Sperm Toolbox – A selection of small molecules to study human spermatozoa

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Abstract

Male contraceptive options and infertility treatments are limited. To help overcome these limitations we established a small molecule library as a toolbox for assay development and screening campaigns using human spermatozoa. We have profiled all compounds in our automated high-throughput screening platform and provide the dataset, which allows direct side-by-side comparisons of compound effects and assays using live human spermatozoa.

Main

One of the grand challenges for science and society is the development of novel contraceptives that are safe and deliver control of reproduction to men and women all over the world. In parallel, a deeper understanding of the sperm function and possible interventions for male infertility is required to counter declining birth rates. Recently, the application of advanced technologies has helped to move the human fertility field forward, revealing new potential targets for both contraception and fertility, and new compounds as contraceptive candidates (reviewed by(Anderson and Johnston, 2023; Norcross et al., 2022; Service et al., 2023). A key part of this effort is the development of mechanistic insight and drug candidates that affect the behaviour and properties of human spermatozoa(Balbach et al., 2023; Carlson et al., 2022; Faber et al., 2023; Hau et al., 2022). Towards this end, we have recently developed an automated live human sperm phenotypic, target-agnostic screening platform that can screen 1000s of compounds and identify positive and negative modifiers of sperm function (Gruber et al., 2020; Gruber et al., 2022). These effects can be either positive or negative and therefore starting points for either fertility treatments (including medical assisted reproductive technologies) or contraceptive development. An advantage of using a high-throughput platform is the ability to efficiently compare many compounds under the same assay conditions, within a short amount of time.

To facilitate drug discovery approaches related to contraception or infertility, we assembled a small library containing 84 small molecules, which we have coined the Sperm Toolbox (STB). The idea of the STB is in concordance with similar efforts e.g. the MMV Pandemic Response Box (Samby et al., 2022), the SGC Epigenetic Chemical Probe Collection (Brown and Muller, 2015), or the Drug Repurposing Hub (Corsello et al., 2017) which facilitate deeper understanding of biology or pathology or repurpose approved drugs. We tested the STB compounds in multiple functional sperm assays, for general cytotoxicity and aqueous solubility (Figure 1A). The STB has been assembled to contain previously published compounds and compounds detected in our own screening campaigns (Gruber et al., 2020; Gruber et al., 2022). In addition, we included a few compounds which have been inferred from patent applications or studies of proteins potentially relevant for sperm function (Figure 1B). The focus has been mainly on literature investigating human systems, but compounds tested in animal models, cell-based, or biochemical systems have also been included. The compounds selected in the STB have been described to effect crucial sperm functions e.g. motility, capacitation, acrosome reaction, Ca^{2+} signalling, viability, or are related to other processes (e.g. spermatogenesis, liquefaction, or ejaculation) (Figure 1C). Compound annotations are included in the STB dataset and indicate that Enzymes/Kinases, Receptors, Channels and Transporters are the most represented compound classes. Using information from the drug repurposing hub (Corsello et al., 2017), we generated a protein-protein interaction network of targets related to STB compounds (Figure 1E). This network consists of multiple subclusters related to functions in spermatozoa (Figure 1F) and other biological processes, functions, and pathways (Figure 1G).

Figure 1

(A) The Sperm Toolbox is a collection of 84 small molecules with published, observed or inferred effect on multiple biological processes in or generation of spermatozoa. Human sperm cells have been tested in various assays, which allows comparison of compounds under the same experimental conditions. (B) Summary of the sperm toolbox compound compositions. (C) Summary of annotated (i.e. published, observed, inferred) sperm function of Toolbox compounds. (D) Coarse classification of Sperm Toolbox target classes. (E) StringDB Protein-Protein interaction networks (Full network, confidence 0.7) of putative targets of Sperm toolbox compounds. Protein targets have been inferred from the repurposing hub. Network has been clustered using MCL clustering in Cyotscape. (F) Sperm related terms (GeneOntology, Reactome) within the network shown in (E). Marker size indicates false discovery rate (FDR). (G) Enriched terms within the biggest subclusters in (E). Redundant terms have been filtered using Cytoscape (cutoff 0.5). Color matches subcluster color in (E)

To compare the effects of STB compounds on specific sperm functions, we screened them in multiple
phenotypic functional assays. Each sperm function assay has been repeated in multiple donor pools (see
Material and Methods), where each pool consists of cells donated from at least 3 different donors to address
donor to donor variability. This generates datasets that are more representative of a more general
population. Each compound has been tested at two concentrations 10 and 30 μM and normalized to
vehicle controls (DMSO). We have modified our assays from the previously published workflow
(Gruber et al., 2020) to generate a deeper understanding of compound action (e.g., by increasing
incubation time) and to better model *in vivo* conditions (e.g. by introducing conditions which
support capacitation, which is a sperm maturation process required for fertilization). Our motility
assays, use a high-content microscope to record short timelapse movies and can run in different
modes. The first mode, denoted 'motility assay', utilises non-capacitating assay conditions that
models the state of spermatozoa after ejaculation. The second mode, denoted 'capacitation assay',
utilises capacitating conditions (Extended Figure 1A). Both modes allow sperm motility to be
measured. In addition, the capacitation assay also scores hyperactivation (i.e. distinct movement
patterns concomitant with capacitation which are crucial for fertilization) and is therefore a marker
of capacitation.

The acrosome assays utilize a high-throughput flow cytometer to score for compounds inducing the
acrosome reaction, using peanut agglutinin conjugated to a fluorescent dye (labelling the inner
acrosomal membrane). As with the motility assays, we have developed two different screening
modes, named 'acrosome 1' and 'acrosome 2' (Extended Figure 1A). Both modes are capable of
measuring induction of the acrosome reaction. However, in the acrosome 2 assay, a physiological
agonist mix of the acrosome reaction is used thus we also also measures inhibition of acrosome
reaction (Prajapati et al., 2022).

Additionally, we tested the effect of STB compounds on sperm viability using a complementary live-
cell flow-cytometer approach and propidium iodide, which does not permeate intact cell
membranes (Extended Figure 1B).

In addition to functional assays using human spermatozoa, we also profiled each STB compound for
general cytotoxicity in two cell-lines (HeLa and HepG2). The HeLa-based assay uses the cell painting
assay (Bray et al., 2016), while the second assay (HepG2) utilizes a resaruzin based read-out
(Baragana et al., 2015). To ensure usability of STB compounds, we also measured aqueous solubility.
An overview of additional assays is given in Extended Figure 1C.

This multi-assay compound profiling dataset has revealed a broader picture of the action of
individual compounds, helps find similarities between compounds, and provides an opportunity to
compare results from different screening assays. Computational analysis of the profile dataset has
the potential to elucidate further sperm biology. Using unsupervised clustering we observed clusters
of compounds with a significant reduction of sperm motility and/or increased amounts of acrosome
reacted cells (e.g. Alexidine dihydrochloride, Tafenoquin or A23187) (Figure 2A). Some of these
compounds also show significant levels of cytotoxicity in HeLa and/or HepG2 cells as well as
decreased sperm viability suggesting that their effect on motility and acrosome reaction could be
non-specific. However, other clusters show a significantly increased acrosome reaction and
hyperactive motility but do not show effects on sperm viability or general cytotoxicity (e.g. LRRK2-
IN-1, Clofarabine, Linsitinib, Trequinsin). One example, LRRK2-IN-1, which enhances motility
(progressive and hyperactivated), has been described as a selective inhibitor of LRRK2 kinase, which
is involved in Parkinson's disease (Deng et al., 2011). This compound shares some structural
similarities with two kinase inhibitors in the STB, which decrease sperm motility: Compound 19,

described as a potent Testis-Specific Serine/Threonine Kinase 2 (TSSK2) inhibitor (Hawkinson et al.,
2017) and CZC 25146, annotated as a potent LRRK2 inhibitor.

Overall, we observed that a number of compounds show weak or no effects in our assays (Extended
figure 2), which stresses an important aspect of the STB: comparing compounds using the same
assay conditions. Our screening system is not limited to the buffer system, incubation times or
screening concentration used in this study. This flexibility provides an excellent start point to
establish control compounds and assay conditions for novel drug discovery campaigns related to
contraception and infertility. Our profiled dataset captures well described compounds from the
literature and allows direct comparisons to compounds identified in our own screening. We provide
the complete dataset as well as web interface for data analysis
(https://spermtoolbox.shinyapps.io/spermtoolbox/).

This work represents the first version of the STB. Future revisions could contain newly published
compounds modulating functions in spermatozoa e.g., a sAC inhibitor TDI-11861 (Balbach et al.,
2023), a CatSper inhibitor RU1968 (Schierling et al., 2023), a SLO3 inhibitor (Lyon et al., 2023) or
other contributions from the research community. In addition, the STB could present an important
resource for testing and benchmarking newly developed drug screening assay.

In summary the STB is a small library intended to facilitate contraceptive and infertility drug
discovery. We have established a unique reference dataset which allows comparing the performance
of compounds in multiple assays. This will ultimately give a broader picture of the compounds effect
on sperm function.

A   Sperm Motility assays

Motility
Non-capacitating media

Capacitation
Capacitating media

◆ Microscope read-out

B   Sperm Acrosome assays

Acrosome 1
Capacitating media

Acrosome 2
Capacitating media

Sperm Viability
Non-capacitating media

● Flow-cytometer read-out

C   Additional assays

HeLa cytotoxicity — 24 h with compounds — ◆ Microscope read-out

HepG2 cytotoxicity — 70 h with compounds — ◇ Fluorometric read-out

Aqueous solubility — 24 h with compounds — ◇ uHPLC read-out

Extended Figure 1
Overview of assays

(A) Diagram showing sperm motility assays run on high-content microscope with compound incubation time/read-out time. Motility assay run under non-capacitating conditions, with a 1 hour recovery phase after preparation of spermatozoa. Capacitation assay run under capacitating conditions. Spermatozoa are capacitated for 30 min prior to compound incubation.

(B) Diagram showing assays run on high-throughput flow cytometer to measure acrosome status and sperm viability. Incubation time with compound, agonist and read-out times are indicated. Acrosome assays run under capaciting conditions. Sperm viability assay run under non-capacitating condition.

(C) Additional assays performed on sperm toolbox compounds.

Extended Figure 2

    (A) Vulcano plots of Acrosome, Capacitation and Motility assays. Upper panel indicates 10 µM, lower plot panels indicate 30 µM. Incubation times for assays are 3h with compound for Acrosome assay and Classic Motility (PM = progressive motility), and 30 min for the Capacitation assay (HA = hyperactive motility, PM = progressive motility). Dotted line indicates significance levels of 0.05. Any point above dotted line is indicated in magenta.

Figure 2

    (A) Heatmap showing standardized results (z-score) for every Toolbox compound screened at 30 μM in selected assays: Acrosome 1 (3h with compound then induction with acrosome reaction using an agonist mix), Motility Hyperactive (30 min capacitation then 30 min incubation with compound), Motility Progressive (3h incubation with compounds under non-capacitating conditions), Motility Total (3h incubation with compound under non-capacitating conditions)), Solubility (aqueous solubility of compounds after 24h incubation), Sperm viability (3h with compound then propidium iodide assay), Toxicity HeLa (24h compound incubation then cell painting assay), Toxicity HepG2 (70h incubation

with compound then resaruzin based assay). Heatmap color indicates decrease (blue) or increase (red).

(B) UMAP plot showing groups of compounds with similar assay profile. Color indicates annotated sperm function.

(C) (C) Structures and zoom-in of three examples related to LRRK2 kinase.

Material and Methods

Ethical approval

152 Written consent was obtained from each donor in accordance with under local ethical approval
153 (University of Dundee, SMED REC 20/45).

Sperm handling

Donated human spermatozoa with normal semen characteristics (concentration, motility; WHO
2010) from healthy volunteers with no known fertility problems were used in this study. Samples
were obtained by masturbation after ≥ 48 h of sexual abstinence, liquefied for 30 min at 37 °C, and
processed using density gradient centrifugation, to separate cells using 40/80% Percoll (Sigma
Aldrich, UK) fractions. Every experiment has been performed on pooled spermatozoa from ≥ 3
donors each.

For experiments in non-capacitating conditions, we used a buffer system slightly modified from
(Tardif et al., 2014) using Minimal Essential Medium Eagle (Sigma), supplemented with HEPES (1 M
solution, Gibco), sodium lactate (DL-solution, Sigma), sodium pyruvate (100 mM solution, Gibco) and
bovine serum albumin (7.5 % solution, Sigma).

For experiments in capacitating conditions, we used a buffer system slightly modified from the HTF
from (Prajapati et al., 2022) to a final composition of 97.8 mM NaCl, 4.69 mM KCl, 0.2 mM $MgSO_4$,
0.37 mM KH_2PO_4, 2.04 mM $CaCl_2$, 0.33 mM Na-pyruvate, 12.4 mM Na-lactate, 2.78 mM glucose, 21
mM HEPES, 25 mM $NaHCO_3$ and 3 mg/mL BSA. All buffer components were supplied by Sigma-
Aldrich unless otherwise stated and all buffer systems were adjusted to pH 7.4.

Compound handling

Compounds were purchased from vendors indicated in supplementary file x. 10 mM stock solutions
in DMSO were generated. Quality control of each compound has been performed (HPLC-MS and
NMR).

Compound plates were generated using 10 mM stock solutions of each STB compound in Echo 384-
LDV plates (LP-0200). Prior to running experiments, assay ready plates have been generated using
Echo acoustic dispensers (550/555). Each compound was screened at 10 and 30 µM final
concentration. Plate types used for assays: Motility, HeLa cell painting and Sperm viability
(PerkinElmer 384-well PhenoPlate), Acrosome (Greiner 384-PP V-bottom plates).

Motility assays

Classic motility assay:

Cells were rested for 1 h post density gradient centrifugation. 10 µL assay buffer was dispensed into assay ready plates, plates were put onto a shaker instrument for 30 seconds using 1,000 rpm, followed by a short pulse centrifugation. Plates were incubated for 15-30 mins at 37 °C prior to addition of 10 µL of pooled cells (at 1 M/mL concentration). Plates were then incubated in a Yokogawa CV7000 microscope set at 37 °C for 10 min prior to imaging. Imaging a 384-well plate requires ≤ 20 min using the following settings: 2 positions per well, 0.5 sec timelapse movies (3x binning; 11 ms exposure time, 22 ms interval time, 500 intervals). A second and a third timepoint was recorded after 3 h, and 6 h incubation at 37 °C. Data has been processed as described in Gruber et al., 2020.

Capacitation assay:

Cells were capacitated for 30 min at 37 °C and 5 % CO_2. 10 µL assay buffer was dispensed into assay ready plates, plates were put onto a shaker instrument for 30 seconds using 1,000 rpm, followed by a short pulse centrifugation. Plates were incubated for 15-30 mins at 37 °C and 5% CO_2 prior to addition of 10 µL of pooled cells (at 1 M/mL concentration). This was followed by a 20 min compound incubation step at 37 °C and 5 % CO_2. Plates were then incubated in our CV7000 microscope set at 37 °C and 5% CO_2 for 10 min prior to imaging. Imaging a 384-well plate requires ≤ 20 min using the following settings: 2 positions per well, 0.5 sec timelapse movies (3x binning; 11 ms exposure time, 22 ms interval time, 500 intervals). Data has been processed as described in Gruber et al., 2020.

Acrosome assays

In both experimental modes, 20 µL of pooled cells (at 1 M/mL concentration) were capacitated for 3 h in presence of compounds at 37 °C and 5% CO_2. In mode a, cells were then stained with PNA-Alexa647 (ThermFisher, 1 mg/mL, final dilution 1:1000) and Hoechst dye for 30 min at 37 °C and 5% CO_2, followed by 10 min fixation at RT by adding 20 µL of 4% paraformaldehyde (Sigma) in PBS. In mode b, a cocktail of progesterone , prostaglandin A and NH_4Cl was added to all compound wells and incubated for an additional 1 h at 37 °C and 5% CO_2 to induce acrosome reaction. This was followed by fixation and staining protocol as for mode a. In both modes fixatives and stains were removed and cells were resuspended in PBS, using a 405 platewasher. Plates were then measured on a Novocyte Advanteon high-throughput flow cytometer. Gating of data has been performed using the flow cytometer software to export counts of gated populations.

Sperm viability assay

Cells were incubated with compounds for a total of 3h at 37 °C. 20 min prior, propidium iodide was added (1.5 mM solution, Sigma, final dilution 1:2000). Plates were analysed using a Satorius iQue Screener with settings to allow for a sampling time of ≤30 min per 384-well plate. Gating of data has been performed using the flow cytometer software to export counts of gated populations.

HeLa cell painting

Cell were incubated with compounds for 24h. Cell painting was performed after Bray et al., 2016 with modifications suggested here (Cimini et al., bioRxiv 2022.07.13.499171; doi: https://doi.org/10.1101/2022.07.13.499171):

- 10 µL of MitoTracker (Life Technologies, M22426, 1 mM stock in DMSO as recommended by the vendor) is added to 50 µL of media (1:2000 final dilution)
- Phalloidin-Alexa594 (Life Technologies, A12381, 66 µM stock in methanol as recommended by the vendor, 1:500 final dilution)
- WGA-Alexa594 (Life Technologies, W11262, 5 mg/mL stock, 1:250 final dilution) was used
- DAPI (5 mg/mL stock; 1:1000 final dilution) was used to stain DNA
- 20 µL of staining solution was used
- PBS was used for washing steps

HepG2 cytotoxicity assay

HepG2 assay was performed as described previously (Baragana et al., 2015).

Aqueous solubility

The aqueous solubility of test compounds was measured using UHPLC, as previously described in (Smith et al., 2022) .

Data analysis

Data was normalized to DMSO control wells. Each plate had 16 DMSO wells. A median value of all 16 wells was used to calculated percentage change (pct_ch = ((value / DMSO_median) -1) * 100). For sperm viability we calculated fold-change (fc = 1 - (value / DMSO_median)). For each compound we calculated a p-value using a Welch's t-test implemented in scipy (scipy.stats.ttest_ind) comparing a compounds effect to DMSO controls.

The following packages have been used for data analysis and visualization:

R: Tidyverse, plotly, pHeatmap

Python: pandas, numpy, scipy, seaborn, matplotlib, umap

Acknowledgements

The authors acknowledge support by the Bill & Melinda Gates Foundation (INV-007117).

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