

In Silico docking of Influenza-Interleukin 6 interactions and the role of HDAC-6 in its modelling

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Abstract: Influenza virus infections have been seen to be persistent throughout the year seasonally claiming several lives. IL-6/IL-2 receptors have been identified as crucial mediators for clearance of influenza by up regulating several intracellular defense mechanisms. Associated with IL-6 signalling is the expression acceleration of sequestrome 1(SQSTM1)/ aggresome and colocalization of HDAC-6 to the cytoplasm. The key player HDAC6 is investigated for modelling several intracellular processes that come into action to bring out the viral clearance. The shuttling of HDAC6 takes place from nucleus to cytoplasm and vice versa controlling the overexpression of IFN γ and ISGs which subsequently triggers virus specific immune response.

Keywords: Histone Deacetylases (HDACs), Influenza virus, Interferon gamma (IFN γ), IFN γ stimulated genes (ISGs), Interleukin 6 (IL-6).

Introduction:

Around the globe, influenza virus induced flu has been the cause of rising mortality in the past years, with India witnessing a total of 8-12% registered cases per year [1]. Studies have proved that of several types of cytokines involved in the immune response against influenza, Interleukin 6 (IL-6) and its receptor (IL-6R) play a crucial role in the fight against the disease and in the efficiency of viral clearance [2]. IL-6 is expressed upon recognition of the viral glycoprotein and RNA strands by pattern recognition receptors like Toll like receptors (TLRs) and Retinoic acid Inducible Gene-1 (RIG) like receptors (RLRs). Downstream to IL-6/IL-6R stabilization, the viral genome undergoes replication and synthesis of several proteins which preferentially layer at the periphery, beneath the plasma membrane [3]. The formation of the sequestrome (SQSTM-1) or aggresome induces the expression of histone deacetylase 6 (HDAC6).

HDAC6, a class II histone deacetylase is one of the least studied HDACS with special reference to its shuffling activity between nucleus and cytoplasm. HDAC6, a transcriptional co-repressor ; deacetylates histone and non histone proteins changing the expression pattern of the genes and their protein product. It contains two catalytic domains in between (DD1 and DD2), a SE14 (serine/ glutamate rich tetradecapeptide repeat) and a zinc finger binding domain (BUZ) at the C terminus as well as a nuclear localization signal (NLS) and nuclear export signal (NES) towards the N terminus [4].

BUZ is known to bind to monoubiquitin of the hitherto polyubiquitinated protein aggresome. Studies have proved that it also co-purifies with ubiquitin specific proteases (USPs) [4]. Further, HDAC catalytic domain (DD1 and DD2) share similarity with BRAP-2 (BRAC-1 associated protein -2) and thus sense any DNA damage induced by integration of viral genome and subsequent replication [4]. So, both aggresome and DNA damage induce HDAC6 expression in flu conditions. HDAC6 known to be predominantly cytoplasmic, is known being understood to efficiently shuttle between the nucleus and cytoplasm [5]. The cytoplasmic anchorage of HDAC6 depends on the SE14 repeats [6] as well as the deacetylation of the lysine residue at the nuclear export signal (NES) at the N-terminus [7].

The two catalytic domains of HDACs share a distinct homology and are placed intermediately in the sequence. The nuclear localization signal is known to be activated upon destabilization of SE14 repeats along with BUZ as well as the acetylation of NES at the N terminal [7]. The C-terminus BUZ (zinc finger binding domain) binds to the ubiquitinated protein aggregates. However, the effect of BUZ upon viral infection is least studied and thus is one of our focus of investigation. HDAC 6 out of all other HDACs has been explicitly central to disease induced cellular modifications, the reason being its importance in α -tubulin dependent deacetylase, that brings about increased cell motility, immune synapse improvisation and engulfment of viral particles and subsequent apoptosis of infected cells by caspases [11] (Fig1). Caspase-3 has been identified as a viral nucleocapsid protein released into the host cell cytosol upon infection [12].

Fig.1. HDAC6 centrality to biological functions,e.g Viral recognition,Immune synapse modification etc.

In the process IL-6, also activates MyD88 dependent pathway, which further renders an active NF- κ B transcription factor that translocates into the nucleus to express the Interferon Stimulated Genes (ISGs) which form IFN γ as product released in the vicinity of the affected cell to inhibit the spread of viral infection [8]. The IFN γ expression is accompanied by a wide range of cytoskeletal rearrangement and lowered expression of global protein content, subjecting it to the attack of Natural killer cells (NK cells) [10].

In this paper, we have tried to illustrate the cascade of events that underlie the IL-6 and HDAC6 interactions and subsequent clearance of the influenza virus infection.

Materials and Methods:

The data for HDAC6, IL-6 and Caspase-3 have been obtained from National Centre of Biotechnology Information (NCBI) database. All these protein molecules have *Homo sapiens* origin. The accession numbers are AAH69243.1 (HDAC6, 1215aa), CAG29292.1 (IL-6, 212aa) , CAC88866.1 (Caspase-3, 277 aa).

The bioinformatics softwares used for the sequence alignment is CLUSTALW Omega (accessible at www.ebi.c.uk/Tools/msa/clustalwo) provided by European Molecular Bioinformatics Laboratory- European Bioinformatics Institute (EMBL-EBI) and blastP (NCBI, accessible at blast.ncbi.nlm.nih.gov).

The interactome pattern has been studied using Protinfo PPC (accessible at protinfo.compbio.washington.edu/PPC).

Results and Discussion:

HDAC-6 sequence analysis: There are two catalytic domains of HDAC6 (DD1-domain1 and DD2- domain2). DD1 spans 286-374 and DD2 spans 485-835 amino acids (Fig.2,3).

The putative active sites of DD-1 in HDAC are – 215,216,224, 225, 253, 255,346 and 384 amino acid(aa) residues. Only one active site 346aa lies within DD-1. The putative active sites for domain 2 are identified as 610,611,614, 620, 649,651,742, 780,622,624, 630,634 aa which all span in the DD2 region. 891-1048 aa in HDAC6 in the viral G glycoprotein recognition domain and thus caspase3 binds to this domain, and cleaves it at 1088 bp at the site of the zinc finger binding domain (BUZ).

Fig.2. Homology between yeast Hda1 and human HDAC6

Fig.3. HDAC6 functional domain

Fig.4. The amino acid residue of the homologous regions and the active sites of HDAC6.

Interaction of IL-6 and HDAC-6: The homology prediction of IL-6 and HDAC6 shows very few conserved regions, but regions of similarity are between 1-131 aa (IL-6) and 621-1066 aa (in HDAC 6). The 485-835 aa of DD-2 of HDAC6 also shows the very few sequence alignment, other than a few active site residues (610, 611, 619,620, 649, 651, 742, 780, 622, 624, 630,634). Further, protein blast (BlastP) available at NCBI, confirmed some common functional product (Fig.4). However, the sequence similarity indicates that IL-6 leads to HDAC-6 overexpression via a mediator molecule as like sequestrome (SQSTM1) or aggresome, instead of direct spatial interaction. The interaction is also temporally defined as the presence of the former, leads to the expression of the latter in the proposed model.

Fig.5. Multi protein alignment of HDAC6 and IL-6 using CLUTALWO.

Interaction of Caspase-3 and HDAC6: Caspase-3 shares homology with 286-374 aa residue of HDAC-6. The most representative homologous aa residues of caspase-3 are 10,11,23-24,28, 37, 40, 48, 51, 53, 54,55, 61,64 to 156. The other region of the similarity is between 157-490 aa of caspase-3 and 527-922 aa of HDAC-6(Fig.5,7). The high similarity of both indicate a potential spatial interaction of both, as well as a possible case of colocalized expression giving a temporal profiling.

Interaction of Caspase-3 and IL-6: Caspase -3 and IL-2 had very few regions of sequence based homology and therefore we examined both for protein blast using (BLASTP) available at NCBI(Fig.6,7). The functional product similarity test also confirmed no direct correlation of both and thus denying the possibility of a spatial interaction of both .

Fig.6. CLUSTALWO between HDAC-6 and Caspase 3.

Fig.7. CLUSTALWO between IL-6 and Caspase 3.

Fig.8. Color code used in the CLUTALWO

Modelling the cascade of events: We designed an algorithm based on due interaction patterns and the known literature on the behavior of each of the key proteins (HDAC-6, IL-6). The cascade has been represented (Fig.10,11).

The aggresome included HDAC-6 expression co-localized with α -tubulin in cytosol, leads to increased acetylation of polymerized α -tubulin. This causes increased motility and endocytosis, which helps in higher infiltration of viral particles into the same cell

due to ease of access (Fig.9). The NES at N-terminal is simultaneously deacetylated leading to the activation of NLS and repression of NES. Prior to this the monoubiquitin bound BUZ gets cleaved at 1088bp by USPs (ubiquitin specific protease) upon caspase-3 binding at metaviral in glycoprotein recognition site of domain 2 (Fig.10). The C-terminal truncated version of HDAC, translocates into the nucleus where it acetylates the histones for upregulated expression of most of the housekeeping proteins and deacetylates for downregulation of accessory protein and major histocompatibility protein class I (MHC I). This makes the infected cell subject to programmed cell death by apoptosis via Natural killer cell (NK) action. The HDAC-6 simultaneously gets activated at the same NES domain of N-terminus, causing its shuttling back to the cytosol and repetition of the same process till viral clearance of the infected cell is achieved. The IL-6 mediated activation of MyD88 dependent pathway upregulates Interferon Stimulated genes (ISGs) via active NF- κ B transcription factor, leading to expression of Interferon ($\text{IFN}\gamma$), which limits the spread of viral pathogens to the cell in vicinity (Fig.11).

Fig.9. Sequence comparison of different tubulin and HDAC 6 action site.

Fig. 10.Cascade of events post Viral infection at the cytosol- nucleus interface and in the cytosolic periphery.

Fig. 11.Cascade of events post Viral infection inside the nucleus and production of $\text{IFN}\gamma$.

Interaction of HDAC6 and other proteins: Using Protinfo software, we deciphered a range of different proteins either colocalizing or spatially interacting with HDAC6. To list, a few of them are Tubg1, Axin 1, Mapre 1, APC, Clip 2, SS 18, Clasp which mainly regulate cell cytoskeletal rearrangement, cell growth and survivability (Fig.12).

Fig.12. Interaction of HDAC6 with other putative proteins in stressed condition using Protinfo.

Phylogenetic relation of HDAC-6/IL-6/Caspase3: The bootstrap analysis method of phylogenetic relation between the three key protein molecule also shows significant similarity of HDAC-6 and caspase-3, that in contrast to IL-6. However IL-6 and HDAC-6 have few regions of homology. (Fig.13)

Fig.13. Phylogenetic relation between IL-6, HDAC6 and caspase3 in chronological order.

Conclusion:

The proposed model is based on the interaction patterns of the key protein molecules like HDAC-6 and IL-6 in influenza infection condition. The in-silico docking gives an early insight to the possible pathway taken up by the immune system to evade the

pathogen. However, sufficient experimental evidences can establish the proposed model. The future outcomes of this model promises for epigenetic modulation of HDACs for treating diseases of different virulence.

Conflict of Interest:

This is an independent project carried out in collaboration of both the authors. All softwares used for the project work are open sourced and reference has been quoted wherever applicable.

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