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Fluoxetine as an Anti-Inflammatory Therapy in SARS-CoV-2 Infection - Protocol v1.1

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1 Works for me dx.doi.org/10.17504/protocols.io.bscjnaun

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SUBMIT TO PLOS ONE

ABSTRACT

Hyperinflammatory response caused by infections such as Severe Acute Respiratory Syndrome Coronavirus 2 (SARS-CoV-2) increase organ failure, intensive care unit admission, and mortality. Cytokine storm in patients with Coronavirus Disease 2019 (COVID-19) drives this pattern of poor clinical outcomes and is dependent upon the activity of the transcription factor complex nuclear factor kappa-light-chain-enhancer of activated B cells (NF- κ B) and its downstream target gene interleukin 6 (IL6). In this study, we compare transcriptomic signatures from a variety of drug-treated or genetically suppressed (i.e. knockdown) cell lines in order to identify a mechanism by which antidepressants such as fluoxetine demonstrate non-serotonergic anti-inflammatory effects. Our results demonstrate a critical role for the IL6 signal transduction protein (IL6ST or gp130) in fluoxetine's ability to act as a potential therapy for hyperinflammatory states such as asthma and sepsis.

THIS PROTOCOL ACCOMPANIES THE FOLLOWING PUBLICATION

Creeden, Justin and Imami, Ali Sajid and Eby, Hunter M. and Gillman, Cassidy and Becker, Kathryn N. and Reigle, Jim and Andari, Elissar and Pan, Zhixing K. and O'Donovan, Sinead M. and McCullumsmith, Robert E. and McCullumsmith, Cheryl B., Fluoxetine as an Anti-Inflammatory Therapy in SARS-CoV-2 Infection. Available at SSRN: <https://ssrn.com/abstract=3736012> or <http://dx.doi.org/10.2139/ssrn.3736012>

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PROTOCOL CITATION

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MANUSCRIPT CITATION please remember to cite the following publication along with this protocol

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KEYWORDS

iLINCS, LINCS, Drug Repurposing, Bioinformatics

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IMAGE ATTRIBUTION

Thumbnail Designed by Justin Fortune Creeden

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GUIDELINES

Please ensure that you have the appropriate amount of time, computational resources and access before executing this workflow.

MATERIALS TEXT

R programming language 3.3.3 of later

[source](#) by The R Foundation

R Studio Desktop 1.1.463

by The R Studio, Inc.

ssri_il6 1.1

[source](#) by Ali Sajid Imami, Justin Fortune Creeden

iLINCS

SAFETY WARNINGS

No Applicable Warnings.

BEFORE STARTING

Please ensure that you have the following tools installed:

1. R v 3.6 or later
2. RStudio v 1.2 or later
3. Rtools appropriate to the version of R if using Windows
4. Command Line Tools with XCode if working on macos

Follow the instructions on the [README](#) for running.

Workflow

1 Identify Drug Signatures

We searched iLINC5 for the L1000 drug signatures for Fluoxetine, Paroxetine, Bupropion and Dexamethasone.

Fluoxetine Signature List

Paroxetine Signature List

Dexamethasone Signature List

Bupropion Signature List

curate_signature.R v1.1 [↗](#)

[source](#) by Ali Sajid Imami, Justin Fortune Creeden

2 Download Drug Signatures

We downloaded all the 436 identified signatures for further processing.

Signature To Drug Mapping

process_signatures.R v1.1 [↗](#)

[source](#) by Ali Sajid Imami, Justin Fortune Creeden

Downloaded L1000 Signatures

3 Generating High Confidence Signatures

We filtered all signatures to keep only the genes that had a Log₂ Fold Change value greater than 0.85 or less than -0.85 to generate a high confidence signature

process_signatures.R v1.1 [↗](#)

[source](#) by Ali Sajid Imami, Justin Fortune Creeden

Filtered L1000 Signatures

4 Identifying Concordant Signatures

The generated high confidence signatures were uploaded to iLINCS and searched against the Consensus Gene Knockdown Signature database for concordance against 27 inflammation related genes.

process_signatures.R v1.1 [↗](#)

[source](#) by Ali Sajid Imami, Justin Fortune Creeden

Concordant Gene Knockdown Signature List

5 Cell Line Matching

The resulting list of concordant signatures was matched with the list of input signatures and only those signatures were kept that had the input and concordant signature in the same cell line. This resulted in 779 total signatures.

analyse_data.R v1.1 [↗](#)

[source](#) by Ali Sajid Imami, Justin Fortune Creeden

Cell Line Matched Concordance Scores

6 Maximising Absolute Concordance

The list of 779 total signatures was further simplified by only keeping the match with the maximum absolute concordance score in a given combination of drug, gene and cell line. This reduced the list of signatures to 395.

analyse_data.R v1.1 [↗](#)

[source](#) by Ali Sajid Imami, Justin Fortune Creeden

Cell Line Matched Maximum Absolute Concordance Scores

7 Summarising Concordance

The concordance scores were then further summarised by calculating an arithmetic mean of the concordance scores across multiple cell lines for the same drug-gene combination.

analyse_data.R v1.1 [↗](#)

[source](#) by Ali Sajid Imami, Justin Fortune Creeden

Averaged Concordance Scores

