Bionatura
Latin American Journal of Biotechnology and Life Sciences

Bionatura Issue 4 Vol 8 No 1 2023

Article

Determination of molecular genotype of human respiratory syncytial virus in respiratory patients in Thi-Qar Province

Sally Salih Jumaa[1]
[1] *National University of Science and Technology, Thi-Qar, Iraq*
* *Correspondence: SallySalih901@gmail.com*
Available from: http://dx.doi.org/10.21931/RB/CSS/2023.08.04.47

ABSTRACT
The current study has targeted the detection of one important pathogenic virus responsible for respiratory tract illness (RTI) that involves Human Respiratory syncytial viruses (HRSV), association with demographics, and some parameters including age, sex, and clinical symptoms. The clinical specimens that were preferred in this study were throat swabs and blood specimens that were taken from 100 patients who experienced respiratory tract illness during the period from January to May 2019 in Thi-Qar Province, south of Iraq. The techniques used in this study are Nested RT-PCR for RSV-A and RT-PCR for RSV-B. The results attained from this study are summarized in the following points: 1- Out of 100 patients suffering from respiratory tract infection, 38(38%) were detected with Respiratory syncytial virus, 24(24%) were detected with RSV type A, and 14(14%) detected with RSV type B.
Keywords: molecular genotype, human respiratory syncytial virus, acute respiratory infection

INTRODUCTION

Human Respiratory syncytial virus (HRSV) is a major cause of acute respiratory infection (ARI) in children worldwide [1, 2, 3]. It is responsible for seasonal outbreaks [4] and is associated with substantial morbidity and mortality rates, especially in people with some underlying conditions [5]. Every year, HRSV is a source of significant hospital admissions in young children, with a considerable rate of mortality in high-risk groups [6, 7]. HRSV ARI has a major impact on healthcare resources and costs [8, 9]. Furthermore, there is growing evidence that HRSV ARI in childhood and adults is linked to long-term impaired lung function that can manifest as recurrent wheezing or asthma [10]. RSV virus is classified according to antigenic differences in virion structural proteins into 2 subtypes, A and B [11]. Both subtypes usually circulate during epidemic seasons, following an irregular, alternating prevalence pattern, with subtype A having a cumulative higher prevalence than subtype B [12]. Although RSV-A is thought to have a more severe clinical course [13], several papers reported no significant differences in disease severity between the 2 subtypes [14] or found that RSV-B causes more severe disease than RSV-A [15]. This inconsistency could result from bias due to inclusion in these studies of infants with different respiratory diseases, differing

ages, coming from different climates, or other confounding factors. Equally important, a different disease course may also reflect different RSV genotypes [16].

MATERIALS AND METHODS

Study Population

A total of 100 throat swab specimens were collected from patients suffering from respiratory tract illness (RTI), the database of them was registered in this study which involved the name of the patient, age; gender and the major clinical symptoms of RTI, such as fever, cough, sneezing, nasal discharge rhinorrhea, the age of selected patients was from 6 years to 65 years old of both genders in Thi-Qar Province south of Iraq during four Months (from February to May 2019) specimens including 39 males and 61 females suffering from acute respiratory tract illness (RTI).

Samples collections

Throat swab samples were ideally collected within 24 hours of patients with respiratory disease; Swab specimens were preserved in viral transport media (VTM), then the throat swab was stored at –20 c until examined by PCR - Technologies for RSV in throat swab specimens.

RESULTS

Table 1. demonstrates RSV-A-positive in the patient group according to gender. The patient group by RSV-A shows that (50%)of them are males and (50%) are females.

Variable	Rsv- A Group	
Sex groups	**No. of +ve cases**	**% of +ve cases**
Male	**12**	**50**
Female	**12**	**50**
Total	**24**	**100**

Cal.X2:0.01 df: 1 Tab. X2:6.63 p_value: 0.01

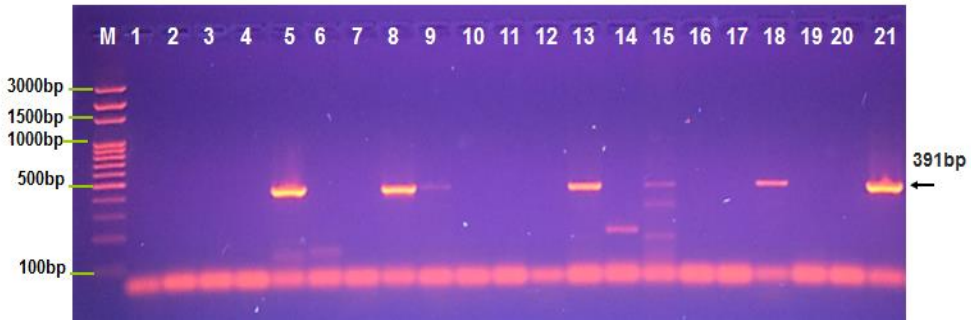

Fig 1: Agarose gel electrophoresis image that showed Nested PCR product analysis for the attachment glycoprotein (G) gene in respiratory syncytial virus genotype A (RSVA). M (Marker ladder 3000-100bp). Lane (1-21) showed positive RSVA at 391bp product size.

Variable	Rsv- B Group	
Sex groups	**No. of +ve cases**	**% of +ve cases**
Male	**5**	**36**
Female	**9**	**64**
Total	**14**	**100**

Cal.X^2: 1.14 df: 1 Tab. X^2:6.63 p_value: 0.01

Table 2. demonstrates RSV-B-positive in the patients' group according to gender. The percentage of females infected with RSV-B is higher than males. The patients group by RSV-B shows that (36%) of them are males and (64%) are females.

Fig 2. Agarose gel electrophoresis image that showed RT-PCR product analysis for the attachment glycoprotein (G) gene in respiratory syncytial virus genotype B (RSVB). M (Marker ladder 3000-100bp). Lane (1-22) showed positive RSVB at 772bp product size.

DISCUSSION

RSV is among the most frequent etiological agents causing LRTI, especially among young infants and adults [17]. RSV epidemics occur yearly but may alternate between midwinter and early spring. Its distribution varies in different countries and seasons in the current study. Of 100 samples, 38% are positive with RSV using RT-PCR and Nested-RT-PCR analyses. This result is comparable with several studies conducted in different areas, such as a study done by [18] recorded (18.75%) in patients who used real-time polymerase chain reaction in Wasit City, and [28] revealed a seroconversion rate of RSV (20.4%) among patients in the Kurdistan region. The results in the present study are higher than those obtained by [19], who indicated that among 150 samples, 26 % were positive for RSV infections, and lower compared with data reported in Baghdad by [20]; the percentage reached 79% among patients with respiratory tract infections. In neighboring countries, the infection of RSV was (36.8%) by [21] hospitalized children with respiratory tract infection in Kuwait, and a study done by [22] shows 31.1% of RSV infections among Iranian patients In this study, the infection rate seems to be higher with than other studies such as study done by [23] who recorded

(6.6%) in Baghdad, These variations in incidence among studies might reflect different epidemiological patterns of RSV infection in different countries, which in turn might be related to environmental factors, geographical factors, differences in host genetic susceptibility, immune status, sampling size, detection techniques, and different viral strains circulating in different geographical areas [24]. Sex Distribution of Respiratory Syncytial Virus-Positive in the Respiratory Infections group showed The prevalence of respiratory syncytial virus A+B in the present study among females is 21 cases higher than those in males, 17 cases with significant differences between them. This finding corresponds with other previous studies by [25], which revealed that the gender, females (53.2%) were higher than males, and the results also match with [26] in Iran (62.5%) were female and the rest (37.5%) were males and While the current study is inconsistent with a study conducted by(Rodriguez-Fernandez et al., 2017) in Texas [27] in Egypt [28] in Iraq. And [29] males were at higher risk of severe RSV infection as compared to females in Denmark.

CONCLUSIONS

The study found that 100 patients had respiratory illnesses. The percentage of females infected with RSV-A is equal to that of males. The patient group by RSV-A shows that (50%)of them are males and (50%) are females. This result shows statistically significant differences between males and females ($P<0.01$). While the percentage of females infected with RSV-B is higher than males. The patient's group by RSV-B shows that (36%) of them are males and (64%) are females. This result shows there are statistically significant differences between males and females ($P<0.01$).

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Received: May 15, 2023/ Accepted: June 10, 2023 / Published: June 15, 2023
Citation: Jumaa, S.S. Determination of molecular genotype of human respiratory syncytial virus in respiratory patients in Thi-Qar Province. Revista Bionatura 2023;8 (4) 63. http://dx.doi.org/10.21931/RB/CSS/2023.08.04.47