Available online on 15.02.2021 at http://jddtonline.info

Journal of Drug Delivery and Therapeutics

Open Access to Pharmaceutical and Medical Research

© 2011-21, publisher and licensee JDDT, This is an Open Access article which permits unrestricted non-commercial use(CC By-NC), provided the original work is properly cited

Open Access Full Text Article

Research Article

Corona Viruses and Human Leukocyte Antigen (HLA) alleles

Alsadig Gassoum[1,2], Nihad Elsadig Babiker[1,3]*, Sawsan A. Hamed[1], Sara Elsadig Babiker[1,4], Imad Fadl-Elmula[5]

[1] *National Center for Neurological Sciences, Khartoum, Sudan*

[2] *Almadein University College, Sudan*

[3] *Darfur University College, Sudan*

[4] *MRCOG, Sultan Qaboose Hospital, Slalah, Oman*

[5] *Al Neelain University, Sudan*

Article Info:

Article History:

Received 13 Dec 2020;
Review Completed 27 Jan 2021
Accepted 07 Feb 2021;
Available online 15 Feb 2021

Cite this article as:

Gassoum A, Babiker NE, Hamed SA, Babiker SE, Fadl-Elmula I, Corona Viruses and Human Leukocyte Antigen (HLA) alleles, Journal of Drug Delivery and Therapeutics. 2021; 11(1-s):83-85
DOI: http://dx.doi.org/10.22270/jddt.v11i1-s.4742

*Address for Correspondence:

Nihad Elsadig Babekir Ismail, National Center for Neurological Sciences, Khartoum, Sudan

Abstract

Major histocompatibility complex **(**MHC) is consisted of cluster of genes known as human leukocyte antigen HLA, these genes are committed to process and present antigens to T lymphocyte. Corona viruses, belonging to a genus of the corona viridae family, are enveloped viruses containing single stranded RNA 27-32 kb. This study was conducted to highlight some observations that may help other researcher for rapid research advances; the new corona virus genome sequence was obtained from Virus pathogen database, the spike protein (surface glycoprotein) was aligned with SPIKE_CVHSA Spike glycoprotein OS=Human SARS coronavirus OX=694009 GN=S PE=1 SV=1 which was retrieved from Uniprot data base Distribution of HLA alleles was obtained from allele frequencies database, IEDB server was used for MHC 1 prediction. The distribution of HLA-A alleles among population revealed that, the most common wasHLA-A*11:01. The affinity prediction of HLA-A*03:01(AAAYFVGYLK) and HLA-A*11:01(AAYFVGYLK) alleles to the spike peptide were positive. The two positive predicted peptides for both 2 alleles showed mutation of K245Q, This mutation may affect the binding affinity of the protein peptides to HLA-A alleles.

Keywords: HLA. MHC, alleles, Corona viruses, SARS, APS

INTRODUCTION

In human MHC is consisted of cluster of genes known as HLA, these genes are committed to process and present antigens to T lymphocyte. The encoded protein by these genes is termed MHC class 1 heavy chain which display peptide on the cell surface, accessory protein with the heavy chain and peptide generate peptide class 1 complexes. In human MHC contains a hundreds of alleles that located at each three loci that encoding class1 heavy chain, each allele has acapacity to bind specific variety of peptides.[1] The binding is based on the interaction between two to three residues of side chain with pocket in the binding groove of MHC 1 molecule.[2] Class 1 molecules (heavy chain) bound non-covalently to small non glycosylated protein known as B2 microglobulin. The prence of peptide in agroove of class 1 molecule increasing the affinity of B2m to heavy chain, in the absence of peptide, B2m will dissociate from cell surface class 1 molecule in a short time not exceeding minutes at 37C.[3] other molecules and proteins are involving glycosylation of class 1 heavy chain, which is typically membrane protein, glycosylation is occurring in ER with presence of calnexin and/or calreticulin, highly related ER-resident molecular chaperones that bind to nascent proteins with monoglucosylated N-linked oligosaccharides. [4,5,6] Recognition of foreign antigens is based on binding to a class I molecule bearing a foreign peptide at an affinity higher than this threshold, but still not very impressive (compared with immunoglobulins), with a K_D in the range of 10^{-4} to 10^{-6} M .[7,8] The activation of naïve TCD8+ is resulting in proliferation and production of effecter molecules with anti-viral activity, and the triggering of TCD8+ is generated by viral infected cell to release effecter molecules. The previous process can be accomplished by cells that harboring proper co-stimulatory molecules, these cells are known as antigen presenting cells (APC). [9]

Coronaviruses, belonging to a genus of the coronaviridae family, are enveloped viruses containing single stranded RNA 27-32 kb. This virus have been isolated from rats, chichins, swine, turkeys, dogs, cats, rabbits, horses, cattle and human.[10,11] SARS CoV-2 are spherical in shape, have a protein called spikes, which protruding from their surface. The spikes attached onto human cells, then changing their structure to facilitate the viral membrane to fuse with the cell membrane, after this the viral genetic material can enter the cell to be copied and producing a huge number of viruses, the virus spikes bind to receptors on the human cells surface called angiotensin converting enzyme 2 (ACE2).[12]

METHODOLOGY

This study was conducted to highlight some observations that may help other researcher for rapid research advances;the new corona virus genome sequence was obtained from Virus pathogen database, the spike protein (surface glycoprotein) was aligned with SPIKE_CVHSA Spike glycoprotein OS=Human SARS coronavirus OX=694009 GN=S PE=1 SV=1 which was retrieved from Uniprot database. Distribution of HLA alleles was obtained from allele frequencies database, IEDB server was used for MHC 1 prediction, the new corona virus protein for spike gene was subjected for peptide affinity to HLA-A allele, then according to percentile rank prediction, positive peptides were selected, the selected peptides were searched among the population to find the percentage of the predicted positive alleles. Moreover, the positive peptide was searched in the aligned two sequences (spike sequence from new corona virus with human SARS coronavirus), to detect possible mutations that may affect the binding affinity to HLA-A allele.

RESULTS AND DISCUSSION

HLA-A*03:01 allele was observed in 30.2% of Belgium, India Delhi 30.2%, Sudan 9% , Hong Kong Chinese 1.6%, Singapore Chinese 1.3%, Malaysia Peninsular Chinese 0.5%, USA African American Bethesda 24%, USA Caucasian 20%, Spain 20%, Italy North19%. The affinity prediction of HLA-A*03:01 allele to the spike peptide (AAAYFVGYLK) was positive. The HLA-A*11:01 was detected in 50% Malaysia Peninsular Chinese, Hong Kong Chinese 49%, Singapore Chinese 48%, India Delhi 19%, Spain 14%, USA 16%, USA Caucasian 14%, Italy North 15% and Sudan Central Shaigiya Mixed 2.7%.the spike protein peptide (AAYFVGYLK) was predicted positive to HLA-A*11:01. The percentage of the allele distribution among population was obtained from population frequency database. Table 1

In this study, the Spike glycoprotein of the new corona virus (Strain Name: Wuhan-Hu-1|Protein Name:surface glycoprotein) and Spike glycoprotein OS=Human SARS coronavirus OX=694009 GN=S PE=1 SV=1 were aligned.The alignment showed that, K amino acid residue was substituted by Qaa, the amino acid change was occurring in (AAAYFVGYLK and AAYFVGYLK)peptides, which were predicted positive affinity for HLA-A*03:01 and HLA-A*11:01 alleles respectively. Figure 1

Table 1: shows, the affinity prediction for the wild and mutant alleles of HLA-A*03:01and HLA-A*11:01

Wild allele			
Allele	**Length**	**Peptide**	**Percentile rank**
HLA-A*03:01	10	AAAYFVGYLK	0.24
HLA-A*11:01	10	AAAYFVGYLK	0.13
Mutant allele			
HLA-A*03:01	10	AAAYFVGYLQ	29
HLA-A*11:01	10	AAAYFVGYLQ	13.5

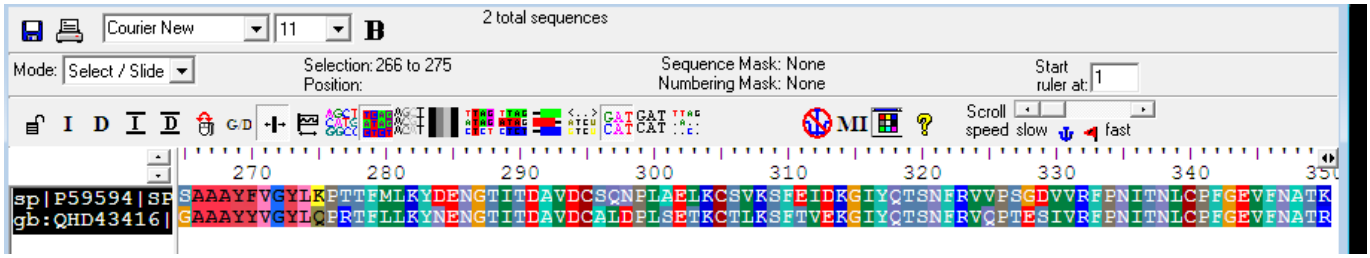

Figure 1: The alignment showed: K amino acid residue was substituted by Qaa, the amino acid change was occurring in (AAAYFVGYLK and AAYFVGYLK) peptides.

The distribution of HLA-A alleles among population revealed that, the most common allele among Chinese was HLA-A*11:01 (50%), HLA-A*03:01 was seen in 24% of American Black, 20% Spain and 19% in Italy. On the other hand Sudan and India expressed 19% and 2.7% HLA-A*11:01 allele, HLA-A*03:01 was detected in 30% of Indian population and 9% of Sudanese. The two positive predicted peptides for both 2 alleles showed mutation of K245Q, this mutation indicated that, the wild type residue (K) was positive charge while the mutant residue was neutral, the mutant residue was occurring near highly conserved region.This mutation may affect the binding affinity of the protein peptides to HLA-A alleles.

CONCLUSION

Spike glycoprotein of the new corona virus, which were predicted positive affinity for HLA-A*03:01 and HLA-A*11:01 alleles, both 2 alleles showed mutation of K245Q, this mutation may affect the binding affinity of the protein peptides to HLA-A alleles for that more researches are needed to confirm this results

List of abbreviations

MHC: Major histocompatibility complex

HLA: Human leukocyte antigen

RNA: ribonucleic acid

CoV: corona viruses

ACE: Angiotensin Converting Enzyme

SARS: Severe acute respiratory syndrome

APC: antigen presenting cells

Competing interests: Nil

References

1- Rammensee H -G, Friede T, Stevanovic S. MHC ligands and peptide motifs: first listing. Immunogenetics, 1995; 41:178–228.
2- Madden D R. The three-dimensional structure of peptide-MHC complexes. Annu. Rev. Immuno, 1995; l13:587–622.
3- Pamer E, Cresswell P. Mechanisms of MHC class I-restricted antigen processing. Annu. Rev. Immuno, 1998; l16:323–58
4- Lindquist J A, Jensen O N, Mann M, Hammerling G J. ER-60, a chaperone with thiol-dependent reductase activity involved in MHC class I assembly. EMBO J, 1998; 17:2186–95.
5- Hughes E A, Cresswell P. The thioloxidoreductase ERp57 is a component of the MHC class I peptide-loading complex. Curr. Bio, 1998; l8:709–12.
6- Morrice N A, Powis S J. A role for the thiol-dependent reductase ERp57 in the assembly of MHC class I molecules. Curr. Bio, 1998; l8:713–16.
7- Kiselow P, von Boehmer H. Development and selection of T cells: facts and puzzles. Adv. Immuno, 1995; l58:87–210.
8- Davis M M, Boniface J J, Reich Z, Lyons D, Hampl J. et al.Ligand recognition by alpha beta T cell receptors. Annu. Rev. Immuno, 1998; l16:523–44.
9- Yewdell J W, Norbury C C, Bennink J R. Mechanisms of exogenous antigen presentation by MHC class I molecules in vitro and in vivo: implications for generating $CD8^+$ T cell responses to infectious agents, tumors, transplants, vaccines. Adv. Immuno, 1999; l73:1–77.
10- Tyrrell, D.A.J. &Bynoe, M.L. Cultivation of novel type of common-cold virus in organ cultures. Br. Med. J, 1965; 1: 1467–1470.
11- Bradburne, A.F., Bynoe, M.L. & Tyrrell, D.A. Effects of a “new” human respiratory virus in volunteers. Br. Med. J, 1967; 3:767–769 .
12- Wrapp, Daniel; Wang, Nianshuang; Corbett, Kizzmekia S.; Goldsmith, Jory A.; Hsieh, Ching Lin; Abiona,Olubukola; Graham, Barney S.; McLellan, Jason S. Cryo-EM structure of the 2019-nCoV spike in the prefusion conformation. Science 2020; pii: eabb2507. doi: 10.1126/science.abb2507.