

Zinc Finger Activators restore normal gene and protein expression in a mouse model of SCN2A haploinsufficiency

Jenny Hodges, Ph.D. Senior Scientist, Neuroscience

Presented at ESGCT October 24th, 2023 Yolanda Santiago¹, Andrew Olin¹, Jason Eshleman¹, Luke Bogart², Jack Hsiao², Mary Gulino², Madison Riley², Stephanie Hromadka², Stephanie Petit², Patrick Dunn¹, Jisoo Lee¹, Dan Chung¹, Giulia Cisbani³, Chiara Melis³, Finn Peters³, Toufan Parman¹, Eloise Hudry², Katie Worringer², Bryan Zeitler¹, Greg Davis¹, and Amy Pooler¹

¹SangamoTherapeutics, ²Novartis, ³Evotec



I am a full-time employee of Sangamo Therapeutics



SCN2A haploinsufficiency





Loss of function mutations in the SCN2A reduce $Na_v 1.2$ expression and alter neuronal excitation

- Na_v1.2 is a voltage gated sodium channel expressed primarily in excitatory neurons in the brain
- Reduced Na_vI.2 expression impairs neuronal excitation and synaptic plasticity
- Restoring normal levels of Nav1.2 is expected to correct neuronal function





Zinc Finger Activator approach to treating haploinsufficiency disorders





Zinc fingers are nature's solution for highly specific DNA binding



Zinc Fingers are natural proteins that bind DNA sequences with high specificity At least 782 human genes encode for Zinc Finger Proteins Most natural Zinc Finger Proteins function to regulate the epigenetic state of other genes



Zinc finger-mediated activation of Nav1.2 as a potent and specific therapeutic avenue for treating SCN2A haploinsufficiency





Active ZF-As were found at all three Scn2a transcription start sites



• 123/550 ZF-As >1.5-fold Scn2a activation in Neuro2a cells



ZF-As upregulate Scn2a long transcript in a dose-dependent manner in WT mouse cortical neurons



• Upregulation of Scn2a long transcript causes a dose-dependent repression of the middle Scn2a transcript



ZF-A mediated activation of the long *Scn2a* transcript increases Na_v1.2 in WT mouse cortical neurons





Early ZF-A leads were evaluated in vivo for Scn2a upregulation



Sangame

Im

Treatment (ZF-A)	Dose Level (vg/kg)	No. of Mice	
Vehicle	0	8	
hSynI-ZF-A I	3.16E+13	8	
hSynI-ZF-A I	1.00E+14	8	
hSynI-ZF-A 3	3.16E+13	8	
hSynI-ZF-A 3	1.00E+14	8	
3-week in-life		Right Hem	isohere
In-situ hybridization/		micro-di	sected
nmunohistochemistr	Y	for RT-q	PCR



Transgene is expressed throughout the CNS 3 weeks post-administration

ZF-As upregulate Scn2a long transcript in several brain regions and spinal cord

1.00E+14 vg/kg



- ZF-A-mediated dose-dependent repression of the middle Scn2a transcript was observed in all brain regions except the cerebellum
- Long Scn2a transcript is expressed at 5-fold higher absolute levels than the middle Scn2a transcript in all brain regions of vehicle treated animals

3.16E+13 vg/kg



Sangame

ZF-As elicit a dose-dependent increase in Na_v1.2 expression





RNAScope shows ZF-As increase *Scn2a* levels by more than two-fold in single neurons





Sangame I-Way ANOVA, Dunnett's multiple comparisons test, p-values represent a comparison to vehicle, *p<0.01, **p<0.005 ***p<0.001 14

Lead ZF-As candidates increase *Scn2a* expression and restore Na_v1.2 levels in *Scn2a* haploinsufficient mouse cortical neurons





Neurons were transduced on day 2 and harvested 6 days later for RT-qPCR and western blot. RT-qPCR data normalized to mean of Atp5b and Eif4a2. Western blot data normalized to mean of Na⁺K⁺-ATPase. Mean +/- SD.

Lead candidate ZF-A restores *Scn2a* expression to normal in *Scn2a*^{+/-} mice *in vivo*





RT-qPCR data normalized to mean of Atp5b and Eif4a2. I-Way ANOVA, Dunnett's multiple comparisons test, p-values represent a comparison to Scn2a^{+/+} vehicle, ****p<0.0001.BLOQ – Below Limit of Quantitation.

Conclusion



 ZF-As targeting mouse Scn2a increase Scn2a long transcript expression and Na_vI.2 levels in Scn2a^{+/+} and Scn2a^{+/-} mouse cortical neurons in vitro



- In vitro to in vivo translation achieved with ZF-As targeting Scn2a
- Na_vI.2 levels are elevated in several brain regions of WT mice following ZF-A treatment
- Lead ZF-A restores normal Scn2a long transcript levels in the brains of Scn2a^{+/-} mice



- Demonstrated proof-of-concept that ZF-As can be utilized to potentially to treat diseases caused by haploinsufficiency
- PoC also achieved for ZF-As targeting mouse Shank3 as a therapeutic approach for treating Phelan-McDermid syndrome. See Daniel Chung's poster – P415 (Wednesday 5pm and Thursday 830pm)





Thank you

Jenny Hodges

Senior Scientist, Neuroscience

Sangamo Therapeutics Inc.