Felix Horns

Helen Hay Whitney & Chen Postdoctoral Fellow, California Institute of Technology

Division of Biology and Bioengineering
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Education

Ph.D. in Biophysics 2013 - 2019
Stanford University
Advisor: Stephen R. Quake
Thesis: *Origins of Somatic Diversity in Human Antibodies and the Brain*

M.Phil. in Computational Biology 2012 - 2013
University of Cambridge

B.A. in Biology, *summa cum laude* with highest honors 2007 - 2011
Amherst College
Advisor: Michael E. Hood

Honors & Awards

Burroughs Wellcome Fund Career Award at the Scientific Interface	2023 - 2028
NIH Pathway to Independence Award K99/R00, NIBIB (offered, but declined)	2023
Chen Postdoctoral Fellowship	2023 - 2025
Howard Hughes Medical Institute Fellow of the Helen Hay Whitney Foundation	2020 - 2023
National Science Foundation Graduate Research Fellowship	2013 - 2016
Fulbright Scholarship	2011 - 2012
George A. Plimpton Fellowship, Amherst College	2011 - 2013
Oscar E. Schotte Prize for best undergraduate thesis in Biology, Amherst College	2011
Phi Beta Kappa	2011
Doelling Undergraduate Research Awards	2010 & 2011
William C. Young Prize in Biology, Amherst College	2008

Research Experience

California Institute of Technology, Division of Bioengineering 2019 - present
Helen Hay Whitney & Chen Postdoctoral Fellow
Advisor: Michael B. Elowitz

- Invented RNA export systems for measurement and manipulation of living mammalian cells.
- Independent research published in *Cell*.

Stanford University, Program in Biophysics 2013 - 2019
National Science Foundation Graduate Research Fellow
Advisor: Stephen R. Quake; Key collaborators: Liqun Luo

- Developed genomic and computational tools, and used them to reveal the dynamics of B cell evolution, antibody class switching, and cell states in living humans.
- Established and led collaboration between Quake and Luo labs using single-cell transcriptomics to discover how neurons diversify to enable neural circuit assembly during brain development.
- Thesis research published in *Cell*, *Science*, *PNAS*, *Cell Reports*, and *eLife*.

University of Helsinki, Metapopulation Research Group 2011 - 2012
Fulbright Scholar
Advisor: Anna-Liisa Laine

- Uncovered how spatial structure impacts the evolution of disease and immunity.
- Research published in *Evolution*.

Amherst College, Department of Biology 2009 - 2011
Undergraduate Researcher
Advisor: Michael E. Hood

- Discovered a genome defense mechanism in basidiomycete fungi, a burst of retrotransposition in a fungal genome, and a theoretical limit on the evolution of disease resistance.
- Thesis research published in *Genome Biology and Evolution* and *Ecology and Evolution*.

PUBLICATIONS

18. **F Horns**†, JA Martinez, C Fan, M Haque, JM Linton, V Tobin, L Santat, AO Maggiolo, PJ Bjorkman, C Lois, MB Elowitz†, "Engineering RNA export for measurement and manipulation of living cells." ***Cell***, 186(17), 3642-3658.E32 (2023).

17. EL Shrock, RT Timms, T Kula, EL Mena, AP West Jr, R Guo, I-H Lee, AA Cohen, LGA McKay, C Bi, Keerti, Y Leng, E Fujimura, **F Horns**, M Li, DR Wesemann, A Griffiths, BE Gewurz, PJ Bjorkman, SJ Elledge, "Germline-encoded amino acid–binding motifs drive immunodominant public antibody responses." ***Science***, 380(6640), eadc9498, (2023).

16. M Swift, **F Horns**, SR Quake, "Lineage tracing reveals fate bias and transcriptional memory in human B cells." ***Life Science Alliance***, 6(3), e202201792, (2023).

15. S Lee, EC Lai, and the Fly Cell Atlas Consortium, including **F Horns**, "Diverse cell-specific patterns of alternative polyadenylation in *Drosophila*." ***Nature Communications***, 13, 5372 (2022).

14. D Yang*, MG Jones*, S Naranjo, WM Rideout III, KHJ Min, R Ho, W Wu, JM Replogle, JL Page, JJ Quinn, **F Horns**, X Qiu, MZ Chen, WA Freed-Pastor, CS McGinnis, DM Patterson, ZJ Gartner, ED Chow, TG Bivona, MM Chan, N Yosef, T Jacks, JS Weissman, "Lineage tracing reveals the phylodynamics, plasticity, and paths of tumor evolution." ***Cell***, 185(11), 1905-1923 (2022).

13. H Li*, J Janssens*, and the Fly Cell Atlas Consortium, including **F Horns**, "Fly Cell Atlas: A single-nucleus transcriptomic atlas of the adult fruit fly." ***Science***, 375(6584), eabk2432 (2022).

12. CN McLaughlin*, M Brbic*, Q Xie, T Li, **F Horns**, SS Kolluru, JM Kebschull, D Vacek, A Xie, J Li, RC Jones, J Leskovec, SR Quake, L Luo, H Li, "Single-cell transcriptomes of developing and adult olfactory receptor neurons in Drosophila." ***eLife***, 10, e63856 (2021).

11. Q Xie, M Brbic, **F Horns**, SS Kolluru, RC Jones, J Li, AR Reddy, A Xie, S Kohani, Z Li, CN McLaughlin, T Li, C Xu, D Vacek, DJ Luginbuhl, J Leskovec, SR Quake, L Luo, H Li, "Temporal evolution of single-cell transcriptomes of Drosophila olfactory projection neurons." ***eLife***, 10, e63450 (2021).

10. **F Horns**, SR Quake, "Cloning antibodies from single cells in pooled sequence libraries by selective PCR." ***PLoS ONE***, 15(8), e0236477 (2020).

9. H Li*, T Li*, **F Horns**, J Li, Q Xie, C Xu, B Wu, JM Kebschull, CN McLaughlin, SS Kolluru, RC Jones, D Vacek, A Xie, DJ Luginbuhl, SR Quake, L Luo, "Single-cell transcriptomes reveal diverse regulatory strategies for olfactory receptor expression and axon targeting." ***Current Biology***, 30(7), 1189-1198 (2020).

8. **F Horns**, CL Dekker, SR Quake, "Memory B cell activation, broad anti-influenza antibodies, and bystander activation revealed by single-cell transcriptomics." ***Cell Reports***, 30(3), 905-913 (2020).

7. **F Horns**, C Vollmers, CL Dekker, SR Quake, "Signatures of selection in the human antibody repertoire: selective sweeps, competing subclones, and neutral drift." ***Proceedings of the National Academy of Sciences***, 116(4), 1261-1266 (2019).

6. H Li*, **F Horns***, B Wu, Q Xie, J Li, T Li, DJ Luginbuhl, SR Quake, L Luo, "Classifying Drosophila olfactory projection neuron subtypes by single-cell RNA sequencing." ***Cell***, 171(5), 1206-1220 (2017).

5. **F Horns**, E Petit, ME Hood, "Massive expansion of Gypsy-like retrotransposons in Microbotryum fungi." ***Genome Biology and Evolution***, 9(2), 363-371 (2017).

4. **F Horns***, C Vollmers*, D Croote, SF Mackey, GE Swan, CL Dekker, MM Davis, SR Quake, "Lineage tracing of human B cells reveals the in vivo landscape of human antibody class switching." ***eLife***, 5, e16578 (2016).

3. AJM Tack, **F Horns**, AL Laine, "The impact of spatial scale and habitat configuration on patterns of trait variation and local adaptation in a wild plant parasite." ***Evolution***, 68(1), 176-189 (2014).

2. **F Horns**, E Petit, R Yockteng, ME Hood, "Patterns of repeat-induced point mutation in transposable elements of basidiomycete fungi." ***Genome Biology and Evolution***, 4(3), 240-247 (2012).

1. **F Horns**, ME Hood, "The evolution of disease resistance and tolerance in spatially structured populations." ***Ecology and Evolution***, 2(7), 1705-1711 (2012).

* denotes equal contribution
† denotes co-corresponding author

Patents

3. **F Horns**, MB Elowitz, "Exported RNA reporters for live-cell measurement" (U.S. Patent Application 17/820,235) (2021).

2. **F Horns**, JA Martinez, MB Elowitz, "Cell-to-cell delivery of RNA circuits" (U.S. Patent Application 17/820,232) (2021).

1. **F Horns**, SR Quake, "Methods and compositions for selective PCR and cloning of antibody sequences" (U.S. Patent Application 63/039,113) (2020).

Presentations

Invited Seminars

SY-Stem Symposium on Stem Cell Research	Mar 2024
Caltech, Biology and Bioengineering Annual Retreat	Nov 2023
Caltech, Center for Molecular and Cellular Medicine Seminar	Oct 2023
Systems Virology Journal Club	Oct 2023
Extracellular Vesicle Club	Sep 2023
Helen Hay Whitney Foundation Annual Meeting	Nov 2022
10X Genomics, Global Immunology Virtual Summit	May 2020
Chan-Zuckerberg Biohub, Immunology Seminar	Jan 2019
Stanford University, Program in Biophysics, Student Seminar	Oct 2018
University of California, San Francisco, Systems Immunology Seminar	Sep 2018
A-STAR, Singapore, Infectious Disease Workshop	Oct 2016

Talks at International and Regional Meetings

American Society for Virology Annual Meeting	Jun 2023
Allen Discovery Center for Lineage Tracing Retreat	May 2023
Cold Spring Harbor Laboratory, Systems Immunology	Apr 2023
Winter Q-Bio	Feb 2023
Ettore Majorana Foundation, Italy, Frontiers in Biophysics	Aug 2018
Stanford University, Immunology Retreat	Sep 2017
Stanford University, Human Systems Immunology Center Meeting	Jul 2016

Posters at International and Regional Meetings

Stanford University, Bioengineering Retreat	Nov 2018
Stanford University, Biophysics Retreat	Sep 2018
Gordon Research Conference, Molecular Mechanisms in Evolution	Jun 2015
ETH Zurich, Switzerland, Evolutionary Biology Workshop	Jun 2012
CNRS, France, Theoretical and empirical advances in evolutionary genomics	Apr 2012

Teaching Experience

Amherst College, Departments of Physics and Biology
Teaching Assistant

- Physics 46: Molecular and Cellular Biophysics — Spring 2011
- Biology 18/19: Introductory Biology Laboratory — Fall 2008, Spring 2009

Amherst College, Departments of Physics, Chemistry, and Biology
Peer Tutor

- Classical mechanics, electromagnetism, chemistry, molecular genetics — 2009 - 2011

Mentorship

Graduate Students
Victoria Tobin (Caltech Bioengineering), NIH F30 awardee
Joe Martinez (Caltech Bioengineering)
Linjing Fang (Caltech Bioengineering)
Michael Swift (Stanford Chemical & Systems Biology), NSF GRFP awardee
Ana Jimena Pavlovitch-Bedzyk (Stanford Immunology)

Undergraduate Students
Maggie Sui (Caltech Bioengineering), now Fulbright Scholar

Research Technicians
Mehernaz Haque (Caltech)

Service

Invited Journal Referee
eLife, *Molecular Biology and Evolution*, *PLoS Computational Biology*

Contributed Journal Reviews
Nature, *Science*, *Cell*, *Neuron*

Societies (current and past membership)
Sigma Xi, American Physical Society, Biophysical Society, American Society for Virology, Society for Neuroscience

Outreach

Community Outreach

Teacher and demonstrator, Caltech Diversity in Chemistry Initiative	2022 - present
Reviewer, Caltech Summer Undergraduate Research Fellowship program	2023
Responder, Santa Clara County Rapid Response Network	2015 - 2019
Mentor, Stanford Science Penpals	2014 - 2018

Science Communication

Writer and editor, *Hawkmoth*	2015 - 2016
Science columnist, *The Amherst Student*	2009 - 2011

Harnessing RNA export to monitor and manipulate living cells

Overview: As a central information carrier of the cell, RNA provides a powerful interface for reading and writing cell states, but *current RNA-based technologies have critical limitations*. Although RNA analysis reveals the states of individual cells[1], existing techniques typically must destroy the cell to access its RNA. This limits our ability to observe how individual cells change over time, which is a major drawback because these cell dynamics lie at the heart of important biomedical questions, such as how embryos develop, immune cells fight pathogens, tumors spread, and bodies age. In parallel, delivery and expression of engineered RNA promises programmable control over cell behavior[2]. However, delivering RNA to target cells in tissue remains challenging, which impedes the use of RNA therapeutics[3] to repair or remove diseased cells within the body.

My research seeks to overcome these limitations by engineering cells to export RNA, which unlocks new ways to monitor and manipulate living cells. I invented RNA export systems, inspired by viruses, that package and secrete RNA from mammalian cells within protective nanoparticles[4]. Exporting and sequencing RNA enables molecular information to be obtained non-destructively from living cells. These systems also deliver RNA cargos from cell to cell. Building on this foundation, *my goal is to create and use RNA-based reporter and delivery systems to monitor and manipulate cells within animals* (Fig. 1). I will uncover principles of cell secretion and harness them to engineer RNA exporters with new capabilities, such as tunable transport, stability, and immunogenicity (Aim 1). I will develop RNA-based reporters to monitor dynamic cell states, providing new forms of "liquid biopsy" with improved sensitivity and information content, and apply them to reveal tumor and immune dynamics (Aim 2). Finally, I will create "RNA delivery" cells to precisely manipulate cells in vivo for immunotherapy and regenerative medicine (Aim 3). This plan leverages my background of interdisciplinary research at the interface of biophysics, genomics, and synthetic biology.

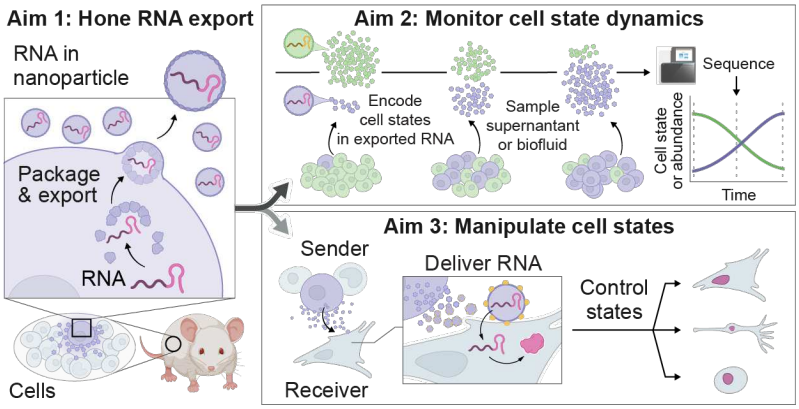

Fig. 1. Summary of aims. Exporting RNA enables non-destructive monitoring of cell dynamics and cell-to-cell delivery of RNA therapeutics.

Selected graduate work: With Dr. Stephen Quake, I developed and applied single-cell and antibody repertoire sequencing techniques to reveal how human antibodies and immune cells diversify and respond to challenges. I charted the first comprehensive map of antibody class switching in living humans[5] and uncovered genetic signatures of somatic antibody evolution, revealing that both selective and neutral processes shape human antibodies[6]. I also profiled dynamic B cell responses to influenza vaccination, resulting in the discovery of activated B cell states underlying memory recall, broadly binding anti-influenza antibodies, and widespread "bystander" activation of antibodies that do not bind vaccines[7]. The antibody repertoire and phylogenetic analysis approaches I developed have been adopted across immunology (e.g., to discover SARS-CoV-2 antibodies[8] and public antibodies[9]) and to study evolution in other contexts, such as tumor growth[10]. Finally, to understand how brains are built, in collaboration with Dr. Liqun Luo, I developed and used single-cell transcriptomics techniques to discover how neurons transiently diversify and express combinations of cell-surface proteins during development to precisely assemble neural circuits[11,12]. The single-cell genomic and computational methods I developed also enabled us to generate the first organism-wide cell atlas of the fruit fly[13] and have been broadly adopted in the invertebrate community (e.g., [14,15]).

Postdoctoral work: Recognizing untapped potential of RNA for both analysis and control of cells, I resolved to overcome both the destructive nature of RNA measurements and the difficulty of precisely delivering RNA by harnessing synthetic biology. With Dr. Michael Elowitz, I engineered RNA exporters, based on capsids and designed protein nanocages, that efficiently package and secrete specific RNA molecules from cells with virus-like particles or vesicles[4]. By combining viral genetic barcoding with RNA export and sequencing, I demonstrated non-destructive monitoring of cell population dynamics with clonal resolution[4]. Further, export systems efficiently delivered RNA from cell to cell[4], enabling manipulation of cell states. Importantly, RNA

exported from tumor xenografts is detectable in blood, laying the foundation for monitoring and manipulating cells in animals. I am extending these systems to models of cancer and immunity, including tumors and T cells. I have also established collaborations to apply RNA export to understand hematopoiesis and neurodevelopment in animals and organoids, which I will continue in my independent career. This work shows the potential and feasibility of RNA-based reporter and delivery systems.

Short- and medium-term plans: *I will develop RNA export systems to measure and manipulate dynamic cell states in living animals* (Fig. 1). Using these exporter, reporter, and delivery platforms, I will answer longstanding questions in cancer immunology and establish cell-based RNA therapeutics.

Aim 1. Engineer improved RNA exporters for in vivo operation. Using RNA exporters in vivo raises new technological demands. For example, packaging RNA in small vesicles (<100 nm diameter) that transport readily through tissues[16,17] into blood and evade phagocytosis[18] should improve RNA detection via liquid biopsy. Rationally tuning these properties of secreted vesicles and how they interact with cells in turn requires answering basic questions in biophysics, cell biology, and immunology, such as how protein architecture governs vesicle size and how immune cells recognize vesicles. The goal of this aim is to endow RNA exporters with new capabilities by uncovering and harnessing the rules that govern synthetic vesicle design and function.

(1) Establish strategy to characterize RNA exporters at high throughput. Learning the rules of exporter design requires exploration of a large design space, as exporters are composed of combinations of capsid or nanocage, membrane-binding, and secretion domains[4] (Fig. 2A, left). To explore this space efficiently, leveraging the ability of RNA exporters to package their own RNA, I will establish sequencing-based, pooled assays to measure biophysical and functional properties, such as vesicle size, secretion rate, and stability, of >10^4 exporters per experiment (Fig. 2B).

(2) Learn the design rules of RNA exporters. Deciphering the rules that link nanoscale protein architecture (e.g., size, shape, degree of oligomerization) to mesoscale properties of secreted vesicles (e.g., size, secretion rate, stability) would reveal principles of cell secretion and facilitate expansion of exporter functionality (Fig. 2A). To uncover these rules, I will systematically vary protein architecture, drawing upon natural capsids[19,20] and computationally designed proteins[21,22], and characterize the physical and functional properties of secreted vesicles using ultrastructural imaging and sequencing.

(3) Cloak exporters from immunity. Minimizing exporter immunogenicity would unlock diagnostic and therapeutic utility. I will exploit the diversity of human proteins, including endogenous viral capsids[23–25], to humanize exporters. I will also cloak exporter vesicles by surface display of immunomodulators[18].

Together, these studies will reveal the molecular logic of cell secretion and provide a set of RNA exporters tailored for varying research and therapeutic applications.

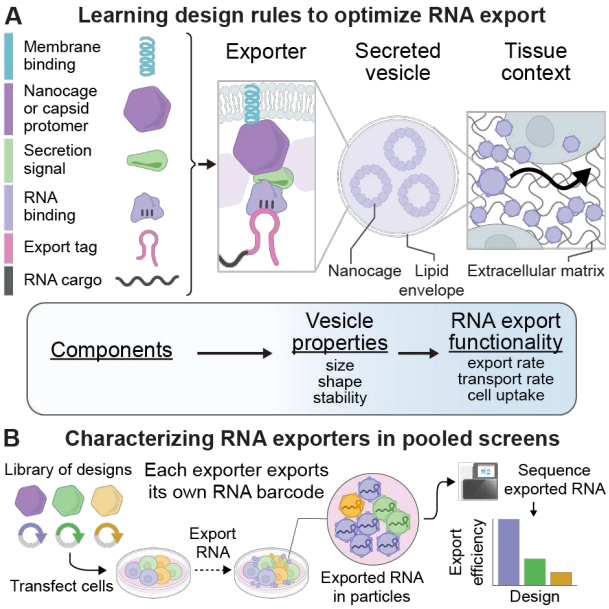

Fig. 2. Engineering RNA exporters. (**A**) Design rules link exporter protein architectures to vesicle properties and functionality. (**B**) High-throughput measurement of exporter properties via "self-export" of RNA barcodes.

Aim 2. Monitor cell state dynamics by exporting and reading RNA in vivo. The dynamics of cell populations and states underlie diverse biological processes. For example, in cancer, cells clonally expand, contract, mutate, and change states over time, which drives growth, evolution, and metastasis[26]. If one could track these cell dynamics within living animals, then central questions could be addressed, such as how clonal competition impacts tumor growth[27,28], what cell states promote metastasis[29], and when immune suppression arises[26]. However, current analysis methods are destructive and reveal only snapshots of cell population structures and states[10,30,31], from which dynamics must be inferred. By contrast, exporting and sequencing RNA enables non-destructive molecular monitoring of cell populations and states[4]. Exporters efficiently secrete RNA barcodes from cells (10^3-fold faster than natural secretion), endowing reporter systems with single-cell

sensitivity (reliable detection of RNA from each cell) and daily time resolution in cell culture[4]. Importantly, RNA secreted by tumor xenografts is detectable in blood, raising the possibility of monitoring cells in living animals via minimally invasive, longitudinal "liquid biopsy". The goal of this aim is to expand RNA-based reporters to monitor single-cell states and to use them to reveal cancer and immune dynamics in animals.

(1) Monitor cell states via RNA editing. Beyond monitoring cell population dynamics[4], the information content of exported RNA barcodes could be expanded to encompass cell states. To encode defined cell states into RNA, I will use state-responsive promoters (e.g., for Wnt[32] or Notch[33] signaling, or T cell[34] activity) to drive RNA editing[35] within sequences alongside a cell barcode that identifies the cell of origin. Exporting and sequencing this RNA will reveal single-cell state trajectories in a non-destructive, scalable manner (Fig. 3A).

(2) Monitor single-cell transcriptomes. Recovering transcriptome samples over time from barcoded cells would provide genome-scale measurements of single-cell state trajectories. Endogenous transcripts and cell barcodes are already both present in exporter particles[4], and I will detect both together in single particles using in situ hybridization[36], thus revealing single-cell transcriptome dynamics (Fig. 3B).

(3) Characterize tumor and immune cell dynamics. The dynamic interplay of tumor and immune cells underpins cancer but is challenging to measure by existing methods. I will use my established population dynamics reporter system[4] in tumor xenograft models[37] to monitor the clonal dynamics of tumor growth and immune responses (Fig. 3C). As I develop tools to monitor cell states, I will use them to reveal tumor and immune cell state dynamics underlying tumor growth or clearance. The results will address longstanding questions in cancer immunology, including whether clones compete or cooperate[27,28], what signals drive metastasis[29], and how tumors suppress immunity[26].

Taken together, these studies will establish a set of broadly applicable "liquid biopsy" reporters for monitoring cell dynamics in cell culture and animal models.

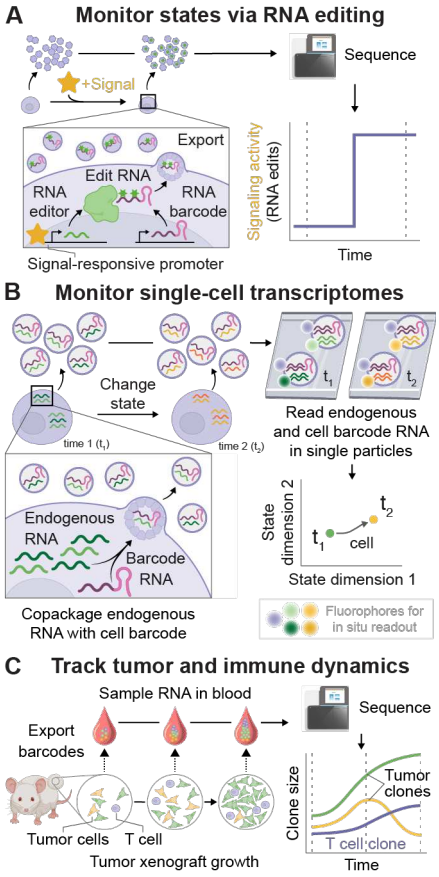

Fig. 3. Measuring cell state dynamics using RNA export. (**A**) Encoding and reading cell states by editing RNA. (**B**) Reading transcriptome samples from single cells over time. (**C**) Monitoring tumor and immune dynamics in vivo.

Aim 3. Manipulate cells using "RNA delivery" cells. RNA is a promising therapeutic[2] but is held back by the challenge of delivery[3]. Efficient cell-to-cell RNA transfer[4] unlocks the possibility of engineering an "RNA delivery" cell that is engineered ex vivo then infused, explores tissues, detects diseased cells, and locally delivers RNA circuits to repair or clear those cells. I will establish this strategy, which combines the versatility of RNA with the sensing, logic, and tissue penetration capabilities of cell therapies.

(1) Precisely control RNA delivery. Cell-based RNA delivery offers targeting at three levels. First, I will use synthetic receptors[38] to activate RNA export when the delivery cell recognizes a target cell (Fig. 4A). Second, by pseudotyping particles with natural[39,40] or engineered[41–43] fusogens, I will target entry to specific cell types (Fig. 4B). Third, I will use RNA[44–46] and protein[47] sensors and circuits encoded in the cargo RNA itself to conditionally regulate cargo activity based on the intracellular state of the recipient cell.

(2) Regenerate cell types by delivering transcription factor (TF) mRNA. Reprogramming cells in vivo is a longstanding goal in regenerative medicine[48], but efficient and specific delivery remains a roadblock. Tissue-resident RNA delivery cells could overcome this roadblock by providing sustained local transmission of mRNA encoding reprogramming factors to target cells. I have shown that cell-to-cell delivery of TF mRNA reprograms cells in culture (fibroblast to myocyte conversion by MyoD[49]). I will harness RNA delivery cells to regenerate cell types in vivo in progressively more challenging conversions, including pancreatic alpha to beta cells[50] to address diabetes and glia to dopamine neurons[51,52] to address Parkinson's disease (Fig. 4C).

(3) Modulate immune cell states to enhance anti-tumor immunity. Tumors suppress immunity by inhibiting immune cells[53], but tumor killing can be restored by reprogramming immune cell states[54]. To enhance tumor clearance through local immune activation, having shown that T cells can export RNA[4], I will engineer T cells to deliver TF mRNA to convert Th2 to Th1 cells[55] and M2 to M1 macrophages[56] (Fig. 4C).

Together, this work will establish a platform that unifies cell and gene therapy for refined manipulations of target cells in vivo.

Training environment: My group will provide *unique interdisciplinary training opportunities for diverse scientists*, who will help to define the emerging interface of biophysics, genomics, and synthetic biology and address central biomedical questions. Having mentored individuals from underrepresented groups throughout my career, I will continue leveraging my experiences to recruit diverse scientists and foster a supportive environment where everyone is empowered to explore their boldest ideas, learn from one another, and thrive.

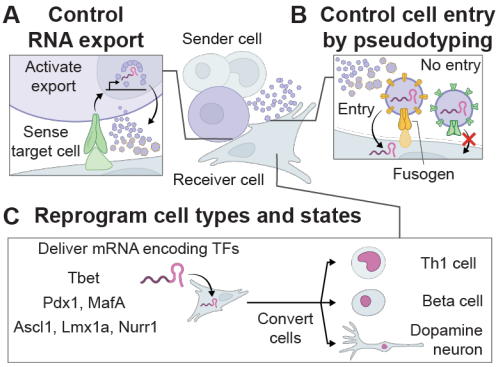

Fig. 4. Manipulating cell states using controlled cell-to-cell delivery of RNA. (A, B) Strategies to control delivery. **(C)** Examples of manipulations.

Broader impacts and career outlook: This work will enable tracking of cell states within animals in varied biological contexts. After refining the platforms, I will use them to address longstanding questions in immunology (how do the collective dynamics of immune cells underpin healthy immunity versus disease?), development (how do tissues assemble?), and aging (how do individual cells and tissues change with age?). This work will also establish cell-based delivery of RNA as a new therapeutic modality. I will expand the platform's effector outputs to include genome editing and selective cell ablation. I am eager to provide my colleagues and collaborators with reporting and delivery systems to accelerate discovery and therapeutics in diverse biological settings. Finally, having benefited from exceptional mentorship myself, I look forward to nurturing the next generation of creative scientific thinkers in my lab. Taken together, our work will unlock better understanding and control of cells to advance human health.

References

1. Aldridge, S., and Teichmann, S.A. (2020). Single cell transcriptomics comes of age. Nat. Commun. *11*, 4307.
2. Dykstra, P.B., Kaplan, M., and Smolke, C.D. (2022). Engineering synthetic RNA devices for cell control. Nat. Rev. Genet. *23*, 215–228.
3. Dammes, N., and Peer, D. (2020). Paving the Road for RNA Therapeutics. Trends Pharmacol. Sci. *41*, 755–775.
4. Horns, F., Martinez, J.A., Fan, C., Haque, M., Linton, J.M., Tobin, V., Santat, L., Maggiolo, A.O., Bjorkman, P.J., Lois, C., et al. (2023). Engineering RNA export for measurement and manipulation of living cells. Cell *186*, 3642-3658.e32.
5. Horns, F.*, Vollmers, C.*, Croote, D., Mackey, S.F., Swan, G.E., Dekker, C.L., Davis, M.M., and Quake, S.R. (2016). Lineage tracing of human B cells reveals the in vivo landscape of human antibody class switching. Elife *5*, e16578.
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9. Shrock, E.L., Timms, R.T., Kula, T., Mena, E.L., West, A.P., Jr, Guo, R., Lee, I.-H., Cohen, A.A., McKay, L.G.A., Bi, C., et al. (2023). Germline-encoded amino acid-binding motifs drive immunodominant public antibody responses. Science *380*, eadc9498.
10. Yang, D., Jones, M.G., Naranjo, S., Rideout, W.M., 3rd, Min, K.H.J., Ho, R., Wu, W., Replogle, J.M., Page, J.L., Quinn, J.J., et al. (2022). Lineage tracing reveals the phylodynamics, plasticity, and paths of tumor evolution. Cell *185*, 1905-1923.e25.
11. Li, H.*, Horns, F.*, Wu, B., Xie, Q., Li, J., Li, T., Luginbuhl, D.J., Quake, S.R., and Luo, L. (2017). Classifying Drosophila Olfactory Projection Neuron Subtypes by Single-Cell RNA Sequencing. Cell *171*, 1206-1220.e22.
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13. Li, H., Janssens, J., De Waegeneer, M., Kolluru, S.S., Davie, K., Gardeux, V., Saelens, W., David, F.P.A., Brbić, M., Spanier, K., et al. (2022). Fly Cell Atlas: A single-nucleus transcriptomic atlas of the adult fruit fly. Science *375*, eabk2432.
14. Xu, J., Liu, Y., Li, H., Tarashansky, A.J., Kalicki, C.H., Hung, R.-J., Hu, Y., Comjean, A., Kolluru, S.S., Wang, B., et al. (2022). Transcriptional and functional motifs defining renal function revealed by single-nucleus RNA sequencing. Proc. Natl. Acad. Sci. U. S. A. *119*, e2203179119.

15. Feng, M., Xia, J., Fei, S., Huang, Y., Lai, W., Swevers, L., and Sun, J. (2023). Single-nucleus sequencing of fat body reveals distinct metabolic and immune response landscapes in silkworm larvae after Bombyx mori nucleopolyhedrovirus infection. J. Immunol. *211*, 140–153.
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