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Epitope finding in Zika virus molecule: The first world report

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ABSTRACT

Zika virus infection is a new problematic virus infection that becomes the present public health problem. Now this mosquito borne infectious disease can be seen worldwide and can cause dengue-like infection. In addition, it can also induce transplacental infection and result in congenital neurological defect. To prevent this infection, there is still no specific vaccine. To find a new vaccine, finding epitope is the first step. Here, the authors report the study to find epitope within Zika virus molecule. According to this study, the appropriate epitopes can be seen. This is the first world report on epitope finding for Zika virus. The data can be useful for further vaccine development.

1. Introduction

Zika virus infection is a new problematic arboviral virus infection that becomes the present public health problem [1,2]. Since its first discovery in Africa, it expands to several areas including Pacific and South America causing many problematic outbreaks. Now this mosquito borne infectious disease can be seen worldwide and can cause dengue-like infection causing acute febrile illness and thrombocytopenia [1,2]. In addition, it can also induce transplacental infection and result in infant with microcephaly and ocular defect [3]. To prevent this infection, the basic concept for prevention of arboviral infection, prevention of mosquito, can be applied but it seems to be very difficult. A better means should be specific prevention by vaccination. However, there is still no specific vaccine. In biomedicine, to find a new vaccine, finding epitope is the first step. Here, the authors report the study to find epitope within Zika virus molecule using standard bioinformatics approach. According to this study, the appropriate epitopes can be seen. This is the first world report on epitope finding for Zika virus. The data can be useful for further Zika virus vaccine development.

2. Materials and methods

This study aims at finding epitope within the Zika virus molecule. The primary template is the protein of Zika virus isolate Brazil-ZKV2015, complete genome (GenBank: KU497555.1). The sequence is shown in Table 1. The authors used standard bioinformatics technique for prediction of the epitope within the mentioned primary template molecule. The technique used is namely "SVMTriP". "SVMTriP" is the standard bioinformatics technique described by Yao *et al.* [4]. Combined tri-peptide similarity and propensity scores techniques are used for epitope prediction. The sensitivity of this technique is equal to a sensitivity of 80.1% [4].

3. Results

According to the searching, the first 10 positions in molecule that has good epitope properties are shown in Table 2. Nevertheless, the two positions with the best epitope score (score more than 8.0) which are suggested for using as epitopes are 784YIMDEAHFTDPSSIAARGYI1803 (score = 1.000) and 157YIQIMDLGHMCDATMSYECP176 (score = 0.839).

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Table 1

Protein of Zika virus isolate Brazil-ZKV2015, complete genome.

Position	Sequence
1	MKNPKKKSGG FRIVNMLKRG VARVSPFGGL KRLPAGLLLG HGPIRMVLAI LAFLRFTAIK
61	PSLGLINRWG SVGKKEAMEI IKKFKKDLAA MLRIINARKE KKRRGADTSV GIVGLLLTTA
121	MAAEVTRRGS AYYMYLDRND AGEAISFPTT LGMNKCYIQI MDLGHMCDAT MSYECPMLDE
181	GVEPDDVDCW CNTTSTWVVY GTCHHKKGEA RRSRRAVTLP SHSTRKLQTR SQTWLESREY
241	TKHLIRVENW IFRNPGFALA AAAIAWLLGS STSQKVIYLV MILLIAPAYS IRCIGVSNRD
301	FVEGMSGGTW VDVVLEHGGC VTVMAQDKPT VDIELVTTTV SNMAEVRSYC YEASISDMAS
361	DSRCPTQGEA YLDKQSDTQY VCKRTLVDRG WGNGCGLFGK GSLVTCAKFA CSKKMTGKSI
421	QPENLEYRIM LSVHGSQHSG MIVNDTGHET DENRAKVEIT PNSPRAEATL GGFGSLGLDC
481	EPRTGLDFSD LYYLTMNNKH WLVHKEWFHD IPLPWHAGAD TGTPHWNNKE ALVEFKDAHA
541	KRQTVVVLGT QEGAVHTALA GALEAEMDGA KGRLSSGHLK CRLKMDKLRL KGVSYSLCTA
601	AFTFTKIPAE TLHGTVTVEV QYAGTDGPCK VPAQMAVDMQ TLTPVGRLIT ANPVITESTE
661	NSKMMLELDP PFGDSYIVIG VGEKKITHHW HRSGSTIGKA FEATVRGAKR MAVLGDTAWD
721	FGSVGGALNS LGKGIHQIFG AAFKSLFGGM SWFSQILIGT LLMWLGLNTK NGSISLMCLA
661	NSKMMLELDP PFGDSYIVIG VGEKKITHHW HRSGSTIGKA FEATVRGAKR MAVLGDTAWD
721	FGSVGGALNS LGKGIHQIFG AAFKSLFGGM SWFSQILIGT LLMWLGLNTK NGSISLMCLA
781	LGGVLIFLST AVSADVGCSV DFSKKETRCG TGVFVYNDVE AWRDRYKYHP DSPRRLAAAV
841	KQAWEDGICG ISSVSRMENI MWRSVEGELN AILEENGVQL TVVVGSVKNP MWRGPQRLPV
901	PVNELPHGWK AWGKSYFVRA AKTNNSFVVD GDTLKECPLK HRAWNSFLVE DHGFGVFHTS
961	VWLKVREDYS LECDPAVIGT AVKGKEAVHS DLGYWIESEK NDTWRLKRAH LIEMKTCEWP
1021	KSHTLWTDGI EESDLIIPKS LAGPLSHHNT REGYRTQMKG PWHSEELEIR FEECPGTKVH
1081	VEETCGTRGP SLRSTTASGR VIEEWCCREC TMPPLSFRAK DGCWYGMEIR PRKEPESNLV
1141	RSMVTAGSTD HMDHFSLGVL VILLMVQEGL KKRMTTKIII STSMAVLVAM ILGGFSMSDL
1201	AKLAILMGAT FAEMNTGGDV AHLALIAAFK VRPALLVSFI FRANWTPRES MLLALASCFL
1261	QTAISALEGD LMVLINGFAL AWLAIRAMVV PRTDNITLAI LAALTPLARG TLLVAWRAGL
1321	ATCGGFMLLS LKGKGSVKKN LPFVMALGLT AVRLVDPINV VGLLLLTRSG KRSWPPSEVL
1381	TAVGLICALA GGFAKADIEM AGPMAAVGLL IVSYVVSGKS VDMYIERAGD ITWEKDAEVT
1441	GNSPRLDVAL DESGDFSLVE DDGPPMREII LKVVLMTICG MNPIAIPFAA GAWYVYVKTG
1501	KRSGALWDVP APKEVKKGET TDGVYRVMTR RLLGSTQVGV GVMQEGVFHT MWHVTKGSAL
1561	RSGEGRLDPY WGDVKQDLVS YCGPWKLDAA WDGHSEVQLL AVPPGERARN IQTLPGIFKT
1621	KDGDIGAVAL DYPAGTSGSP ILDKCGRVIG LYGNGVVIKN GSYVSAITQG RREEETPVEC
1681	FEPSMLKKKQ LTVLDLHPGA GKTRRVLPEI VREAIKTRLR TVILAPTRVV AAEMEEALRG
1741	LPVRYMTTAV NVTHSGTEIV DLMCHATFTS RLLQPIRVPN YNLYIMDEAH FTDPSSIAAR
1801	GYISTRVEMG EAAAIFMTAT PPGTRDAFPD SNSPIMDTEV EVPERAWSSG FDWVTDHSGK
1861	TVWFVPSVRN GNEIAACLTK AGKRVIQLSR KTFETEFQKT KHQEWDFVVT TDISEMGANF
1921	KADRVIDSRR CLKPVILDGE RVILAGPMPV THASAAQRRG RIGRNPNKPG DEYLYGGGCA
1981	ETDEDHAHWL EARMLLDNIY LQDGLIASLY RPEADKVAAI EGEFKLRTEQ RKTFVELMKR
2041	GDLPVWLAYQ VASAGITYTD RRWCFDGTTN NTIMEDSVPA EVWTRHGEKR VLKPRWMDAR
2101	VCSDHAALKS FKEFAAGKRG AAFGVMEALG TLPGHMTERF QEAIDNLAVL MRAETGSRPY
2161	KAAAAQLPET LETIMLLGLL GTVSLGIFFV LMRNKGIGKM GFGMVTLGAS AWLMWLSEIE
2221	PARIACVLIV VFLLLVVLIP EPEKQRSPQD NQMAIIIMVA VGLLGLITAN ELGWLERTKS
2281	DLSHLMGRRE EGATIGFSMD IDLRPASAWA IYAALTTFIT PAVQHAVTTS YNNYSLMAMA
2341	TQAGVLFGMG KGMPFYAWDF GVPLLMIGCY SQLTPLTLIV AIILLVAHYM YLIPGLQAAA
2401	ARAAQKRTAA GIMKNPVVDG IVVTDIDTMT IDPQVEKKMG QVLLIAVAVS SAILSRTAWG
2461	WGEAGALITA ATSTLWEGSP NKYWNSSTAT SLCNIFRGSY LAGASLIYTV TRNAGLVKRR
2521	GGGTGETLGE KWKARLNQMS ALEFYSYKKS GITEVCREEA RRALKDGVAT GGHAVSRGSA
2581	KLRWLVERGY LQPYGKVIDL GCGRGGWSYY AATIRKVQEV KGYTKGGPGH EEPVLVQSYG
2641	WNIVRLKSGV DVFHMAAEPC DTLLCDIGES SSSPEVEEAR TLRVLSMVGD WLEKRPGAFC
2701	IKVLCPYTST MMETLERLQR RYGGGLVRVP LSRNSTHEMY WVSGAKSNTI KSVSTTSQLL
2761	LGRMDGPRRP VKYEEDVNLG SGTRAVVSCA EAPNMKIIGN RIERIRSEHA ETWFFDENHP
2821	YRTWAYHGSY VAPTQGSASS LINGVVRLLS KPWDVVTGVT GIAMTDTTPY GQQRVFKEKV
2881	DTRVPDPQEG TRQVMSMVSS WLWKELGKHK RPRVCTKEEF INKVRSNAAL GAIFEEEKEW
2941	KTAVEAVNDP RFWALVDKER EHHLRGECQS CVYNMMGKRE KKQGEFGKAK GSRAIWYMWL
3001	GARFLEFEAL GFLNEDHWMG RENSGGGVEG LGLQRLGYVL EEMSRIPGGR MYADDTAGWD
3061	TRISRFDLEN EALITNQMEK GHRALALAII KYTYQNKVVK VLRPAEKGKT VMDIISRQDQ
3121	RGSGQVVTYA LNTFTNLVVQ LIRNMEAEEV LEMQDLWLLR RSEKVTNWLQ SNGWDRLKRM
3181	AVSGDDCVVK PIDDRFAHAL RFLNDMGKVR KDTQEWKPST GWDNWEEVPF CSHHFNKLHL
3241	KDGRSIVVPC RHQDELIGRA RVSPGAGWSI RETACLAKSY AQMWQLLYFH RRDLRLMANA
3301	ICSSVPVDWV PTGRTTWSIH GKGEWMTTED MLVVWNRVWI EENDHMEDKT PVTKWTDIPY
3361	LGKREDLWCG SLIGHRPRTT WAENIKNTVN MVRRIIGDEE KYMDYLSTQV RYLGEEGSTP
3421	GVL

Table 2
Predicted epitopes directly derived from SVMTriP analysis.

Positions	Epitopes
1784–1803	YIMDEAHFTDPSSIAARGYI
157–176	YIQIMDLGHMCDATMSYECP
2701–2720	IKVLCPYTSTMMETLERLQR
2138–2157	ERFQEAIDNLAVLMRAETGS
573–592	RLSSGHLKCRLKMDKLRLKG
1911–1930	TDISEMGANFKADRVIDSRR
440–459	GMIVNDTGHETDENRAKVEI
2544–2563	FYSYKKSGITEVCREEARRA
1491–1510	GAWYVYVKTGKRSGALWDVP
2298–2317	SMDIDLRPASAWAIYAALTT

4. Discussion

The advanced bioinformatics technique help find answers to many complex questions in tropical biomedicine and the finding of the epitope for further vaccine production is a good example [5]. Indeed, finding vaccine becomes the bid issue in dealing with many new infectious diseases. For Zika virus infection, there is still no available vaccine [6]. To correspond to the worldwide situation, finding the new vaccine should have the high priority. In this work, the authors report the first world data on the epitopes within Zika virus molecule.

In fact, finding new epitopes to use as vaccine candidates is the acceptable concept. The examples of previous attempts are during the emerging atypical influenza infections [7]. In the present work, the similar attempt is done to find the epitope to correspond to the problem of Zika virus infection. Using standard bioinformatics technique, the two parts of the molecules with the best epitopes property can be found. These two epitopes can be used for further biosynthesis and evaluation as a new Zika virus vaccine candidate.

Conflict of interest statement

We declare that we have no conflict of interest.

References

[1] Joob B, Wiwanitkit V. Zika virus infection and dengue: a new problem in diagnosis in a dengue-endemic area. *Ann Trop Med Public Health* 2015; **8**: 145-6.
[2] Wiwanitkit S, Wiwanitkit V. Acute viral hemorrhage disease: a summary on new viruses. *J Acute Dis* 2015; **4**: 277-9.
[3] Ioos S, Mallet HP, Leparc Goffart I, Gauthier V, Cardoso T, Herida M. Current Zika virus epidemiology and recent epidemics. *Med Mal Infect* 2014; **44**(7): 302-7.
[4] Yao B, Zhang L, Liang S, Zhang C. SVMTriP: a method to predict antigenic epitopes using support vector machine to integrate tri-peptide similarity and propensity. *PLoS One* 2012; **7**(9): e45152.
[5] Wiwanitkit V. Utilization of multiple "omics" studies in microbial pathogeny for microbiology insights. *Asian Pac J Trop Biomed* 2013; **3**(4): 330-3.
[6] Oster AM, Brooks JT, Stryker JE, Kachur RE, Mead P, Pesik NT, et al. Interim guidelines for prevention of sexual transmission of Zika virus – United States, 2016. *MMWR Morb Mortal Wkly Rep* 2016; **65**(5): 120-1.
[7] Wiwanitkit V. Predicted epitopes of H5N1 bird flu virus by bioinformatics method: a clue for further vaccine development. *Chin Med J (Engl)* 2006; **119**(20): 1760.