Apabetalone Downregulates Fibrotic, Inflammatory and Calcific Processes in Renal Mesangial Cells: Mechanism for Reduced Cardiac Events in CKD Patients

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DISCLOSURES FROM PAST 12 MONTHS

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Employed by and owns stock and/or stock options in Resverlogix, who funded this study.

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Member of a clinical steering committee for Resverlogix







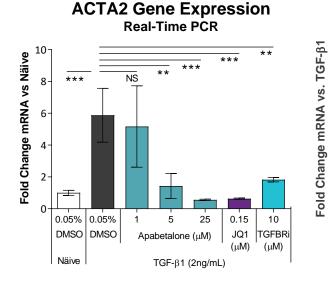
- Patients with chronic kidney disease (CKD) have elevated risk of <u>major adverse cardiac events</u> (MACE)
- Apabetalone is an orally available inhibitor of BET proteins epigenetic readers that modulate expression
 of genes involved in <u>fibrosis</u>, <u>inflammation</u> & <u>calcification</u>.
 - Am J Respir Crit Care Med. 2019, 200:910-920, Cardiovasc Ther. 2020, 2020:9397109, Atherosclerosis. 2019, 280:75-84
- In the phase 3 BETonMACE trial, apabetalone reduced MACE by half in patients with CKD (eGFR < 60 mL/min/1.73m²; HR 0.50 95% CI 0.26,0.96 p=0.04]), implying major benefit along the kidney-heart axis.
 - Clin J Am Soc Nephrol. 2021, 16:705-716
- This study examines effects of apabetalone treatment on primary human renal mesangial cells (HRMCs) in culture on pathways that contribute to renal pathology.



Apabetalone Opposes Fibrotic Activation of HRMCs



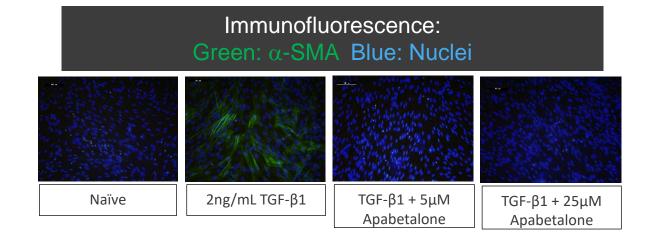
TGF-β1 is a fibrotic stimulus that promotes overproduction of extracellular matrix (ECM)



p<0.01, *p< 0.001, NS not significant. ANOVA followed by Dunnett's

ACTA2 Gene Expression RNA-seq 1.4 1.2 *** *** 1.0 0.8 0.6 0.4 0.2 0.0 5uM 25uM 0.15µM 0.05% 0.05% 0.1µM DMSO DMSO MZ1 JQ1 Apabetalone Naïve TGF-β1 (2ng/mL)

***p< 0.001, Benjamini-Hochberg adjusted p value



Method:

HRMCs from donors without kidney dysfunction were stimulated 24 hours with pro-fibrotic TGF- β 1 ±

- Apabetalone
- JQ1: BET inhibitor [BETi] with chemical scaffold different than apabetalone
- MZ1: BETi that promotes degradation of BET proteins

Gene expression measured by real-time PCR or RNA-seq

Robust induction of smooth muscle actin gene expression (ACTA2) with TGF-β1 stimulation as expected; white vs **black** bars - *Marker of fibrotic activation*

An **inhibitor of TGF-\beta receptors** reduced or abolished the response to TGF- β , indicating expected signal transduction pathways mediate this pro-fibrotic stimulation (**light blue** bar)

Apabetalone, JQ1 and MZ1 all suppress TGF-β stimulated ACTA2 expression, confirming on-target BETi effects

Apabetalone blocked TGF- β induced α -SMA protein production, indicating block to fibrotic state

Apabetalone counters pro-fibrotic activation of TGF- β stimulated HRMCs

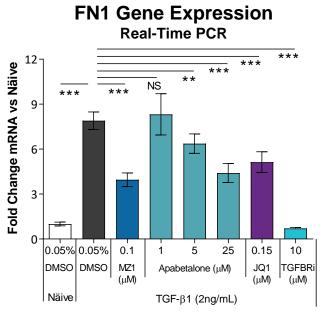
Anti-Fibrotic Effects of Apabetalone



Gene Ontology (GO) analysis of differential gene expression 5μ M Apabetalone vs TGF- β 25μ M Apabetalone vs TGF- β extracellular matrix (n=147) cell-substrate junction (n=219) collagen-containing extracellular matrix (n=120) cell-substrate adherens junction (n=218) cell-substrate junction (n=129) focal adhesion (n=218) focal adhesion (n=128) cytosolic part (n=129) cell-substrate adherens junction (n=128) cvtosolic ribosome (n=69) nuclear-transcribed mRNA catabolic ... (n=77) actin cytoskeleton (n=132) tracellular matrix structural constituent (n=60) lysosomal lumen (n=58) extracellular matrix organization (n=107) collagen-containing extracellular matrix (n=168) xtracellular structure organization (n=116) SRP-dependent cotranslational protein ... (n=63) actin binding (n=111) extracellular matrix (n=203) cell-cell junction (n=111) cotranslational protein targeting ... (n=64) extracellular matrix organization (n=165) cell leading edge (n=106) cell adhesion molecule binding (n=215) cell adhesion molecule binding (n=125) vacuolar lumen (n=83) angiogenesis (n=123) protein targeting to ER (n=65) sarcolemma (n=45) xtracellular structure organization (n=176) cell-substrate adhesion (n=95) ameboidal-type cell migration (n=167) actin filament bundle (n=31) cell leading edge (n=172) ameboidal-type cell migration (n=98) skeletal system development (n=208) egative regulation of cell migration (n=73) stress fiber (n=28) establishment of protein ... (n=65) 15 10 15 0 5 10 0 0.15μ M JQ-1 vs TGF- β $0.1\mu M MZ1 vs TGF-\beta$ focal adhesion (n=233) focal adhesion (n=250) cell-substrate adherens junction (n=234) cell-substrate junction (n=253) cell-substrate junction (n=236) cell adhesion molecule binding (n=279) cell adhesion molecule binding (n=249) angiogenesis (n=267) agen-containing extracellular matrix (n=188) ribonucleoprotein complex biogenesis (n=259) extracellular matrix organization (n=184) ribosome biogenesis (n=175 extracellular matrix (n=225) cadherin binding (n=188 rix structural constituent (n=89) skeletal system development (n=273) cell leading edge (n=194) 90S preribosome (n=26) cadherin binding (n=163) preribosome (n=55 extracellular structure organization (n=196) rRNA metabolic process (n=147 sarcolemma (n=75) rRNA processing (n=126) ameboidal-type cell migration (n=186) esponse to topologically incorrect protein (n=122) angiogenesis (n=227) collagen fibril organization (n=40 regulation of cellular protein localization (n=245) cell growth (n=219) extracellular matrix (n=251 regulation of vasculature development (n=173) axon part (n=174) tissue migration (n=142) actin cytoskeleton (n=260) epithelial cell migration (n=139) bone development (n=126) regulation of vasculature development (n=152) actin filament organization (n=213 0 10 15 5 8 10 4 6 log10(padj) log10(padj) n is the number of differentially expressed genes in each GO term

GO analysis of RNA-seq shows multiple gene sets associated with ECM (red arrows) in the top 20 affected by BET inhibitors, supporting anti-fibrotic properties

Fibronectin (FN1) is a component of the ECM that contributes to fibrosis

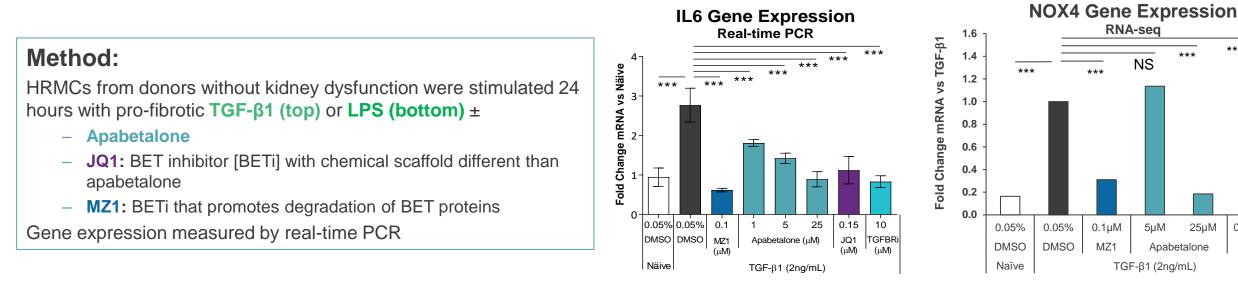


p<0.01, *p< 0.001, NS not significant. ANOVA followed by Dunnett's

Apabetalone counters TGF-β stimulated production of a pro-fibrotic ECM component in HRMCs

Anti-Inflammatory Effects of Apabetalone





p<0.01, *p< 0.001, NS not significant. ANOVA followed by Dunnett's

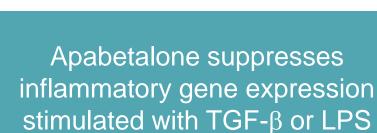
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0.15

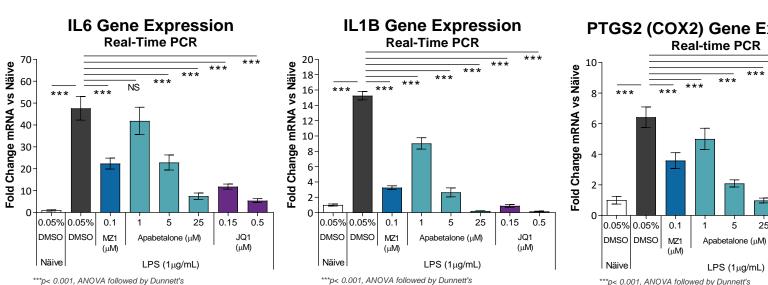
0.5

JQ1

(μM)



***p< 0.001, Benjamini-Hochberg adjusted p value



PTGS2 (COX2) Gene Expression

5

LPS (1µg/mL)

25

6

0.15µM

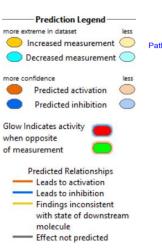
JQ1

25µM

Upstream Regulator of Inflammation is Inhibited by Apabetalone



Upstream Regulator	Human Renal Mesangial Cells (HRMC) 24h BETi + 2ng/mL TGF-β5μM Apabetalone25μM Apabetalone0.15μM								
Blue – inhibition Orange – activation Green p<0.05	Predicted Activation State	z-score	p-value	Predicted Activation State	z-score	p-value	Predicted Activation State	z-score	p-value
NfkB-RelA	No prediction	-1.18	4.49E-03	Inhibited	-2.533	4.10E-03	Inhibited	-2.00	4.98E-03
NFkB complex	No prediction	-0.443	4.63E-13	Inhibited	-3.142	1.25E-09	Inhibited	-2.00	4.98E-03



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NfkB-RelA and NFkB complex are upstream regulators of inflammation. Both were predicted to be inhibited by apabetalone.

NFkB complex

Differential gene expression by RNA-seq

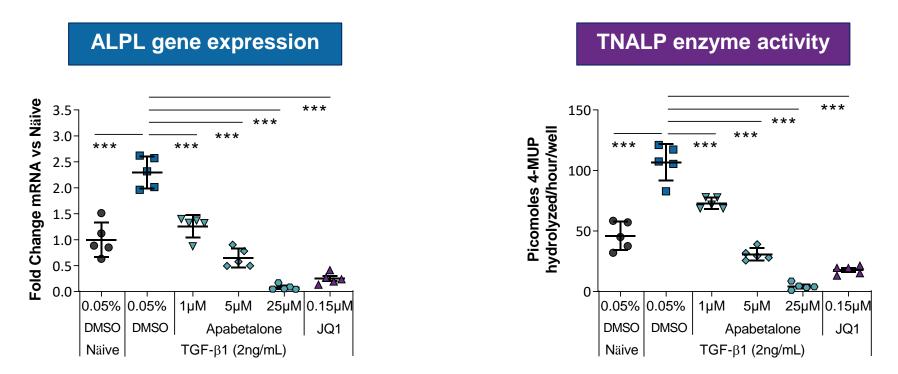
Ingenuity Pathway Analysis (IPA) predicts apabetalone inhibits NF-KB, a master upstream regulator of inflammatory processes

Apabetalone counters inflammatory TGF-β stimulation of HRMCs, and may suppress inflammation associated with renal pathology



RESVERLOGIX

Tissue non-specific alkaline phosphatase (TNALP; gene symbol ALPL) is a key driver of calcification – a process associated with kidney dysfunction *Curr Opin Nephrol Hypertens. 2020, 29:4–15, Nat Rev Nephrol. 2017, 13:429-442*

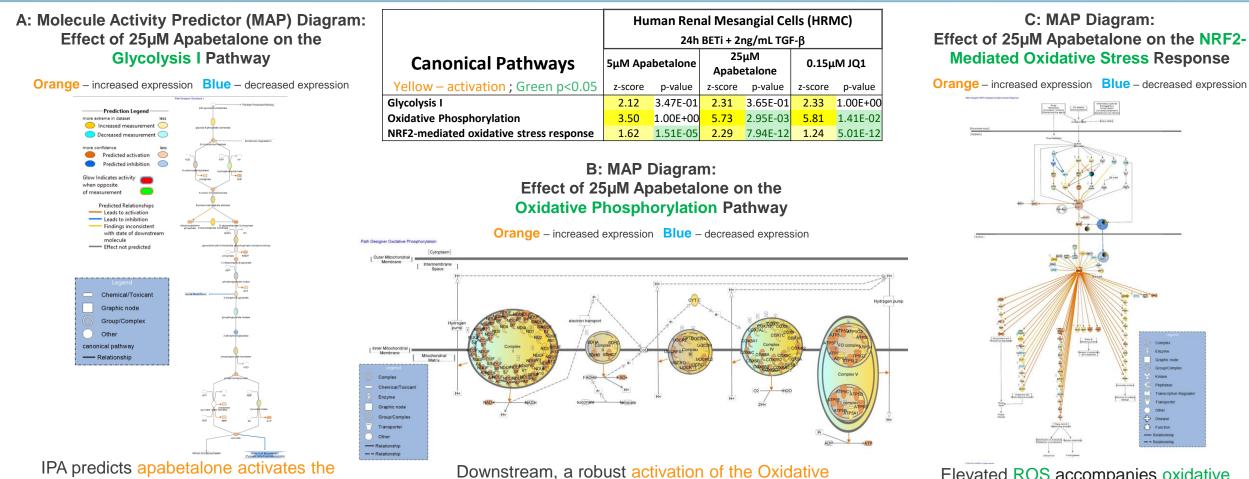


Apabetalone downregulates ALPL expression & enzyme activity in HRMCs, which may suppress calcification prevalent in CKD



Apabetalone's Effects on Canonical Pathways of Energy Metabolism





IPA predicts apabetalone activates the Glycolysis I pathway in HRMC, indicating increased glucose utilization. This may allow adaptation to high glucose in T2DM

Downstream, a robust activation of the Oxidative Phosphorylation pathway was predicted with apabetalone treatment, intuitively because of increased flux of pyruvate into the Krebs cycle. Elevated ROS accompanies oxidative phosphorylation. IPA predicts apabetalone activates the NRF2-mediated oxidative stress response pathway, a protective adaptation

Canonical pathways of energy metabolism predict apabetalone increases glucose utilization, and may allow kidney cells to cope with high glucose in T2DM to ameliorate diabetic nephropathy



- Apabetalone downregulates fibrotic, inflammatory and calcific pathways in HRMCs, which are associated with renal dysfunction.
- Changes in energy metabolism pathways predicted apabetalone facilitates adaptation to high glucose in the kidney in diabetic conditions that lead to diabetic nephropathy.
- Our results provide mechanistic insight into profound reductions in MACE in CKD patients receiving apabetalone in the phase 3 BETonMACE trial.
- The effect of apabetalone on MACE in patients with diabetes and CKD will be further evaluated in the upcoming phase 3 trials.

