wang

#### Chemistry

Lin Yang Lingying Leng Wenbin Tu Rohan Rej Srinivasa Rao Allu

Biochemistry/Cell Biology Liyue Huang Mi Wang Wenbin Tu

#### In vivo Pharmacology

Wei Jiang Yu Wang Wen Bo Duxin Sun **Computational design** Jelena Tosovic Paul Kirchoff

Structural Biology Jeanne Stuckey

**SK** life science labs