Application of ADAR-mediated RNA Editing to Modulate Gene Expression

Chikdu Shivalila, Ian Harding, Prashant Monian, Genliang Lu, Keith Bowman, Michael Byrne, Arindom Chatterjee, Jigar Desai, Jason Dufresne, Frank Favaloro, Stephen Friend, Jack Godfrey, Naoki Iwamoto, Jayakanthan Kumarasamy, Pachamuthu Kandasamy, Tomomi Kawamoto, Anthony Lamattina, Gina Lein, Amber Lindsey, Richard Looby, Leah McCarthy, Andrew McGlynn, Allison Molski, Qianli Pan, Erin Purcell-Estabrook, Jeff Rossi, Stephany Standley, Alexandra Walen, Hailin Yang, Yuan Yin, Hui Yu, Paloma H. Giangrande, Chandra Vargeese

Summary

- AIMers can be applied to modulate gene expression by altering protein-protein interactions or transcript stability.
- AIMers were designed to modulate Nrf2-Keap1 protein-protein interactions and activate Nrf2-dependent gene expression. The AIMers directed up to 80% editing of Nrf2 or Keap1 transcripts in multiple cell types in vitro and led to dose-dependent activation of Nrf2-dependent gene expression.
- In mice expressing human ADAR1, AIMers led to ≥40% transcript editing and activation of Nrf2-dependent gene expression in the liver.
- AIMers were designed to modify regulatory elements in RNA that impact transcript stability. The AIMers increased mRNA expression 2-15-fold in vitro in cultured cells.
- GalNAc-AIMers that supported 40-60% editing in the mouse liver resulted in a corresponding ~5-fold increase in mRNA and protein expression 1-week after treatment.

Introduction

- AIMers are chemically modified oligonucleotides that direct sequence-specific adenosine (A) to inosine (I)/guanosine (G) RNA editing using endogenous ADAR enzymes (Figure 1A).
- In addition to correcting disease-causing mutations, application of AIMers to modulate protein-protein, protein-RNA, and RNA-RNA interactions can impact numerous biological outcomes (**Figure 1B**).

Figure 1. AIMers direct RNA editing with endogenous ADAR enzymes



Figure 2. Applying AIMers to modulate protein-protein interactions



We developed AIMers to modify the Nrf2-Keap1 interface (Figure 2A).

• Nrf2 is an antioxidant transcription factor negatively regulated by Keap1 through Nrf2-Keap1 binding (Figure 2B, C).

(B) adapted from Ref 2. (C) adapted from Ref 3. Note: Q26, D27, and I28 appear on the Nrf2 DLG motif; E82 appears on the Nrf2 ETGE motif.

References: 1. Monian et al., 2022. Nat Biotechnol DOI: 10.1038/s41587-022-01225-1; 2. Francisqueti-Ferron et al., 2015. Free Radic Biol. Med DOI: 10.1016/j.freeradbiomed.2015.05.034. Acknowledgments: Editorial and graphical support provided by Amy Donner (Wave Life Sciences) and Eric Smith, respectively.

Presented at The American Society of Gene and Cell Therapy 26th Annual Meeting, May 16-20, 2023 – Los Angeles. CA

Wave Life Sciences, Cambridge, MA, USA

Figure 3. Dose-dependent modulation of Nrf2-Keap1 interaction *in vitro*



Primary mouse hepatocytes treated gymnotically with the indicated concentration of AIMer. RNA was collected 48 h later. Editing was quantified by PCR and Sanger sequencing. Gene expression was quantified by qPCR (n=2).

• Keap1 interacts directly with Nrf2, leading to its degradation. When this protein-protein interaction is disrupted, Nrf2 translocates to the nucleus and activates gene expression (Figure 3A).

• We generated GalNAc-AIMers to target mouse *Nrf2* mRNA, altering amino acids at the Nrf2-Keap1 interface.

• In cultured primary mouse hepatocytes, AIMers supported dose-dependent editing of either mouse Ugp2 (control RNA) or Nrf2 mRNA (Figure **3B**). In the same cells, treatment with AIMers targeting *Ugp2* had no effect on expression of *Nqo1*, a gene downstream of Nrf2 (**Figure 3B**).

• The AIMers targeting *Nrf2* led to dose-dependent increases in *Nqo1* expression (**Figure 3B**) consistent with disruption of the protein-protein interaction in mouse cells.

Figure 4. AIMers enable gene expression changes *in vivo* with a single edit



RNA-seq Transcriptome Analysis Confirms Disruption of Nrf2 Protein Interaction with Upregulation of Key Factors



C57BL/6 mice expressing human ADAR1 were dosed with 10 mg/kg of the indicated GalNAc-AIMer subcutaneously on days 0, 2, and 4. Livers were harvested (day 7) and analyzed for (A) RNA editing and (B) Nqo1 and Gstm1 expression via Sanger sequencing and qPCR, respectively. Data were analyzed via One-way ANOVA with Tukey's multiple comparisons test. * p<0.05; ** p<0.01; *** p<0.001; **** p<0.0001 (C) RNA-seq was performed on livers from mice treated as indicated. Expression of each gene was assigned a z-score based on mean expression and the number of sequencing reads. A higher z-score indicates more expression relative to other groups.

• In mouse liver 1-week after first dose, GalNAc-AIMers led to ~50% editing of the targeted mRNA (*Nrf2* or *Ugp2*) (Figure 4A).

• At the same time, expression of Nrf2-dependent RNAs Nqo1 and Gstm1 increased significantly after GalNAc-Nrf2 AIMer treatment compared with PBS, whereas expression of these same RNAs did not increase after treatment with GalNAc-Ugp2 AIMer (Figure 4B)

• RNA-seq evaluation of liver gene expression 1-week after first dose shows that Nrf2-dependent genes generally increased after GalNAc-Nrf2 AIMer treatment, whereas the expression of these same genes did not increase in response to PBS or GalNAc-Ugp2 AIMer treatment (Figure **4C**).

• These data provide preclinical proof-of-concept that AIMer-mediated RNA editing can be applied to modulate PPIs in mice.



Upregulation

Figure 6. AIMers can edit RNA motifs to upregulate gene expression in hepatocytes and T cells *in vitro*







Figure 5. Applying AIMers to edit RNA motifs to restore or upregulate gene expression



We developed AIMers to upregulate mRNA expression (Figure 5A).

• Multiple sequence-dependent regulatory elements in RNA can be edited to impact gene expression (Figure 5B)

AIMers were designed to edit RNA sequence elements that impact mRNA stability, with the aim of upregulating gene expression (Figure 5C).



Primary Human Hepatocytes

(A-C) Primary human hepatocytes were treated with 10 µM AIMer or water (mock treatment) for 48 hours. (D) Primary human T cells were treated with 10 µM AIMer for 48 hours. In all panels, mRNA expression was quantified by gPCR.

• In cultured primary human hepatocytes, AIMers designed to edit regulatory elements in different transcripts led to increased expression of the edited transcripts (2->10-fold upregulation) compared with mock-treated cells (Figure 6A-C).

• In cultured primary human T cells, multiple AIMers that edit RNA regulatory elements led to increased expression of the edited transcript (4-6fold) compared with mock treatment (Figure 6D)

Figure 7. AIMers upregulate mRNA and downstream serum protein *in vivo*

(A) Human or mouse primary hepatocytes were treated with 10 µM GalNAc-AIMers for 48 hours. (B-D) Mice expressing human ADAR (n=5) were treated subcutaneously with 10 mg/kg GalNAc-AIMer or PBS on days 0, 2, and 4. Editing (Sanger sequencing), mRNA expression (qPCR), and protein expression (ELISA), were evaluated on day 7. Data were analyzed via the Kruskal-Wallis test followed by a Dunn post hoc test comparing to PBS-treated samples with Bonferroni adjustment for multiple comparisons. * p<0.05

 We compared Transcript A expression in response to RNA editing in cultured mouse and human cells. After GalNAc-AIMer treatment, Transcript A expression is increased more in human hepatocytes (~14-fold more than mock) compared to mouse hepatocytes (~2-fold more than mock), indicating that the mouse model may underpredict the impact of AIMers on this transcript (**Figure 7A**).

• We evaluated mouse AIMers in vivo in mice expressing a human ADAR transgene. One-week after the first dose, we detected 40-60% RNA editing in the liver (Figure 7B), which corresponded to a ~5-fold upregulation of Transcript A expression (Figure 7C) and a ~5-fold upregulation of protein expression (Figure 7D).