

Chapter 6

LABORATORY GUIDELINES FOR THE SAMPLE COLLECTION OF NOVEL CORONAVIRUS

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Abstract

This work can be utilized by the administration/ wellbeing specialists/ emergency clinical clinicians/ research centres to gather proper clinical examples as demonstrated for the conclusion of 2019-nCoV. This section portrays the data for assortment, bundling, and transport of clinical examples to the SARS bunch at ICMR-National Organization of Virology (NIV), Pune, Maharashtra for the analysis of 2019 Novel Coronavirus (2019-nCoV). The clinician should choose the need for assortment of clinical examples for research centre testing of 2019-nCoV directly after following the case definition as given by the wellbeing specialists. By following all bio-safety safeguards and utilizing proper defensive gear (PPEs), clinical sample should be sent to the assigned research facility (ICMR-NIV, Pune) by adhering to standard triple bundling.

INTRODUCTION

Coronaviruses are a gathering of exceptionally differing RNA infections in the Coronaviridae family that is separated in 4 genera: alpha, beta, gamma, and delta that cause sickness changing from gentle to extreme in human and other creatures (1-3). There are endemic human coronavirus as alpha coronaviruses 229E and NL63 and beta coronaviruses OC43 and HKU1 that can cause flu-like ailment or pneumonia in people (Azhar et al., 2019; Drosten et al., 2003; Hui & Zumla, 2019). Be that as it may, two zoonotic coronaviruses have developed, causing extreme ailment in people: SARS-CoV in 2002-2003 and MERS-CoV in 2012 (De et al., 2016; Hilgenfeld & Peiris 2013). In January 2020, the etiologic operator answerable for a bunch of extreme pneumonia cases in Wuhan, China, was recognized just like the novel beta coronavirus, unmistakable from SARS-CoV and MERS-CoV (Global Initiative on Sharing All Influenza Data (GISAI), 2020). On 11 February 2020, the Global Board on Scientific Classification of Infectious Diseases (ICTV) declared that the infection was named extreme acute respiratory condition coronavirus -2 (SARS-CoV-2) (Gorbalenya et al., 2016) while, around the same time

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