Advancements in Genetic Engineering
ISSN: 2169-0111
Short Communication

CORONAVIRUS & COVID-19

Senanur Uslu
Istanbul Medeniyet University, Turkey.

Abstract:

Coronaviruses are a large family of viruses known to cause more serious diseases from the common cold, such as Middle East Respiratory Syndrome (MERS) and Severe Acute Respiratory Syndrome (SARS). Coronaviruses were identified in the mid-1960s. Sars-Corona Virus (SARS-CoV) is a coronavirus that was first seen in China in February 2003 and causes severe acute respiratory failure. As the largest known RNA viruses (because coronaviruses have the largest genome of RNA viruses), CoVs are further divided into four types: alpha coronavirus (Ⅰ-CoV), beta coronavirus (Ⅱ-CoV), gamma coronavirus (Ⅲ-CoV), and deltacoronavirus (Ⅳ-CoV); the first two only infect mammals, including bats, pigs, cats and humans. Gammacoronavirus mostly infects birds and Deltacoronavirus can infect both birds and mammals. This novel coronavirus is now the seventh member of the Coronaviridoe, which is known to infect humans. All Coronaviruses belong to a genus. All of these genuses are in the Coronaviridae family, making up one of the two subfamilies. Coronavirus, Nidovirales, which causes infections mainly in the respiratory and gastrointestinal tract, belongs to the Orthocoronavirinae subfamily, respectively in the Coronaviridae family. Previously, with serological analysis, the differences in the Coronavirus species used were understood and the Coronaviridae family was examined by dividing it into 4 antigenic groups. But then, by examining the monoclonol antibody analysis and nucleotide sequences in the species and divisio groups, the classification was reduced to 3 antigenic groups. Viruses in the coronavirus family have only slight differences in their genomes, with only five nucleotide differences between the three of the viruses. Regardless of the structure of the protein chains, the same results in the same groups showed that this classification is more accurate. Coronaviruses responsible for %30 of upper respiratory tract diseases in humans are included in group 1 (HCoV-229E) and group 2 (HCoV-OC43). TGEV (Porcine transmissible gastroenteritis virus), FCV (Feline coronavirus), CCV (Canine coronavirus) in group 1 and all members of group 2 are genetically very close to each other. IBV, the only member of the 3rd group, is not different from other coronaviruses, but it shows variations within its species. Group 1 and group 2 coronaviruses include mammalian viruses.

Biography:

she has Done Msc –Biology from Istanbul Medeniyet University, Turkey.., Trained in molecular genetics. Undergone training In molecular genetics at Asia Pacific School of genome and genetics in Istanbul Medeniyet University..