216 countries and regions from all six continents had

reported more than 20 million cases of COVID-19, and

more than 733,000 patients had died’'. High mortality

occurred especially when health-care resources were

overwhelmed. The USA is the country with the larges

number of cases so far.

Although genetic evidence suggests that SARS-CoV-2

is a natural virus that likely originated in animals, there is

no conclusion yet about when and where the virus firs!

entered humans. As some of the first reported cases

in Wuhan had no epidemiological link to the seafood

market”, it has been suggested that the market may not be

the initial source of human infection with SARS-CoV-2.

One study from France detected SARS-CoV-2 by PCR

in a stored sample from a patient who had pneumonia

at the end of 2019, suggesting SARS-CoV-2 might have

spread there much earlier than the generally known

starting time of the outbreak in France”\*. However, this

individual early report cannot give a solid answer to the

origin of SARS-CoV-2 and contamination, and thus a

false positive result cannot be excluded. To address this

highly controversial issue, further retrospective inves-

tigations involving a larger number of banked samples

from patients, animals and environments need to be

conducted worldwide with well-validated assays.

Genomics, phylogeny and taxonomy

As a novel betacoronavirus, SARS-CoV-2 shares

79% genome sequence identity with SARS-CoV and

50% with MERS-CoV™. Its genome organization is

shared with other betacoronaviruses. The six functional

open reading frames (ORFs) are arranged in order from

5’ to 3’: replicase (ORFla/ORF 1b), spike (S), envelope

(E), membrane (M) and nucleocapsid (N). In addition,

seven putative ORFs encoding accessory proteins are

interspersed between the structural genes”. Most of

the proteins encoded by SARS-CoV-2 have a similar