



VCU

Virginia Commonwealth University
VCU Scholars Compass

Graduate Research Posters

Graduate School

2020

DYRK1A and the Cell Cycle

Holly Byers
Virginia Commonwealth University

Larisa Litovchick, MD, PhD

Follow this and additional works at: <https://scholarscompass.vcu.edu/gradposters>



Part of the [Medicine and Health Sciences Commons](#)

Downloaded from

Byers, Holly and Litovchick, MD, PhD, Larisa, "DYRK1A and the Cell Cycle" (2020). *Graduate Research Posters*. Poster 72.

<https://scholarscompass.vcu.edu/gradposters/72>

This Poster is brought to you for free and open access by the Graduate School at VCU Scholars Compass. It has been accepted for inclusion in Graduate Research Posters by an authorized administrator of VCU Scholars Compass. For more information, please contact libcompass@vcu.edu.

DYRK1A and the Cell Cycle

Holly A. Byers¹, Larisa Litovchick, Ph.D.^{1,2}

Virginia Commonwealth University School of Medicine, 1. Department of Human Genetics, 2. Department of Internal Medicine



Background

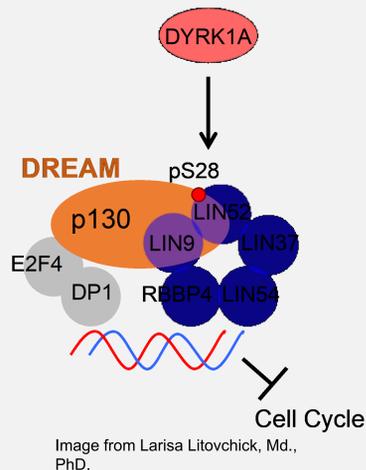
DREAM is a key regulator of cell cycle quiescence

- DREAM (DP1, the Rb-related protein p130, E2F4, and the MuvB core complex)
- Multi-subunit repressor complex of cell cycle-promoting genes
- Switch from DREAM to BMYB-MuvB (MMB) is highly regulated

DYRK1A (dual specificity tyrosine-(Y)-phosphorylation regulated kinase 1A)

- nervous system development, cell growth and division, and neuronal differentiation
- Cytogenetic Location: 21q22.13
- Putative tumor suppressor** and important regulator of many proteins through its kinase activity
- DYRK1A phosphorylates Serine residue 28 on LIN52 of the MuvB core, allowing p130 to bind to LIN52.

Necessary for formation of DREAM complex.



Lab observation: T98G DYRK1A-KO cells appear slightly smaller, and proliferate more slowly than control cells.

Unexpected phenotype. DYRK1A is a **putative tumor suppressor** through phosphorylation of LIN52 (required for binding of p130 for DREAM assembly).

Research Questions: Is there **slower, encumbered DNA synthesis** happening in DYRK1A-KO cell lines to explain the **slower proliferation** observed in T98G cells? What is the underlying mechanism of the delayed proliferation of the DYRK1A-KO cells?

Methods

Cell Line: T98G cells

- Human astrocytes, glioblastoma multiforme cells (originally derived from a 61 year-old Caucasian male)
- Hyperpentaploid, and typically carry three copies of the DYRK1A gene

Two mutant lines used in these experiments:

- CRISPR **DYRK1A-KO** lines (labeled as 3.1.A6 and 4.1.A1)
- Grown in Dulbecco's Modified Eagle Medium (DMEM) + FBS, + penicillin/streptomycin, + glutamax. Starvation media in these experiments contained 0% FBS

Experimental protocol for starvation and release of cells back into cell cycle: plate equal numbers of cells → replace media with starvation media for 48 hours → Induces cells to enter quiescence/temporary arrest in G1/G0 → Release cells back into the cell cycle through addition of 15% FBS → Collect samples at 0, 16, and 22 hr timepoints.

•Three methods used to gauge cell cycle progression in T98G cells following starvation and release:

- Cell cycle FACS using propidium iodide (Canto flow cytometry)
- Western blot for cell cycle (especially S phase) protein markers
- EdU (Ethylnyl deoxyuridine) staining to measure active DNA synthesis across time points

Results

Figure 1: Using student's T tests between each group (using JMP statistical software) both DYRK1A-KO lines' 5 day cell count means were significantly different from the control line mean cell count ($p=0.001$ for both mutant lines).

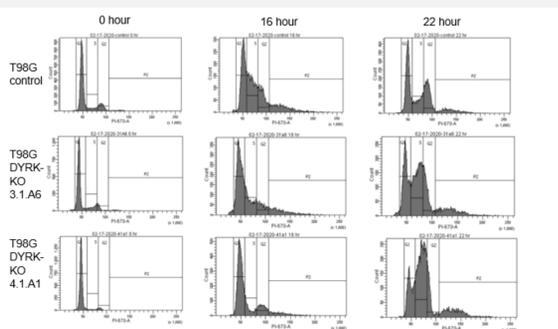
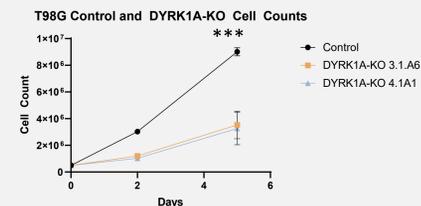


Figure 2: T98G and T98G DYRK1A-KO lines were starved and then released back into the cell cycle. WT T98G proceeds through cell cycle checkpoints normally, while DYRK1A-KO lags, entering S phase at 22 hours. Quantification on right panel. $N=3$ biological repeats.

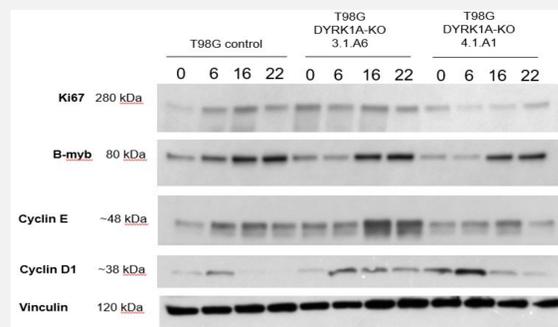
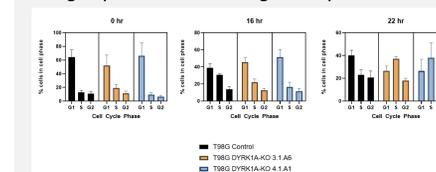
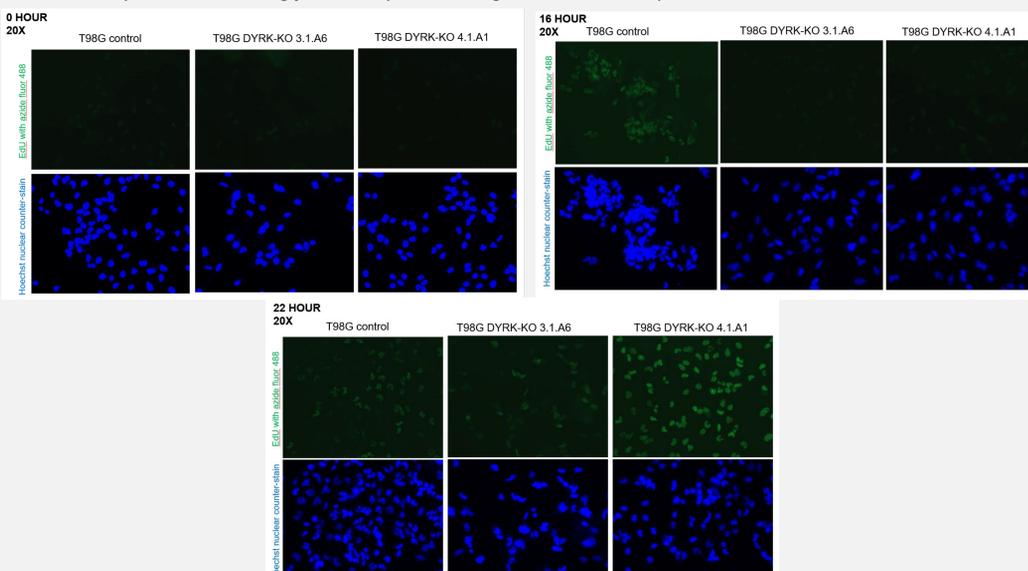


Figure 3: Cell Cycle protein markers after starvation and release at 0-22 hr timepoints. $N=3$ biological repeats.

Figure 4: EdU staining (30 minute pulse) for T98G control and DYRK1A-KO cells at 0, 16, 22 hr in the cell cycle. EdU staining for DNA synthesis in green, and lower panels Hoechst nuclear stain.



Discussion

Conclusions

DYRK1A T98G mutants are growing more slowly, entering and proceeding through S phase more slowly than control T98G cells. This is evidenced by:

- FACS cell cycle data: *DYRK1A-KO* cells enter S phase around the 22 hour mark rather than 16-18 hours.
- EdU staining: *DYRK1A-KO* cells do not begin to complete active DNA synthesis until ~22 hrs
- Cell Cycle markers with WB: Cyclin E, B-myb accumulates later in the cell cycle in KO lines

DYRK1A may be having an unexpected, but significant effect on the cell cycle. Further investigation is needed to fully elucidate and understand the roles of *DYRK1A* in cell cycle regulation and arrest.

Future Directions

- Quantification of EdU staining, EdU Cell Cycle FACS
- Probing for additional cell cycle markers (Cyclin A, Cyclin B for S/G2 transition)
- Delving deeper into what is happening with Ki67 and DYRK1A, potentially IP at various time points in the cell cycle for Ki67/DYRK1A interaction
 - Additionally, Ki67 staining in T98G control and *DYRK1A* mutant cells at time points throughout the cell cycle following synchronization
- Cell line-dependent observation? Use of additional cell lines for repeated experiments (Litovchick lab currently works with multiple non-cancer and cancer lines with *DYRK1A-KO*)

Acknowledgements

Dr. Larisa Litovchick (PI)

Varsha Ananthapadmanabhan

Breanna Jeffcoat

Supriya Joshi

Fatmata Sesay

Hayley Walston

VCU Massey Cancer Center Flow Cytometry Shared Resource

Julie Farnsworth

