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RESEARCH ARTICLE

DETECTION OF VARICELLA-ZOSTER VIRUS IN RASH [SAMPLES BY] GENETICS [ANALYSIS THAT COLLECTED FROM] PATIENTS IN [BABYLON PROVINCE]

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Abstract

The Varicella-zoster virus (VZV), also known as human herpesvirus 3 (HHV-3), is any_-herpesvirus that is the etiological agent of varicella (chickenpox) as a primary infection and herpes zoster (shingles) as a recurring infection. The 185 samples from two patients were subjected for specimen which include both skin sites for the sampling was forehead from both sexes and the age of patient was 17 and 18 years. These patients were diagnosed by dermatology doctor , rendering to the signs and indications,, in addition to be having hazard reasons that were determined by the evidence almost patients. In this study, patients with recent custom of local antibiotic treatment and usage beautifying substantial were excluded from sampling. The results was in total of 185 sample collected from patients suffering from rash. Detected the viruses were 107(57,8%)samples and other microorganisms were 78 (42,2%). The other microorganisms may by bacteria such as Streptococcus, Staphylococcus, Coranybacterum And Clostridium. But the 57,8% samples detected as a DNA viruses by viral infection kit.. of percentages for the Varicella-zoster virus was 86(80.37%) but other viruses were 21(19.63%) that detected by metagenomic analysis.

Introduction:-

The Varicella - zoster virus (VZV), also known as human [herpesvirus] 3 (HHV-3), is [anv_-herpesvirus] that is the etiological cause of [varicella] (chickenpox) as a [primary infection] and herpes zoster (shingles) as a recurring infection [1–2]. Varicella - zoster virus is definite to persons [4,3], and is particularly transmissible through airborne broadcast [3,4,6]. Record, [Varicella - zoster virus infections] result in varicella, producing [fever and a generalized pruritic rash], which typically happens through infantile [1,5,3]. Sharing a common feature of herpes – viruses, Varicella - zoster virus undergoes latency and may reactivate. Usually, occurring in adults, Varicella - zoster virus reactivation causes herpes zoster (HZ), producing a localized, painful rash [1,2,4,6]. Both [varicella and zoster] are predominant global [1,3], and can be serious, particularly in kids and adults with weakened [immune systems] [1,4,6]

Varicella - zoster virus is a [Deoxyribose nucleic acid virus] and is a one of the herpes-virus group. Similar other herpes - viruses, Varicella - zoster virus perseveres in the human body as a hidden infection next the[primary (first)] impurity; Varicella-zoster virus perseveres in [sensory nerve ganglia]. first impute Varicella-zoster virus results in [varicella]. Hidden impurity can re-activate causing in [herpes-zoster] (shingles). The Varicella - zoster virus has a little existence period in the ambience**.** Varicella - zoster virus move in the body during the respirational tract and

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[conjunctiva]. It duplicates in location of [entry] in the nose-pharynx and in local immune[lymph knobs]. A firstly [[viremia]] occurs four to six days next impute and distributes organisms to new tissues, at the example [liver, spleen, and sensual knots]. Additional, duplication happens in the intestine, shadowed by a next viremia & virus-related hitting of the skin. Varicella - zoster virus can be growing in [monocytes] of an hitting individual from five days previously to one to two days after the admission of the rash.

Materials and Methods:-

Samples Collection:

The 185 samples from two patients were subjected for specimen which contain both [skin sites] for the sampling was forehead from together genders and the age of patient was [17 and 18 years]. These patients were identified by medical doctor [dermatology], according to the marks and symptoms, in addition to be having danger causes that were [determined by the information about patients]. In this study, patients with recent usage of local antibiotic treatment and custom beautifying substantial were excluded from sampling.

DNA Extraction:

[DNA extraction] was approved out according to the [genomic DNA purification kit] supplemented by industrial company (Gene aid, UK).

Whole Genome Sequencing (WGS) :

The 185 samples of [DNA isolated] from patients with rash were a selection of for full [metagenome sequencing] depended the [next-generation sequencing]method. Next [extraction of Genomic DNA], the isolated DNA [subjected to quantification by NanoDrop] instrument to estimation the [DNA concentration] according to manufacturing's instructions. Furthermore, the condition of the [DNA was assessed by gel electrophoresis] technique to estimate the[presence or absence of DNA in the sample], where [1µl]of [DNA loaded] to [1%] agarose gel and run at [160V] for [30min]. Next this step, only successful samples were submitted to [Macrogen company] (Korea) for [whole metagenome sequencing] (Paired-ends) using the [Illumina NovaSeq] [6000 platform]. The resulted raw reads were [processed by further bioinformatics tools]**.** The raw data were analyzed by numerous [bioinformatics tools]. Wholly bioinformatics methods which used to examine the study [sequences] were hinge on whichever using command-line tools and [bioinformatics softwires] on open-source operating system, Linux (Version: Ubuntu [18.04.3 LTS], Canonical Ltd., UK), Windows-based database (CLC Genomics Workbench version [20.0.3] or using web-based servers such as the Galaxy platform [(https://galaxyproject.org)] (7). Beforehand WGS examination, the raw data undergo quality control by[FastQC][Version, 0.11.5] (8) to evaluate quality of reads and calculating the basic data (for example whole number of bases, reads and [GC content]). Afterward quality controller, raw reads were subjected to preprocessing stages to decrease biases in examination by trimming out [bases of low quality], adapter sequences, the [Poly-G tail and human DNA]. Trimmomatic [version 0.36] tools (9) and [CLC Mapper] [CLC Genomics Workbench version 20.0.3]. The filtered raw data have undergone for further processing steps brief with its [tools and references] in Table (1).

Table (1):- The Bioinformatics tools or programs which used for analyze the filtered raw data.

Processing type	Ref.
Assembly	(10)
Visualizing the de novo assembly	(11)
Ordering contigs	(12)
Taxonomy classification	(13)
Visualizing annotated Taxonomy	(14)
Manipulation of the SAM/BAM files	(15)

Results and Discussion:-

In present study a total of 185 sample collected from patients suffering from rash. Detected the viruses were 107(57,8%)samples and other microorganisms were 78 (42,2%). The other microorganisms may by bacteria such as Streptococcus, Staphylococcus, Coranybacterum And Clostridium. But the 57,8% samples detected as a DNA viruses by viral infection kit. As the table(2).

Table (2):- Viruses detected by viral infection kit.

SPECIMENS	NO. (%)
Vires samples	107(57,8%)
Other Microorganisms samples	78(42,2%).
Total	185(100%)

The result for figure(1) was appearance of percentages for the Varicella-zoster virus was 86(80.37%) but other viruses were 21(19.63%) that detected by metagenomic analysis these results

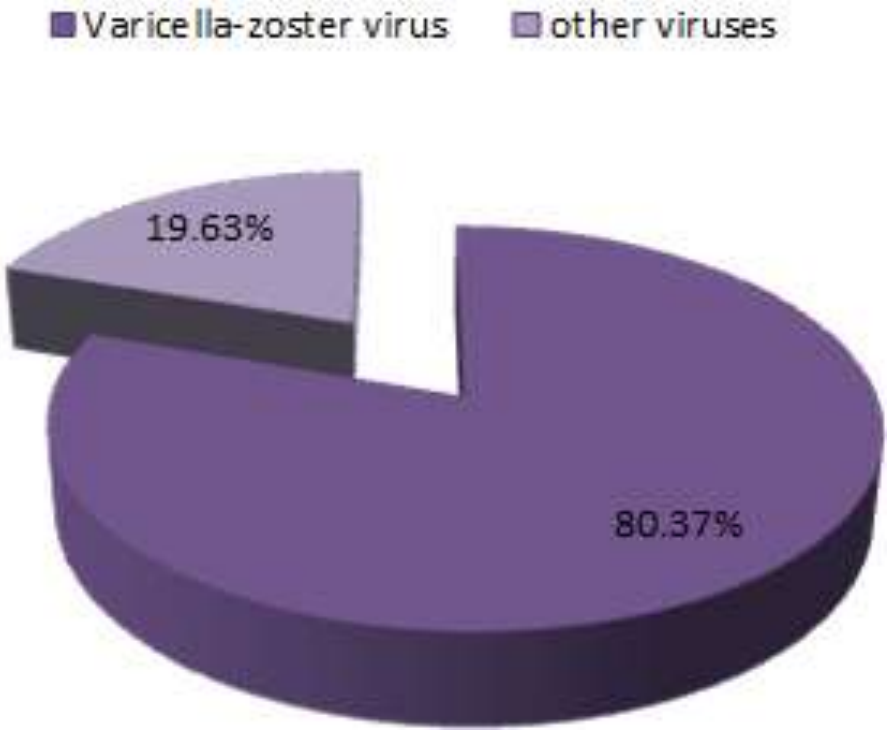

Figure (1):- The percentages of VZV.

In present study The VZV was high percentages of skin samples . so the virus is a Deoxyribose nucleic acid virus] and is a associate of the herpes-virus collection. Similar other herpes viruses, the virus keep it up in the body as a hidden infection afterward the start infection; virus persists in sensory nerve ganglia. start infection with virus marks in **varicella**. Hidden impurity can reactivate resulting in herpes zoster (**shingles**). The virus has a little existence time in the economic.

Conclusion:-

Microbiology studies are essential in infectious rash because different etiologic agents can manifest with similar clinical profiles. Molecular techniques show that herpes virus may be present in patients with bacterial rash and qPCR may be useful in its detection and treatment, so as to avoid steroids, or appropriately administer antiviral drugs to patients who are positive for herpes by PCR. Cost-effective studies should be carried out to evaluate the impact of such molecular techniques.

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