

## Original Article

# The Indinavir Derivate as a Novel Pharmacophore for Treatment of HTLV-1 Viral Infections

Masoud Youssefi<sup>1,2</sup>, Kiarash Ghazvini<sup>1,2</sup>, Carlos Brites<sup>3</sup>, Mohsen Karbalaee<sup>4</sup>, Masoud Keikha<sup>1,2\*</sup>

1. Antimicrobial Resistance Research Center, Mashhad University of Medical Sciences, Mashhad, Iran

2. Department of Microbiology and Virology, Faculty of Medicine, Mashhad University of Medical Sciences, Mashhad, Iran

3. LAPI, Laboratório de Pesquisa em Infectologia, Department of Medicine, Complexo Hospital Universitário Professor Edgard Santos, Universidade Federal da Bahia, Salvador, Brazil

4. Department of Microbiology and Virology, School of Medicine, Jiroft University of Medical Sciences, Jiroft, Iran

## Abstract

**Background and Aims:** Human T-lymphotropic virus type 1 (HTLV-1), is as a type C retrovirus, which was first isolated from a patient with Adult T-cell leukemia/lymphoma (ATLL). Approximately 10-20 million people are infected by HTLV-1 virus worldwide, but only 5-10% of them develop clinical manifestations such as Acute-T lymphoma (ATL), HTLV-1 associated myelopathy/tropical spastic paraparesis (HAM/TSP), uveitis, and infective dermatitis. Indinavir was the first protease inhibitor used for treating HIV-1. It has some activity on HTLV-1, but it is not fully able to inhibit the HTLV-1 protease. Nowadays, design and construction of novel pharmacophore compounds can serve as an appropriate replacement for Indinavir.

**Materials and Methods:** In the present research, we used bioinformatics studies, to evaluate the potential role of four novel pharmacophores with inhibitory function on HTLV-1 protease, so called KMI pharmacophores (Keikha Modified Indinavir).

**Results:** After a detailed structural analysis of each of them, it seems all four designed pharmacophores, (especially KMI-3) could be more effective on HTLV-1 protease than Indinavir.

**Conclusions:** According to exact in silico evaluations of each four pharmacophores, KMI-3 demonstrated a potential for its use on treatment of HTLV-1 infections.

**Keywords:** HTLV-1; Protease; Indinavir; Molecular docking.

## Introduction

The Human T-lymphotropic virus type 1 (HTLV-1) was first isolated by Poiesz et al. from an American young black with cutaneous T cell-lymphoma [1]. HTLV-1, is a human deltaretrovirus type C, and belong to Orthoretrovirinae subfamily [1-2]. So far, four different types of HTLV virus have been

identified, and HTLV-1 is the most prevalent type [3]. HTLV-1 infects approximately 10-20 million people worldwide, 90% of them are asymptomatic HTLV-1 carriers. Nonetheless, only 5-10% of them will develop HTLV-1 associated disorders such as Acute-T leukemia/lymphoma (ATLL), HTLV-1 associated myelopathy/tropical spastic para-paresis (HAM/TSP), HTLV-1 associated dermatitis, and HTLV-1 uveitis [3].

The most HTLV-1 endemic areas are South of Japan, Caribbean basin, central Africa, South America, Melanesian islands, and Iran (especially Mashhad) [2-3]. HTLV-1 infection

\*Corresponding author: Central lab, Imam Reza university hospital, Imam Reza square, Mashad, Iran, Postal code: 9137913316051, Tell: +98 5138022206 Email: masoud.keykha90@gmail.com.

is transmitted by breastfeeding, sexual contact, and receiving blood or blood products [4-5]. Despite the long time since HTLV-1 discovery, and the large number of HTLV-1-infected individuals there is no effective drug against the virus, so far.

In contrast, there are many active drugs against HIV and HCV, capable of controlling HIV viremia, or providing cure, in the case of HCV [6]. Drugs like Zidovudine (ZDV), and interferon- $\alpha$  (IFN- $\alpha$ ) are recommended to treat patients with ATLL [6-7]. However, some available studies show a limited activity of AZT on HTLV-1 infection [8].

The structural differences between HIV and HTLV-1 enzymes are known as the main cause of the lack of efficacy of anti-HIV-1 drugs on HTLV-1. In addition, HTLV-1 able to integrate its genome into the host genome, and usually proliferates by clonally, via duplication of infected cellules. So, targeting effective signaling routes in HTLV-1 pathogenesis, based on the structure of viral enzymes seems to be the best strategy for designing anti-HTLV-1 drugs [6,9].

The HTLV-1 protease (PR) has a pivotal role in propagation and maturation of virus. This enzyme is a homodimer aspartic protease (presence of two Aspartic amino acids in the positions 32 and 36 of active site), and each chain is formed of 125 amino acid residues. The enzyme is responsible for processing of Gag-pro-pol, and Gag polyproteins, which in turn have key role in virus maturation [10].

Like HTLV-1, other viruses such and HIV viruses have specific proteases each. Many protease-inhibitors have been used to treat HIV and HCV, like. Amprenavir, Atazanavir, Darunavir, Fosamprenavir, Indinavir, Lopinavir, Nelfinavir, and Ritonavir, (for HIV) or Asunaprevir, Boceprevir, Grazoprevir, Paritaprevir, Simeprevir, Telaprevir (for treatment of HCV) [6,11]. Considering similarity of spatial shape of HTLV-1 and HIV proteases, is valid to hypothesise that anti-HIV protease inhibitors are also effective for HTLV-1 infection.

Indinavir was approved by FDA in March 1996, but is no longer in use for treating HIV infections. However, it's in vitro activity against HTLV-1 was [12]. Based on Selvaraj et

al. studies, the main reason for the absence of anti-HTLV-1 activity of HIV-1 protease inhibitors is the presence of a Methionine 37 at active site of HTLV-1 protease [13].

Currently, development in pharmacophore field, is considered as the most important approaches in design and synthesis of drugs. In pharmaceutical studies, such approach allows professional designing at lower costs, by using specific softwares and existing patterns, making easy and by initial screening by docking's software analysis and further synthesis of the best compound for testing [14]. The main goal of this study was designing and evaluation of molecular docking of Indinavir-derived pharmacophores against HTLV-1 PR.

## Methods

The low efficacy of Indinavir against HTLV-1 PR, is expected due to the differences in aminoacids sequences in active sites of HTLV-1 and HIV-1 proteases. We retrieved crystallography structure of HIV-1 PR (2UXZ) and HTLV-1 PR (3WSJ) from PDB database ([www.rcsb.org](http://www.rcsb.org)). Superimposition was done to investigate structural differences of enzymes, and aminoacids sequence of enzymes was aligned by Geneious software to determine their differences and active sites. The interaction ratio between Indinavir and HTLV-1 PR was then evaluated by LIGPLOT software. In the next stage, Indinavir structure was taken from Pubchem (<https://pubchem.ncbi.nlm.nih.gov/>) web site, and optimized in terms of energy via Hyperchem software and MM3+ algorithm. The docking process was performed using Molegro virtual docker software, and evolutionary algorithms method [15]. Orientations of docked ligand (Indinavir) was compared to crystallography of HTLV-1 PR in complex with Indinavir (3WSJ). The root-mean-square deviation (RMSD) of closest orientation of docking results with crystallography structure was evaluated 157 Å (angstrom). Finally, using hydrophobic properties, H-bond, and Electric charge of residues in the binding packet of drug, four pharmacophores were suggested. The pharmacologic, toxic, and carcinogenic

properties of designed pharmacophores were assessed by online websites such Molinspiration ([www.molinspiration.com](http://www.molinspiration.com)), Lazar (<https://lazar.in-silico.de/predict>), and Swiss ADME. Each of pharmacophores were separately optimized, and docking analysis in protease active site was done with coordinates X=39.31, Y=0.60, and Z=24.83 in radius=10.

## Results

To review and compare the three dimensional structure, and enzyme active sites in HIV-1 and HTLV-1, crystallography construction of both proteins was superimposed, and their amino acid sequences was aligned (Figures 1a, and 1b). According to alignment results, the rate of sequence similarity was estimated as 38% (Figure 1b). Contrary to differences found in the three-dimensional structure and amino acids position in HTLV-1 and HIV-1 proteases, the active site is preserved in both viruses, and 95% similarity was seen (Figure 1b). Notwithstanding, there is a fundamental difference between two viral proteases; HIV-1

protease 116 amino acids. This difference is as the main factor for failure in treatment, and lack of effective act of anti-HIV proteases against HTLV-1 PR. Studies have shown, there are two main differences between HTLV-1 and HIV-1 proteases: first, presence of some unique amino acids, in the functional domains of HTLV-1 PR, such as Met37, Ser55, Val56, Leu57, and Ala59; second, some amino acids in functional domains of HTLV-1 PR, such Arg10, Leu23, Asp25, Gly27, Asp29, Asp125, Ala128 and Thr131, which are also in HIV-1 PR sequence, but in different positions than their positions in HTLV-1 PR.

These differences lead to the ineffectiveness of Indinavir against HTLV-1 PR. As a general conclusion, in order to more efficacy of this drug on HTLV-1 PR, structural changes must be done on it.

A detailed review shows that there is a relatively weak bond between Indinavir and HTLV-1 protease enzyme (Figure 2).

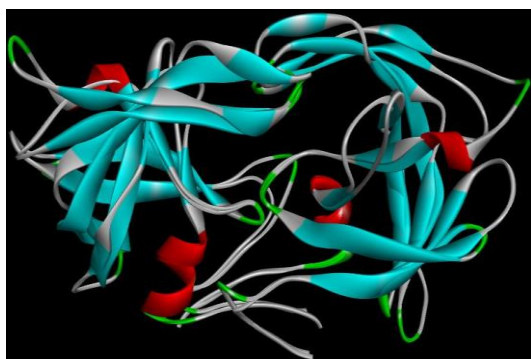


Fig. 1a. Superimposition of HTLV-1 PR vs HIV-1 PR.

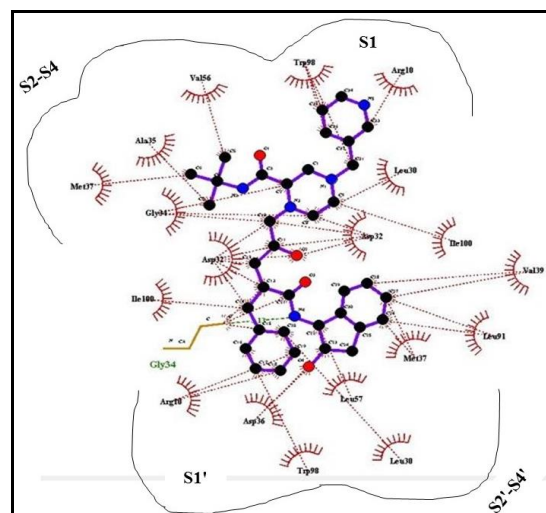


Fig. 2. Indinavir interaction with S1, S2-S4, S1' and S2'-S4' pockets of HTLV-1 PR (3WSJ)

|      | Active site |     |     |     |     |     |     |     |     |     | Flap site |     |     |     |     |     |     |     |     |     |
|------|-------------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----------|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| 2UNZ | 10          | 20  | 30  | 40  | 50  | 60  | 70  | 80  | 90  | 100 | 110       | 120 | 130 | 140 | 150 | 160 | 170 | 180 | 190 | 200 |
| 3WSJ | 10          | 20  | 30  | 40  | 50  | 60  | 70  | 80  | 90  | 100 | 110       | 120 | 130 | 140 | 150 | 160 | 170 | 180 | 190 | 200 |
| 2UNZ | 210         | 220 | 230 | 240 | 250 | 260 | 270 | 280 | 290 | 300 | 310       | 320 | 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |
| 3WSJ | 210         | 220 | 230 | 240 | 250 | 260 | 270 | 280 | 290 | 300 | 310       | 320 | 330 | 340 | 350 | 360 | 370 | 380 | 390 | 400 |

Fig. 1b. Alignment of HTLV-1 PR vs HIV-1 PR amino acid sequences

protease has 99 amino acids, while HTLV-1





## Discussion

20 Iranian Journal of Virology, Volume 13, Number 1, 2019



crystallography complex was evaluated, and then drug orientation into the HTLV-1 PR binding pocket was confirmed. Next, using Molegro virtual docker software, drug bonding energy to HTLV-1 PR was assessed; the energy of closest orientation towards crystallography structure was equivalent of -172.23 KJ/mol-1. Then, considering the electrical charge, H-bond capacity, and HTLV-1 PR hydrophobic binding pocket, some pharmacophore were recommended, and their pharmacologic criteria including lack of toxicity for humans, solubility, low mutagenicity, specificity (protease targeting) were confirmed by online data bases such Swiss ADME, LAZAR, and Molinspiration. The docking information of these compounds showed better results than Indinavir (Table 2).

However, KMI-3 (Keikha modified indinavir-3) with -220.41 KJ/mol-1 energy, had highest capacity for induction of hydrogenous and hydrophobic bonds (Figure 5a-b and Table 2). Based on studies, Met37 is located in the outermost part of binding pocket S4, and is accounted as the main factor for rejection of anti-HIV-1 proteases in HTLV-1 virus.

Selvaraj et al. demonstrated that none of each anti-HIV-1 protease inhibitors cannot interaction with Met37 in HTLV-1 PR structure.

Nonetheless, in present study, KMI-2 and KMI-3 can produce a relatively strong hydrogenous bond with this amino acid [13,18].

Also, KMI-1 can make hydrogenous bond with Asp32 and Leu57; the S3-S3' part has assigned to itself a large volume of HTLV-1 PR binding pocket, so that bond to and inhibition of these residues (Asp32 and Leu57), has important role in the inhibition of HTLV-1 protease enzyme [13,19]. Based on Li et al. studies, Leu57 and Trp98 in binding pocket S3/S3', play a pivotal role in difference between HTLV-1 and HIV-1 protease.

The presence of these amino acids increase in S3/S3' pocket leads to hydrophobicity of pocket, cover of Asn97, and eventually decrease in bond of drug to enzyme [21].

Accordingly, KMI-3 and KMI-4 were designed in a way that cause a hydrophobic bond with Trp98; so are able to block the rejection effect of Trp98 of HTLV-1 PR. Selvaraj et al. proved

that apart from similarities between both active sites, the size of binding pockets of enzymes are different with each. The binding pocket in HTLV-1 protease is Z form, and its most important amino acids include Arg10, Leu30, Asp32, Gly34, Ala35, Asp36, Met37, Val39, Leu57, Ala59, Leu91, Trp98, and L100 [13,22]. Overall, several studies showed that, by creating partial structural changes, anti-HIV-1 PR drugs such as Tipranavir, Indinavir, Darunavir and Amprenavir, can inhibit effectively HTLV-1 PR [13,23].

So far, numerous anti-HTLV-1 PR compounds such as peptido-mimetics (peptoids, peptido-sulfanomids), statine based inhibitors, HIV-1 Protease inhibitors, MES13-099, JG-365, and etc. have synthesized and studied. However, each one has some disadvantages; for example, statin compounds are only active in micromole concentrations; as well reduction in solubility and bioavailability of peptidomimetics, and insufficient specificity of MES13-099 [6, 18, 23-24]. As a rule of thumb, with a little change in the structure of FDA approved anti-HIV-1 proteases, they exchange to specific anti-HTLV-1 protease [13, 24].

## Conclusion

In summary, in the present research, first, HIV-1 and HTLV-1 sequences was compared with each other, and unique regions in HTLV-1 protease were identified. In the next step, modified pharmacophores based on Indinavir were constructed, which include better molecular docking outputs. It seems modification of anti-HIV-1 proteases is the best strategies for development of specific anti-HTLV-1 proteases, and probably will be proved in the future in vitro studies.

## Conflict of Interests

None to declared.

## Ethical Considerations

The Ethics Committee of Mashhad University of Medical Sciences was approved the study.

## Funding/Support

None to declared.

## References

- Poiesz BJ, Ruscetti FW, Gazdar AF, Bunn PA, Minna JD, Gallo RC, et al. Detection and isolation of type C retrovirus particles from fresh and cultured lymphocytes of a patient with cutaneous T-cell lymphoma. *Proc Natl Acad Sci U S A*. 1980; 77(12):7415-9.
- Rafatpanah H, Hosseini RF, Pourseyed SH. The Impact of immune response on HTLV-I in HTLV-I-associated myelopathy/tropical spastic paraparesis (HAM/TSP). *Iran J Basic Med Sci*. 2013;16(3):235.
- Gonçalves DU, Proietti FA, Ribas JG, Araújo MG, Pinheiro SR, Guedes AC, Carneiro-Proietti AB, et al. Epidemiology, treatment, and prevention of human T-cell leukemia virus type 1-associated diseases. *Clin Microbiol Rev*. 2010;23(3):577-89.
- Bittencourt AL. Vertical transmission of HTLV-I/II: a review. *Rev Inst Med Trop Sao Paulo*. 1998; 40(4):245-51.
- Azami M, Badfar G, Esmaeli E, Moslemirad M, Rahmati S. Epidemiology of human T-lymphotropic virus type 1 among blood donors and general population in Iran: a meta-analysis. *Future Virol*. 2018;13(08):585-99.
- Keikha M, Karbalaee Zadeh Babaki M, Augusto Marcondes Fonseca L, Casseb J. The Relevance of HTLV-1-associated Myelopathy/Tropical Spastic Paraparesis in Iran: A Review Study. *Rev Clin Med*. 2019;6(2):60-65.
- Alizadeh AA, Bohan SP, Lossos C, Martinez-Climent JA, Ramos JC, Cubedo-Gil E, et al. Expression profiles of adult T-cell leukemia-lymphoma and associations with clinical responses to zidovudine and interferon  $\alpha$ . *Leuk Lymphoma*. 2010;51(7):1200-16.
- Macchi B, Balestrieri E, Ascolani A, Hilburn S, Martin F, Mastino A, et al. Susceptibility of primary HTLV-1 isolates from patients with HTLV-1-associated myelopathy to reverse transcriptase inhibitors. *Viruses*. 2011;3(5):469-83.
- Selvaraj C, Singh P, Singh SK. Molecular modeling studies and comparative analysis on structurally similar HTLV and HIV protease using HIV-PR inhibitors. *J Recept Signal Transduct Res*. 2014;34(5):361-71.
- Kuhnert M, Steuber H, Diederich WE. Structural basis for HTLV-1 protease inhibition by the HIV-1 protease inhibitor indinavir. *J Med Chem*. 2014;57(14):6266-72.
- De Clercq E, Li G. Approved antiviral drugs over the past 50 years. *Clin Microbiol Rev*. 2016; 29(3):695-747.
- Pettit SC, Sanchez R, Smith T, Wehbie R, Derse D, Swanstrom R, et al. HIV type 1 protease inhibitors fail to inhibit HTLV-I Gag processing in infected cells. *AIDS Res Hum Retroviruses*. 1998; 14(11):1007-14.
- Selvaraj C, Singh P, Singh SK. Molecular insights on analogs of HIV PR inhibitors toward HTLV-1 PR through QM/MM interactions and molecular dynamics studies: comparative structure analysis of wild and mutant HTLV-1 PR. *J Mol Recognit*. 2014;27(12):696-706.
- Tian S, Sun H, Li Y, Pan P, Li D, Hou T, et al. Development and evaluation of an integrated virtual screening strategy by combining molecular docking and pharmacophore searching based on multiple protein structures. *J Chem Inf Model*. 2013;53(10):2743-56.
- Kaushik P, Lal Khokra S, Rana AC, Kaushik D. Pharmacophore modeling and molecular docking studies on *Pinus roxburghii* as a target for diabetes mellitus. *Adv Bioinformatics*. 2014;2014:903246.
- Kuhnert M, Steuber H, Diederich WE. Structural basis for HTLV-1 protease inhibition by the HIV-1 protease inhibitor indinavir. *J Med Chem*. 2014;57(14):6266-72.
- Dewan MZ, Uchihara JN, Terashima K, Honda M, Sata T, Ito M, et al. Efficient intervention of growth and infiltration of primary adult T-cell leukemia cells by an HIV protease inhibitor, ritonavir. *Blood*. 2006;107(2):716-24.
- Kheirabadi M, Maleki J, Soufian S, Hosseini S. Design of new potent HTLV-1 protease inhibitors: in silico study. *Mol Biol Res Commun*. 2016;5(1):19.
- Darden T, York D, Pedersen L. Particle mesh Ewald: An  $N \cdot \log(N)$  method for Ewald sums in large systems. *J Phys Chem*. 1993;98(12):10089-92.
- Tozser J, Weber IT. The protease of human T-cell leukemia virus type-1 is a potential therapeutic target. *Curr Pharm Des*. 2007;13(12):1285-94.
- Li M, Laco GS, Jaskolski M, Rozycki J, Alexandratos J, Wlodawer A, et al. Crystal structure of human T cell leukemia virus protease, a novel target for anticancer drug design. *Proc Natl Acad Sci U S A*. 2005;102(51):18332-7.
- Selvaraj C, Omer A, Singh P, Singh SK. Molecular insights of protein contour recognition with ligand pharmacophoric sites through combinatorial library design and MD simulation in valida-

ting HTLV-1 PR inhibitors. Mol Biosyst. 2015;11(1):178-89.

23. Bruno BJ, Miller GD, Lim CS. Basics and recent advances in peptide and protein drug delivery. Ther Deliv. 2013;4(11):14.

24. Karbalaee M, Keikha M. What Is Adult T-Cell Leukemia Pathogenesis? System Virology as a Solution of This Puzzle, Jundishapur J Chronic Dis Care. 2019;8(3):e93351.