

Sphingosine kinase (SPHK), a new drug target for treating schistosomiasis

Ziada Kiwanuka, Bismark Dankwa, Mary Evans, Benjamin Hulme, Sarah Davey, Kristin Lees, Iain Chalmers, Gabriel Rinaldi, Josephine Forde-Thomas, Karl Hoffmann



| Introduction | Objective |
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| • Schistosomiasis is a neglected tropical disease (NTD) affecting 230 million people, and 779 million are at risk of becoming infected globally. | • This study aims to characterise the role of Sphingosine Kinase in the parasite S. mansoni and assess its suitability as a potential drug |
| There are two types of Schistosomiasis infections. Urogenital schistosomiasis caused by Schistosoma haematobium, and intestinal schistosomiasis caused by either Schistosoma mansoni or Schistosoma japonicum. Schistosoma mansoni is a major species responsible for infecting approximately 54 million people appually. | SPHK is an enzyme that phosphorylates the sphingolipid sphingosine to sphingosine 1 phosphate (S1P). |
| Praziquantel (PZQ) is the only World Health Organization's recommended drug for treating all Schistosoma species worldwide In absence of vaccine and documented evidence indicating possible resistance of PZQ, new chemical matter needs to be brought into the drug discovery pipeline to sustain schistosomiasis control. | S1P is involved in the regulation of various cellular processes, such as cell survival, proliferation, migration, and differentiation. Dysregulation of S1P has been implicated in several human diseases, including cancer, inflammation, and autoimmune disorders (Zheng et al., 2019). |
| Bioinformatic Searches | In human diseases, Sphingosine kinase inhibitors have been primarily studied as a potential therapeutic agent for cancer and inflammatory conditions. They have shown promise in preclinical studies and early clinical trials for their ability to suppress tumor growth, induce apoptosis ir |
| Smp_343150 Conserved Blast search Smp_157100 SPHK1 Smp_130110 Smp_157100 Smp_157100 Smp_157100 functional motifs Smp_157100 five motifs that are functionally | cancer cells, and inhibit angiogenesis (Zheng et al., 2019). Thus, the importance of screening these compounds against schistosome parasite. More argumentation of using these compounds is evidenced by the structural protein (3D) structure - see figure D, E, F, and G showir binding of the compounds to the S. <i>mansoni</i> protein. |
| Domain searchSmp_163080Multiple sequence alignmentimportant.Smp_342570Smp_036180• Residues highlighted in boxes are those that are highly conserved within | Adult worm screening of Human Sphingosine Kinase 1 inhibitors |
| Smp_157100 HsSPHK1 HsSPHK2 Motif 1 Motif 2 Motif 2 Motif 3 Motif 3 Mot | 3 chemically distinct compounds known to inhibit HsSPHK were screened against adult <i>S. mansoni</i> Compounds were screened against worm pairs in triplicate on 3 separate occasions Praziquantel (10 µM PZQ) and Auranofin (10 µM AUR) were included as positive controls and DMSO was included as a negative control. First experiment was performed at a final concentration of 50 µM followed by 2 dose response |







Gene expression throughout the life cycle

- Highly expressed in cercaria and schistosomula (Lu et al., 2016)(Protasio et al., 2017)
- Single-cell RNA sequencing (RNA-seq) from adult schistosomes, where this transcript shows enriched expression in neurons, germinal stem cell progenies (GSCs) and male germ cells (Wendt et al., 2020).

Structural Protein Analysis

- This analysis predicts the binding of PF543 and C567731 to *S. mansoni* SPHK using the known crystallographic structures for human sphingosine kinase 1 co-complexed with the compounds (PDB 4V24 PF543 & 3VZD C567731) (J. Wang et al., 2014) (Z. Wang et al., 2013).
 Validation of our analysis tools Repeating the docking of the known human protein (SPHK) crystal structure and the compounds to produce the same pose of compound
 In Auto Dock Vina, the ligands were energy minimized before docking was carried out. The protein's active site was placed with grid box dimensions set at X=12.65 Å, Y=13.4757 Å, and Z=-11.1428 Å for the centre while box size dimensions were set at X=27.0291 Å, Y=23.3081 Å, and Z=23.4367 Å.
 Figure A & B shows the crystal structure of 4V24 & Smp_157100 homology respectively and the binding of compound C567731
- titrations of 25 μM, 12.5 μM, and 6.25 μM concentrations. Worms were scored by microscopy at 24, 48 and 72h using the WHO-TDR scoring metric described in the table below. 50 μM concentration Compound titrations; 50 μM-6.25 μM









PI staining, egg count, EC₅₀ measurements

- At 72h, 15µg/ml of propidium iodide was added to those worms that showed no movement (i.e. scored 0) to distinguish the compounds that caused worm death and those that only immobilized the worms.
- Worms that stained red upon the addition of propidium iodide were confirmed as dead.
- Eggs present in each well were counted using a Cytation 7. Egg production was inhibited in wells treated with compounds when compared to the negative control, (DMSO)



2 °antibody only



| Smp_157100 4V24 3VZD_1 | NFIINLPKANLLRYRAIVTCSGDGLVYEVINGLISRKDYDDVIEEDTIPIGILPGGSANS 240 ELVRSEELGRWDALVVMSGDGLMHEVVNGLMERPDWETAIQKPLCSLPAGSGNA 123 ELVRSEELGRWDALVVMSGDGLMHEVVNGLMERPDWETAIQKPLCSLPAGSGNA 112 | | | |
|---|--|--|--|--|
| Smp_157100 4V24 3VZD_1 | PVSCIHFGTYDTNFHRYGIQSIEWGFIADLDYKSERFRWMGEKRFLLYACYYLMKKPTYR 358 PMNLLS-LHTASGLRLFSVLSLAWGFIADVDLESEKYRRLGEMRFTLGTFLRLAALRTYR 215 PMNLLS-LHTASGLRLFSVLSLAWGFIADVDLESEKYRRLGEMRFTLGTFLRLAALRTYR 204 *:.: : :::::::::::::::::::::::::::::::: | | | |
| Smp_157100 4V24 3VZD_1 | LPETNQHISNHQDKWVTLDKKFVTILVLNHSH <mark>I</mark> TSS <mark>A</mark> VMYPDAHMSDPYLNLLILHENTT 478 VPDEDFVLVLALLHSHLGSEMFAAPMGRCAAGVMHLFYVRAGVS 303 VPDEDFVLVLALLHSHLGSEMFAAPMGRCAAGVMHLFYVRAGVS 292 :* *:.** :*.* ***: * * .: : ::*: :: .:: | | | |
| Smp_157100 4V24 3VZD_1 | RFDLLAL <mark>G</mark> RALSSGQ <mark>G</mark> LQST-SNMDIVKVCALRIEPYSQDSVTTMLD <mark>G</mark> ELVPSGTFQAEV 537 RAMLLRLFLAMEKGRHMEYECPYLVYVPVVAFRLEPKDGKGV-FAVDGELMVSEAVQGQV 362 RAMLLRLFLAMEKGRHMEYECPYLVYVPVVAFRLEPKDGKGV-FAVDGELMVSEAVQGQV 351 * ** * *:*::::::::::::::::::::::::::: | | | |
| Residues in 4VDZ and 3VZD active site (lipid binding pocket) conserved with the Smp_157100 and was used in docking. | | | | |
| Residues invo | olved in binding of PF543 in 4VD2. | | | |
| | | | | |
| а | b | | | |
| | | | | |
| Validation of our analysis tool | | | | |
| a) Compound p | position Alignment of our docking results; PF543: RMS – 0.382 | | | |





| Ser310(A) | ** |
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| | |

| Ligplot was used to observe the interactions of the residues and the compound of our docking results, Hydrogen bond interactions are coloured in green which are Asp 320 and Ser 310 in compound C567731 (Figure E), These compounds are both conserved with the human protein. | Ongoing activities S1P is not detected in the worms treated with SPHK inhibitors, however, further experiments are to be performed to clearly see the localization of S1P on worms |
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| In compound PF543 (Figure F), Ile 308, Gln 309 and Arg 327 shows the hydrogen bond interaction which are also conserved with human protein, and the residues coloured black are the Hydrophobic bonds. | Currently performing long-term culture on schistosomula treated with compounds to observe if SPHK inhibition affects worm development |
| (Dankwa et al., 2022)(Z. Wang et al., 2013)(J. Wang et al., 2014)(Whatley et al., 2019) | Future directions Further titration of the compounds until full recovery of the worms is observed Knock-down of Smp_157100 using RNA interference |
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Adran Y Gwyddorau Bywyd Department of Life Sciences





