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Phosphorylation sites within Ebola virus nucleoprotein

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ABSTRACT

To understand the infection process, the viral multiplication and entry to the cell is widely studied. The Ebola virus nucleoprotein is the important problem for the pathological process. Focusing on the specific biological process, the post translational modification is needed. Here, the authors used the bioinformatics study to find the phosphorylation sites within the Ebola virus nucleoprotein and could identify many new sites.

1. Introduction

The Ebola virus infection is the present focus in the biomedicine. Due to the big outbreak in Africa, there are several attempts to perform research on this virus. To understand the infection process, the viral multiplication and entry to the cell is widely studied. The Ebola virus nucleoprotein is the important problem for the pathological process. Shi *et al.* noted that "a filovirus-unique region of Ebola virus nucleoprotein conferred aberrant migration and mediated its incorporation into virions[1]." Focusing on the specific biological process, the post translational modification is needed. The phosphorylation process is the important process that should be studied. Peyrol *et al.* used high resolution tandem mass spectrometry to study Zaire Ebolavirus nucleoprotein and noted that there were many phosphorylation sites within the molecules. They concluded that "nuclear protein was found to be phosphorylated in two different amino acid stretches: [561-594] and [636-653][2]." and "residues Thr(563), Ser(581), Ser(587) and Ser(647) were accurately identified as phosphorylated sites[2]." Here, the authors used the bioinformatics study to find the phosphorylation sites within the Ebola virus nucleoprotein and could identify many new sites.

2. Materials and methods

The phosphorylation sites within the Ebola virus nucleoprotein were assessed using a standard bioinformatics tool, namely, "NetPhos 2.0 Server"[3]. Blom *et al.* noted that this method was "an artificial neural network method that predicted phosphorylation sites in independent sequences with a sensitivity in the range from 69% to 96%[3]." Focusing on the template, the Ebola virus nucleoprotein sequence was derived from PubMed database.

3. Results

According to this study, there are 47 identified phosphorylation sites. Classifying by specific amino acid group, there are 19 serine, 17 threonine and 11 tyrosine specific sites. The details for positioning within sequence are shown in Figure 1.

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739 Sequence

MDSRPQKIWMAPSLTESDMDYHKILTAGLSVQQGIVRQRVIPVYQVNNLEEICQLIIQAFEAGVDFQESADSFLLMLGLH 80
HAYQGDYKLFLESGAVKYLEGHGFRFEVKKRDGVKRLEELLPAVSSGKNIKRTLAAMPEEETTEANAGQFLSFASLFLPK 160
LVVGEKACLEKVQRQIQVHAEQGLIQYPTAWQSVGHMMVIFRLMRTNFLIKFLLIHQGMHMVAGHDANDAVISNSVAQAR 240
FSGLLIVKTVLDHILQKTERGVRLHPLARTAKVKNEVNSFKAALSSLAKHGEYAPFARLLNLSGVNNLEHGLFPQLSAIA 320
LGVATAHGSTLAGVNVGEQYQQLREAATEAEKQLQQYAESRELDHLGLDDQEKKILMNFHQKKNEISFQQTNAMVTLRKE 400
RLAKLTEAITAASLPKTSGHYDDDDDIPEPGPINDDDNPGHQDDDPTDSQDTTIPDVVVDPDDGSYGEYQSYSENGMNAP 480
DDLVLFDLDFDDEDTKPVPNRSTKGGQQKNSQKGQHIEGRQTQSRPIQNVPGPHRTIHHASAPLTDNDRRNEEPSGSTSPR 560
MLTPINEEADPLDDAADDETSSLPPLESDDEEQDDRDGTSNRTRIVAPPAPVYRDHSEKKELPQDEQQDQDHTQEARNQDSD 640
NTQSEHSFEEMYRHILRSQGPFDAVLYYHMMKDEPVVFSTSDGKEYTYPDSLEEEYPPWLTEKEAMNEENRFVILDGQQF 720
YWPVMNHKNKFMAILQHHQ 800
••••••••••••S•••S•••Y••• 80
•••S•••••••••••••••TT••••••••••••••••• 160
•• 240
•S•••••••••••••••T•••••••••••T••••••••S•••••••••••••Y••••••••••••••••••••••••••• 320
•••••••••••••••••••Y•••••••T•••T•••• 400
•••••••••••••••••S••Y•••••••••••••••••••••••••••S••TT•••••••••••SY••Y•SY•••••••• 480
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••T•••••••••••••••••••••••••••••••••••TS••T•••••••••Y•••S••••••••••••••••••••••• 640
•T••••S••••Y•••••S••••••••••••••••••••S••••••Y•Y••S•••••••••T•••••••••T••••••••• 720
••••••••••••••••••• 800

Phosphorylation sites predicted: Ser: 19 Thr: 17 Tyr: 11

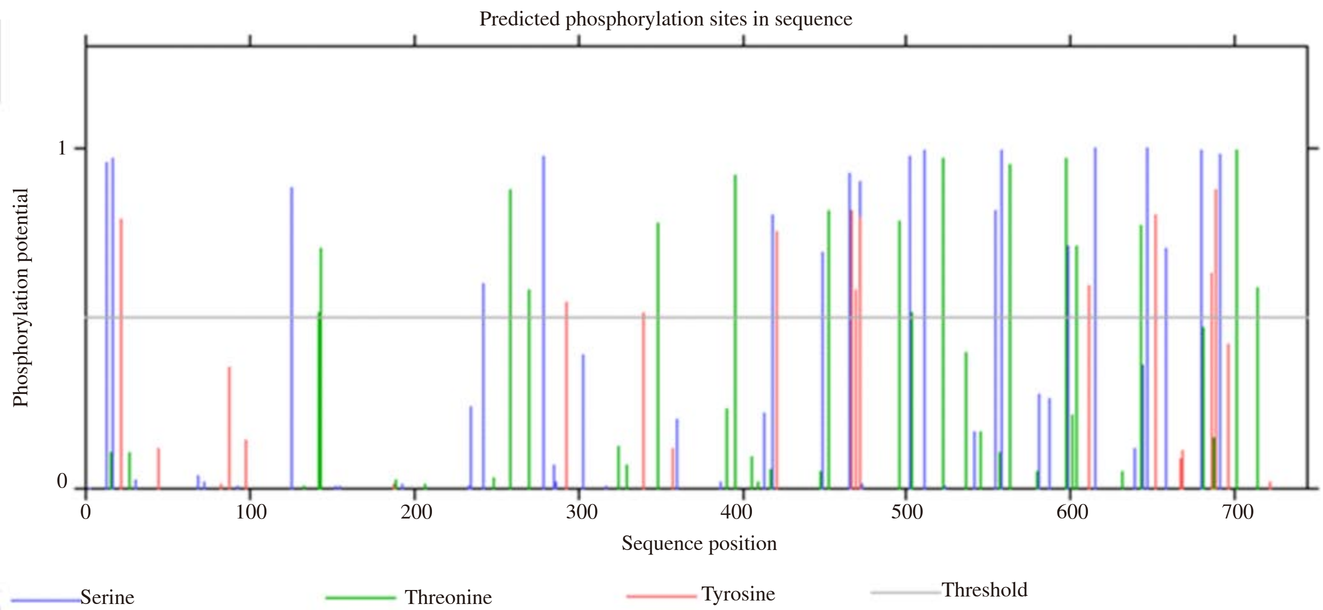

Figure 1. Predicted phosphorylation sites within the Ebola virus nucleoprotein.

4. Discussion

The post translational modification is an important process to be studied for clarifying the pathogenesis of the virus infection. For the Ebola virus infection, this process is not well clarified. The phosphorylation of the Ebola virus nucleoprotein is very interesting. García *et al.* noted that understanding the phosphorylation of the Ebola virus was very important since it could be useful information in new drug search[4]. There is an interesting previous report on this topic[2]. Peyrol *et al.* recently found 4 phosphorylatable sites that were conserved among Ebolavirus and Marburgvirus nuclear proteins and mentioned that "their modification may play a modulatory role in viral RNA synthesis[2]." Based on our present report, there are many new identified phosphorylation sites that should be further studied in details.

Conflict of interest statement

We declare that we have no conflict of interest.

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