**Methods:** 1-Viral diagnostic methods: Four lower respiratory samples were collected from the patients with pneumonia of unknown cause who were identified in Wuhan including the bronchoalveolar-lavage fluid, also Seven bronchoalveolar-lavage fluid specimens were collected from the patients in Beijing hospitals with pneumonia of a known cause to serve as control samples,nucleic acids were extracted from clinical samples by the high Pure Viral Nucleic Acid Kit also extracted nucleic acid samples were tested for bacteria and viruses by PCR and finally unbiased high-throughput sequencing was used to discover microbial sequences.

2- Isolation of virus: The bronchoalveolar-lavage fluid samples were collected in the sterile cups to which the virus transport medium was added, to remove the cellular debris, the Samples were centrifuged.Also supernatant was inoculated on the human airway epithelial cells and also expanded on a plastic substrate to generate the passage and the apical surfaces of the human airway epithelial cells were washed three times with the phosphate-buffered saline.

3- Transmission electron microscopy:The supernatant from the human airway epithelial cell cultures was collected and showed the cytopathic effects,The human airway epithelial cells were collected which show the cytopathic effects and was fixed. And sections were cut from the resin block and stained with the uranyl acetate and lead citrate, separately.

4- Viral genome sequencing: RNA was extracted from the bronchoalveolar-lavage fluid and the culture supernatants was used as a template to clone and sequence the genome, A combination of Illumina sequencing was used and a nanopore sequencing to characterize the virus genome. Also sequence reads were assembled into a contig maps.And a multiple-sequence alignment of the 2019-nCoV and the reference sequences was performed with the use of Muscle.

**Results:1-patients**: Three adult patients presented with a severe pneumonia and were admitted to a hospital in. First patient was a 49-year-old woman, second was a 61-year-old man, and third was a 32-year-old man. The clinical profiles were available for the first and second. The first was reported by no underlying chronic medical conditions but reported fever and cough with chest discomfort.After 4 days her cough and chest discomfort worsened, but the fever was reduced and the respiratory distress developed 7 days after the onset of illness and worsened over the next 2 days, so at the end,the first and the third recovered and were discharged from the hospital on January 16, 2020. second died on January 9, 2020. **2-Detection and isolation of a novel coronavirus:** A three bronchoalveolar-lavage samples were collected from Wuhan Jinyintan Hospital, RNA extracted from the bronchoalveolar-lavage fluid from the patients was used as a template to clone and sequence the genome using a combination of the Illumina sequencing and the nanopore sequencing.The infected human airway epithelial cultures were examined with the light microscopy daily and with transmission the electron microscopy 6 days after the inoculation to determine whether the virus particles could be visualized in 2019-nCoV, After some processes at the end no specific cytopathic effects were observed in the Vero E6 and Huh-7 cell lines until 6 days after inoculation. To characterize the virus, de novo sequences genome from the clinical specimens and human airway epithelial cell virus isolates were obtained by the Illumina and nanopore sequencing, The novel coronavirus was identified from all the three patients. Two nearly full-length coronavirus sequences were obtained from the bronchoalveolar-lavage fluid and one full-length sequence was obtained from the virus isolated from a patient.