



Check for updates

Temperature does matter—an additional dimension in kinase inhibitor development

Miriam Strauch and Florian Heyd 🗈

Laboratory of RNA Biochemistry, Institute of Chemistry and Biochemistry, Freie Universitaet Berlin, Germany

Keywords

body temperature; CLK; high-throughput inhibitor screen; inhibitor; kinase; malaria; *Plasmodium falciparum*

Correspondence

F. Heyd, Laboratory of RNA Biochemistry, Institute of Chemistry and Biochemistry, Freie Universitaet Berlin, Takustr. 6, Berlin 14195, Germany Tel: +49-30-83862938 E-mail: florian.heyd@fu-berlin.de

[Correction added on 15 December 2020, after first online publication: Peer review history is not available for this article, so the peer review history statement has been removed.]

(Received 7 June 2020, revised 8 September 2020, accepted 11 September 2020)

doi:10.1111/febs.15564

Introduction

Pharmacological modulation of kinase activity using small molecules has been a central endeavor in drug development, in particular in the treatment of cancer [1]. Countless targeted studies and high-throughput screens in academia and industry have led to the identification of numerous inhibitors, some of which have made their way into the clinic [2]. In many cases, three-dimensional structures of target kinases in complex with small molecule inhibitors have been solved and used to chemically modify and improve inhibitors [3]. However, recent work suggests an additional dimension that has been neglected in previous screening campaigns and validations: the impact of temperature, more specifically body temperature. In fact, common high-throughput screening platforms perform a kinase reaction at room temperature or 30 °C (e.g., [4–6] also see http://www.kinase-screen.mrc.ac.uk/), which is obviously below human body temperature,

Abbreviations

°C, degree Celsius; ³²P-γ-ATP, adenosine triphosphate, labeled on the gamma phosphate withnonbreakingspace32P; *Anopheles* spec., Anopheles species; CLK, CDC2-like kinases; CLK1, CDC2-like kinase 1; CLK3, CDC2-like kinase 3; Kd, kinase domain; MBP, myelin basic protein; *P. falciparum*, Plasmodiumnonbreakingspacefalciparum; *Pf*, Plasmodiumnonbreakingspacefalciparum; *Plasmodium* spp., Plasmodium species; SD, standard deviation; SR protein, serine/arginine-rich protein; SRPK, SR protein kinase; SRSF1, serine/arginine-rich splicing factor 1.

The FEBS Journal **288** (2021) 3148–3153 © 2020 The Authors. *The FEBS Journal* published by John Wiley & Sons Ltd on behalf of Federation of European Biochemical Societies This is an open access article under the terms of the Creative Commons Attribution License, which permits use,

distribution and reproduction in any medium, provided the original work is properly cited.

Kinase inhibitors are a major focus in drug development. Recent work shows that subtle temperature changes in the physiologically relevant temperature range can dramatically alter kinase activity and specificity. We argue that temperature is an essential factor that should be considered in inhibitor screening campaigns. In many cases, high-throughput screening is performed at room temperature or 30 °C, which may lead to many false positives and false negatives when evaluating potential inhibitors in the physiological temperature range. As one example, we discuss a new antimalaria compound that inhibits the highly temperature-sensitive kinase CLK3 (CDC2-like kinase 3) from *Plasmodium falciparum*.

that is, the environment where the inhibitor should eventually be used. Here we suggest that this discrepancy in temperature may contribute to false positives and false negatives in high-throughput inhibitor screens and argue that temperature is an important variable that should be considered when screening for and validating kinase inhibitors.

The molecular basis for kinase temperature sensitivity

Recent work shows that the activity and/or specificity of at least two kinase families, p38alpha and CDC2like kinases (CLKs), is highly responsive to temperature changes in the physiological temperature range [7,8]. P38alpha belongs to the family of mitogen-activated kinases [9], whereas CLKs phosphorylate SR proteins, a family of proteins that control pre-mRNA processing, for example, alternative splicing [10]. Recent work has shown that circadian oscillations in core body temperature of only 1-2 °C are sufficient to control CLK activity, which then alters the phosphorylation state of SR proteins and globally controls alternative splicing and gene expression [11,12]. This temperature-dependent change in CLK activity is mediated through subtle and reversible structural changes in the kinase activation segment, which in addition to controlling kinase activity is also involved in substrate binding and could thus alter substrate specificity and inhibitor binding [8]. Available CLK inhibitors have been identified in screens at 30 $^{\circ}$ C or room temperature [13–16], whereas a screen at 37 $^{\circ}$ C or 38 $^{\circ}$ C, which induces the alternative conformation, has not been performed.

Similarly, a substrate-specific change in activity between 33 °C and 39.5 °C has been reported for p38alpha, which is caused by a temperature-dependent conformational change, in this case in the substrate binding domain, which alters the affinity for different substrates [7]. Such structural rearrangements in close proximity to the substrate and nucleotide binding site switch these kinases on and off or change substrate specificity in a temperature range between 34 °C and 38 °C and will obviously affect the binding of potential inhibitors. Interestingly, altered conformational dynamics of the activation segment has been suggested to contribute to the emergence of tumors that display resistance to the kinase inhibitor imatinib through altered inhibitor binding [17]. This provides strong evidence that conformational dynamics of the activation segment, which is temperature-dependent, can indeed influence inhibitor binding. Screening at room temperature will thus result in a different set of hits than screening at 30 °C or 37 °C. This ambiguity will on the one hand contribute to the low percentage of initial hits that also perform at physiological temperatures at 37 °C. On the other hand, screening at room temperature may result in false negatives, as there may be promising candidates that only bind to the kinase in the 37 °C conformation and that are thus scored

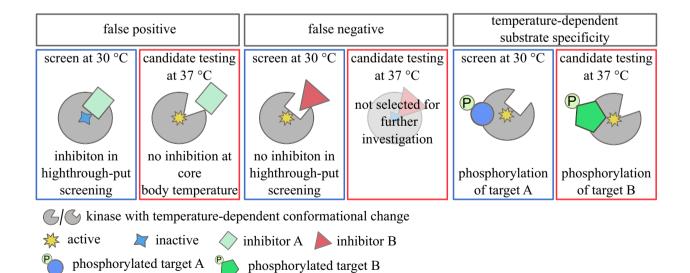


Fig. 1. Temperature-dependent conformational changes can influence the results of high-throughput screens. Model how temperaturedependent conformational changes in kinases can lead to false positives (left) and false negatives (middle) when performing high-throughput screening at room temperature or 30 °C; the right panel shows a temperature-dependent change in substrate specificity.

negative at lower temperatures (Fig. 1). Notably, comparing inhibitor activity *in vitro* (between room temperature and 30 °C) and in cell culture (at 37 °C) revealed in several cases strong differences [18,19], which is in line with the hypothesis discussed above. It should also be noted that the recombinant kinases used for inhibitor screens are in most cases expressed in bacteria and thus may lack functionally important post-translational modification. While this is a general concern, the CLK and p38 proteins in the examples discussed above were bacterially expressed and maintained temperature sensitivity, suggesting this trait to be independent of additional modifications.

Plasmodium falciparum CLK3 and an antimalaria compound as an example

Interestingly, CLKs from different organisms have adapted to the physiologically relevant temperature range of the respective species, from mammals to flies, reptiles, and parasites ([8] and see below). We will discuss one example in detail, the CLK3 homolog from Plasmodium falciparum, to highlight the importance of considering temperature when screening for kinase inhibitors. Malaria is one of the most frequent infectious diseases, and, with more than 200 million new infections and 405 000 deaths per year (WHO malaria report 2019), represents a global health threat. There is an urgent need to develop new antimalaria therapeutics, especially due to developing resistance against conventional treatments [20]. The disease is transmitted via the mosquito Anopheles from which the protozoan parasite Plasmodium spp. is transferred into the human host (reviewed in Ref. [21]). The parasite has a complex life cycle and needs to undergo dramatic morphological changes to adapt to the different hosts, which in turn requires massive changes in gene expression. Some of these changes appear to be mediated through alternative splicing, as, for example, the splicing regulatory protein PfSR1, a homolog of human SR protein SRSF1, is required for *Plasmodium* spp. proliferation in human red blood cells [22-25]. Thus, alternative splicing is increasingly recognized as potential point for therapeutic intervention. Alternative splicing is globally controlled through the phosphorylation status of SR proteins, which are phosphorylated by two classes of kinases, CLKs and SRPKs. In P. falciparum, the importance of CLK3 (PfCLK3) has been highlighted by the finding that it plays an essential role in maintaining the asexual blood stage of the parasite [26]. In recent work, Alam et al. [22] identified and validated a potential new antimalaria drug that specifically inhibits PfCLK3. A high-throughput screen (kinase reaction

performed at room temperature) revealed the compound TCMDS-135051 as a highly selective and specific PfCLK3 kinase inhibitor. This was confirmed *in vivo* by the finding that parasite strains that developed resistance against TCMDS-135051 acquired mutations in PfCLK3. Gene expression analysis showed that upon inhibitor treatment transcription was impaired and intron-containing genes were overrepresented in the downregulated genes, pointing to a potential connection of PfCLK3 and splicing, which, however, was not further analyzed [22].

As mentioned above, the best-characterized substrates of CLKs are SR proteins. To further elucidate the role of PfCLKs in controlling SR protein phosphorylation, we used our established in vitro kinase assay with an SR repeat as substrate. We have previously shown that the in vitro activity faithfully mimics the activity of the respective kinase in living cells [8]. Our assays demonstrate that the activity of both, PfCLK1 and PfCLK3, strongly responds to temperature changes in the physiologically relevant temperature range (Fig. 2). The temperature optima of both kinases are around 22 °C and remarkably, both kinases are basically inactive toward phosphorylating an SR repeat at 37 °C. Interestingly the optimal temperature for Anopheles populations is 20-26 °C [27], which is also the optimal temperature for P. falciparum development and transmission to humans [28]. This temperature range will induce maximal CLK activity, whereas the activity is switched off upon transmission into the human host simply by the altered temperature (Fig. 2). We hypothesize that P. falciparum uses the different host temperature leading to altered CLK activity and SR protein phosphorylation to induce the massive changes in gene expression required in different life cycle stages, but this idea awaits experimental validation.

The PfCLK temperature-response curve raises the question, how TCMDS-135051 can be active as an antimalaria compound, if its target, PfCLK3, is not active when the parasite is in the human host. The answer may lie in changed substrate specificity conferred by higher temperature. Alam et al. [22] used myelin basic protein (MBP) as in vitro substrate, which is not an SR protein and may thus not be the physiologically relevant substrate, but they clearly observed phosphorylation by PfCLK3 at 37 °C. Furthermore, autophosphorylation of PfCLK3 was still weakly active at 37 °C (Fig. 2, also see Ref. [22]), suggesting that higher temperature primarily affects the phosphorylation of SR proteins but that other targets may still be phosphorylated. This could point to a temperature-dependent change in substrate selectivity.

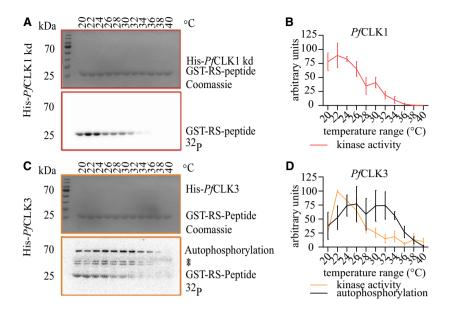


Fig. 2. Kinase activity of *Pf*CLK1 and *Pf*CLK3 is temperature-dependent in the physiological relevant temperature range of the vector *Anopheles* spec. (A) An *in vitro* kinase assay with bacterially expressed His-tagged *Pf*CLK1 kinase domain (kd) and a GST-RS-peptide as substrate. Kinase and substrate were incubated at the indicated temperatures with ${}^{32}P-\gamma$ -ATP as described in Ref. [6]. A representative gel is shown. The top gel is the Coomassie stain after SDS/PAGE to confirm equal loading and the bottom gel the autoradiograph (${}^{32}P$) of the same gel. (B) Quantification of substrate phosphorylation (red) relative to the highest activity (*n* = 3, mean \pm SD); autophosphorylation was not detectable. (C) *In vitro* kinase assays with bacterially expressed His-tagged *Pf*CLK3 full length performed as in (A). *Pf*CLK3 degradation products are marked with asterisks. (D) Quantification of substrate (orange) and autophosphorylation (black) relative to the highest activity (*n* = 3, mean \pm SD).

Interestingly, PfCLK3 autophosphorylation happens at tyrosine 526 [26] and MBP has two predicted tyrosine phosphorylation sites and these substrates were both phosphorylated at 37 °C. In contrast, an SR repeat was not phosphorylated at 37 °C, pointing to a temperature-dependent change in target amino acid specificity. This could be controlled through conformational changes of the activation segment, which makes direct contact to the substrate and could thus inhibit of favor binding of specific substrates. A similar phenomenon has been described for p38alpha, where changes in the physiological temperature range alter substrate affinity and specificity by subtle conformational changes [7], suggesting this to be a general phenomenon. Thus, while TCMDS-135051 is clearly acting as an antimalaria agent, it may do so by inhibiting the phosphorylation of noncanonical and as of yet unknown targets with equally unknown functionality.

Conclusion

Together these data emphasize that temperature should be considered as an important variable in kinase inhibitor screening campaigns, as even subtle changes within the physiologically relevant temperature range can have a dramatic impact on kinase activity and substrate specificity. Furthermore, we hypothesize that repeating screens at 37 °C will yield new promising lead structures that were false negatives in screening campaigns at lower temperature.

Acknowledgements

We thank Bernhard Loll and Marco Preussner for comments on the manuscript. We thank Andrew B. Tobin for providing *Pf*CLK expression plasmids. We thank the DFG (HE5398/4-2 and the SFB973) for funding. Open access funding enabled and organized by Projekt DEAL.

Conflict of interest

The authors declare no conflict of interest.

Author contributions

MS performed experiments. MS and FH analyzed and interpreted data and wrote the manuscript. FH conceived and supervised the work.

References

- Knight ZA, Lin H & Shokat KM (2010) Targeting the cancer kinome through polypharmacology. *Nat Rev Cancer* 10, 130–137.
- 2 Ferguson FM & Gray NS (2018) Kinase inhibitors: the road ahead. *Nat Rev Drug Discov* **17**, 353–377.
- 3 Fedorov O, Sundstrom M, Marsden B & Knapp S (2007) Insights for the development of specific kinase inhibitors by targeted structural genomics. *Drug Discov Today* **12**, 365–372.
- 4 Anastassiadis T, Deacon SW, Devarajan K, Ma H & Peterson JR (2011) Comprehensive assay of kinase catalytic activity reveals features of kinase inhibitor selectivity. *Nat Biotechnol* **29**, 1039–1045.
- 5 Davis MI, Hunt JP, Herrgard S, Ciceri P, Wodicka LM, Pallares G, Hocker M, Treiber DK & Zarrinkar PP (2011) Comprehensive analysis of kinase inhibitor selectivity. *Nat Biotechnol* 29, 1046–1051.
- 6 Imamura RM, Kumagai K, Nakano H, Okabe T, Nagano T & Kojima H (2019) Inexpensive highthroughput screening of kinase inhibitors using one-step enzyme-coupled fluorescence assay for ADP detection. *SLAS Discov* 24, 284–294.
- 7 Deredge D, Wintrode PL, Tulapurkar ME, Nagarsekar A, Zhang Y, Weber DJ, Shapiro P & Hasday JD (2019) A temperature-dependent conformational shift in p38alpha MAPK substrate-binding region associated with changes in substrate phosphorylation profile. J Biol Chem 294, 12624–12637.
- 8 Haltenhof T, Kotte A, De Bortoli F, Schiefer S, Meinke S, Emmerichs AK, Petermann KK, Timmermann B, Imhof P, Franz A *et al.* (2020) A conserved kinase-based body-temperature sensor globally controls alternative splicing and gene expression. *Mol Cell* 78, 57–69.e4.
- 9 Martinez-Limon A, Joaquin M, Caballero M, Posas F & de Nadal E (2020) The p38 pathway: from biology to cancer therapy. *Int J Mol Sci* 21,1913.
- 10 Ghosh G & Adams JA (2011) Phosphorylation mechanism and structure of serine-arginine protein kinases. *FEBS J* **278**, 587–597.
- 11 Preussner M, Goldammer G, Neumann A, Haltenhof T, Rautenstrauch P, Muller-McNicoll M & Heyd F (2017) Body temperature cycles control rhythmic alternative splicing in mammals. *Mol Cell* 67, 433– 446.e4.
- 12 Preussner M, Wilhelmi I, Schultz AS, Finkernagel F, Michel M, Moroy T & Heyd F (2014) Rhythmic U2af26 alternative splicing controls PERIOD1 stability and the circadian clock in mice. *Mol Cell* 54, 651–662.
- 13 Muraki M, Ohkawara B, Hosoya T, Onogi H, Koizumi J, Koizumi T, Sumi K, Yomoda J, Murray MV, Kimura H et al. (2004) Manipulation of alternative

splicing by a newly developed inhibitor of Clks. *J Biol Chem* **279**, 24246–24254.

- 14 Ohe K & Hagiwara M (2015) Modulation of alternative splicing with chemical compounds in new therapeutics for human diseases. *ACS Chem Biol* **10**, 914–924.
- 15 Prak K, Kriston-Vizi J, Chan AW, Luft C, Costa JR, Pengo N & Ketteler R (2016) Benzobisthiazoles represent a novel scaffold for kinase inhibitors of CLK family members. *Biochemistry* 55, 608–617.
- 16 Walter A, Chaikuad A, Helmer R, Loaec N, Preu L, Ott I, Knapp S, Meijer L & Kunick C (2018) Molecular structures of cdc2-like kinases in complex with a new inhibitor chemotype. *PLoS One* 13, e0196761.
- 17 Lovera S, Morando M, Pucheta-Martinez E, Martinez-Torrecuadrada JL, Saladino G & Gervasio FL (2015) Towards a molecular understanding of the link between imatinib resistance and kinase conformational dynamics. *PLoS Comput Biol* **11**, e1004578.
- 18 Seong YS, Min C, Li L, Yang JY, Kim SY, Cao X, Kim K, Yuspa SH, Chung HH & Lee KS (2003) Characterization of a novel cyclin-dependent kinase 1 inhibitor, BMI-1026. *Cancer Res* 63, 7384–7391.
- 19 Smyth LA & Collins I (2009) Measuring and interpreting the selectivity of protein kinase inhibitors. J Chem Biol 2, 131–151.
- 20 Hemingway J, Ranson H, Magill A, Kolaczinski J, Fornadel C, Gimnig J, Coetzee M, Simard F, Roch DK, Hinzoumbe CK *et al.* (2016) Averting a malaria disaster: will insecticide resistance derail malaria control? *Lancet* **387**, 1785–1788.
- 21 Phillips MA, Burrows JN, Manyando C, van Huijsduijnen RH, Van Voorhis WC & Wells TNC (2017) Malaria. *Nat Rev Dis Primers* 3, 17050.
- 22 Alam MM, Sanchez-Azqueta A, Janha O, Flannery EL, Mahindra A, Mapesa K, Char AB, Sriranganadane D, Brancucci NMB, Antonova-Koch Y *et al.* (2019) Validation of the protein kinase PfCLK3 as a multistage cross-species malarial drug target. *Science* **365**, eaau1682.
- 23 Eshar S, Allemand E, Sebag A, Glaser F, Muchardt C, Mandel-Gutfreund Y, Karni R & Dzikowski R (2012) A novel *Plasmodium falciparum* SR protein is an alternative splicing factor required for the parasites' proliferation in human erythrocytes. *Nucleic Acids Res* 40, 9903–9916.
- 24 Otto TD, Wilinski D, Assefa S, Keane TM, Sarry LR, Bohme U, Lemieux J, Barrell B, Pain A, Berriman M *et al.* (2010) New insights into the blood-stage transcriptome of *Plasmodium falciparum* using RNA-Seq. *Mol Microbiol* **76**, 12–24.
- 25 Sorber K, Dimon MT & DeRisi JL (2011) RNA-Seq analysis of splicing in *Plasmodium falciparum* uncovers new splice junctions, alternative splicing and splicing of antisense transcripts. *Nucleic Acids Res* 39, 3820–3835.

- 26 Solyakov L, Halbert J, Alam MM, Semblat JP, Dorin-Semblat D, Reininger L, Bottrill AR, Mistry S, Abdi A, Fennell C *et al.* (2011) Global kinomic and phospho-proteomic analyses of the human malaria parasite *Plasmodium falciparum. Nat Commun* 2, 565.
- 27 Beck-Johnson LM, Nelson WA, Paaijmans KP, Read AF, Thomas MB & Bjornstad ON (2013) The effect of temperature on *Anopheles* mosquito population

dynamics and the potential for malaria transmission. *PLoS One* **8**, e79276.

28 Mordecai EA, Paaijmans KP, Johnson LR, Balzer C, Ben-Horin T, de Moor E, McNally A, Pawar S, Ryan SJ, Smith TC *et al.* (2013) Optimal temperature for malaria transmission is dramatically lower than previously predicted. *Ecol Lett* 16, 22–30.