

Identification of Novel genotypes of Human Respiratory Syncytial Virus (RSV) A strain circulating in Sudan

Sahar O Khalil^{1*}, Hisham N Altayb², Khalid A Enan³, Ali. Y. H⁴, Isam M Elkhidir⁵ and Mohamed A. Hassan⁶

¹ Department of Microbiology, University of science and technology, P.O. Box: 30, Omdurman, Sudan.

² College of medical laboratory Science, Sudan. University of Science and Technology, Sudan.

³ Department of Virology, Central Laboratory, Ministry of science and Technology, P.O. Box 7099, Khartoum, Sudan.

⁴ Department of Virology, Veterinary research Institute, P.O. Box 80 67, Khartoum, Sudan.

⁵ Department of Microbiology and Parasitology, Faculty of Medicine, University of Khartoum, Khartoum, Sudan.

⁶ Department of Bioinformatics, Africa City of Technology. Division of Molecular Genetics, Institute of Human Genetics, University of Tubingen, Germany.

* Corresponding author: Sahar O Khalil; e-mail: saharosmankhalil@yahoo.com

Received: 27 April 2016

Accepted: 21 May 2016

Online: 26 May 2016

ABSTRACT

Respiratory syncytial virus (RSV) is the major cause of acute lower respiratory tract infection in children and vulnerable adults, but little is known regarding RSV infection in Sudan. 224 throat swab specimens were collected from children less than 5 years old, with respiratory tract infections admitted at Khartoum Hospitals in winter season (2011- 2012), were screened for RSV using direct immunofluorescence assay (DFA), Reverse transcription-polymerase chain reaction (RT-PCR) and Nested RT-PCR. Nucleotide sequencing and bioinformatics analysis based on the G gene were done for nine cell culture isolated of RSV strains and were positive by DFA, RT-PCR and Nested RT-PCR. Out of 224 patients, RSV infections were detected in 136 (60.7%) patients, using DFA technique, 44 (19.6%) patients using RT-PCR and 14 (41.2%) patients, using Nested RT-PCR. Multiple sequence alignment of Sudanese RSV sequences showed, substitution of amino acid serine (S) to Cysteine (C) at position 11 in isolate 176, In isolate 316 also there was substitution of amino acid Asparagine (N) to lysine (K) at position 73. Insertion of G at position 84 and A at position 103 in isolate 377 cause frame shift mutations, when compared to other RSV G genes from database. The G protein novel mutations in isolates 176, 316 and 377 were damaging the protein in addition to change in functions and 3D structure of mutant protein of the Sudanese RSV strains, this may have implications for RSV vaccine development in Sudan.

Keywords: Respiratory tract infection, respiratory syncytial viruses, reverse transcription polymerase chain reaction, direct immunofluorescence assay.

young children, and the elderly worldwide, However, there is no safe and effective RSV vaccine licensed for human use [1, 2, 3]. RSV has two antigenic subgroups (A and B) exist with partial cross-protection [4, 5]. In general, subtype A strains are thought to be more virulent and usually the predominant circulating strains compared with subtype B strains [6, 7]. The most two immunogenic RSV proteins are the Fusion (F) and

1. INTRODUCTION

Respiratory syncytial virus (RSV), a *Pneumovirus*, family *Paramyxoviridae*, remains the most significant cause agent of severe lower respiratory tract disease in infants,